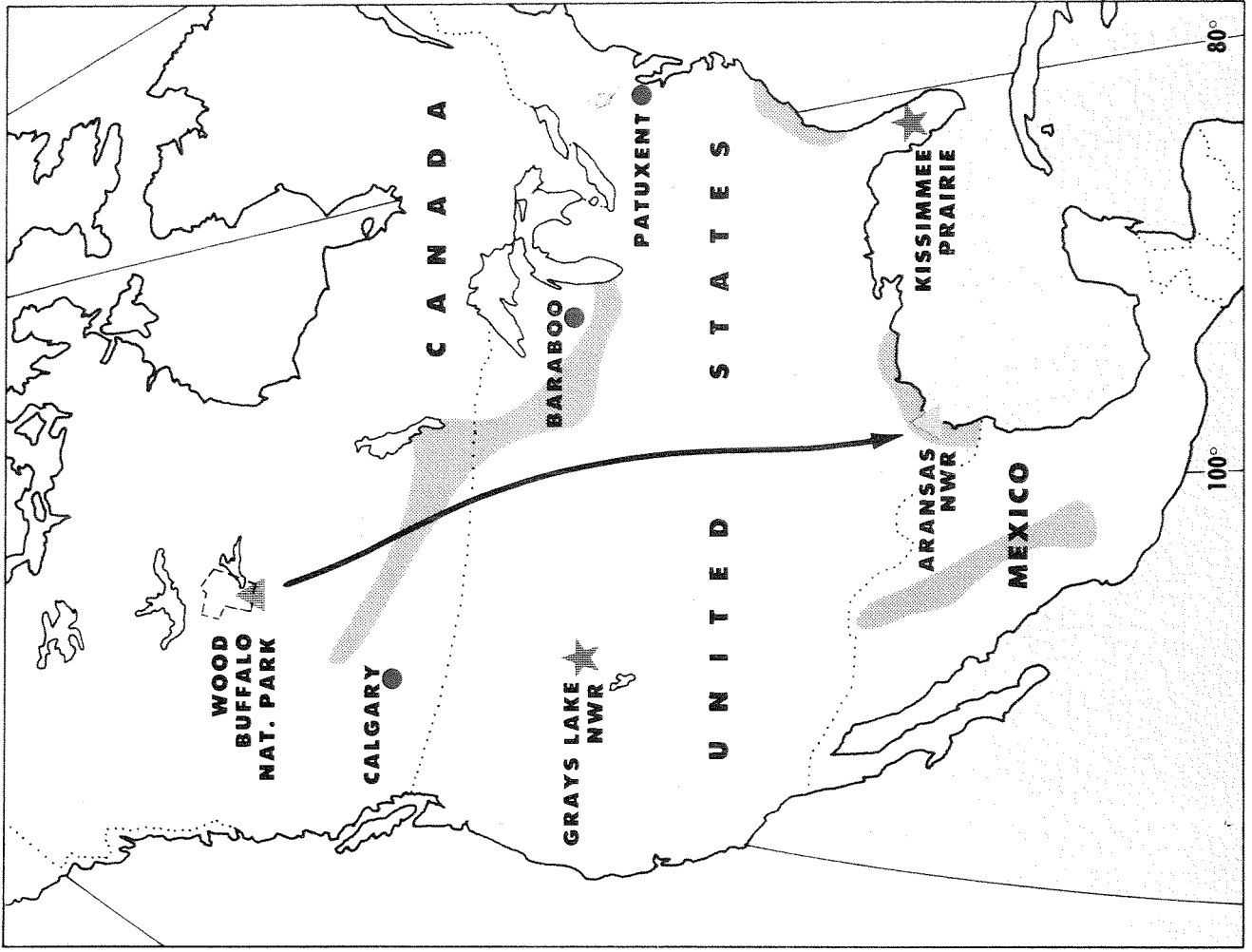


# Whooping Crane

## Conservation Viability Assessment





- ▨ Former range
- ▴ Breeding area
- ◁ Winter area
- Captive breeding centers
- ★ Experimental release site
- ➔ Major migration route

# ***GRUS AMERICANA***

## **WHOOPING CRANE**

### **CONSERVATION VIABILITY ASSESSMENT WORKSHOP REPORT**

**Compiled by C. Mirande, R. Lacy, and U. Seal**

**Fossil Rim Wildlife Center  
Glen Rose, Texas, USA  
6-8 August 1991**



**A Publication of the  
CAPTIVE BREEDING SPECIALIST GROUP (CBSG/SSC/IUCN)**

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## **TABLE OF CONTENTS**

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<b>GOALS &amp; OBJECTIVES</b>	<b>SECTION 1</b>
<b>SUMMARY &amp; RECOMMENDATIONS</b>	<b>SECTION 2</b>
<b>WILD POPULATIONS</b>	<b>SECTION 3</b>
<b>CAPTIVE POPULATIONS</b>	<b>SECTION 4</b>
<b>SMALL POPULATION BIOLOGY</b>	<b>SECTION 5</b>
<b>VORTEX</b>	<b>SECTION 6</b>
<b>DISEASE</b>	<b>SECTION 7</b>
<b>REINTRODUCTION</b>	<b>SECTION 8</b>
<b>GENETICS</b>	<b>SECTION 9</b>
<b>STUDBOOKS</b>	<b>SECTION 10</b>
<b>CBSG \ IUCN SSC</b>	<b>SECTION 11</b>
<b>REFERENCES</b>	<b>SECTION 12</b>
<b>MINUTES</b>	<b>SECTION 13</b>
<b>PARTICIPANTS</b>	<b>SECTION 14</b>



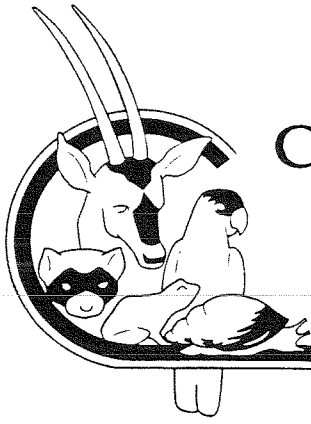
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***GRUS AMERICANA***

**WHOOPIING CRANE**

**CONSERVATION VIABILITY ASSESSMENT  
WORKSHOP REPORT**

**SECTION 1  
GOALS & OBJECTIVES**



# Captive Breeding Specialist Group<sup>1</sup>

Species Survival Commission  
IUCN -- The World Conservation Union

U. S. Seal, CBSG Chairman

## WHOOPING CRANE

*Grus americana*

### POPULATION VIABILITY ANALYSIS WORKSHOP

6-8 August, Fossil Rim

#### Workshop Goals:

The overall purpose of the workshop is to develop a Captive Conservation Strategy that will assure, with high probability, the continued survival and adaptive evolution of the Whooping Crane. The final document will include specific recommendations and priorities for research and management of captive populations. The plan will be developed by detailed examination of natural history, biogeography, life-history characteristics, status in the wild and captivity, and threats to continued existence. Computer models will be used to assist in evaluating the vulnerability of these populations to extinction.

The PVA Document will be prepared in draft form during the workshop. It is a goal of the workshop that this document be reviewed and revised by all participants during the workshop as many times as necessary to achieve agreement on its content before departure.

The goals of the Population Viability Analysis (PVA) Workshop include:

- (1) Conduct population viability analyses of the Whooping Crane.
- (2) Formulate quantitative strategies with risk assessments to prevent extinction and achieve the establishment or maintenance of viable, self-sustaining populations within the historic range of the birds.



**PVA Objectives:**

1) Determine numbers of Whooping Crane subpopulations required for various probabilities of survival and preservation of genetic diversity for specified periods of time (i.e. 25,50,100,200 years).

(2) Consider how possible interventions in the wild population might increase the rate of growth and maximize retention of genetic diversity.

(3) Consider how possible interventions in the captive population might increase the rate of growth and maximize retention of genetic diversity.

(4) Assess potential and anticipated needs of birds for release studies. Develop goals for the captive populations to provide birds for release to the wild without compromising the genetic diversity and demographic stability of the captive population.

(5) Project the potential expansion or decline of Whooping Crane population numbers under various management regimes.

(6) Outline metapopulation structure needed to establish viable populations. Indicate management consequences of this approach.

(7) Formulate quantitatively and evaluate the role of captive propagation as a component of the strategy for this species. In particular, consider how captive propagation can:

- a) accelerate expansion of the population,
- b) enhance preservation of genetic diversity,
- c) protect population gene pool against fluctuations due to environmental vicissitudes in the wild, and
- d) provide birds for reinforcement of wild populations or establishment of new populations.
- e) enhance conservation efforts through public education.

(8) Identify problems or issues that need continuing analysis and research.

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***GRUS AMERICANA***

**WHOOPING CRANE**

**CONSERVATION VIABILITY ASSESSMENT  
WORKSHOP REPORT**

**SECTION 2  
SUMMARY & RECOMMENDATIONS**

## SUMMARY & RECOMMENDATIONS

An endangered species is (by definition) at risk of extinction. The dominant objective in the recovery of such a species is to reduce its risk of extinction to some acceptable level - as close as possible to the background, "normal" extinction risk all species face. We need to improve estimation of risk, to rank order better the risk due to different potential management options, to improve objectivity in assessing risk, and to add quality control to the process (through internal consistency checks). Among the risks to be evaluated are those of extinction, and loss of genetic diversity. The most fundamental threat is, of course, declining population size. If a population is declining in numbers, and no action is taken to reverse the trend, then extinction is imminent. However, even if a small population is not declining or even if it is increasing, its fate is uncertain. Small populations are challenged by a number of factors that increase the likelihood of the population going extinct simply because the population is small.

The concept of risk is used to define the targets for recovery, and is used to define recovery itself. Risk, not surprisingly, is a central issue in endangered species management. A set of tools to evaluate risk, loosely known as "Population Viability Analysis" has appeared. These techniques are already powerful enough to improve recognition of risk, rank relative risks, and evaluate options. They have the further benefit of changing part of the decision making process from unchallengeable internal intuition to explicit (and hence challengeable) quantitative rationales.

The Population Viability Assessment Workshop for the Whooping Crane (*Grus americana*) was a collaborative endeavor of the USFWS and CWS Whooping Crane Recovery Team, the International Crane Foundation and the Captive Breeding (Small Population) Specialist Group, SSC/IUCN. The purpose of the workshop was to review ecological, demographic and genetic data from the wild and captive populations of the Whooping Crane as a basis for developing stochastic simulation models allowing risk of extinction and rates of genetic loss estimates for the wild and captive populations as a tool for ongoing adaptive management of the species. Goals of the workshop were formulation and evaluation of quantitative management scenarios that could serve as part of a conservation strategy that will assure, with high probability, the continued survival and adaptive evolution of the Whooping Crane.

This Workshop Report includes a set of management scenarios with specific recommendations and priorities for research and management of the wild and captive populations and for their joint management as a meta-population to maximize retention of genetic heterozygosity and minimize the risk of extinction.

Data on the population biology of the whooping cranes for use in population viability modeling was provided at the workshop by Ernie Kuyt, from his records on the breeding population at Wood Buffalo National Park (data from 1969 to 1991), and Tom Stehn, from records on the arrivals of birds at Aransas (data from 1938 to 1991). Stephen Nesbitt and Jane Nicolich provided data on the histories of releases of sandhill cranes in Florida and Mississippi. In addition, consensus of workshop participants was obtained on the likely values, or the range of plausible values, of parameters that could not easily be estimated from existing data.

We know from the size of the population at the 1941 bottleneck that the current population is derived from at most 12 and more likely 6 or 8 founding lineages. Currently 95.8% of the wild genetic diversity is retained in the captive flocks. This can be brought up to 98.6% with improved genetic representation in the captive flock. It is important to keep this number as high as possible since a significant amount of genetic diversity was lost during the bottleneck.

The model indicates that, if the population biology parameters estimated for the population are accurate and continue to pertain into the future, the Aransas/Wood Buffalo population is large enough to sustain fairly steady, though not invariant, growth ( $r = .046$ , with annual variation of  $SD(r) = .081$ ) Table 2). At this rate of growth, the population would be expected to reach 500 individuals in about 27 years, and to reach 1,000 individuals in about 42 years, if habitat is not limiting and inbreeding does not depress viability. The population is projected to have no measurable probability of extinction within the next 100 years. In spite of the optimism reasonably engendered by these predictions, it might be noted that the standard deviation in population growth is expected to be about double the mean growth. Thus, in many years the population will decline temporarily, even though the long-term growth and stability may continue to be very good.

The Gray's Lake experimental population had declined to just 13 cranes (4 females and 9 males, all adult) by mid 1991. None of the released birds have bred at Gray's Lake. It is uncertain whether the remaining whooping cranes should be recaptured and used in captive propagation. Disease risks also exist, complicating the decision about whether to move the 13 birds to another site. Even if the Gray's Lake cranes begin to breed, it is possible that the remaining birds do not constitute a sufficiently large founder stock to allow population growth to stable levels.

The potential fate of a population perhaps to be introduced to central Florida was examined also with the use of the VORTEX simulation program. Initially, and optimistically, it was assumed that reproduction and mortality in a Florida population would mirror that observed in the Wood Buffalo/Aransas population. Modelling was used to examine the likely success of a new population established with releases of 10 or 20 birds per year for 10 years, or with releases of 10 or 20 birds every 4 years for 40 years. The habitat in Florida was predicted to be able to support as many as 500 cranes (based on the densities of sandhill cranes in similar habitats), but the management plans presently call for the establishment of a population with at least 25 breeding pairs (about 100 birds).

The models here represent a first attempt to evaluate the effects of historic and future growth on the size and genetic diversity of the captive whooping crane population. Deterministic life table analysis of the entire history of the captive population (1967-1991) shows a mean population growth rate of  $r = 0.011$  (stochastic  $r$ ) with high variability between years (standard deviation = 0.114). The population size at the end of 100 years with a carrying capacity of 200 was only 127 birds. Only 89% of the initial heterozygosity ( $H$ ) was retained.

Currently only 12.040 of the 34 founders are effectively represented in the captive population. With reproduction in the remaining 11 founders and balancing of genetic representation, this can be brought up to 35.3 of the potential 45 founders. The remaining 9.7 founders have already been lost due to deaths. Additional founders or better representation of founder lines may be obtained by bringing additional eggs from Wood Buffalo or birds from Gray's Lake into captivity.

Analysis of the reproductive history of whooping cranes and comparison to other species of cranes indicates that improvement in management should be achievable over the next 1 to 5 years. To evaluate the impacts of improved management, reasonable estimates of improvement were chosen (see above) and modelled individually to compare effects (Models 4-9). These factors were then combined to provide a more optimistic, but hopefully realistic prediction of achievable growth rates in the future. All models reached carrying capacity within the 100 year period, all had 92-94% of the initial heterozygosity retained.

If historic population biology parameters remain constant, the captive population is unable to consistently provide the numbers of birds targeted for release in Florida under the Analyses of Wild Population section of this report. Seven of the eight models showed a negative growth rate unless harvest rates are limited to 10 birds per year and are delayed for five years before initiation. Since harvests were only conducted for 10 years, the populations all eventually reached carrying capacity, but between 14.4 and 43.9% of the harvests could not be completed due to inadequate numbers of young for individual years. The amount of heterozygosity retained drops from 93% to 88 or 89% and the amount of rare alleles retained drops from 25 to 16.

The results indicate, that with improved management, that it is possible for the captive population to sustain release efforts. Harvest rates of 10 to 20 per year are sustainable if the captive population is allowed to grow for three more years before regular harvest and improved management goals are achieved. This may take a few years. This model does not include supplementation of the captive population or the release population with eggs from Wood Buffalo National Park. Several offspring per founding line should be retained in captivity before offspring are released. At least two offspring per founder, or more for rare lineages, was recommended at the workshop. This number should be examined more closely.



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***GRUS AMERICANA***

**WHOOPING CRANE**

**CONSERVATION VIABILITY ASSESSMENT  
WORKSHOP REPORT**

**SECTION 3  
WILD POPULATIONS**

# WHOOPING CRANE

## ANALYSES OF WILD POPULATIONS

### Population Biology Parameters

Data on the population biology of the whooping cranes for use in population viability modeling was provided at the workshop by Ernie Kuyt, from his records on the breeding population at Wood Buffalo National Park (data from 1969 to 1991), and Tom Stehn, from records on the arrivals of birds at Aransas (data from 1938 to 1991). Stephen Nesbitt and Jane Nicolich provided data on the histories of releases of sandhill cranes in Florida and Mississippi. In addition, consensus of workshop participants was obtained on the likely values, or the range of plausible values, of parameters that could not easily be estimated from existing data.

### *Population Size and Carrying Capacity*

The Aransas-Wood Buffalo population has been counted upon arrival at Aransas each year since fall 1938, at which time the population consisted of only 18 cranes. In winter 1990-91, 146 cranes arrived at Aransas and 135 cranes departed for Wood Buffalo. Habitat in the vicinity of Wood Buffalo does not appear to be limiting, and workshop participants estimated that prairie habitat could support as many as 1,000 whooping cranes. However, it was also recognized that some potential habitat will probably be converted to agriculture, especially if the crane population does not expand rapidly to use available wetlands. For the purposes of modeling, the present population size was set at 150 cranes, carrying capacity was set at 1,000, and habitat (and, therefore, carrying capacity) was expected to decrease by 1% per year during the next 50 years. To test the viability of a much more restricted population, we also modelled populations with final carrying capacities of 50, 100, and 150. (Initial carrying capacities were double these values.) Simulations with an initial population size of 18 cranes (and  $K = 500$ ) were run for 52 years to determine whether the simulation model and the parameters used accurately predicted the population fate as it had been observed from 1938 through 1990. In each case, the population was started at the expected stable age distribution calculated from the life table.

### *Reproductive Rates*

Whooping cranes are monogamous, annual breeders. The sex ratio at hatching and of adults appears to be about 1:1. It was assumed that all adult males are potential mates (i.e., none are excluded from the breeding population because of an inability to establish or hold territories). For the initial modeling of the wild population, it was assumed that both males and females begin breeding at 5 years of age. Kuyt and Goossen (1987) reported a mean age of first breeding among 14 color-banded cranes at Wood Buffalo of 5.0 years (range 3-7). Because of uncertainty in the mean age of first breeding, additional scenarios were examined with first breeding delayed until 6 years of age.

At the workshop, the view was expressed that cranes might not typically begin breeding until about 7 years of age (although some would breed earlier, others might not breed until even later ages). However, a first of age breeding of 7 years is inconsistent with the data on nesting at Wood Buffalo. If cranes did not breed until 7, the population would not have contained enough



breeding-age birds to account for the numbers of nests observed each year since 1967. (See below for explanation of the calculation of the percent of the adult population breeding each year.)

From 1976 through 1989, the years for which the most complete data are available, a total of about 310 nests were observed at Wood Buffalo. These nests yielded an estimated .76 hatchlings per nest, although more hatchlings may have been produced if eggs had not been removed for stocking of other populations (Patuxent and Grays Lake). **[Note to workshop participants: we are working with Ernie Kuyt to refine these numbers for the ultimate draft. Don't expect any major changes, however.]**

Of an estimated 125 young arriving at Aransas between 1939 and 1966 (prior to egg-pulling at Wood Buffalo), 30 were twins from 15 nests and 95 were singletons. Assuming 73.3% survival from hatching to arrival at Aransas, as estimated from recent data (see below), it can be calculated that about 171 hatchlings gave rise to the 125 survivors ( $171 \times 73.3\% = 125$ ). These hatchlings would have consisted of 56 twins (28 twin pairs  $\times 73.3\% \times 73.3\% = 15$  surviving pairs of twins) and 115 singletons (56 twins + 115 singletons = 171 hatches). Thus, about 20% of nests [ $28 / (28 + 115) = 20\%$ ] would be expected to hatch twins, and 80% to produce singletons. The percent of young birds arriving at Aransas with a twin would be less than the percent of twins at hatching, because one of a pair of twins often dies, even if mortality of birds hatched with a twin is no different than singleton hatches.

Some early deaths of hatchlings in nests may have gone unrecorded. If so, reproduction would be greater than estimated, but so would nestling mortality. Similarly, if twins are more likely to die during the first year than are singletons, the frequency of twinning would have been underestimated, but the additional (unknown) mortality of twin hatchlings would compensate to produce a number of surviving twins as estimated.

The percent of adults establishing nesting territories each year cannot be determined directly, because ages cannot be determined after the first year (except for banded birds, many of which have not yet reached breeding age). To estimate the number of adult birds (5 years and older) in the population, we assumed that the population was typically close to the stable age distribution determined from the life table. (The fecundity estimate used in the life table depends in turn on the percent of adults breeding, so these calculations must be done iteratively in order to find a fit to the data.) From the estimated number of adults during the years 1976 through 1989 (1302 bird-years  $\times .60$  adults/birds = 781 adults), and the approximately known number of nests during those years (310), it was calculated that about 79% of the adults nest each year ( $310 \times 2 / 781 = .79$ ), and about 60% successfully produce hatchlings ( $79\% \times .76$  hatches/nest). If cranes do not typically breed until reaching 6 years of age, then a smaller fraction of the population would be adult (51%), a greater fraction of adults (93%) would be nesting, and 70% of adults ( $93\% \times .76$ ) would be successful breeders. If cranes do not nest, on average, until 7 years of age, there would not have been enough adult birds (about 46% adult  $\times 1302$  birds = 599 cranes 7 years or older) to account for the 310 nests observed over the 14 years of observation.

Environmental (annual) variation in reproductive success is similarly difficult to estimate because, although the numbers of nest and hatchlings have been recorded at Wood Buffalo since 1976, the number of breeding age birds is not known for each year. However, if we assume that the percent of the population consisting of adults is constant over time, we can calculate the variation in reproductive success (number of hatchlings / adult) for each year since 1976. That variation observed between years is slightly less than the binomial variation expected due simply to random sampling from the pool of breeders with a constant probability of reproductive success. Any variation in the percent of the population that is adult would increase further the variation expected with random sampling. Thus, over the past 14 years, all variation in reproduction could be accounted for by demographic (intrinsic random) variation and there is no evidence of additional environmental variation in the wild.

### *Mortality*

Survival rates can be estimated either from recorded sightings of banded birds or from changes in counts of all birds. From 1976 through 1989, about 234.5 cranes were observed to hatch at Wood Buffalo (taking the midpoint of the possible range in those few years in which counts were imprecise), of which 172 arrived at Aransas the following winter, yielding an estimated survival of 73.3%. Because the most consistent censuses of the population are taken when the cranes arrive at Aransas each year, the population was modeled with arrival at Aransas delimiting annual increments in the life cycle of the cranes. Thus, the first "year" in the model consists of only about 6 months, and the first year survival was set at 73.3%. During the 14 years of close monitoring of the Wood Buffalo population, the observed variance around the mean survivorship of 0.733 was 0.047. The variance expected from random binomial sampling would be 0.013. The difference ( $V = .034$ , or  $SD = .184$ ) can be attributed to environmental variation.

Examining just the subset of cranes that were banded at Wood Buffalo from 1976 through 1990, 76.3% were sighted at Aransas the following winters. The observed annual variation in survival was  $V = .046$ , and the expected binomial variation is  $V = .022$ , the difference yielding an estimated environmental variation of  $V = .024$  or  $SD = .155$ . The slight differences between the estimates based on banded birds vs. all observed hatchlings are easily accounted for by sampling error. We chose to use the slightly more conservative estimates (mean = 73.3%, environmental variation = 18.4% SD) based on all hatchlings for the modeling.

Mortality after the first year can similarly be determined from either data on banded birds of known age, or from winter census reports from Aransas since 1938. (Young of the year are distinguishable from older birds when they arrive at Aransas.) Since 1938, cumulatively 2359 birds greater than 1 year of age returned to Aransas of the 2594 cranes that departed from Aransas the previous spring, yielding an estimated annual mortality after the first year of 9.06%. Among the banded birds, 89.9% annual survival was observed in 386 bird-years, but band loss after several years could have accounted for some of the "mortality" recorded among banded birds. No variation was detectable statistically among mortality rates calculated separately for each age class beyond the first year.

Examination of annual variation in the percent of cranes returning to Aransas revealed 7 years during which survival was significantly less than the mean (see Figure 1). Including those 7 years in the distribution of survival rates produced a distribution that was significantly different from both a binomial and a normal distribution. Omitting those 7 outliers resulted in a distribution that fits either a normal or a binomial distribution well. The VORTEX program used to model the population assumes that annual variation in survival follows a binomial distribution (or the equivalent normal approximation), and treats outliers as "catastrophes". The causes of the depressed survival during those seven years are not known, but can be assumed to be phenomena that are outside of the "normal" range of variation that produces typical year-to-year variation. Omitting the 7 outlier years from the data (treating them in the analysis as catastrophes) yields a mean annual survival after the first year of 92.7%. The seven catastrophe years had a mean survival of 72.3%, or 78% of the mean of "normal" years.

The estimated survivorship schedule (above) would result at the stable age distribution in a population with about 12% of the over-wintering birds at Aransas being young-of-the-year. This is very close to the 13% young that have been observed among Aransas arrivals since 1938.

The observed annual variation in survival rates from 1938 through 1990, but excluding the 7 outlier years, was  $V = .00255$ ; the variation expected due to binomial sampling from a constant probability is  $V = .00220$ . The difference can be attributed to environmental variation in the probability of surviving (see Figure 1), with  $V = .00035$ , or  $SD = .019$ . Similar calculations for comparing the observed to expected variation in annual survival of banded cranes yields an estimate of  $SD = .022$  for environmental variation. Both of these values are very close to the intuitive estimate provided by participants at the workshop that annual fluctuations in mortality probabilities would be about  $\pm 2\%$ .

Mortality rates are not certain to remain at historic levels. Increasing development along migration routes, increase commercial shipping traffic near wintering grounds, increased exposure to enzootic or epizootic diseases of waterfowl, or other factors could impact whooping cranes. We tested the stability of the population under assumptions of 25% or 50% increased mortality (with proportional increases in the environmental variation affecting mortality), and also under an assumption that increasing enzootics would cause a 2%  $\pm 2\%$  (EV) increase in mortality, relative to historic levels.

### *Lifespan*

From records of continuously breeding pairs at Wood Buffalo, the oldest birds recorded are at least 28 years. Cranes of other species are known to have lived for longer than 70 years in captivity, but field biologists at the workshop expressed the belief that whooping cranes would not typically live beyond 30 in the wild. Based on the above mortality estimates, about 3% to 5% (depending on the estimated frequency of disease epidemics or other catastrophes) of cranes would live beyond 30 years of age. For modelling the wild population, we conservatively used the estimate of 30 years for an upper limit to age.

## *Catastrophes*

As described above, in 7 of the past 52 years adult mortality was significantly greater than the mean across years, with an average depression in survival of 22% relative to non-catastrophe years. This would suggest a frequency of catastrophes of about 14%. Most of those catastrophe years were early in the data set, perhaps suggesting that the causes of the catastrophes, whatever they may have been, could have diminished in recent decades. Workshop participants suggested, based on experience with other bird populations, that a frequency of catastrophes due to disease epidemic, toxic contamination of the environment, or other causes might be about 10%, typically causing loss of about 15% of the population. It was also suggested that the probability of a hurricane striking the Aransas population at the time that birds were in residence (which is later in the year than most hurricanes would hit) might be about 0.33%, and that such a storm could kill about 50% of the cranes. Recognizing considerable uncertainty in these estimates, the population was modeled also with frequencies of catastrophes twice as great (20% and 0.66%). The addition of the above rates of catastrophes to a mean adult survival of 92.7% in non-catastrophe years would result in overall probabilities of adult survival (in catastrophe and non-catastrophe years) of 91.2% and 89.6%, respectively, for the lower and higher catastrophe frequencies. These estimates bracket the overall mean survival rate of 90.9% observed since 1938.

Although no catastrophes are known to have impacted breeding at Wood Buffalo, a few simulations were run to examine the likely impact of catastrophes that affect breeding, rather than survival of adults. For those scenarios, we examined the effect of catastrophes occurring at the above frequencies (10% and 0.33%, or 20% and 0.66%), and which depress breeding success by 50% and 100%, respectively.

## *Inbreeding depression*

There are no data from which we could estimate the effects that inbreeding would have on fecundity or survivorship of whooping cranes. Inbreeding data exist for very few populations of any bird species. Lacking empirical estimates for cranes, the wild population was modelled both under the optimistic assumption that inbreeding would not impact fitness, and also under the assumption that inbreeding would cause an increase in juvenile survivorship due to a genetic load of 3.0 "lethal equivalents" (Morton et al. 1956), a value typical of mammalian populations (Ralls et al. 1988). This severity of inbreeding depression would result in a 31% reduction in the survival of offspring of full-sib or parent-offspring matings.

## **Gray's Lake Population**

The Gray's Lake experimental population had declined to just 13 cranes (4 females and 9 males, all adult) by mid 1991. None of the released birds have bred at Gray's Lake. It is uncertain whether the remaining whooping cranes should be recaptured and used in captive propagation. Disease risks also exist, complicating the decision about whether to move the 13 birds to another

site. Even if the Gray's Lake cranes begin to breed, it is possible that the remaining birds do not constitute a sufficiently large founder stock to allow population growth to stable levels.

To explore the possible fate of that flock, we modelled the population under the optimistic assumptions that they begin to breed at the same rate as does the Wood Buffalo flock, and that the population suffers mortality comparable to the Wood Buffalo/Aransas population. Mortality has been greater at Gray's lake in the past (Garton et al. 1989 report to USFWS), and we modelled also the expected fate if future mortality remains as high as in the past (79% first-year mortality of hatchlings, 15.5% annual mortality thereafter). We also modelled the population under the assumption that, as the reproduction by the Grays Lake cranes begins, chick mortality declines to the level observed at Wood Buffalo (26.7%), but that adult mortality remains higher (15.5%). The carrying capacity of the population was set at 100; the concern is not whether sufficient habitat exists, but rather whether the released birds will expand to populate the habitat. The scenarios were tested under the assumption that inbreeding will have no effect on survival, and also under the assumption that mortality of inbred chicks is elevated due to a genetic load of 3.0 lethal equivalents.

Although the data from the experimental flock at Gray's Lake shows no evidence of fluctuations between years in mortality rates (Garton et al. 1989), we modelled the population under the assumption that the flock would experience environmental variation comparable to that observed at Aransas/Wood Buffalo (18% SD in first-year mortality, 1.9% SD in annual mortality subsequent to the first year). The frequency and severity of catastrophes was similarly assumed to mirror those estimated for the Aransas/Wood Buffalo population.

### **Florida (potential) Population**

The potential fate of a population perhaps to be introduced to central Florida was examined also with the use of the VORTEX simulation program. Initially, and optimistically, it was assumed that reproduction and mortality in a Florida population would mirror that observed in the Wood Buffalo/Aransas population. Modelling was used to examine the likely success of a new population established with releases of 10 or 20 birds per year for 10 years, or with releases of 10 or 20 birds every 4 years for 40 years. The habitat in Florida was predicted to be able to support as many as 500 cranes (based on the densities of sandhill cranes in similar habitats), but the management plans presently call for the establishment of a population with at least 25 breeding pairs (about 100 birds). Simulations were therefore examined with carrying capacities of  $K = 100$ ,  $K = 250$ , and  $K = 500$ .

It was assumed that young birds would be released. First-year mortality of released birds might be greater than first-year mortality in the established population at Wood Buffalo (26.7%). Sandhill cranes released in Florida suffered 43% first-year mortality (data provided by Stephen Nesbitt, FL GFWFC). Mortality between fledging and 1 year of age among hatched by parents in the newly established Florida population averaged only 12.8% (data from S. Nesbitt), suggesting that newly released juveniles suffered approximately 35% additional mortality relative to birds subsequently hatched within the new population (87.2% "natural" survival x 65%

survival related to the release = 57% survival through 12 months following release). Although juvenile mortality among sandhill chicks produced by the new non-migratory Florida population (12.8%) was lower than juvenile mortality in the Wood Buffalo-Aransas flock of whooping cranes (26.7%), adult mortality was greater in the Florida sandhills (10%) than in the whooping cranes (7.3%). Until releases are conducted, it is impossible to know whether the differences in mortality are due to differences between the species, differences between the environments, or both.

Sandhill cranes released in Mississippi suffered 27% mortality in the first year after release (data provided by Jane Nicolich, Patuxent), almost identical to first-year mortality among the Wood Buffalo-Aransas whooping cranes. Combining data from Mississippi and Florida, sandhill cranes suffered an average of 37.7% mortality in the 12 months following release (data summary provided by Stephen Nesbitt, FL GFWFC).

Acknowledging the uncertainty in mortality rates to be expected in a future non-migratory flock of whooping cranes, two plausible scenarios were examined: mortality as in the Wood Buffalo-Aransas population (26.7% juvenile, 7.3% adult mortality), and mortality as in the non-migratory Florida sandhills (12.8% and 10%). In addition, the assumption was made that 40% of released birds died as a result of the release, probably during the first year. This was modelled by assuming that just 6 or 12 of the 10 or 20 released birds were effectively added to the population.

Recognizing that a reintroduced population may not breed as well as does the established population at Wood Buffalo (the Gray's Lake population has had no successful breeding), scenarios with breeding delayed to 6 or 7 years of age (with 60% adults breeding per year) were also examined.

#### **Simulation Duration, Number, and Output**

The workshop chose to model the whooping crane population(s) for 100 years, and most scenarios were tested with 1,000 simulations each. The simulations proceed much more slowly when inbreeding depression is included in the analysis (because genetic relationships must be calculated between all pairs of animals in the simulated populations), so simulations testing the effects of inbreeding were repeated only 100 times for each scenario. The results examined included the probability of extinction within 100 years, the median time to extinction when at least 50% of the simulated populations went extinct, the mean population size at 100 years of those populations not going extinct, the mean population growth rate ( $r$ ), and the mean gene diversity (percent of initial heterozygosity) remaining after 100 years.

## RESULTS

### Fit of the basic model to the experience of the Aransas/Wood Buffalo population

From late 1938 to 1991, the Aransas/Wood Buffalo population of whooping cranes had grown at a mean exponential rate of  $r = 0.040$ , with annual fluctuations in the growth rate of  $SD(r) = 0.141$  ( $N[1990] / N[1938] = \lambda^{52} = 8.111$ ;  $\lambda = 1.041$ ;  $r = \ln(\lambda) = 0.040$ ). Deterministic life table analysis with the birth and death rates used in the modelling projects a mean population growth rate of  $r = .052$  ( $\lambda = 1.053$ , or 5.3% growth per year) if no eggs are removed from nests (allowing some twins to be reared) and breeding begins at age 5. Population growth is projected to be  $r = .036$  if second eggs are removed,  $r = .040$  if breeding begins at 6 years, and  $r = .025$  if second eggs are removed and breeding is delayed until 6. (See Table 1.)

The match of the observed population growth rate to the rate calculated from the life table if it is assumed that cranes begin breeding at 6 years of age could suggest that 6 is the typical age of first breeding for cranes in the wild. However, life table analyses use mean birth and death rates to calculate a single estimate of the population growth rate. When birth and death rates are fluctuating, it is more to average the population growth rates calculated separately from birth and death rates for each year. This mean growth rate would be lower than the growth rate estimated from mean life table values. Thus, in a fluctuating environment, or even in the presence of demographic stochasticity in birth and death rates, standard life table analysis can overestimate long-term population growth.

When started with the 18 individuals present in 1938, the stochastic simulations yielded a mean growth rate of  $r = .032$ , with annual fluctuations in growth of  $SD(r) = .112$ , if cranes breed at 5 and inbreeding is assumed to have no impact on viability. The stochastic simulation of the population into the future (beginning population size = 150) yielded a mean growth rate of  $r = .046$ , with  $SD(r) = .081$  (Table 2). The lower value of the growth when starting with only a few cranes presumably results from a reduction in mean population growth caused occasionally by a lack of mates (temporarily imbalanced sex ratio). The greater variation in growth across years reflects the lesser stability of a small population. Projected mean population growth is lower if the cranes do not breed until 6, or if inbreeding depresses juvenile survival (Tables 1, 2, and 3).

Recognizing some uncertainty of parameters and expected results, the similarities among the observed population growth, the mean growth calculated from the life table, and the means produced by stochastic simulations suggests that the population dynamics has been modelled reasonably accurately. Moreover, when the simulation model was started with the 18 cranes present in 1938, it projected a population size in 1991 ( $N = 151 \pm 123$  SD) almost exactly the same as that observed ( $N = 146$ ). However, it should be noted that 3.6% of the simulated populations went extinct within the 52 years from 1938 through 1990 (Table 1). It is the negative mean growth of the extinct populations that brings the overall mean population growth yielded in the simulations down below the value ( $r = .041$ ) that would be calculated from a population increase to 151 from 18 over 52 years.

The model slightly under-predicted the annual fluctuations in population growth (model  $SD(r) = .112$  vs. actual  $SD(r) = .141$ ). This may reflect a lack of full incorporation of all aspects of stochasticity into the model, or it may simply reflect the sampling error inherent in stochastic phenomena. Because the data input to the model necessarily derive from analysis of past trends, such retrospective analysis should be viewed as a check of consistency, not as proof that the model correctly describes current population dynamics. Providing another confirmation of consistency, both deterministic calculations and the simulation model project an over-wintering population of whooping cranes consisting of 12% juveniles (less than 1 year old), while the observed frequency of juveniles at the wintering grounds in Texas has averaged 13%.

The stochastic simulation under-predicted the population growth rate and the final population size if either breeding was delayed until 6 or inbreeding depressed first-year survival. The observed population performance is still within the range of results projected under these scenarios, however, so they cannot be rejected as being unrealistically pessimistic. The actual population might have been fortunate, performing better than the median of the simulated populations. In another way, the Aransas/Wood Buffalo population was fortunate: each of the simulations predicted a modest probability (3.6% to 19.0%) that the population of 18 cranes in 1938 would not have survived.

Two other aspects of the results shown in Table 1 are worth noting. Genetically, the simulations predict that the whooping crane population would have lost 13% to 16% of its heterozygosity. This amount of loss would not likely be noticed in any molecular genetic survey, as several-fold variation in the amount of heterozygosity is observed among healthy populations of vertebrates. The loss of this amount of gene diversity has been observed to be damaging to some species (Ralls et al. 1988; Lacy et al. in press), however, and is greater than that recommended as acceptable for many endangered species conservation programs (Soulé et al. 1986).

Finally, although relatively few cranes successfully rear two chicks, the cumulative depression in population growth that would be caused by a continual removal of second eggs is substantial. If second eggs had been removed for the entire history of the population since 1938, population growth would have been lower, the expected final (1990-1991) population size would have been about half what it is today, and the probability of extinction during the past 52 years would have been greater.

#### **Predicted future stability of the Aransas/Wood Buffalo population**

The model indicates that, if the population biology parameters estimated for the population are accurate and continue to pertain into the future, the Aransas/Wood Buffalo population is large enough to sustain fairly steady, though not invariant, growth ( $r = .046$ , with annual variation of  $SD(r) = .081$ ) (Table 2). At this rate of growth, the population would be expected to reach 500 individuals in about 27 years, and to reach 1,000 individuals in about 42 years, if habitat is not limiting and inbreeding does not depress viability. The population is projected to have no measurable probability of extinction within the next 100 years. In spite of the optimism reasonably engendered by these predictions, it might be noted that the standard deviation in



population growth is expected to be about double the mean growth. Thus, in many years the population will decline temporarily, even though the long-term growth and stability may continue to be very good.

The population is not destabilized if reproduction is delayed until 6 years of age. The population is projected to show strong growth (albeit at a slower pace than if breeding occurs at 5) and to stay near carrying capacity.

Losses of genetic diversity over the next century under these scenarios would be minimal (about 2% to 3% of the heterozygosity present in 1991), and the incorporation of inbreeding depression in the modelling has very little impact on scenarios using the baseline demographic parameters (compare Table 2 to Table 3). Because the earlier bottleneck likely caused significant losses in genetic variation (see Table 1), the population might now have lower fecundity, higher mortality, or be more susceptible to disease and other disturbances than would have been the case prior to the decline in numbers. The continued growth of the population indicates that genetic deterioration did not proceed so far as to preclude recovery of the population, however. If the population grows to 1,000 or more, the recovery of genetic variation by mutation would be expected to outpace further losses by random drift, and variation would be slowly restored.

#### *Effect of egg removals*

If eggs continue to be harvested from the population (limiting each nest to at most one chick), the growth rate would be reduced to  $r = .028$ , with annual fluctuations of  $SD(r) = .081$ . The population would be projected to reach 500 birds in about 44 years. The reduced population growth would not make the population unstable: There was no greater variance expected in  $r$ , and none of the 1,000 simulated populations went extinct. If the population is destabilized by increased mortality or by severely restricted habitat, however, the continued collection of eggs would amplify that instability.

#### *Effect of habitat limitations*

If habitat limits the Aransas/Wood Buffalo population at numbers well below those estimated at the workshop, the population is projected to be somewhat less stable (greater  $SD(r)$ ) and to have a measurable, but low, probability of extinction due to random fluctuations (see lines 5 - 10 of Tables 2 and 3). Genetic drift results in moderate and perhaps damaging losses of genetic diversity when the population is kept below 50 or 100. For example, 12% to 14% of present gene diversity can be expected to be lost from a population of 50 in the next 100 years. If inbreeding reduces juvenile survival by an amount typical for vertebrates, the genetic loss could cause a reduction in population growth from about 3.6% to about 2.9% per year (line 9 of Tables 2 and 3).

### *Effect of increased mortality*

If mortality increases by 50%, the population is not self-sustaining in a deterministic sense ( $r$  is negative), nor in the models (lines 13 and 14 of Table 2). Lesser increases in mortality allow for a slow positive average growth rate (lines 11, 12, 15, and 16), but leave the population vulnerable to chance extinctions and result in losses of genetic variability greater than if mortality remains as estimated from the 1938 - 1990 data. These effects are exacerbated if inbreeding impacts juvenile survival.

### *Effects of catastrophes*

The frequency and severity of catastrophes are difficult to predict with accuracy. Within the range of catastrophes modelled, the population maintained positive population growth and remained fairly stable. Catastrophes affecting breeding were less damaging than those affecting survival, as expected for a long-lived, slowly reproducing species.

### **Potential for Flock Establishment in Florida**

If breeding and mortality rates at a Florida site mirror those observed in the Aransas/Wood Buffalo flock, the suggested rates of release is adequate to assure establishment (see top 4 lines of Tables 4 and 5), with a minimal probability of failure to establish a population. The new population is expected to expand rapidly to fill available habitat. Either number of releases (10 per year or 40 per year) and either rate of release (every year for 10 years or every 4 years for 40 years) would appear adequate to establish a population, *assuming that population parameters in the new population are the same as those in the Aransas/Wood Buffalo population*. These projections account for an estimated 40% loss of newly released birds to the multiple dangers of release (for example, predation on unwary birds, or dispersal out of suitable habitat). The retention of genetic variability is expected to be related directly to the numbers of birds released and to the ultimate carrying capacity of the habitat.

Marginally more genetic variation is retained for 100 years if the releases are spread over more years, because fewer generations lapse between releases and the end of the time period monitored in the simulation. A slower rate of release leaves the population small and therefore highly vulnerable to stochastic fluctuations for more years during establishment, however, resulting in slower population growth (lower mean  $r$ ) with greater annual fluctuations (larger  $SD(r)$ ).

If breeding at a new site is delayed until 6 or 7 years of age, population growth would be slower, the population would be less stable, and there would be some probability of failure of the introduction. Moreover, the slower population growth results in greater losses of genetic variation and, consequently, more noticeable impacts of inbreeding depression (compare lines 9-12 in Table 4a, 4b, and 4c to Table 5a, 5b, and 5c).

If a non-migratory flock in Florida experiences birth and death rates more similar to the sandhill cranes in Florida, rather than the whooping cranes in Aransas/Wood Buffalo flock, establishment

is still likely. The greater adult, but lower juvenile, mortality among the Florida sandhill cranes results in lower population growth and somewhat higher probabilities of extinction (failure to become established). Genetic variation is lost more quickly than if mortality is as in Aransas/Wood Buffalo cranes, both because of the slower population growth and because of a more rapid replacement of generations (due to higher infant survival coupled with lower adult survival).

A combination of higher adult mortality with delayed breeding (bottom four lines of Tables 4 and 5) does not allow for effective establishment. Although many of the populations simulated under that scenario persisted for 100 years, the extant population were, on average, declining, and often contained fewer cranes than had been released. Genetic losses were large and inbreeding depression could accelerate the decline of the released populations (last four lines of Table 5). Considering the lack of reproduction in the Gray's Lake experimental flock, even poorer breeding performance (or higher mortality) must be recognized as a possibility among birds released in any site. Close monitoring of released birds should provide data for use in refined modelling of the population at regular intervals (perhaps yearly), guiding the program through a strategy of adaptive management (Holling 1978).

#### **Future Viability of the Gray's Lake Flock**

If reproduction and survival in the remnant experimental flock at Gray's Lake immediately match those of Aransas/Wood Buffalo, the population has a moderate probability of surviving (line 1 of Table 6), even if the likely effects of inbreeding on the small flock are considered (line 7). However, if mortality of adults and/or juveniles remains as high as it has been in the past, the small remnant population will continue its decline toward extinction. Initiation of reproduction would not be sufficient to allow population growth; a decrease in mortality is required as well. The flock could disappear quite soon, within 11 years even if reproduction begins.

If the Gray's Lake population does begin breeding, achieves positive population growth, and seems to be on the way to becoming established, it would likely need additional genetic diversity to thrive. Among those simulated populations that expanded and survived for 100 years, the cumulative decrease in heterozygosity (about 25%) was comparable to that caused by a generation of matings between siblings or between parents and offspring. Most vertebrate species suffer substantial decreases in survival and fecundity under such severe inbreeding (Ralls et al. 1988). Given the long generation time of cranes, and the low probability that the Gray's Lake population will reverse its decline, it would be logical to await population growth before any further genetic supplementation would be attempted.

## **Explanation of Tables**

The following tables summarize the results from the simulation analyses of various scenarios describing possible fates over 100 years of populations of whooping cranes (52 years for Table 1). Except for those input parameters listed in the tables, life history parameters estimated, as described above, for the Aransas/Wood Buffalo population were input into the models. Blank cells of the table indicate that parameters are unchanged from the previous line.

The last seven columns of each table present results of the analyses. The exponential rate of population growth ( $r$ ) is given from deterministic life table analyses, and the mean  $r$  resulting from the simulations is given with the standard deviation (a measure of the fluctuations in population growth in the simulated populations). The probabilities (frequencies) of extinction in the simulations and, if at least 50% of the simulated populations went extinct, the median times to extinction are given. Of those simulated populations not going extinct during the simulations, the mean population size ( $N$ ) and percent of initial genetic variance ( $H$ , expected heterozygosity) remaining at 100 years (52 years in Table 1) are given.

In scenarios not incorporating inbreeding depression, inbreeding was assumed to have no impact on fitness, and 1,000 simulations were run for each scenario. In scenarios incorporating inbreeding depression, inbreeding was assumed to reduce juvenile survival due to a genetic load of 3.0 lethal equivalents, and 100 simulations of each scenario were run.

### **Table 1. Aransas/Wood Buffalo population, 1938-1990.**

Results of 1,000 simulations each of various scenarios describing possible population dynamics of the Aransas/Wood Buffalo population of whooping cranes from late 1938 through 1990. Inbreeding was assumed either to have no impact on fitness or to reduce juvenile survival due to a genetic load of 3.0 lethal equivalents. The carrying capacity was set at 500. Age of first breeding was set at either 5 or 6 years of age. Either 20% of nests were assumed to produce twin hatchlings (2nd eggs not removed) or all nests were assumed to produce singletons (2nd eggs removed). Mortality rates, frequencies and severities of catastrophes, and environmental variation in demographic parameters were as estimated from available records, as explained in the text.

### **Table 2. Aransas/Wood Buffalo population, without inbreeding depression.**

Results of 1,000 simulations each of various scenarios describing possible fates over 100 years of the Aransas/Wood Buffalo population of whooping cranes. Inbreeding was assumed to have no impact on fitness. Input parameter columns are: final carrying capacity of the simulation (Final  $K$ ), after a 50% total decline over the 100 years; age of first breeding; indication of whether 20% of nests were assumed to produce twin hatchlings (2nd eggs not removed) or whether all nests produce singletons (2nd eggs removed); adjustments to mortality of none, multiplied by 125%, multiplied by 150%, or (additively) incremented by 2%; and hurricane and disease catastrophes either at the projected frequencies (0.33% and 10%) and severities (50% and

15% mortality), double the projected frequencies, impacting breeding rather than survival, or impacting breeding with double the frequency. Other input parameters are as described in text.

**Table 3. Aransas/Wood Buffalo population, with inbreeding depression.**

Results of 100 simulations each of various scenarios describing possible fates over 100 years of the Aransas/Wood Buffalo population of whooping cranes. Inbreeding was assumed to reduce juvenile survival due to a genetic load of 3.0 lethal equivalents. Other input parameters are as in Table 2.

**Table 4. Future Florida population, without inbreeding depression.**

Results of 1,000 simulations each of various scenarios describing possible fates over 100 years of a population to be established in central Florida. Inbreeding was assumed to have no impact on fitness. Reproduction was assumed to be the same as at Wood Buffalo. Frequency and severity of catastrophes was set to be the same as estimated for the Aransas/Wood Buffalo population. Mortality schedules were set to match Aransas/Wood Buffalo (26.7% juvenile, 7.3% adult annual mortality), or to match Florida sandhill cranes (12.8% juvenile, 10.0% adult mortality). The numbers of released birds listed for each scenario (6 or 12 per release over 10 or 40 years) is 40% lower than the 10 or 20 birds planned per release, in expectation that about 40% would fail to become established, as has been the case with sandhill cranes released in Florida. Tables 4a, 4b, and 4c present results for populations with carrying capacities of 100, 250, and 500, respectively.

**Table 5. Future Florida population, with inbreeding depression.**

Results of 100 simulations each of various scenarios describing possible fates over 100 years of a population to be established in central Florida. Inbreeding was assumed to decrease juvenile survival due to a genetic load of 3.0 lethal equivalents. Other input parameters are as in Table 4.

**Table 6. Gray's Lake Population.**

Results of 1,000 simulations each of several scenarios describing possible fates over 100 years of the whooping crane population at Gray's Lake. Carrying capacity was set at 100. Inbreeding was assumed either to have no impact on fitness or to decrease juvenile survival due to a genetic load of 3.0 lethal equivalents. Reproduction was assumed to become the same as at Wood Buffalo. Frequency and severity of catastrophes were set to be the same as estimated for the Aransas/Wood Buffalo population. Mortality schedules were set to match Aransas/Wood Buffalo (26.7% juvenile, 7.3% adult annual mortality), the rates observed at Gray's Lake (79.0%/15.5%), or the juvenile mortality rate observed at Wood Buffalo (26.7%) and the adult mortality rate experience to date at Gray's Lake (15.5%).

**Table 1. ARANSAS/WOOD BUFFALO POPULATION, 1938-1990**

Description	Input Parameters			Population Growth			Extinc Prob	Final Population		
	Inbreeding Depression	Breeding Age	2nd egg removed	Deter r	Stochastic r	SD(G)		N	SD(N)	H
Best estimate	No	5	No	.052	.032	.112	.036	151	123	87
			Yes	.036	.012	.118	.092	58	46	83
Breed at 6		6	No	.040	.017	.120	.069	76	65	84
			Yes	.025	.000	.124	.153	36	29	80
Inbreeding depression	Yes	5	No	.052	.023	.113	.051	101	82	86
			Yes	.036	.003	.122	.136	40	33	82
Inbr. depression Breed at 6		6	No	.040	.009	.122	.102	55	49	84
			Yes	.025	-.007	.127	.190	26	24	81

Table 2. ARANSAS/WOOD BUFFALO POPULATION, WITHOUT INBREEDING DEPRESSION

Description	Input Parameters						Population Growth		Extinction		Final Pop.	
	Final K	Breeding Age	2nd egg removed	Mort. adjust	Catastrophes: Freq. Repr. Sevrity Surv	Defer r	Stochastic r	SDX(t)	Prob	Median time	N	H
Best estimate	500	5	No	None	.33% 1.0 .50 10% 1.0 .85	.052	.046	.081	0	--	490	98
			Yes			.036	.028	.081	0	--	474	97
Breed at 6		6	No			.040	.033	.080	0	--	482	98
			Yes			.025	.017	.080	0	--	434	97
Limited habitat	150	5	No			.052	.042	.086	0	--	145	95
			Yes			.036	.027	.081	0	--	143	95
	100		No			.052	.041	.088	0	--	96	93
			Yes			.036	.025	.084	.001	--	94	93
	50		No			.052	.036	.095	0	--	46	86
			Yes			.036	.020	.091	.005	--	45	87
Increased mortality	500		No	x 1.25		.025	.016	.095	0	--	403	96
			Yes			.009	-.003	.097	.026	--	181	93
			No	x 1.50		-.003	-.021	.126	.202	--	57	84
			Yes			-.018	-.042	.142	.616	92	15	74
			No	+ 2%		.030	.022	.089	.001	--	448	97
			Yes			.013	.003	.090	.009	--	256	94
Double freq. of catastrophes			No	None	.66% 1.0 .50 20% 1.0 .85	.035	.025	.104	.002	--	446	97
			Yes			.019	.007	.104	.014	--	312	94
Breeding catastrophes			No		.33% 0.0 1.0 10% .50 1.0	.064	.059	.055	0	--	503	98
			Yes			.048	.043	.051	0	--	502	98
Breeding catastrophes, double freq.			No		.66% 0.0 1.0 20% .50 1.0	.059	.054	.059	0	--	502	98
			Yes			.043	.038	.054	0	--	500	98

Table 3. ARANSAS/WOOD BUFFALO POPULATION, WITH INBREEDING DEPRESSION

Description	Input Parameters						Population Growth		Extinction		Final Pop.	
	Final K	Breeding Age	2nd egg removed	Mort. adjust	Catastrophes: Freq. Repr. Surv	Delet r	Stochastic r	SD(t)	Prob	Median time	N	H
Best estimate	500	5	No	None	.33% 1.0 .50 10% 1.0 .85	.052	.043	.081	0	--	488	98
			Yes			.036	.026	.081	0	--	462	97
Breed at 6		6	No			.040	.031	.079	0	--	483	98
			Yes			.025	.016	.081	0	--	412	97
Limited habitat	150	5	No			.052	.039	.087	0	--	146	95
			Yes			.036	.025	.082	0	--	140	95
	100		No			.052	.038	.087	0	--	93	93
			Yes			.036	.022	.083	0	--	93	94
	50		No			.052	.029	.094	0	--	45	87
		Yes			.036	.015	.091	.01	--	41	88	
Increased mortality	500		No	x 1.25		.025	.012	.096	.01	--	374	96
			Yes			.009	-.006	.100	.04	--	136	92
			No	x 1.50		-.003	-.030	.133	.37	--	47	81
			Yes			-.018	-.046	.139	.71	83	14	77
			No	+ 2%		.030	.019	.089	0	--	434	97
		Yes			.013	-.004	.093	.03	--	177	92	
Double freq. of catastrophes			No	None	.66% 1.0 .50 20% 1.0 .85	.035	.024	.102	0	--	431	97
			Yes			.019	.006	.101	0	--	292	95
Breeding catastrophes			No		.33% 0.0 1.0 10% .50 1.0	.064	.058	.055	0	--	504	98
			Yes			.048	.042	.051	0	--	501	98
Breeding catastrophes, double freq.			No		.66% 0.0 1.0 20% .50 1.0	.059	.054	.058	0	--	503	98
			Yes			.043	.037	.054	0	--	503	98



Table 4a. FUTURE FLORIDA POPULATION, WITHOUT INBREEDING DEPRESSION

Description	Input Parameters				Population Growth			Extinction		Final Pop.		
	K	Breeding Age	Mortality juv adult	Release schedule	Deter r	Stochastic r	SD(r)	Prob	Median time	N	H	
Low K Breed at 5 Mortality as at Arkansas/WBPNP	100	5	26.7	7.3	6/yr for 10yr	.052	.037	.093	.002	--	93	90
					12/yr for 10yr	.052	.039	.090	0	--	94	91
					6/4yr for 40yr	.052	.026	.106	.001	--	93	90
					12/4yr for 40yr	.052	.028	.097	0	--	94	92
Breed at 6		6			6/yr for 10yr	.040	.025	.094	.007	--	89	89
					12/yr for 10yr	.040	.026	.080	.001	--	90	91
					6/4yr for 40yr	.040	.012	.106	0	--	87	90
					12/4yr for 40yr	.040	.014	.098	0	--	90	92
Breed at 7		7			6/yr for 10yr	.029	.013	.100	.025	--	77	87
					12/yr for 10yr	.029	.016	.090	.001	--	84	91
					6/4yr for 40yr	.029	-.002	.111	.027	--	76	88
					12/4yr for 40yr	.029	.003	.097	.002	--	84	92
Breed at 5 Mortality as in FL sandhills		5	12.8,10.0		6/yr for 10yr	.042	.023	.097	.025	--	88	86
					12/yr for 10yr	.042	.026	.089	.001	--	90	89
					6/4yr for 40yr	.042	.009	.115	.013	--	86	87
					12/4yr for 40yr	.042	.013	.099	0	--	91	91
Breed at 6		6			6/yr for 10yr	.027	.006	.106	.075	--	68	82
					12/yr for 10yr	.027	.011	.093	.014	--	78	89
					6/4yr for 40yr	.027	-.010	.124	.063	--	66	84
					12/4yr for 40yr	.027	-.004	.104	.005	--	80	90
Breed at 7		7			6/yr for 10yr	.015	-.012	.128	.316	--	44	78
					12/yr for 10yr	.015	-.003	.100	.059	--	60	86
					6/4yr for 40yr	.015	-.029	.137	.208	--	37	79
					12/4yr for 40yr	.015	-.019	.107	.041	--	61	88

Table 4b. FUTURE FLORIDA POPULATION, WITHOUT INBREEDING DEPRESSION

Description	Input Parameters				Population Growth		Extinction		Final Pop.	
	K	Breeding Age	Mortality juv, adult	Release schedule	Deter r	Stochastic r	Prob	Median time	N	H
Medium K Breed at 5 Mortality as at Aransas/WBNP	250	5	26.7,7.3	6/yr for 10yr	.052	.041	0	--	235	93
				12/yr for 10yr	.052	.042	0	--	237	95
				6/4yr for 40yr	.052	.029	0	--	236	93
				12/4yr for 40yr	.052	.032	0	--	238	96
Breed at 6		6		6/yr for 10yr	.040	.027	.009	--	218	92
				12/yr for 10yr	.040	.029	0	--	231	95
				6/4yr for 40yr	.040	.013	.007	--	207	92
				12/4yr for 40yr	.040	.017	0	--	231	95
Breed at 7		7		6/yr for 10yr	.029	.014	.028	--	163	89
				12/yr for 10yr	.029	.019	.002	--	212	94
				6/4yr for 40yr	.029	-.002	.023	--	143	89
				12/4yr for 40yr	.029	.005	.003	--	212	95
Breed at 5 Mortality as in FL sandhills		5	12.8,10.0	6/yr for 10yr	.042	.026	.091	--	214	89
				12/yr for 10yr	.042	.031	.001	--	233	94
				6/4yr for 40yr	.042	.010	.013	--	201	89
				12/4yr for 40yr	.042	.017	.095	--	231	95
Breed at 6		6		6/yr for 10yr	.027	.008	.103	--	137	85
				12/yr for 10yr	.027	.014	.089	--	197	93
				6/4yr for 40yr	.027	-.009	.067	--	114	85
				12/4yr for 40yr	.027	.000	.098	--	192	93
Breed at 7		7		6/yr for 10yr	.015	-.009	.122	--	58	78
				12/yr for 10yr	.015	-.001	.097	--	113	88
				6/4yr for 40yr	.015	-.029	.137	--	46	79
				12/4yr for 40yr	.015	-.018	.106	--	104	90

Table 4c. FUTURE FLORIDA POPULATION, WITHOUT INBREEDING DEPRESSION

Description	Input Parameters				Population Growth		Extinction		Final Pop.		
	K	Breeding Age	Mortality juv, adult	Release schedule	Deter r	Stochastic r	SD(r)	Prob	Median time	N	H
High K Breed at 5 Mortality as at Aransas/WBNP	500	5	26.7,7.3	6/yr for 10yr	.052	.042	.087	.002	--	471	94
				12/yr for 10yr	.052	.044	.083	0	--	478	97
				6/4yr for 40yr	.052	.029	.102	0	--	451	93
				12/4yr for 40yr	.052	.033	.092	0	--	480	97
Breed at 6		6		6/yr for 10yr	.040	.028	.089	.005	--	400	92
				12/yr for 10yr	.040	.031	.082	.001	--	461	96
				6/4yr for 40yr	.040	.013	.106	.005	--	342	92
				12/4yr for 40yr	.040	.018	.093	0	--	450	96
Breed at 7		7		6/yr for 10yr	.029	.015	.095	.031	--	241	89
				12/yr for 10yr	.029	.020	.084	.002	--	386	95
				6/4yr for 40yr	.029	.000	.109	.016	--	193	89
				12/4yr for 40yr	.029	.005	.095	.002	--	344	95
Breed at 5 Mortality as in FL sandhills		5	12.8,10.0	6/yr for 10yr	.042	.028	.090	.014	--	396	90
				12/yr for 10yr	.042	.032	.079	0	--	463	95
				6/4yr for 40yr	.042	.012	.112	.011	--	336	90
				12/4yr for 40yr	.042	.018	.095	0	--	450	95
Breed at 6		6		6/yr for 10yr	.027	.008	.104	.082	--	177	84
				12/yr for 10yr	.027	.015	.086	.006	--	329	93
				6/4yr for 40yr	.027	-.011	.126	.068	--	124	84
				12/4yr for 40yr	.027	.000	.098	.002	--	298	93
Breed at 7		7		6/yr for 10yr	.015	-.009	.123	.241	--	60	78
				12/yr for 10yr	.015	-.001	.097	.059	--	142	89
				6/4yr for 40yr	.015	-.029	.138	.224	--	49	79
				12/4yr for 40yr	.015	-.018	.107	.030	--	112	89

Table 5a. FUTURE FLORIDA POPULATION, WITH INBREEDING DEPRESSION

Description	Input Parameters				Population Growth		Extinction		Final Pop.		
	K	Breeding Age	Mortality juv, adult	Release schedule	Deiter r	Stochastic r	SD(r)	Prob	Median time	N	H
Low K Breed at 5 Mortality as at Arkansas/WBNP	100	5	26.7,7.3	6/yr for 10yr	.052	.031	.090	0	--	92	90
				12/yr for 10yr	.052	.034	.087	0	--	91	91
				6/4yr for 40yr	.052	.019	.107	0	--	90	91
				12/4yr for 40yr	.052	.023	.100	0	--	92	92
Breed at 6		6		6/yr for 10yr	.040	.019	.094	.01	--	82	89
				12/yr for 10yr	.040	.022	.089	.01	--	83	91
				6/4yr for 40yr	.040	.006	.105	.01	--	82	90
				12/4yr for 40yr	.040	.012	.094	0	--	89	92
Breed at 7		7		6/yr for 10yr	.029	.005	.101	.06	--	61	87
				12/yr for 10yr	.029	.013	.087	.01	--	82	91
				6/4yr for 40yr	.029	-.005	.111	.05	--	70	89
				12/4yr for 40yr	.029	.001	.094	0	--	83	92
Breed at 5 Mortality as in FL sandhills		5	12.8,10.0	6/yr for 10yr	.042	.012	.106	.07	--	73	86
				12/yr for 10yr	.042	.020	.091	0	--	86	89
				6/4yr for 40yr	.042	.000	.119	.06	--	77	86
				12/4yr for 40yr	.042	.008	.101	0	--	82	91
Breed at 6		6		6/yr for 10yr	.027	-.005	.118	.23	--	53	82
				12/yr for 10yr	.027	.007	.088	.02	--	72	90
				6/4yr for 40yr	.027	-.020	.129	.15	--	47	82
				12/4yr for 40yr	.027	-.006	.100	0	--	72	90
Breed at 7		7		6/yr for 10yr	.015	-.020	.131	.41	--	28	76
				12/yr for 10yr	.015	-.009	.102	.07	--	42	85
				6/4yr for 40yr	.015	-.036	.139	.30	--	28	78
				12/4yr for 40yr	.015	-.024	.112	.06	--	53	88

Table 5b. FUTURE FLORIDA POPULATION, WITH INBREEDING DEPRESSION

Description	Input Parameters				Population Growth		Extinction		Final Pop.		
	K	Breeding Age	Mortality juv, adult	Release schedule	Deter r	Stochastic r	SD(r)	Prob	Median time	N	H
Medium K Breed at 5 Mortality as at Aransas/WBNP	250	5	26.7,7.3	6/yr for 10yr	.052	.036	.086	0	--	234	93
				12/yr for 10yr	.052	.039	.085	0	--	233	95
				6/4yr for 40yr	.052	.024	.098	0	--	231	93
				12/4yr for 40yr	.052	.029	.091	0	--	235	96
Breed at 6		6		6/yr for 10yr	.040	.021	.093	.03	--	194	92
				12/yr for 10yr	.040	.026	.085	0	--	223	95
				6/4yr for 40yr	.040	.008	.106	.01	--	181	92
				12/4yr for 40yr	.040	.015	.094	0	--	233	96
Breed at 7		7		6/yr for 10yr	.029	.006	.101	.08	--	124	87
				12/yr for 10yr	.029	.015	.088	0	--	197	94
				6/4yr for 40yr	.029	-.006	.112	.05	--	116	90
				12/4yr for 40yr	.029	.003	.092	0	--	202	95
Breed at 5 Mortality as in FL sandhills		5	12.8,10.0	6/yr for 10yr	.042	.015	.101	.07	--	174	90
				12/yr for 10yr	.042	.027	.083	.02	--	226	94
				6/4yr for 40yr	.042	.001	.115	.01	--	148	87
				12/4yr for 40yr	.042	.014	.094	0	--	225	95
Breed at 6		6		6/yr for 10yr	.027	-.008	.119	.21	--	69	81
				12/yr for 10yr	.027	.010	.085	.01	--	176	92
				6/4yr for 40yr	.027	-.022	.134	.19	--	67	83
				12/4yr for 40yr	.027	-.003	.098	.02	--	170	94
Breed at 7		7		6/yr for 10yr	.015	-.020	.134	.43	--	34	78
				12/yr for 10yr	.015	-.003	.094	.06	--	101	89
				6/4yr for 40yr	.015	-.036	.138	.30	--	30	78
				12/4yr for 40yr	.015	-.023	.111	.08	--	80	88

Table 5c. FUTURE FLORIDA POPULATION, WITH INBREEDING DEPRESSION

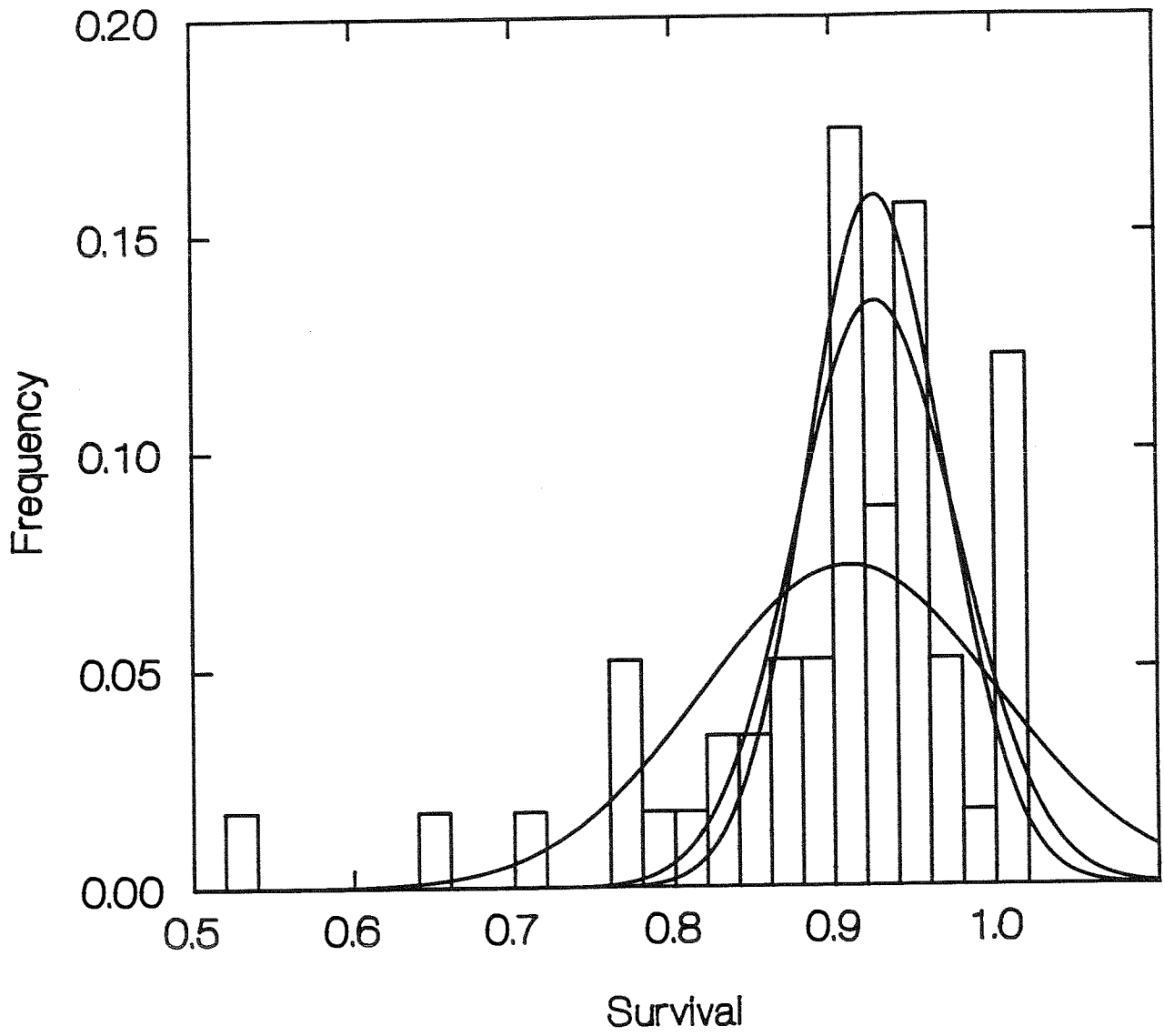
Description	Input Parameters				Population Growth		Extinction		Final Pop.		
	K	Breeding Age	Mortality juv. adult	Release schedule	Deter r	Stochastic r	SD( $\lambda$ )	Prob	Median time	N	H
High K Breed at 5 Mortality as at Arkansas/W/BNP	500	5	26.7,7.3	6/yr for 10yr 12/yr for 10yr 6/4yr for 40yr 12/4yr for 40yr	.052	.035	.089	0	--	431	94
					.052	.041	.083	0	--	477	97
					.052	.026	.099	0	--	443	94
					.052	.030	.093	0	--	477	97
Breed at 6		6		6/yr for 10yr 12/yr for 10yr 6/4yr for 40yr 12/4yr for 40yr	.040	.020	.094	.03	--	321	91
					.040	.029	.081	0	--	453	96
					.040	.010	.106	0	--	285	92
					.040	.016	.093	0	--	422	96
Breed at 7		7		6/yr for 10yr 12/yr for 10yr 6/4yr for 40yr 12/4yr for 40yr	.029	.008	.097	.07	--	163	89
					.029	.015	.086	.01	--	333	95
					.029	-.004	.107	.02	--	142	89
					.029	.003	.092	0	--	317	95
Breed at 5 Mortality as in FI sandhills		5	12.8,10.0	6/yr for 10yr 12/yr for 10yr 6/4yr for 40yr 12/4yr for 40yr	.042	.019	.093	.03	--	298	90
					.042	.027	.084	0	--	426	95
					.042	.002	.117	.05	--	235	89
					.042	.016	.091	.01	--	432	95
Breed at 6		6		6/yr for 10yr 12/yr for 10yr 6/4yr for 40yr 12/4yr for 40yr	.027	-.003	.112	.19	--	122	84
					.027	.011	.089	.01	--	287	92
					.027	-.018	.127	.13	--	69	83
					.027	-.004	.095	.01	--	233	93
Breed at 7		7		6/yr for 10yr 12/yr for 10yr 6/4yr for 40yr 12/4yr for 40yr	.015	-.023	.135	.51	98	45	78
					.015	-.010	.101	.08	--	66	86
					.015	-.036	.146	.37	--	32	79
					.015	-.023	.109	.06	--	77	88

Table 6. GRAY'S LAKE POPULATION

Description	Input Parameters			Population Growth		Extinction		Final Pop.	
	Inbreeding depression	Breeding Age	Mortality juv, adult	Deter r	Stochastic r	Prob	Median time	N	H
No inbreeding depression Breed at 5	No	5	26.7, 7.3	.052	.029	.158	--	88	76
			26.7, 15.5	-.032	-.084	1.00	19	--	--
			79.0, 15.5	-.133	-.164	1.00	11	--	--
Breed at 6		6	26.7, 7.3	.040	.015	.244	--	72	73
			26.7, 15.5	-.045	-.099	1.00	17	--	--
			79.0, 15.5	-.137	-.162	1.00	11	--	--
Moderate inbreeding depression Breed at 5	Yes	5	26.7, 7.3	.052	.011	.27	--	67	75
			26.7, 15.5	-.032	-.097	1.00	16	--	--
			79.0, 15.5	-.133	-.166	1.00	11	--	--
Breed at 6		6	26.7, 7.3	.040	-.004	.47	--	38	73
			26.7, 15.5	-.045	-.106	1.00	18	--	--
			79.0, 15.5	-.137	-.170	1.00	12	--	--

**Figure 1.** Frequency histogram of proportion of cranes surviving for one year, from each arrival at Aransas until the following fall arrival. The broadest curve is the normal distribution that most closely fits the histogram. Statistically, this curve is a poor fit to the data. The second highest and second broadest curve is the normal distribution that most closely fits the histogram excluding the five leftmost bars (7 outlier "catastrophe" years). The narrowest and tallest curve is the normal approximation to the binomial distribution expected from demographic stochasticity. The difference between the tallest and second tallest curves is the additional variation in annual survival due to environmental variation.





**FIGURE 1**

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**SUMMARY OF ANNUAL PRODUCTIVITY OF THE WOOD BUFFALO NATIONAL PARK WHOOPING CRANES**

Data collected by Ernie Kuyt, Canadian Wildlife Service, Compiled by Kristi Sprow, Aviculture Intern, International Crane Foundation  
31 July 1991

YR	# NEST	# HATCH	% HATCH	# FLEDGE	% FLEDGE	# CHICKS ARRIVED AT ARANSAS	% HATCH TO ARRIVE AT ARANSAS	% NESTS WITH A CHICK AT ARANSAS
67	9	9	100	9	100	9	100	100
68	10	-	-	-	-	6	-	60
69	11	-	-	-	-	8	-	72.7
70	13	-	-	-	-	6	-	46.2
71	13	-	-	-	-	5	-	38.5
72	15	-	-	-	-	5	-	33.3
73	14	-	-	-	-	2	-	14.3
74	15	-	-	-	-	2	-	13.3
75	16	-	-	-	-	8	-	50.0
76	16	13	81.3	12	75	12	92.3	75
77	17	13	75.6	10	58.8	10	76.9	58.8
78	15	11-15	73.3-	8-11	53.3-	7	46.7	46.6
			100		73.3		63.6	
79	18	14	77.7	6-14	33.3-	6	42.9	33.3
					77.8			
80	19	14-15	73.7-	6	40.0-	6	40.0-	31.6
			78.9		42.9		42.9	
81	17	9	52.9	3-9	17.4-	3	33.3	17.6
					52.9			
82	17	12	70.6	8	47	6	50	35.3
83	24	13	54.2	10	41.7	7	53.8	29.2
84	16-22	16-22	57.1-	16-18	57.1-	15	68.2	53.6
			78.6		75.0			
85	28	20	71.4	16-20	80.0-	16	80	57.1
					100			
86	28	22-24	78.6-	20-24	71.4-	20	83.3-	71.4
			92.9		85.7		90.9	
87	32	25-26	78.2-	25-26	78.2-	25	96.2-	78.1
			81.2		81.2		100	
88	30	22	73.3	22	68.8	19	86.4	63.3
89	30	20-27	66.7-	-	-	20	74.1-	66.6
			90.0				100	
90	32	-	-	-	-	-	-	-
<b>AVERAGE %</b>			72.3-		58.7-		68.3-	49.8
<b>(1967-89)</b>			78.6		70.0		72.1	

## 1990 - 1991 WHOOPING CRANE POPULATION

Peak Population: 146 (89 adults, 44 subadults, 13 juveniles).

Number Banded Cranes: 67 (45 adults, 22 subadults).

% Population Banded: 1990-91 - 45.9%  
1989-90 - 49.6%  
1988-89 - 59.4%

Winter Territories: 45

Average distribution: Aransas Refuge - 70  
Lamar/Egg Point - 7  
San Jose - 18  
Matagorda - 36  
Welder - 15

Number territories: Aransas - 20  
Lamar/Egg Point - 3  
San Jose - 5  
Matagorda - 13  
Welder - 4

Winter Mortality - 11 (3 adults, 3 subadults, 5 juveniles)

Spring 1991 Population - 135

Population at Start of Breeding Season - 133

(one adult female shot in spring migration, one crane found dead on nesting grounds)

### THREATS TO POPULATION AT ARANSAS

Erosion of Habitat

Oil Spills & Toxins

Dredging of GIWW (spoil placement)

Global Warming (rise in sea level)

Human Disturbance (tour boats, airboats, etc.)

Reduction of Freshwater Inflows increasing bay salinities

Disease

Hunting

Poaching

Contaminants in Ecosystem

Survival of Color-banded Whooping Cranes (1 November to 1 November) .

Hatching year	<1a	Age (years)												
		1	2	3	4	5	6	7	8	9	10	11	12	13
1977	9/10	9/9	8/9	7/8	6/7	6/6	5/6	3/5	3/3	2/3	2/2	2/2	2/2	2/2
1978	7/8	5/7	5/5	5/5	5/5	4/5	4/4	4/4	4/4	4/4	3/4	3/3	3/3	2/2
1979	5/6	5/5	5/5	5/5	4/5	4/4	4/4	4/4	4/4	4/4	3/4	2/3		
1980	4/6	3/4	3/3	3/3	3/3	2/3	2/2	2/2	2/2	2/2	2/2			
1981	2/3	1/2	1/1	1/1	1/1	1/1	1/1	1/1	1/1	1/1				
1982	5/7	3/5	3/3	1/3	1/1	1/1	1/1	1/1	1/1					
1983	6/10	6/6	5/6	4/5	4/4	4/4	4/4	4/4						
1984	10/13	8/10	6/8	6/6	4/6	3/3	3/3							
1985	16/16	16/16	16/16	12/16	12/12	11/12								
1986	18/18	17/18	15/17	11/15	10/11									
1987	21/21	18/21	16/18	16/16										
1988	14/17	12/13	9/12											

a period between banding (late July to mid-August and first arrival at ANWR

These entries are from a combined effort of Ernie Kuyt's WBNP breeding surveys and Tom Stehn's Arkansas winter census compiled during the 1991 WC PVA meeting.

Table 1. Whooping crane peak winter populations, at Aransas NWR and vicinity, in coastal Louisiana, and in New Mexico, 1938-1986.

Year	Wood-Buffalo/Aransas Population (migratory)			Louisiana Pop. (nonmigratory)			
	Adults	Young	Subtotal	Subpop.	Tot.	Wild	
1938-39	14	4	18	11		29	
1939-40	15	7	22	13		35	
1940-41	21	5	26	6		32	
1941-42 <sup>a</sup>	14(13)	2	16	6		22	
1942-43	15	4	19	5		24	
1943-44	16	5	21	4		25	
1944-45	15	3	18	3		21	
1945-46 <sup>a</sup>	18(14)	4(3)	22(17)	2		24	
1946-47	22	3	25	2		27	
1947-48	25	6	31	1		32	
1948-49	27	3	30	1		31	
1949-50	30	4	34			34	
1950-51	26	5	31			31	
1951-52	20	5	25			25	
1952-53	19	2	21			21	
1953-54	21	3	24			24	
1954-55	21	0	21			21	
1955-56	20	8	28			28	
1956-57	22	2	24			24	
1957-58	22	4	26			26	
1958-59	23	9	32			32	
1959-60	31	2	33			33	
1960-61	30	6	36			36	
1961-62	34	5	39			39	
1962-63	32	0	32			32	
1963-64 <sup>b</sup>	26(28)	7	33			33	
1964-65	32	10	42			42	
1965-66	36	8	44			44	
1966-67	38	5	43			43	
1967-68	39	9	48			48	
1968-69	44	6	50			50	
1969-70	48	8	56			56	
1970-71	51	6	57			57	
1971-72	54	5	59			59	
1972-73	46	5	51			51	
1973-74	47	2	49			49	
1974-75	47	2	49	Ad	Young	Subt	49
1975-76	49	8	57		4	4	61
1976-77	57	12	69	3	3	6	75
1977-78	62	10 <sup>d</sup>	72	6	2	8	80
1978-79	68	7	75 <sup>e</sup>	6	3	9	84
1979-80	70	6	76	8	7	15	91
1980-81	72	6	78	15	5	20	98
1981-82	71	2	73	13	0	13	86

1982-83	67	6	73 <sup>f</sup>	10	4	14	87
1983-84	68	7	75	13 <sup>g</sup>	17	30	105
1984-85	71	15 <sup>d</sup>	86 <sup>h</sup>	21 <sup>i</sup>	12 <sup>i</sup>	33	119
1985-86	81	16	97	27	4	31	128
1986-87	89 <sup>k</sup>	21	110	20	1	21	131
1987-88	109	25 <sup>l</sup>	134	16	0	16	150
1988-89	119	19	138	14	0	14	152
1989-90	126	20	146	13	0	13	159
1990-91	133	13	146	13	0	13	159

<sup>a</sup>Where two numbers occur in a column, the one in parenthesis is the original count and the second is the adjusted number as explained in Boyce (1986). The 1945 count of the migratory population on the Aransas NWR and environs was 14 and 3, but 22 adult-plumaged birds returned to the refuge in the fall of 1946. Consequently, it is evident that some birds were not counted in 1945.

<sup>b</sup>One juvenile disappeared in late November.

<sup>c</sup>Efforts to establish the Idaho/New Mexico population were initiated in 1975 when whooping crane eggs from wild pairs in Wood Buffalo National Park, Canada, were transferred to the nests of wild sandhill cranes at Grays Lake NWR in southeastern Idaho. For details of this cross-fostering project, see Drewien and Bizeau (1978) and a later section of the Recovery Plan.

<sup>d</sup>Includes one color-marked juvenile that did not winter at Aransas NWR but was seen in Kansas during spring migration.

<sup>e</sup>One juvenile disappeared soon after arrival on the wintering grounds, and the population peaked at 74 birds.

<sup>f</sup>Two of four juveniles arriving at Aransas NWR subsequently died during the winter.

<sup>g</sup>One ill subadult bird (82-13) was captured for treatment at the Bosque del Apache NWR but died several days later.

<sup>h</sup>Includes one subadult killed by a predator on the wintering grounds. ca. November 14, 1984 and a subadult last seen November 21, 1984.

<sup>i</sup>Numbers represent best estimates available.

<sup>j</sup>One ill 2-year-old subadult was captured at Bosque del Apache NWR for treatment of avian cholera.

<sup>k</sup>One subadult disappeared in winter - presumed dead.

<sup>1</sup>One juvenile wintered in Oklahoma in 1986-87 and one wintered in western Texas in 1987-88. Another wintered in south Texas in 1987-88.





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***GRUS AMERICANA***

**WHOOPING CRANE**

**CONSERVATION VIABILITY ASSESSMENT  
WORKSHOP REPORT**

**SECTION 4  
CAPTIVE POPULATIONS**

## ANALYSES OF CAPTIVE POPULATIONS

### Population Biology Parameters

#### *Breeding Age*

The age of first reproduction was calculated for all female whooping cranes hatched in captivity since the initiation of the breeding program at PWRC in 1966 (see Table 1a). Examining data on females which have reproduced indicate that the median age of first egg was 7.5 years of age and the median egg of first successful chick hatching was age 8. The age of first egg is taken as more relevant to the demographic analyses since fertility and hatchability are often related to management practices. The earliest age of egg laying was 5. The median age for first egg for female hatched since 1975 which have reproduced is 5.

To accurately reflect the entire captive population, data on 11 females (5 living, 6 dead) which have reached sexual maturity and not reproduced should be included in the analyses (see Table 1b). Onset of egg laying in 4 birds may have been delayed by the transfer to ICF. The age of first breeding was set at 6 for the modelling. This is considered a reasonable estimate based on onset of maturity in recent years excluding birds which may have been delayed by the move to ICF. Later age of first reproduction in the past is taken into account in the modelling by adjusting the number of females producing zero young (see Female Reproductive Rates below).

Median age of first offspring for captive males since 1967 was 9 (see Table 1c). This number is higher than expected for the future due to historic artificial insemination practices. The earliest age was 4. The model was run at 6 years of age.

#### *Maximum Age*

The whooping crane program has been running 25 years and thus does not have adequate data on longevity since breeding and life expectancy may be greater than 60 years. White-naped Cranes have been reported to reproduce well into their 60s and a Siberian Crane lived until approximately 80 years old and bred well into his 70s. For the purpose of this modelling, a conservative minimum estimate was set at 30 years. The model was also run to determine the effect of increasing maximum age to 50.

#### *Female Reproductive Rates*

The reproductive records were examined to estimate the percentage of breeding age females producing different numbers of hatchlings each year (see Table 2). The data from 1967 to present indicate that only 29.0% of breeding age females produced young when age of first breeding was set at 6 (see Table 3). As a conservative prediction of what levels of reproduction are reasonable to anticipate in the future, data for 1982-1991 were examined (see Table 3). These data represent historic trends once management efforts were established. Data for the year

1986, 1990, and 1991 were eliminated from the analysis on female reproductive rates due to catastrophic or unusual events which were known to effect reproduction (see Catastrophes below). The results indicate higher reproductive rates with 44.6% of the females producing young. The percentage of females producing larger numbers of offspring per year also increased (Table 4).

To predict probable future trends, an increase to 70% of females breeding at the age of 6 or older was modelled. Improvements in the number of offspring per female were also modelled.

### *Male Reproductive Rates*

Historically, not all males have been in the breeding pool. Priority for breeding was given to good semen producers during artificial insemination (AI). On average, 27% of breeding age males have produced chicks. In the future, the a greater proportion of males can be represented in the breeding pool through improvements in natural copulation and altered AI strategies. The model was run using both historic values and the inclusion of all males in the breeding pool.

### *Breeding Strategy*

Although cranes are behaviorally monogamous, captive management involving artificial insemination (AI) strategies enables insemination by males other than mates. This ensures that a larger number of males are represented in the breeding pool. Therefore, polygyny was chosen as the breeding strategy for the model.

### *Inbreeding Depression*

No data exist on the levels or effects of inbreeding in whooping cranes. The population is estimated to have derived from a maximum of 13 founders. Gee and Mirande estimate that only 6-8 founding lines may be represented in the extant population. Fortunately population numbers recovered within 1-2 generations from the 1941 bottleneck reducing the potential rate of loss of genetic diversity. Gee estimates the degree of relatedness of the living birds to be \_\_\_\_ after \_\_\_\_ generations. The model was generally run with no inbreeding effects. To assess the potential effects of inbreeding, Models 2 and 10 were run with inbreeding set at levels roughly comparable to mammal values (3.0 lethal equivalents) using the heterosis model (see Modelling Results, Inbreeding Depression below). No adequate studies assessing inbreeding levels are known for birds at this time.

### *Age Specific Mortality*

For the purpose of these analyses it was assumed that mortality rates are comparable for males and females since the sex ratio at birth and in the living population are roughly 50:50.

Examination of the genealogy data indicates that from 1967 to present 43.1% of whooping cranes die between hatching and 1 year of age (Table 5). The observed variance is 0.070 and the

expected variance is 0.063. Therefore the standard deviation of first year mortality attributable to environmental variation is 8.5%. Data for the last 10 years (1982-1991) indicate that chick mortality rates have dropped to 38.0% with an environmental variation is 8.7% (see Table 5).

Mortality rates were assumed to be the same for all age classes once birds reached 1 year of age. Data for 1979-1989 indicate that on average 8.3% of whooping crane entering a given age class die before reaching the next age class (eg. 8.3% of 7 year old birds die before reaching 8, see Table 6). The environmental variation associated with reproduction was calculated at 6.8%.

These data include mortality associated with four "catastrophes" encountered at PWRC during this period (see Catastrophes below). The model was initially run with the above mortality data and no catastrophes. Analysis of annual mortality excluding deaths associated with these catastrophes indicates an average annual mortality of 5.3% with an environmental variation of 1.0%. The model was then run with the revised mortality values and the four catastrophes included. Finally, the model was run with the revised mortality values and a prediction of future catastrophes.

### *Catastrophes*

Four events occurred during the 1980s which cause significant changes in the annual mortality or fecundity rates. These are:

	EEE Outbreak <u>1984</u>	Construction <u>1986</u>	Mycotoxin <u>1987</u>	Transfer to ICF <u>1989</u>
Frequency (%)	4	4	4	4
Effect on reproduction	1.0	0	1.0	0.5
Effect on survival	0.825	1	0.95	0.95

The model was initially run with these effects factored into the mortality rates (see above). The model was also run with the mortality rates adjusted to what would have occurred without these catastrophes and the catastrophe data entered directly.

In the modelling of the wild population, years with high mortality rates which were identified as statistical outliers were eliminated from the calculations of environmental variation in mortality. In captivity, three of the above events had documentable effects on survival which were considered to be outside of normal variation, although they were not statistically significant. Consequently, only deaths during those years which were not attributable to these events were included in the calculations of environmental variation (see Table 6).

Predictions were also made on future catastrophes. One disease outbreak was anticipated at one of the three captive centers every 5 years (once every 15 years per site, frequency = 20%). The

effect on reproduction was estimated at 0.89 and on survival at 0.95. One major construction project was anticipated at one of the three centers every 5 years (once every 15 years per site, frequency = 20%) with a 0.83 effect on reproduction and no effect on survival (1.0).

### *Harvest Rates*

The models were examined to evaluate the ability of the captive population to sustain harvest rates adequate to support reintroduction programs. Data on historic trends (Model 2) and predictions for the future based on improvements in management Model 10) were both evaluated.

Only first year birds were harvested. Harvest rates of 10 or 20 juveniles per year of harvest were examined (half male, half female). These numbers correspond to the model for release into Florida under the Wild Population Modelling section of this report. Nesbitt estimated mortality rates of approximately 40% between transfer to the release site and release of the birds. Consequently the captive centers need to produce 10 or 20 offspring to produce 6 or 12 released birds respectively. Each model included ten years of harvest.

The first year of harvest was modelled at one, three, and five years to determine the effect of allowing the captive population to increase in size before harvesting young. The frequency of harvest was also run at one year or four year intervals.

### *Carrying Capacity*

The carrying capacity was set at 200 for the initial modelling. Models 2 and 10 were run examining the effect of dropping the carrying capacity to 100. Once a third center is established, the captive carrying capacity will expand from 70 to 100 individuals. The harvest models were run at 100 since plans call for early initiation of release attempts.

### *Non-variable Parameters*

The following parameters were used in all of the model runs:

- Sex ratio = .5
- Maximum litter size = 5
- Stable age distribution = yes
- Initial population size = 70

### **Results**

The models here represent a first attempt to evaluate the effects of historic and future growth on the size and genetic diversity of the captive whooping crane population. This is viewed as a dynamic process and readers are encouraged to contact the genealogist to recommend additional variables of management strategies to be examined.

### *Predicted Future Stability of the Captive Population Based on Historic Data*

The modelling results for the captive whooping crane population without inbreeding effects and with carrying capacity set at 200 are summarized in Tables 7-8. Deterministic life table analysis of the entire history of the captive population (1967-1991) shows a mean population growth rate of  $r = 0.011$  (stochastic  $r$ ) with high variability between years (standard deviation = 0.114). The population size at the end of 100 years with a carrying capacity of 200 was only 127 birds. Only 89% of the initial heterozygosity ( $H$ ) was retained. All models were run with a starting population of 70 animals with two unique alleles assigned to each individual for a total of 140 alleles. The results show the number of these "rare alleles" (RA) remaining after 100 years. Based on continuation of historic data, only 20 alleles would be retained.

Model 2 examines a subset of the historic data (1982-1991) during which pairs were established and reproducing as a reasonable predictor of what can be expected in the future based on continuation of historic data. Events which were known to significantly impact on birth or death rates were modelled as catastrophes. Years during which these events occurred were eliminated from fecundity and mortality calculations. The results indicate a higher growth rate of  $r = 0.071$  with lower variation ( $SD = 0.078$ ). The population reaches carrying capacity, 93% of the heterozygosity is retained, and 28 rare alleles are preserved. A self-sustaining captive population can be established if we are able to maintain this level of growth.

### *Predicted Future Stability Based on Improved Management*

Analysis of the reproductive history of whooping cranes and comparison to other species of cranes indicates that improvement in management should be achievable over the next 1 to 5 years. To evaluate the impacts of improved management, reasonable estimates of improvement were chosen (see above) and modelled individually to compare effects (Models 4-9). These factors were then combined to provide a more optimistic, but hopefully realistic prediction of achievable growth rates in the future. All models reached carrying capacity within the 100 year period, all had 92-94% of the initial heterozygosity retained.

Altering historic artificial insemination (AI) and natural copulation strategies will ensure that all males are included in the breeding pool. This decrease the growth rate slightly to  $r = 0.069$ , but increases the number of rare alleles preserved. Using AI to maintain a polygynous breeding strategy by inseminating females other than mates yields a slightly higher growth rate than strict monogamy.

Increasing the number of breeding age females reproducing to 70% has the most significant effect on growth rate ( $r = 0.109$ ). Increasing the number of offspring produced by each female and lowering chick mortality also increased growth rates to 0.088 and 0.082 respectively. Increasing reproductive lifespan from 30 to 50 years and predicting levels of future catastrophes had no notable effect on the growth rate or status of the captive population in 100 years.

If all of these improvements are achieved, an annual growth rate of about 0.143 is possible (Model 10). Steady, gradual improvement is expected over the next several years. Efforts are underway to include all males in the breeding pool, especially under-represented lineages. The number of females breeding should increase as a cohort of young birds mature. Attempts have been made to pair these birds at an earlier age and to minimize disturbances and moves. The development of pair bonds in the young birds has been encouraging. Rearing techniques have been refined and fewer problems are being seen with improper sexual imprinting.

Fertility rates should improve as the number of naturally fertile pairs increases. This may be slightly offset by efforts to insure reproduction in males with poorer histories of semen production during AI. The number of eggs laid by individual females may be increased by reducing disturbance and pulling eggs singly in experienced pairs. However, this may be offset by leaving later clutches to increase rates of parent rearing for release.

Reduced chick mortality rates should be achievable as parasite problems are controlled and prevention and treatment of leg problems improves.

#### *Inbreeding Effects*

Assuming standard mammalian levels of inbreeding, the main impact of inbreeding is to reduce growth rates ( $r$ ) by 0.005 for the historic model (Model 11) and 0.003 for the model based on improved management (Model 12) (Table 8). There was no reduction in the final population size, level of heterozygosity, or number of rare alleles retained. Growth rates were reduced by 0.007 for the historic model (Model 15) and 0.009 for the improved management model (Model 16).

#### *Carrying Capacity*

Reducing carrying capacity from 200 to 100 had little impact on growth rates, but the levels of heterozygosity retained dropped from 93 to 88% for the historic model (Model 13) and from 92 to 86% for the improved management model (Model 14) (Table 8). The number of rare alleles dropped from 28 to 15 for the historic model and from 25 to 13 for the improved management model. This finding is extremely noteworthy since current recovery goals target three captive centers whose current capacity is about 100 animals. The target captive population size should be examined more closely at the upcoming masterplan meeting.

#### **Potential to Sustain Harvest to Support Release Program in Florida**

If historic population biology parameters remain constant, the captive population is unable to consistently provide the numbers of birds targeted for release in Florida under the Analyses of Wild Population section of this report (Table 9). Seven of the eight models showed a negative growth rate unless harvest rates are limited to 10 birds per year and are delayed for five years before initiation. Since harvests were only conducted for 10 years, the populations all eventually reached carrying capacity, but between 14.4 and 43.9% of the harvests could not be completed



due to inadequate numbers of young for individual years. The amount of heterozygosity retained drops from 93% to 88 or 89% and the amount of rare alleles retained drops from 25 to 16.

If management is improved as predicted in Model 10, positive growth rates are achieved for all models except harvest rates of 20 birds once every four years starting at present (Table 10). If harvest rates of 10 per harvest year are adequate, almost all harvests can be completed (97.3 to 98.9%). If harvest rates of 20 are desirable, it is better to wait three years before starting harvests, with 94% of the harvest possible. Waiting five years has little added benefit. Under this model, only 87% of the heterozygosity is retained and 13 rare alleles.

The results indicate that it is possible for the captive population to sustain release efforts. Harvest rates of 10 to 20 per year are sustainable if the captive population is allowed to grow for three more years before regular harvest and improved management goals are achieved. This may take a few years. This model does not include supplementation of the captive population or the release population with eggs from Wood Buffalo National Park. Several offspring per founding line should be retained in captivity before offspring are released. At least two offspring per founder, or more for rare lineages, was recommended at the workshop. This number should be examined more closely at the masterplanning meeting.

The genealogist is available to run additional model for the recovery team to explore varying reproductive and mortality rates for the release population or to evaluate the potential of the captive population to support harvest under various management regimes.

## STATUS OF THE CAPTIVE POPULATION

Significant steps have been made towards the development of a masterplan for the captive population. The preliminary results are summarized in this report. Mirande will travel to Patuxent in March to prepare for a workshop to be held at ICF during the fall of 1992. Staff from Patuxent, the Calgary Zoo, the San Antonio Zoo, and ICF will meet to develop a captive masterplan for the whooping cranes.

### Genealogy

The establishment of a genealogy was the necessary first step in conducting genetic and demographic analyses. Data were compiled by the International Crane Foundation (ICF) using SPARKS software (International Species Inventory System). A studbook-like report was provided by ISIS. The data set was incomplete and contained many errors. Data were obtained from in-house records at Patuxent, ICF, and the San Antonio Zoo, and from Dr. James Lewis, published literature, unpublished reports, and when all else failed -- from memory. Many records were incomplete or difficult to locate. The process has contributed to the organization of record systems. The genealogy is believed to be close to completion. There are still 7 cases of unresolved paternity (Table 11 and discussion below). Date and cause of death still need to be determined for a number of individuals. Roger Barr developed a preliminary necropsy database at Patuxent. Pat Klein will be consolidating lab and histology reports currently in different locations and completing interpretations of cause of death. Assumptions on omissions or duplications of individual animals need to be verified.

### Demographic Analysis

#### *Age Structure*

The age structure of the population is reasonably stable (see Figure 1). There are adequate numbers of young entering the population, although this is partially attributable to the input of eggs from Wood Buffalo. The number of young recruited into the captive population will likely be stabilized once releases are initiated, although harvesting for release every 10 years will destabilize the population. Retention of some young in captivity should provide replacement for deaths and balance the genetic representation of the captive flock.

#### *Generation Length*

The whooping crane is a long lived species and estimates of generation time for the captive population vary from \_\_\_ to \_\_\_ years (will be provide in next draft due to software problems). Since genetic diversity is lost in proportion to the number of generations a species passes through during a recovery program, the long generation time for whooping crane results in slower rates of loss.

### *Population Growth Rates*

Predictions of historic growth rates under different management regimes from will be provided in the final draft due to software difficulties due to small sample size. They will include:

- (1) Growth rate for all years
- (2) Growth rate for recent years
- (3) 1967-1985 growth rate with eggs from Wood Buffalo and with eggs sent to Gray's Lake
- (4) 1967-1985 growth rate without eggs from Wood Buffalo and with eggs sent to Gray's Lake
- (5) 1967-1985 growth rate without eggs from Wood Buffalo and Gray's Lake eggs retained at Patuxent

The number of births exceeded the number of deaths for each of these management scenarios, but the rate of growth was or would have been very different.

### **Genetic Analyses**

#### *Founder Representation*

For the purpose of these analyses, eggs taken from separate nesting areas in Wood Buffalo National Park have been assumed to be unrelated to each other and are designated as founders. We know from the size of the population at the 1941 bottleneck that the current population is derived from at most 12 and more likely 6 or 8 founding lineages, so this assumption is clearly invalid. Mitochondrial DNA research by Krajewski will hopefully provide additional cues on the relatedness of birds or eggs taken from the wild. Banding and genealogy data on the wild population provide additional valuable information on the relatedness of birds taken from the wild. Eggs taken from the same wild nest are assumed to be related unless a pair or mate change was documented in the wild population. Studbook numbers are assigned for their wild parents to indicated relatedness for the genetic analyses.

Based on these assumptions 1,000 "gene drop" simulations were run using GENES software developed by Bob Lacy to evaluate the amount of diversity likely to be retained based on the reproductive history of the captive population. There are 45 potential founders in the captive population, 34 have currently reproduced (Table 12). The one unknown listed in this table represents captive sires listed as unknown due to artificial insemination practices. Several measures are given on the effectiveness of founder representation. Founder genome equivalents describe the number of founders it would take to obtain the current level of genetic representation of the wild flock if all founders bred randomly. Currently only 12.040 of the 34 founders are effectively represented in the captive population. With reproduction in the remaining 11 founders and balancing of genetic representation, this can be brought up to 35.294 of the potential 45 founders. The remaining 9.706 founders have already been lost due to deaths. Additional

founders or better representation of founder lines may be obtained by bringing additional eggs from Wood Buffalo or birds from Gray's Lake into captivity.

Currently 95.8% of the wild genetic diversity is retained. This can be brought up to 98.6% with improved genetic representation in the captive flock. It is important to keep this number as high as possible since a significant amount of genetic diversity was lost during the bottleneck.

Currently there has been no inbreeding of lineages based on assumptions of relatedness. Clearly inbreeding is occurring in the captive population, although the degree is unknown.

Table 13 shows the degree of representation of birds designated as founders. The birds with studbook numbers starting with 999 are the wild parents of the captive flock assigned when more than one offspring is represented in the captive population. Founder representation is highly skewed with 11 founders having no offspring and three pairs accounting for the majority ( %) of captive offspring. It is very important to balance representation, Table 13 shows existing and target founder representation. There is some variation in target founder representation due to deaths.

### *Mean Kinship*

Mean kinship is a measure of the amount of an individual's genes which are shared by the rest of the population (see Table 14). Unrepresented founders have mean kinship values of zero. Mean kinship values are a useful tool for assigning mates. Birds with low mean kinship values are most important to breed and should be bred with mates of comparable mean kinship rank. All matings should be checked to insure inbreeding coefficients of zero.

### **Captive Population Management Objectives**

- (1) Establish an adequate number of pairs to provide the numbers of offspring required to sustain release efforts.
- (2) Obtain adequate representation of Wood Buffalo flock through egg collections to insure preservation of 90% of genetic diversity represented in the wild flock for 100(?) years should catastrophe strike the Wood Buffalo population.
- (3) Captive carrying capacity will be approximately 100 animals with the addition of Calgary. The suitability of this population size needs to be evaluated once long-term objectives are determined.

### **Individual Management Objectives**

Short term breeding priorities have been recommended for pairs at Patuxent, ICF, and San Antonio. Recommendations incorporate genetic value, location, research objective, age, and behavior.

These objectives need to be evaluated annually to meet long term goals.

## **Management Problems or Issues to be Addressed**

Delayed sexual maturity

Abnormal eggs

Egg breaking by pairs

Improving fertility

Nutrition

Leg problems

Pseudomonas infections

Cryobanking

Blood banking

- health management

- DNA banks

Effects of stress on health and reproduction

Weight monitoring to establish medical and reproductive normals

Stimulating reproduction

- egg or chick adoptions

- artificial photoperiod

Pair formation

- stimulating and balancing dominance (eg.- calling mounds)

- promoting pair interactions (eg.-pen flooding)

Hormonal research

Genetic defects

Movements of birds between centers

Pre-release protocols

Management of Gray's Lake birds if brought into captivity

Completion of husbandry manual

Table 1a. Sexual maturity of captive whooping crane breeding females (1976 - present).

<u>Female ID</u>	<u>Name</u>	<u>Hatch Year</u>	<u>Year of First Egg</u>	<u>Age at First Egg</u>	<u>Year of First Chick</u>	<u>Age at First Chick</u>
1022	Ektu	1967	1978	11	1978	11
1026	Tex	1967	1977	10	1982	15
1027	Ursula	1968	1977	9	1977	9
1030	"263"	1968	1975	7	1975	7
1036	"259"	1968	1977	9	1978	10
1040	Klewi	1969	1982	13	-	-
1050	Ms. Scrb	1971	1976	5	1977	6
1053	Mrs. C.	1971	1979	8	1981	10
1068	Hanna	1977	1982	5	1983	6
1098	Riva	1982	1988	6	1989	7
1101	Ginger	1982	1987	5	-	-
1110	Wanda	1983	1991	8	-	-
1136	Lazarus	1985	1990	5	1991	6

Average age of first breeding

First egg: mean age = 7.6      median age = 7.5      (N=12)  
 First chick: mean age = 8.7      median age = 8      (N=10)

Table 1b. Captive whooping crane females over 5 years old which have not bred (1967 - present).

<u>Female ID</u>	<u>Name</u>	<u>Hatch Year</u>	<u>Age at Death</u>	<u>Age</u>
1039	"219"	1969	9	-
1058		1974	7	-
1075	Too Nice	1978	6	-
1085		1979	5	-
1096	Lumpy	1982	9	-
1097	Matagorda	1982	6	-
1112		1983	-	8
1119	Kate	1983	-	8
1135		1985	-	6
1137	Faith	1985	-	6
1140	Stella	1985	-	6

Table 1c. Age of captive male whooping cranes at first chick production (1976 - present).

<u>Male ID</u>	<u>Name</u>	<u>Hatch Year</u>	<u>Year of First Chick</u>	<u>Age of First Reproduction</u>
1019	Canus	1964	1981	17
1020	Screwbill	1967	1977	10
1031	Rattler	1968	1978	10
1032	Killer	1968	1976	8
1041	Ulysses	1969	1977	8
1063	Hal	1974	1990	16
1086	Fred	1979	1987	8
1139	Stump	1985	1989	4
1144	Alta	1986	1991	5

Average age of first breeding

First chick: mean age = 9.6      median age = 8      (N=9)

Table 2. Life lines and reproductive summaries for captive female Whooping Cranes, 1975-1991.

STUD BOOK #	YEAR																	
	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	
1022	$\frac{0^a}{0^0}$	$\frac{0}{0}$	$\frac{0}{0}$	$\frac{0}{1}$	$\frac{1}{2}$	$\frac{0}{0}$	$\frac{0}{0}$	$\frac{1}{4}$	$\frac{3}{9}$	$\frac{4}{7}$								
1026	$\frac{0}{0}$	$\frac{0}{0}$	$\frac{0}{1}$	$\frac{0}{1}$	$\frac{0}{1}$	$\frac{0}{0}$	$\frac{0}{0}$	$\frac{1}{1}$										
1027	$\frac{0}{0}$	$\frac{0}{0}$	$\frac{1}{9}$	$\frac{4}{10}$	$\frac{3}{7}$	$\frac{0}{4}$	$\frac{2}{6}$	$\frac{2}{5}$	$\frac{4}{6}$	$\frac{1}{8}$	$\frac{5}{5}$	$\frac{0}{0}$	$\frac{1}{2}$	$\frac{3}{6}$	$\frac{3}{4}$	$\frac{0}{0}$	$\frac{0}{2}$	
1030	$\frac{1}{3}$	$\frac{1}{2}$	$\frac{0}{4}$	$\frac{0}{4}$	$\frac{0}{2}$													
1036	$\frac{0}{0}$	$\frac{0}{0}$	$\frac{0}{6}$	$\frac{3}{9}$	$\frac{5}{11}$	$\frac{0}{2}$	$\frac{0}{0}$	$\frac{4}{7}$	$\frac{2}{7}$	$\frac{1}{2}$								
1039	$\frac{0}{0}$	$\frac{0}{0}$	$\frac{0}{0}$	$\frac{0}{0}$														
1040	$\frac{0}{0}$	$\frac{0}{0}$	$\frac{0}{0}$	$\frac{0}{0}$	$\frac{0}{0}$	$\frac{0}{0}$	$\frac{0}{0}$	$\frac{0}{3}$	$\frac{0}{2}$	$\frac{1}{2}$	$\frac{0}{2}$	$\frac{0}{0}$	$\frac{0}{1}$	$\frac{0}{1}$	$\frac{0}{2}$	$\frac{0}{4}$	$\frac{0}{3}$	
1050	$\frac{0}{3}$		$\frac{2}{3}$															
1053	$\frac{0}{0}$	$\frac{0}{0}$	$\frac{0}{0}$	$\frac{0}{1}$	$\frac{0}{0}$	$\frac{0}{5}$	$\frac{1}{7}$	$\frac{2}{8}$	$\frac{3}{10}$	$\frac{4}{6}$	$\frac{2}{0}$	$\frac{0}{1}$	$\frac{1}{3}$	$\frac{2}{7}$	$\frac{2}{7}$	$\frac{3}{7}$		
1058					$\frac{0}{0}$	$\frac{0}{0}$	$\frac{0}{0}$											
1061																		
1066																		
1068								$\frac{0}{5}$	$\frac{2}{4}$	$\frac{0}{4}$	$\frac{0}{0}$	$\frac{0}{0}$	$\frac{0}{1}$	$\frac{2}{3}$	$\frac{1}{3}$	$\frac{1}{2}$	$\frac{1}{2}$	$\frac{0}{0}$
1075								$\frac{0}{0}$	$\frac{0}{2}$									
1078									$\frac{0}{0}$									
1080																		
1082																		
1084																		
1085										$\frac{0}{0}$								
1088																		
1089																		
1091																		
1092																		
1096													$\frac{0}{0}$	$\frac{0}{0}$	$\frac{0}{0}$	$\frac{0}{0}$	$\frac{0}{0}$	

<sup>a</sup> Figure above line denotes number of chicks hatched by each female in a given year.

Table 3. Summary of production of captive female Whooping Cranes six years or older.

Years	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91
Total Females of Breeding Age	8	10	10	7	8	7	7	7	7	9	4	4	8	11	10	14	14
Females Producing Eggs	1	2	5	5	6	2	2	7	5	6	3	0	5	5	5	4	6
% Females Not Producing Eggs	.875	.800	.500	.286	.250	.714	.714	0.00	.286	.333	.250	1.00	.375	.545	.500	.714	.571
Females Producing Chicks	1	1	2	3	3	0	2	5	5	5	2	0	2	3	3	2	3
% Females Not Producing Chicks	.875	.900	.800	.571	.625	1.00	.714	.286	.286	.444	.500	1.00	.750	.727	.700	.857	.786

All years:

n = 17  
 p producing = 42/145 = .290  
 p not producing = .710  
 Expected (Variance) = .021 SD = .145  
 Observed (Variance) = .048 SD = .218  
 Env Variance = Square root of Obs(V) - Exp(V) = .164

Best years (1982-1985):

n = 4  
 p producing = 17/27 = .630  
 p not producing = .370  
 Exp (V) = .037 SD = .192  
 Obs (V) = .012 SD = .109  
 Env (V) = 0

Representative years used as basis for future modelling (1982-85, 87-89) (1986, 1990, and 1991 were eliminated from the analyses due to events which were known to impact on reproduction):

n = 7  
 p producing = 25/56 = .446  
 p not producing = .554  
 Exp (V) = .030 SD = .173  
 Obs (V) = .041 SD = .201  
 Env (V) = .105



Table 4. Percentage of breeding age female Whooping Cranes (six years or older) producing different numbers of offspring per year.

# C h i c k s	Years								
	1967-1991			1982-85			1982-85, 87-89		
	N	%	Adjusted %	N	%	Adj. %	N	%	Adj. %
0	90	68.7	71.0 <sup>a</sup>	10	37.0	37.0 <sup>a</sup>	31	54.4	55.4 <sup>a</sup>
1	15	11.4	10.6	5	18.5	18.5	9	15.8	15.4
2	11	8.4	7.8	5	18.5	18.5	8	14.0	13.7
3	8	6.1	5.7	2	7.4	7.4	4	7.0	6.9
4	6	4.6	4.2	4	14.8	14.8	4	7.0	6.9
5	1	0.8	0.7	1	3.7	3.7	1	1.8	1.7

<sup>a</sup> Percentage of females producing zero young as calculated in Table 3.

**Table 5. Percentage First Year Mortality for Captive Whooping Cranes (Both Sexes)**

YEAR	NUMBER HATCHED	NUMBER SURVIVED	NUMBER OF DEATHS	p
1967	7	5	2	28.6
1968	10	6	4	40.0
1969	8	5	3	37.5
1970	1	0	1	100.0
1971	9	3	6	66.6
1972	0	0	0	----
1973	0	0	0	----
1974	9	4	5	55.5
1975	1	0	1	100.0
1976	1	1	0	0
1977	3	2	1	33.3
1978	7	2	5	71.4
1979	9	3	6	66.6
1980	0	0	0	----
1981	3	2	1	33.3
1982	12	9	3	25.0
1983	16	10	6	37.5
1984	13	5	8	61.5
1985	8	7	1	12.5
1986	2	2	0	0
1987	9	6	3	33.3
1988	15	9	6	40.0
1989	15	9	6	40.0
1990	15	11	4	26.7
1991	15	6	9	60.0

**Environmental Variance (1967-1991):**

n = 22  
 p = 81/188 = 0.43085  
 Exp (V) = 0.0628  
 Obs (V) = 0.0700  
 Env (V) = square root of Obs (V) - Exp (V) = 0.085

**Environmental Variance (1982-1991):**

n = 10  
 p = 46/121 = 0.38017  
 Exp (V) = 0.02886  
 Obs (V) = 0.03645  
 Env (V) = square root of Obs (V) - Exp (V) = 0.087

**Table 6. Percentage Mortality for Captive Whooping Crane > 1 Yr (Both Sexes)**

YEAR	79	80	81	82	83	84	85	86	87	88	89	TOTAL S
# at start of year	22	24	21	22	30	31	34	38	38	40	48	348
total deaths	1	2	3	1	1	10	1	2	3	3	2	29
p	4.5	8.3	14.3	4.5	3.3	32.2	2.9	5.3	7.9	7.5	4.2	
non-catastrophe deaths	1	2	3	1	1	3	1	2	1	3	0	18
p	4.5	8.3	14.3	4.5	3.3	9.7	2.9	5.3	2.6	7.5	0	

**Environmental Variance Calculations:**

1979-1989:

n = 11  
 p = 29/348 = 0.0830  
 Exp (V) = 0.002585 SD = 0.0508  
 Obs (V) = 0.007157 SD = 0.0846  
 Env (V) = square root of Obs (V) - Exp (V) = 0.0676

1979-1989 with catastrophic deaths eliminated from analysis:

n = 11  
 p(non-cat) = 18/337 = 0.0534  
 Exp (V) = 0.00194 SD = 0.0421  
 Obs (V) = 0.00159 SD = 0.0398  
 Env (V) = 0.01

Note - Years run from 1 July of previous year to 30 June of listed year to correspond to hatching dates.

Table 7. Simulation of Captive Population with no inbreeding and a carrying capacity K = 200.

Model	Input Parameters													Population Growth			Final Pop.					
	All males in breeding pool, % producing young	Proportion of breeding age females producing 0-5 young per year					Mortality (both sexes)			Catastrophes			Deer r	Stochastic		N	H	RA				
		EV	0	1	2	3	4	5	<1 yr	EV	>1 yr	EV		Freq	Severity				r	SD(r)		
															Repr						Surv	
HISTORIC DATA																						
1) 1967-1991	No, 27	16.4	71.0	10.6	7.8	5.7	4.2	0.7	43.2	8.5	8.3	6.9	-	-	-	.017	.011	.114	127	89	20	
2) Predictor years (1982-91) adjusted for catastrophes		10.6	55.4	15.4	13.7	6.9	6.9	1.7	38.5	8.7	5.3	0	4	1.0	.825	.072	.071	.078	196	93	28	
PREDICTIONS BASED ON IMPROVED MGMT																						
4) Increased representation of males a) polygynous b) monogamous	Yes																					
5) > % mature females breeding		10.5	30.0	24.2	21.5	10.8	10.8	2.7								.112	.109	.081	197	93	25	
6) > # offspring per female		10.6	55.4	10.0	10.0	10.0	10.0	4.6								.090	.088	.083	197	93	26	
7) Lower chick mortality									30							.083	.082	.079	198	93	27	
8) Longer lifespan (50 yrs)													20	.83	1.0	.075	.072	.077	198	93	29	
9) Prediction of future catastrophe													20	.89	.95	.074	.071	.077	198	93	28	
10) Models 4-9 combined	Yes	10.5	30.0	15.7	15.7	15.7	15.7	7.2	30				20	.83	1.0	.146	.143	.067	200	92	25	



Table 9. Harvest potential based on historic data (1982-1991), carrying capacity K = 100

Description	Input Parameters				Population Growth				% Harvests which could not be completed	Final Population		
	First Year	Last Year	Harvest Interval	# Harvested	During	r		SD		N	H	RA
						SD	without					
10/year start now	1	10	1	10	-.002	.091	.070	.086	98	89	16	
20/year start now	1	10	1	20	-.063	.070	.072	.090	97	89	16	
10/4 years start now	1	40	4	10	-.015	.083	.072	.090	96	89	16	
20/4 years start now	1	40	4	20	-.058	.060	.074	.090	98	89	16	
10/year start in 3 yrs	3	12	1	10	-.002	.095	.070	.088	98	89	16	
20/year start in 3 yrs	3	12	1	20	-.052	.068	.071	.089	99	89	16	
10/year start in 5 yrs	5	14	1	10	.005	.090	.071	.085	99	89	16	
20/year start in 5 yrs	5	14	1	20	-.052	.074	.070	.088	98	88	15	

**Table 10. Harvest potential based on improved management, carrying capacity K = 100**

Description	Input Parameters				Population Growth				% Harvests which could not be completed	Final Population		
	First Year	Last Year	Harvest Interval	# Harvested	During	r		SD		N	H	RA
						SD	without					
10/year start now	1	10	1	10	.089	.100	.145	.080	100	87	13	2.2
20/year start now	1	10	1	20	.027	.107	.147	.081	100	87	13	11.6
10/4 years start now	1	40	4	10	.054	.085	.150	.081	100	87	13	2.7
20/4 years start now	1	40	4	20	-.012	.071	.152	.082	100	87	13	13.7
10/year start in 3 yrs	3	12	1	10	.093	.095	.143	.081	100	87	13	1.1
20/year start in 3 yrs	3	12	1	20	.050	.104	.146	.082	100	87	13	6.0
10/year start in 5 yrs	5	14	1	10	.093	.092	.145	.081	100	87	13	1.1
20/year start in 5 yrs	5	14	1	20	.050	.105	.146	.080	100	87	13	6.2

Table 11a. Birds with questionable paternity who are alive or reproduced before they died.

UNKNOWN PATERNITY						
CHICK	DAM		POSSIBLE SIRES BASED ON ARTIFICIAL INSEMINATION DATA			ELIMINATED BY
Lumpy PWRC ICF	1096 82-002 130018	Mrs. C PWRC	1053 71-001	Canus PWRC	1019 64-001	A
				Rattler PWRC ICF	1031 68-002 130007	B
				Screwbill PWRC	1020 67-001	C
Riva PWRC ICF	1098 82-003 130008	Ektu PWRC San An	1022 268 760222	Screwbill PWRC	1020 67-001	A
				Rattler PWRC ICF	1031 68-002 130007	B
Ginger PWRC ICF	1101 82-001 130011	"259" PWRC	1036 259	Rattler PWRC ICF	1031 68-002 130007	
				Killer PWRC ICF	1032 68-001 130015	
Napoleon ICF	1118 13-006	Ektu PWRC San An	1022 268 760222	Screwbill PWRC	1020 67-001	A
				Canus PWRC	1019 64-001	B
				I2		C
? PWRC	1112 83-001	Ursula PWRC ICF	1027 68-003 130016	Screwbill PWRC	1020 67-001	A/B
				Canus PWRC	1019 67-001	B/A
				Ulysses PWRC ICF	1041 69-001 130017	v. low
				I2		v. low
? PWRC	1135 85-001	Ursula PWRC ICF	1027 68-003 130016	Ulysses PWRC ICF	1041 67-001 130017	A
				Hal PWRC	1063 74-001	B
				Fred PWRC ICF	1086 79-001 130009	C
				Rattler PWRC ICF	1031 68-002 130007	D
Fred PWRC ICF	1086 79-001 130009	"259" PWRC	1036 259	Rattler PWRC ICF	1031 68-002 130007	
				Patuxent PWRC ICF	1046 425 130004	

Probably not sire,  
MHC analysis  
26.7.91



Table 11b. Birds with questionable paternity who are alive or reproduced before they died.

RESOLVED PATERNITY							
CHICK	DAM		POSSIBLE SIRES BASED ON ARTIFICIAL INSEMINATION DATA			ELIMINATED BY	
Wanda PWRC ICF	1110 83-010 130010	Ursula PWRC ICF	1027 68-003 130016	Screwbill PWRC	1020 67-001	A/B	Only possibility through DNA fingerprinting
				Canus PWRC	1019 64-001	A/B	DNA fingerprinting
				Killer PWRC ICF	1032 68-001 130015	C	DNA fingerprinting
				Ulysses PWRC ICF	1041 69-001 130017	D	DNA fingerprinting
Lazarus PWRC	1136 85-002	Ursula PWRC ICF	1027 68-003 130016	Ulysses PWRC ICF	1041 69-001 130017	A/B	Only possibility through DNA fingerprinting
				Canus PWRC	1019 64-001	A/B	DNA fingerprinting
				Fred PWRC ICF	1086 79-001 130009		DNA fingerprinting
				R51			DNA fingerprinting
Faith PWRC ICF	1137 85-003 130019	Ursula PWRC ICF	1027 68-003 130016	Ulysses PWRC ICF	1041 69-001 130017	A	Only possibility through DNA fingerprinting
				Canus PWRC	1019 64-001	B	DNA fingerprinting
Stella PWRC ICF	1140 85-006 130014	Ursula PWRC ICF	1027 68-003 130016	Ulysses PWRC ICF	1041 69-001 130017		Only possibility through DNA fingerprinting
				Rattler PWRC ICF	1031 68-002 130007		DNA fingerprinting
? PWRC	1142 85-007	Ursula PWRC ICF	1027 68-003 130016	Ulysses PWRC ICF	1041 69-001 130017	low	Only possibility through DNA fingerprinting
				Rattler PWRC ICF	1031 68-002 130007	good	DNA fingerprinting
				Canus PWRC	1019 64-001	good	DNA fingerprinting

Table 11c. Whooping Crane assigned sires in studbook but who need to have AI records reviewed to insure other sires are not possible.

CHICK		HATCH DATE	DAM	
Hanna PWRC	1068 77-001	4 May 1977	Mrs. Screwbill PWRC	1050 71-003
PWRC	1156 88-005	29 April 1988	Ursula PWRC ICF	1027 68-003 130016
PWRC	1160 88-014	16 May 1988	Ursula PWRC ICF	1027 68-003 130016
C.J. PWRC	1161 88-022	21 May 1988	Mrs. C PWRC	1053 71-001
Chesty PWRC ICF	1171 89-031 130021	1 May 1989	Mrs. C PWRC	1053 71-001
Damien PWRC	1172 89-035	3 May 1989	Riva PWRC ICF	1098 82-003 130008
Duncan PWRC ICF	1173 89-038 130022	7 May 1989	Ursula PWRC ICF	1027 68-003 130016
Whitney PWRC ICF	1174 89-039 130023	9 May 1989	Ursula PWRC ICF	1027 68-003 130016
Ellie PWRC ICF	1175 89-052 130024	20 May 1989	Riva PWRC ICF	1098 82-003 130008

Table 12. Founder contributions to the captive whooping crane population.

Founder calculations omit UNKNOWNs.

99904	99905	99906	99907	99908	99909	99910
99911	99912	99913	99914	99915	99916	99917
99918	99921	99922	99923	99924	99925	99926
99928	99929	99930	99931	99932	99933	99937
99941	1002	1006	1019	1032	1042	1102
1144	1145	1147	1148	1179	1180	1190
1192	1210	1213				

Founder contributions

1.0000	1.0000	1.0000	1.5000	3.8750	3.8750	5.0000
5.0000	0.5000	0.5000	1.5000	1.3750	1.3750	1.6250
1.6250	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000
0.7500	0.7500	1.2500	1.2500	4.3750	4.3750	1.5000
1.0000	0.2500	0.2500	5.0000	0.5000	0.0000	0.0000
0.5000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
0.0000	0.0000	0.0000				

Fractional contributions

0.0171	0.0171	0.0171	0.0256	0.0662	0.0662	0.0855
0.0855	0.0085	0.0085	0.0256	0.0235	0.0235	0.0278
0.0278	0.0171	0.0171	0.0171	0.0171	0.0171	0.0171
0.0128	0.0128	0.0214	0.0214	0.0748	0.0748	0.0256
0.0171	0.0043	0.0043	0.0855	0.0085	0.0000	0.0000
0.0085	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
0.0000	0.0000	0.0000				

Number of living descendants

2	2	2	4	17	17	19
19	1	1	3	7	7	8
8	3	3	2	2	2	2
2	2	3	3	17	17	4
2	1	1	10	1	0	0
1	0	0	0	0	0	0
0	0	0				

Table 13. Founder allele representation.

Founder	Retention	%Representation		Target		Difference	
		with unk	w/o	with unk	w/o	with unk	w/o
99904 F	0.759	1.695	1.709	2.122	2.152	0.427	0.443
99905 M	0.734	1.695	1.709	2.051	2.080	0.356	0.371
99906 F	0.747	1.695	1.709	2.087	2.117	0.392	0.407
99907 F	0.839	2.516	2.538	2.343	2.376	-0.173	-0.162
99908 M	0.707	6.553	6.609	1.974	2.002	-4.578	-4.607
99909 F	0.718	6.574	6.630	2.006	2.035	-4.568	-4.595
99910 M	0.872	8.426	8.498	2.437	2.471	-5.990	-6.027
99911 F	0.862	8.522	8.595	2.409	2.443	-6.113	-6.152
99912 M	0.500	0.847	0.855	1.397	1.417	0.550	0.562
99913 F	0.500	0.847	0.855	1.397	1.417	0.550	0.562
99914 F	0.872	2.542	2.564	2.435	2.470	-0.107	-0.095
99915 M	0.582	2.286	2.306	1.625	1.648	-0.662	-0.658
99916 F	0.595	2.405	2.426	1.661	1.685	-0.744	-0.741
99917 M	0.487	2.734	2.757	1.361	1.380	-1.373	-1.377
99918 F	0.483	2.744	2.768	1.350	1.369	-1.394	-1.399
99921 M	0.684	1.680	1.694	1.911	1.938	0.232	0.244
99922 F	0.680	1.709	1.724	1.900	1.927	0.191	0.203
99923 M	0.759	1.695	1.709	2.121	2.151	0.426	0.441
99924 F	0.758	1.695	1.709	2.119	2.149	0.424	0.440
99925 M	0.772	1.695	1.709	2.158	2.189	0.464	0.480
99926 F	0.742	1.695	1.709	2.072	2.101	0.377	0.392
99928 ML	0.630	1.277	1.288	2.794	2.834	1.517	1.546
99929 FL	0.625	1.265	1.276	2.794	2.834	1.529	1.558
99930 M	0.815	2.114	2.132	2.276	2.308	0.162	0.176
99931 F	0.813	2.124	2.142	2.270	2.302	0.147	0.161
99932 M	0.720	7.505	7.569	2.012	2.040	-5.493	-5.529
99933 F	0.723	7.336	7.398	2.020	2.049	-5.315	-5.350
99937 M	0.832	2.569	2.591	2.325	2.358	-0.244	-0.233
99941 M	0.737	1.695	1.709	2.058	2.087	0.363	0.378
1002 M	0.249	0.422	0.426	0.696	0.706	0.274	0.280
1006 F	0.251	0.425	0.429	0.701	0.711	0.276	0.282
1019 ML	0.999	8.475	8.547	2.794	2.834	-5.680	-5.713
1032 M	0.500	0.847	0.855	1.397	1.417	0.550	0.562
1042 ML	0.000	0.000	0.000	2.794	2.834	2.794	2.834
P1027 M U	0.500	0.847	0.000	1.397	0.000	0.550	0.000
1102 ML	0.000	0.000	0.000	2.794	2.834	2.794	2.834
1144 ML	0.500	0.847	0.855	2.794	2.834	1.947	1.979
1145 ML	0.000	0.000	0.000	2.794	2.834	2.794	2.834
1147 ML	0.000	0.000	0.000	2.794	2.834	2.794	2.834
1148 FL	0.000	0.000	0.000	2.794	2.834	2.794	2.834
1179 FL	0.000	0.000	0.000	2.794	2.834	2.794	2.834
1180 ML	0.000	0.000	0.000	2.794	2.834	2.794	2.834
1190 ML	0.000	0.000	0.000	2.794	2.834	2.794	2.834
1192 FL	0.000	0.000	0.000	2.794	2.834	2.794	2.834
1210 UL	0.000	0.000	0.000	2.794	2.834	2.794	2.834
1213 ML	0.000	0.000	0.000	2.794	2.834	2.794	2.834

GENETIC SUMMARY

LIVING DESCENDANT POPULATION

POTENTIAL

	with unknowns	w/o	w/ unk	w/o
Number of founders:	35	34	46	45
Mean retention:	0.673	0.678	0.778	0.784
Founder genomes surviving:	23.543	23.043	35.789	35.289
Founder Equivalents:	19.919	19.611	43.027	42.187
Founder Genome Equivalents:	12.195	12.010	35.789	35.289
Fraction of wild gene diversity retained:	0.959	0.958	0.986	0.986
Fraction of wild gene diversity lost:	0.041	0.042	0.014	0.014
Mean inbreeding coefficient:	0.000			

Table 14. Ordered list of mean kinship by sex.

Rank	MALES	MK	Known	FEMALES	MK	Known	UNKNOWNNS	MK	Known
1	1042	0.0000	1.0000	1148	0.0000	1.0000	1210	0.0000	1.0000
2	1102	0.0000	1.0000	1179	0.0000	1.0000	1204	0.0507	1.0000
3	1145	0.0000	1.0000	1192	0.0000	1.0000			
4	1147	0.0000	1.0000	99929	0.0064	1.0000			
5	1180	0.0000	1.0000	1119	0.0128	1.0000			
6	1190	0.0000	1.0000	1153	0.0128	1.0000			
7	1213	0.0000	1.0000	1163	0.0128	1.0000			
8	1144	0.0043	1.0000	1167	0.0128	1.0000			
9	99928	0.0064	1.0000	1168	0.0128	1.0000			
10	1100	0.0085	1.0000	1194	0.0128	1.0000			
11	1138	0.0085	1.0000	1195	0.0128	1.0000			
12	1127	0.0107	1.0000	1154	0.0171	1.0000			
13	1165	0.0128	1.0000	1197	0.0192	1.0000			
14	1212	0.0128	1.0000	1068	0.0251	1.0000			
15	1054	0.0150	1.0000	1164	0.0326	1.0000			
16	1063	0.0150	1.0000	1193	0.0326	1.0000			
17	1189	0.0150	1.0000	1098	0.0353	1.0000			
18	1162	0.0171	1.0000	1202	0.0406	1.0000			
19	1199	0.0192	1.0000	1040	0.0470	1.0000			
20	1118	0.0288	1.0000	1110	0.0524	1.0000			
21	1128	0.0288	1.0000	1175	0.0537	1.0000			
22	1182	0.0326	1.0000	1101	0.0550	1.0000			
23	1019	0.0427	1.0000	1188	0.0588	1.0000			
24	1130	0.0475	1.0000	1201	0.0588	1.0000			
25	1172	0.0537	1.0000	1053	0.0662	1.0000			
26	1041	0.0556	1.0000	1135	0.0662	1.0000			
27	1031	0.0577	1.0000	1137	0.0662	1.0000			
28	1114	0.0588	1.0000	1140	0.0662	1.0000			
29	1133	0.0588	1.0000	1142	0.0662	1.0000			
30	1139	0.0588	1.0000	1174	0.0662	1.0000			
31	1161	0.0588	1.0000	1178	0.0662	1.0000			
32	1171	0.0588	1.0000	1027	0.0684	1.0000			
33	1185	0.0588	1.0000	1136	0.0684	1.0000			
34	1187	0.0588	1.0000	1156	0.0702	1.0000			
35	1086	0.0636	1.0000	1160	0.0702	1.0000			
36	1173	0.0662	1.0000	1112	0.0726	0.5000			



***GRUS AMERICANA***  
**WHOOPING CRANE**

**CONSERVATION VIABILITY ASSESSMENT  
WORKSHOP REPORT**

**SECTION 5  
SMALL POPULATION BIOLOGY**





## INTRODUCTION

An endangered species is (by definition) at risk of extinction. The dominant objective in the recovery of such a species is to reduce its risk of extinction to some acceptable level - as close as possible to the background, "normal" extinction risk all species face.

The concept of risk is used to define the targets for recovery, and is used to define recovery itself. Risk, not surprisingly, is a central issue in endangered species management. Unfortunately, there is ample reason to suppose that we (as humans) are not "naturally" good at risk assessment. Recovery will be more often successful if we could do this better. There is a strong need for tools that would help managers deal with risk. We need to improve estimation of risk, to rank order better the risk due to different potential management options, to improve objectivity in assessing risk, and to add quality control to the process (through internal consistency checks). Among the risks to be evaluated are those of extinction, and loss of genetic diversity.

In the last several years such tools have been developing. The applied science of Conservation Biology has grown into some of the space between Wildlife Management and Population Biology. A set of approaches, loosely known as "Population Viability Analysis" has appeared.

These techniques are already powerful enough to improve recognition of risk, rank relative risks, and evaluate options. They have the further benefit of changing part of the decision making process from unchallengeable internal intuition to explicit (and hence challengeable) quantitative rationales.



## SMALL POPULATION OVERVIEW

J. Ballou

The primary objective of single-species conservation programs is to reduce the risk of population extinction. A first step in doing this is to identify those factors that can potentially cause extinction in the population. The most fundamental threat is, of course, declining population size. If a population is declining in numbers, and no action is taken to reverse the trend, then extinction is imminent. However, even if a small population is not declining or even if it is increasing, its fate is uncertain. Small populations are challenged by a number of factors that increase the likelihood of the population going extinct simply because the population is small.

### Challenges to Small Populations

Challenges to small populations can be categorized as intrinsic (random variation of genetic and demographic events within the population occurring without reference to environmental events) or extrinsic (environmental events acting on the genetics and demography of a population). At the most basic level, the level of the individual, an intrinsic challenge to the population is Demographic Variation. Demographic variation is the normal variation in the population's birth and death rates and sex ratio caused by random differences among individuals in the population. The population can experience fluctuations in size simply by these random differences in individual reproduction or survival. These randomly caused fluctuations can be severe enough to cause the population to go extinct. For example, one concern in extremely

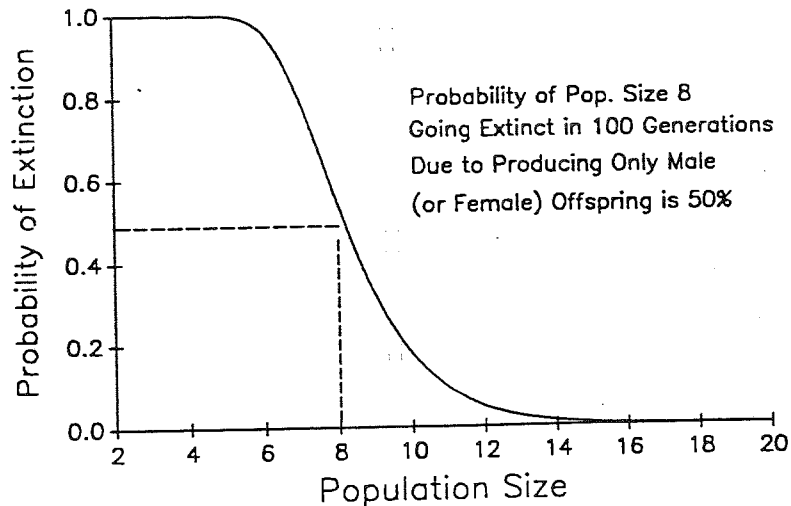


Figure 1. Example of demographic variation: Probability of extinction by 100 generations due solely to producing only one sex of offspring during a generation.

small populations is the possibility that all individuals born into the population during one generation are of one sex, resulting in the population going extinct. Figure 1 illustrates the probability of this occurring over a 100 generation period in populations of different size. There is a 50% chance of extinction due to biased sex ratio in a population of size 8 sometime during this time period.

Similar consequences could result from the coincidental effects of high death rates or low birth rates. However, these risks are practically negligible in large populations. In general, the effect of any one individual on the overall population's trend is significantly less in large populations than small populations. As a result, demographic variation is a relatively minor challenge in all but very small populations (less than 20 animals).

A more significant extrinsic threat to small populations is Environmental Variation. Variation in environmental conditions clearly impact the ability of a population to reproduce and survive. Populations susceptible to environmental variation fluctuate in size more than less susceptible populations, increasing the danger of extinction. For example, reproductive success of the endangered Florida snail kite (*Rostrhamus sociabilis*) is directly affected by water levels, which determine prey (snail) densities: nesting success rates decrease by 80% during years of low water levels. Snail kite populations, as a result, are extremely unstable (Bessinger 1986).

Another level of threat to small populations are Catastrophes such as Disease Epidemics. Catastrophes are similar to other forms of environmental variation in that they are external to the population. However, they are listed separately because of the magnitude of their effects and the difficulty of predicting their occurrence. They can be thought of as relatively rare events that can have devastating consequences for a large proportion of the population. Disease epidemics can have a direct or indirect effect on a population. For example, in 1985 the sylvatic plague had a severe indirect effect on the last, remaining black-footed ferret population by reducing the ferrets prey base, the prairie dog. Later that same year, the direct effect of distemper killed most of the wild population and all of the 6 ferrets that had been brought into captivity (Thorne and Belitsky 1989).

Catastrophes are rare disasters capable of decimating a population. Catastrophic events can include natural events (floods, fires, hurricanes) or human-induced events (deforestation or other habitat destruction). Both large and small populations are susceptible to catastrophic events. Tropical deforestation is the single most devastating 'catastrophe' affecting present rates of species extinction. Estimates of tropical species' extinction rates vary between 20 and 50% by the turn of the century (Lugo 1988).

Small populations are also susceptible to genetic challenges. The primary genetic consideration is the loss of Genetic Variation. Every generation the genes that get passed on to offspring are a random sample of the genes of the parents. In small populations, each random sample of genes is a small sample and represents only a fraction of the genes of the parental generation. Some of the genetic variation present in the parents, may not, just by chance, get passed on to the offspring. This genetic variation is then lost to the population. This process is called genetic drift because the genetic characteristics of the population can drift or vary over time. In small populations, genetic drift can cause rapid loss of genetic variation - the smaller the population, the more rapid the loss of variation.

Conservation programs include the maintenance of genetic diversity as a primary goal for several reasons. If species are to survive over the long-term, they must retain the ability to adapt to changing environments (i.e. evolve). Since the process of natural selection requires the presence of genetic variation, conservation strategies must include the preservation of genetic diversity for long-term survival of species. In addition to long-term evolutionary considerations, the presence of genetic diversity has been shown to be important for maintaining the fitness of the population. A growing number of studies show a general, but not universal, correlation between genetic diversity and various traits related to reproduction, survival and disease resistance (Allendorf and Leary 1986). Individuals with lower levels of genetic variation often have higher mortality rates and lower reproductive rates than individuals with more diversity.

Inbreeding (matings between relatives) also causes populations to lose genetic diversity. All the animals in small populations quickly become related. An offspring produced from related parents are inbred and can get the same alleles from its mother and father. Inbred individuals

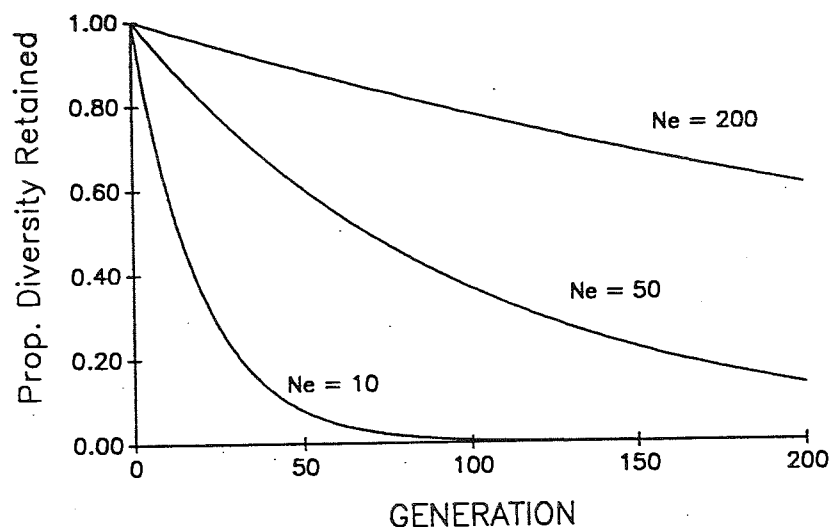


Figure 2. Loss of genetic diversity over 200 generation in populations with different effective sizes ( $N_e$ ).

are therefore more homozygous than non-inbred individuals and they have lower levels of genetic diversity than animals born to unrelated parents.

The loss of genetic variation in populations of different size is shown in Figure 2. The rate of loss is a function of the effective size of the population ( $N_e$ ; the percent of diversity lost each generation is  $1/2N_e$ ). Technically, a population's effective size is the size of an ideal population that loses genetic diversity at the same rate as the real population. There is extensive literature on how to estimate a population's effective size (Lande and Barrowclough 1987); however, the number of animals contributing to the breeding pool each generation can be used as a very rough estimate of the effective size. The effective size of the population is therefore much less than the actual number of animals; estimates suggest that  $N_e$  is often only 10 to 30% of the total population. Seemingly large populations will lose significant levels of genetic diversity if their effective sizes are small.

Data on the effects of inbreeding in exotic species also show the importance of maintaining genetic diversity. Numerous studies have shown that inbreeding can significantly reduce reproduction and survival in a wide variety of wildlife (Ralls and Ballou 1983; Wildt et al, 1987; Figure 3). Inbreeding depression results from two effects: 1) the increase in homozygosity allows deleterious recessive alleles in the genome to be expressed (whereas they are not in non-inbred, more heterozygous individuals); and 2) in cases where heterozygotes are more fit than homozygotes simply because they have two alleles, the reduced heterozygosity

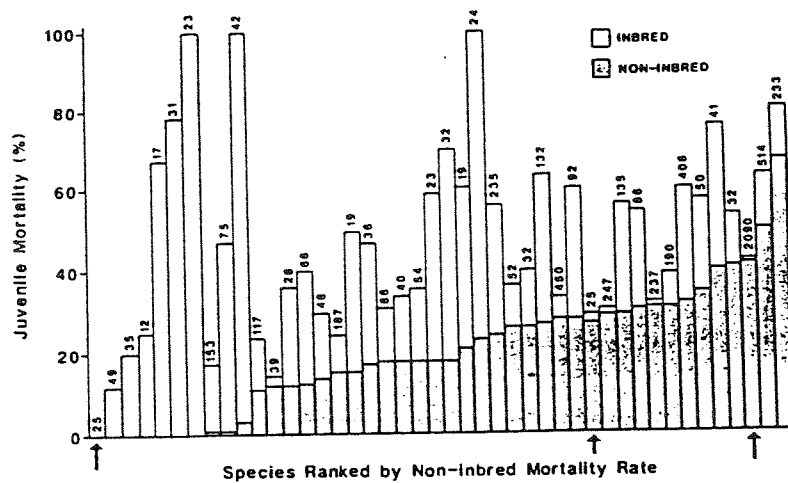


Figure 3. Effects of inbreeding on juvenile mortality in 45 captive mammal populations (From Ralls and Ballou, 1987).3

caused by inbreeding reduces the fitness of the inbred individuals (over dominance). In both cases, the loss of genetic variation due to inbreeding has detrimental effects on population survival.

Small, isolated populations, with no migration from other populations, lose genetic diversity and become increasingly inbred over time. Their long-term survival potential is doubly jeopardized since they gradually lose the genetic diversity necessary for them to evolve and their short-term survival is jeopardized by the likely deleterious effects of inbreeding on survival and reproduction.

The genetic and demographic challenges discussed above clearly do not act independently in small populations. As a small population becomes more inbred, reduced survival and reproduction are likely: the population decreases. Inbreeding rates increase and because the population is smaller and more inbred, it is more susceptible to demographic variation as well as disease and severe environmental variation. Each challenge exacerbates the others resulting in a negative feedback effect termed the "Extinction Vortex" (Gilpin and Soule, 1986). Over time the population becomes increasing smaller and more susceptible to extinction (Figure 4).

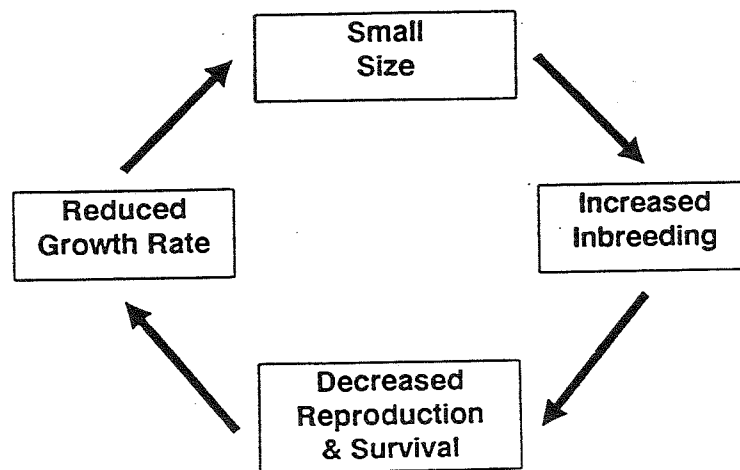


Figure 4. "Extinction Vortex" caused by negative feedback effects of inbreeding in small populations.

### Population Viability Analyses

Many of the challenges facing small populations are stochastic and result from random unpredictable events. Many can generally be assumed to decrease the likelihood of long-term survival of the population. However, because of their stochastic nature, their exact effects on population extinction and retention of genetic diversity can not be predicted with total accuracy. For example although inbreeding depression is a general phenomenon, its effects vary widely between species (Figure 3) and it is not possible to precisely predict how any one population will respond to inbreeding.

Nevertheless, conservation strategies that address these unpredictable issues of extinction and loss of genetic diversity must be developed and implemented. The process that has been developed over recent years to assess extinction probabilities and loss of genetic diversity is called Population Viability Analysis (PVA; Soule 1987). PVA is defined as a systematic evaluation of the relative importance of factors that place populations at risk. It is an attempt to identify those factors that are important for the survival of the population. In some cases, this may be easy - habitat destruction is often a critical factor for most endangered species. But at other times, the effects of single factors, and the interaction between factors, are more difficult to predict.

To try to gain a more quantitative understanding of the effect of these factors, computer models have been developed that apply a combination of analytical and simulation techniques to model the populations over time and estimate the likelihood of a population going extinct and the loss of its genetic variation. The model is first provided with information describing the life-history characteristics of the population. Depending on the model used, this includes data on age of first reproduction, litter size distribution, survival rates, mating structure and age distribution as well as estimates of the variation associated with each of these variables. A number of different external factors may also be considered. This may include levels of environmental variation, change in carrying capacity and severity of inbreeding depression. Models also allow consideration of threats facing the population: probability of catastrophes and their severity, habitat loss and disease epidemics (Figure 5). The models use the life-history variables, the external factors and the potential threats to project the population into the future,

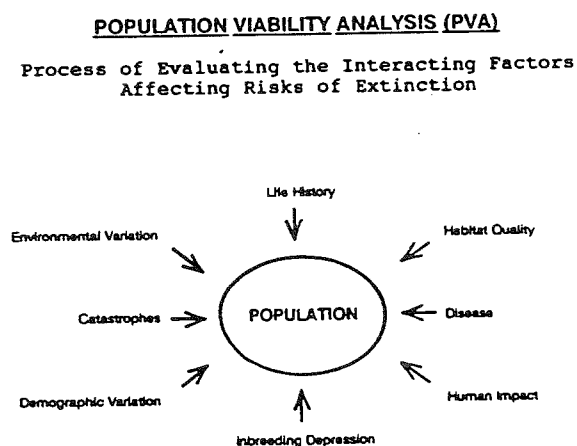


Figure 5. Population Viability Analyses (PVA) model the effects of different life-history, environmental and threat factors on the extinction and retention of genetic diversity in single populations.



measuring the level of genetic variation that is retained over time and recording if and when the population goes extinct (population size goes to zero). The simulations are repeated, often thousands of times, to provide estimates of the statistical variation associated with the results. The probability of extinction at any given time is measured as the number of simulations that the population had gone extinct by that time divided by the total number of simulations run (Figure 6). The levels of genetic variation are recorded as the percent of the original heterozygosity and number of original alleles retained in the population at any particular point.

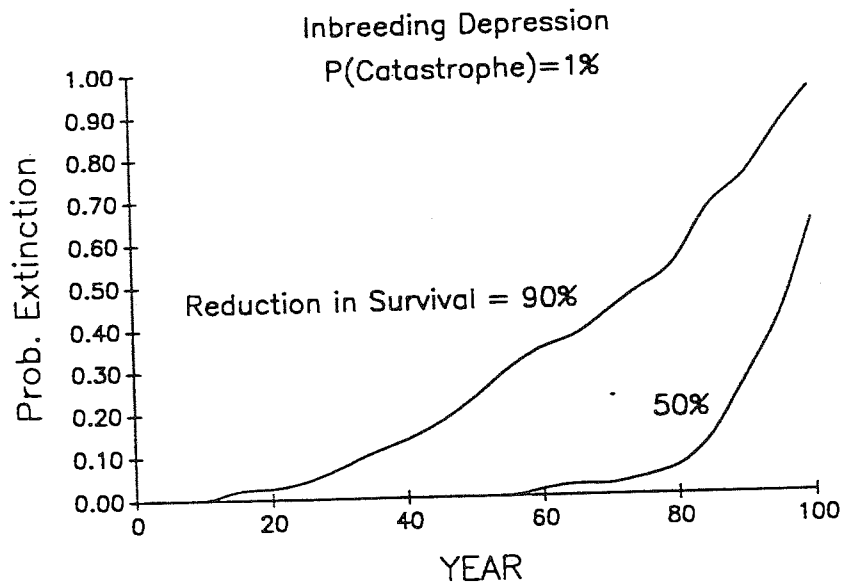


Figure 6. Hypothetical example of population extinction results from the VORTEX PVA model. The model includes negative effects of inbreeding and a catastrophe probability of 1%. The probability of extinction is shown over time for two different levels of catastrophe severity: a 90% reduction in survival vs 50% reduction in survival.

A number of population viability models have been developed. The model used by the Captive Breeding Specialist Group of the IUCN is VORTEX, written by Robert Lacy (Chicago Zoological Society). This model has been used extensively to develop conservation strategies for a number of species including the Black-footed ferret, Florida panther, Puerto Rican Parrot, Javan rhino and the four species of lion tamarins.

The true value of the model is not in trying to examine the effects of all variables simultaneously in the population. The interactions between these many factors is too complex to attempt to interpret the results of population projections based on more than just a few of these considerations. We can gain far more insight into the dynamics of the population by examining only one or two factors at a time - and picking those factors that we believe have an impact on the population and ignoring those that don't.

The primary use of the model in developing conservation strategies is its use in conducting "what if" analyses. For example 'what if' survival were decreased in the wild population as a result of a disease outbreak? How would that effect the extinction of the population and retention of genetic diversity? These 'what if' analyses can also be used to evaluate management recommendations. For example, how would the probability of population extinction change if the carrying capacity of the reserve holding the animals were increased by 10%?

Because the models don't examine all factors potentially contributing to extinction, the model results usually underestimate a population's probability of extinction. However, it is important to stress that the purpose of the PVA is not to estimate exact extinction probabilities but to identify the relative importance of the various factors being considered and to evaluate the effect of a range of management recommendations on the survival of the population.

### **Implications of PVA on Management Goals**

The concepts of population extinction and loss of genetic diversity are based on probabilities rather than certainties. The results from the PVA models provide us with information on the probability of extinction given certain assumptions about the biology and status of the population. As a result, we can not predict or guarantee what will happen to these populations with any absolute certainty.

This has some fairly strong implications when we are trying to develop conservation strategies to reduce the risks of extinction in the populations. We must be able to recognize that we will not be able to formulate and implement recommendations that will guarantee the survival of any population. We can only formulate and implement recommendations that will decrease the likelihood of extinction in populations over a given time period.

A common approach is to develop management strategies that assure a 95% chance of the population surviving for 100 years and maintaining 90% of its genetic variation over the same time period (Shaffer 1987; Soule et al, 1986). This would assure a high probability of survival and retain a large proportion of the population's ability to genetically adapt and evolve to changing environments. This approach defines the Minimum Viable Population (MVP) size to achieve these management objectives. Management strategies can only be fully evaluated if both degree of certainty and time frame for management are specified.

### **Metapopulations**

The discussion to this point has focused on the extinction and genetic dynamics of a single population. However, often managers are faced with a species distributed over several interacting populations. When this is the case and animal movement (migration) between

populations is high enough that the dynamics (extinction or genetic) of any single population is affected by dynamics of other nearby populations, the group of interacting populations is called a Metapopulation (Figure 7). The understanding of metapopulation dynamics has become increasingly important for the development of conservation strategies.

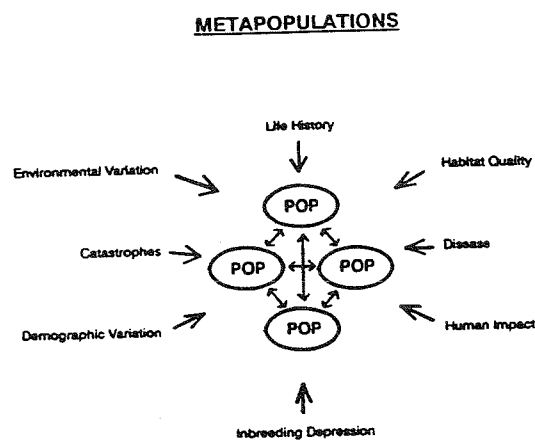


Figure 7. The interaction between population 'patches' results in a Metapopulation structure. Conservation strategies must consider the spatial distribution of the patches and its effect on correlated extinctions and recolonization between patches.

Metapopulation management focuses on the spatial distribution of the populations and how that influences both the genetic and demographic dynamics of the system. The metapopulation system can be thought of as a grouping of populations ('patches') of different sizes and distances from each other, with some patches periodically going extinct and being recolonized by migrants from other patches. The most important conservation considerations are rates of extinction for the individual patches and the recolonization rates between patches (Gilpin 1987).

As we have discussed above, the extinction dynamics of any single patch is affected by any number of factors including size of population, rate of population recovery following a population decline, etc. From a metapopulation perspective, the simplest level is when patch extinction rates are not correlated with each other: the probability of extinction of any one patch is independent of any other patch. Environmental variation and catastrophes increase the extinction correlation between patches and this increases the likelihood of the entire metapopulation going extinct. So considerations of the spatial distribution between patches, and what that means in terms of how similarly they react to environmental variation and catastrophes is an important part of developing management strategies.

On the other side of the coin is the effect of spatial distribution on recolonization rates between patches. The closer patches are to each other, the higher the probability of a patch being recolonized following an extinction by migrants from a neighboring patch. Thus, distances between patches is positively correlated with recolonization and long-term survival of the metapopulation.

Patch extinction and recolonization also effect the retention of genetic diversity in the metapopulation. Small, fragmented and isolated populations rapidly lose genetic diversity. However, with migration between patches, gene flow among patches can be increased and the effective size of the total metapopulation is significantly increased. However, if recolonization following extinction repeatedly involves a very limited number of individuals (one pair or a pregnant female), then individual patches can be genetically invariant as a result of the recurrent founder effects.

The interaction between the positive aspects of recolonization and the negative effects of correlated patch extinction complicate the understanding of metapopulation dynamics, both at the genetic and demographic level. Unfortunately, computer models that combine aspects of single-population extinction and genetic considerations discussed above with considerations of metapopulation theory are not yet available for developing conservation management strategies.

Nevertheless, managers should be cognizant of the complexities of metapopulation systems. In general, populations distributed over several populations are more secure over the long-term than one population located at a single site. This is particularly true if there is gene flow between patches (either natural or through management intervention) and the patches are not susceptible to the same catastrophic threats. In many cases, a captive population can serve as a secure patch that can be used as a source to recolonize other patches through reintroduction efforts and as a reservoir for genetic diversity.

## INTERACTIVE MANAGEMENT OF SMALL WILD AND CAPTIVE POPULATIONS

T. J. Foose

### Introduction

Conservation strategies for endangered species must be based on viable populations. While it is necessary, it is no longer sufficient merely to protect endangered species *in situ*. They must also be managed.

The reason management will be necessary is that the populations that can be maintained of many species under the pressures of habitat degradation and unsustainable exploitation will be small, i.e. a few tens to a few hundreds (in some cases, even a few thousands) depending on the species. As such, these populations are endangered by a number of environmental, demographic, and genetic problems that are stochastic in nature and that can cause extinction.

Small populations can be devastated by catastrophe (weather disasters, epidemics, exploitation) as exemplified by the case of the black footed-ferret and the Puerto Rican parrot, or be decimated by less drastic fluctuations in the environment. Demographically, small populations can be disrupted by random fluctuations in survivorship and fertility. Genetically, small populations lose diversity needed for fitness and adaptability.

### Minimum Viable Populations

For all of these problems, it is the case that the smaller the population is and the longer the period of time it remains so, the greater these risks will be and the more likely extinction is to occur. As a consequence, conservation strategies for species which are reduced in number, and which most probably will remain that way for a long time, must be based on maintaining certain minimum viable populations (MVP's), i.e. populations large enough to permit long-term persistence despite the genetic, demographic and environmental problems.

There is no single magic number that constitutes an MVP for all species, or for any one species all the time. Rather, an MVP depends on both the genetic and demographic objectives for the program and the biological characteristics of the taxon or population of concern. A further complication is that currently genetic and demographic factors must be considered separately in determining MVP's, although there certainly are interactions between the genetic and demographic factors. Moreover, the scientific models for assessing risks in relation to population size are still in rapid development. Nevertheless, by considering both the genetic and demographic objectives of the program and the biological characteristics pertaining to the population, scientific analyses can suggest ranges of population sizes that will provide calculated protection against the stochastic problems.

Genetic and demographic objectives of importance for MVP

*Probability of survival* (e.g., 50% or 95%) desired for the population;

*Percentage of the genetic diversity* to be preserved (90%, 95%, etc.);

*Period of time* over which the demographic security and genetic diversity are to be sustained (e.g., 50 years, 200 years).

In terms of demographic and environmental problems, for example, the desire may be for 95% probability of survival for 200 years. Models are emerging to predict persistence times for populations of various sizes under these threats. Or in terms of genetic problems, the desire may be to preserve 95% of average heterozygosity for 200 years. Again models are available. However, it is essential to realize that such terms as viability, recovery, self-sustainment, and persistence can be defined only when quantitative genetic and demographic objectives have been established, including the period of time for which the program (and population) is expected to continue.

Biological characteristics of importance for MVP

*Generation time:* Genetic diversity is lost generation by generation, not year by year. Hence, species with longer generation times will have fewer opportunities to lose genetic diversity within the given period of time selected for the program. As a consequence, to achieve the same genetic objectives, MVP's can be smaller for species with longer generation times. Generation time is qualitatively the average age at which animals produce their offspring; quantitatively, it is a function of the age-specific survivorships and fertilities of the population which will vary naturally and which can be modified by management, e.g. to extend generation time.

*The number of founders.* A founder is defined as an animal from a source population (the wild for example) that establishes a derivative population (in captivity, for translocation to a new site, or at the inception of a program of intensive management). To be effective, a founder must reproduce and be represented by descendants in the existing population. Technically, to constitute a full founder, an animal should also be unrelated to any other representative of the source population and non-inbred.

Basically, the more founders, the better, i.e. the more representative the sample of the source gene pool and the smaller the MVP required for genetic objectives. There is also a demographic founder effect; the larger the number of founders, the less likely is extinction due to demographic stochasticity. However, for larger vertebrates, there is a point of diminishing returns (Figure 8), at least in genetic terms. Hence a common objective is to obtain 20-30 effective founders to establish a population. If this objective cannot be achieved, then the

program must do the best with what is available. If a pregnant female woolly mammoth were discovered wandering the tundra of Alaska, it would certainly be worth trying to develop a recovery plan for the species even though the probability of success would be low. By aspiring to the optima, a program is really improving the probability of success.

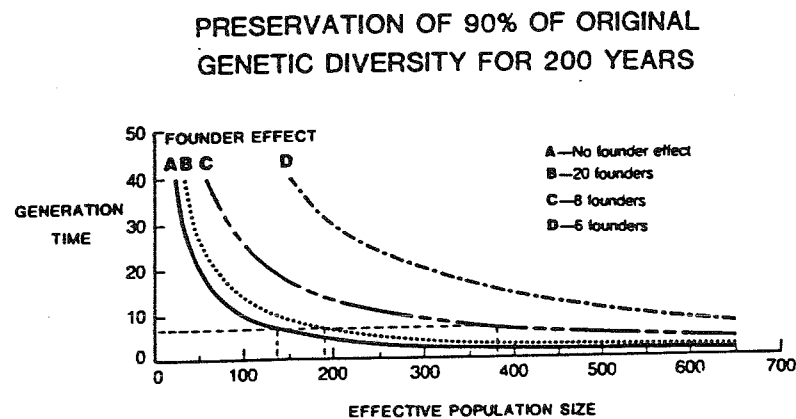


Figure 8. Interaction of number of founders, generation time of the species, and effective population size required for preserving 90% of the starting genetic diversity for 200 years.

*Effective Population Size.* Another very important consideration is the effective size of the population, designated  $N_e$ .  $N_e$  is not the same as the census size,  $N$ . Rather,  $N_e$  is a measure of the way the members of the population are reproducing with one another to transmit genes to the next generation.  $N_e$  is usually much less than  $N$ . For example in the grizzly bear,  $N_e/N$  ratios of about .25 have been estimated (Harris and Allendorf 1989). As a consequence, if the genetic models prescribe an  $N_e$  of 500 to achieve some set of genetic objectives, the MVP might have to be 2000.

*Growth Rate.* The higher the growth rate, the faster a population can recover from small size, thereby outgrowing much of the demographic risk and limiting the amount of genetic diversity lost during the so-called "bottleneck". It is important to distinguish MVP's from bottleneck sizes.

#### Population viability analysis

The process of deriving MVP's by considering various factors, i.e. sets of objectives and characteristics, is known as Population Viability (sometimes Vulnerability) Analysis (PVA). Deriving applicable results in PVA requires an interactive process between population biologists, managers, and researchers. PVA has been applied to a number of species (e.g., Parker and Smith 1988, Seal et al. 1989, Ballou et al. 1989, Lacy et al. 1989, Lacy and Clark, in press).

As mentioned earlier, PVA modelling often is performed separately with respect to genetic and demographic events. Genetic models indicate it will be necessary to maintain populations of hundreds or thousands to preserve a high percentage of the gene pool for several centuries. Recent models allow simultaneous consideration of demography, environmental uncertainty, and genetic uncertainty.

MVP's to contend with demographic and environmental stochasticity may be even higher than to preserve genetic diversity especially if a high probability of survival for an appreciable period of time is desired. For example, a 95% probability of survival may entail actually maintaining a much larger population whose persistence time is 20 times greater than required for 50% (i.e., average) probability of survival; 90%, 10 times greater. From another perspective, it can be expected that more than 50% of actual populations will become extinct before the calculated mean persistence time elapses.

Species of larger vertebrates will almost certainly need population sizes of several hundreds or perhaps thousands to be viable. In terms of the stochastic problems, more is always better.

### **Metapopulations and Minimum Areas**

MVP's imply minimum critical areas of natural habitat, that may be difficult or impossible to maintain single, contiguous populations of the thousands required for viability.

However, it is possible for smaller populations and sanctuaries to be viable if they are managed as a single larger population (a metapopulation) whose collective size is equivalent to the MVP (Figure 9). Actually, distributing animals over multiple "subpopulations" will increase the effective size of the total number maintained in terms of the capacity to tolerate the stochastic problems. Any one subpopulation may become extinct or nearly so due to these causes; but through recolonization or reinforcement from other subpopulations, the metapopulation will survive. Metapopulations are evidently frequent in nature with much local extinction and recolonization of constituent subpopulations occurring.

Unfortunately, as wild populations become fragmented, natural migration for recolonization may become impossible. Hence, metapopulation management will entail moving animals around to correct genetic and demographic problems (Figure 10). For migration to be effective, the migrants must reproduce in the new area. Hence, in case of managed migration it will be important to monitor the genetic and demographic performance of migrants



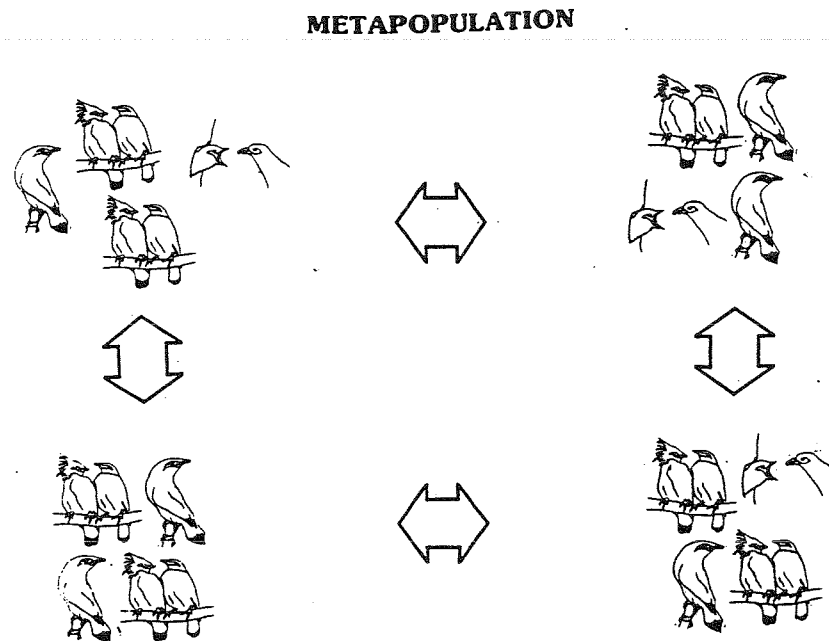


Figure 9. Multiple subpopulations as a basis for management of a metapopulation for survival of a species in the wild.

Managed migration is merely one example of the kinds of intensive management and protection that will be desirable and necessary for viability of populations in the wild. MVP's strictly imply benign neglect. It is possible to reduce the MVP required for some set of objectives, or considered from an alternative perspective, extend the persistence time for a given size population, through management intervention to correct genetic and demographic problems as they are detected. In essence, many of these measures will increase the  $N_e$  of the actual number of animals maintained.

The wolves are already subject to intervention: few animals remain in the wild and they are subject to disturbance by people, it is difficult to protect them in viable populations, potential habitat is fragmented by development, and it is planned to release captive bred animals into the wild. Such interventions are manifestations of the fact that as natural sanctuaries and their resident populations become smaller, they are in effect transforming into megazoos that will require much the same kind of intensive genetic and demographic management as species in captivity.

### MANAGED MIGRATION AMONG POPULATIONS OF BALI MYNAH

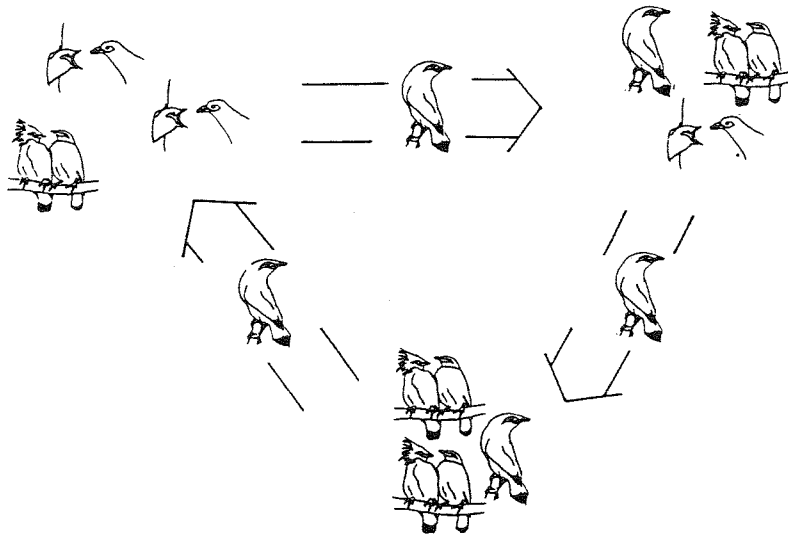


Figure 10. Managed migration among subpopulations to sustain gene flow in a metapopulation.

### Captive Propagation

Another way to enhance viability is to reinforce wild populations with captive propagation. More specifically, there are a number of advantages to captive propagation: protection from unsustainable exploitation, e.g. poaching; moderation of environmental vicissitudes for at least part of the population; more genetic management and hence enhance preservation of the gene pool; accelerated expansion of the population to move toward the desired MVP and to provide animals more rapidly for introduction into new areas; and increase in the total number of animals maintained.

It must be emphasized that the purpose of captive propagation is to reinforce, not replace, wild populations. Captive colonies and zoos must serve as reservoirs of genetic and demographic material that can periodically be transfused into natural habitats to re-establish species that have been extirpated or to revitalize populations that have been debilitated by genetic and demographic problems.

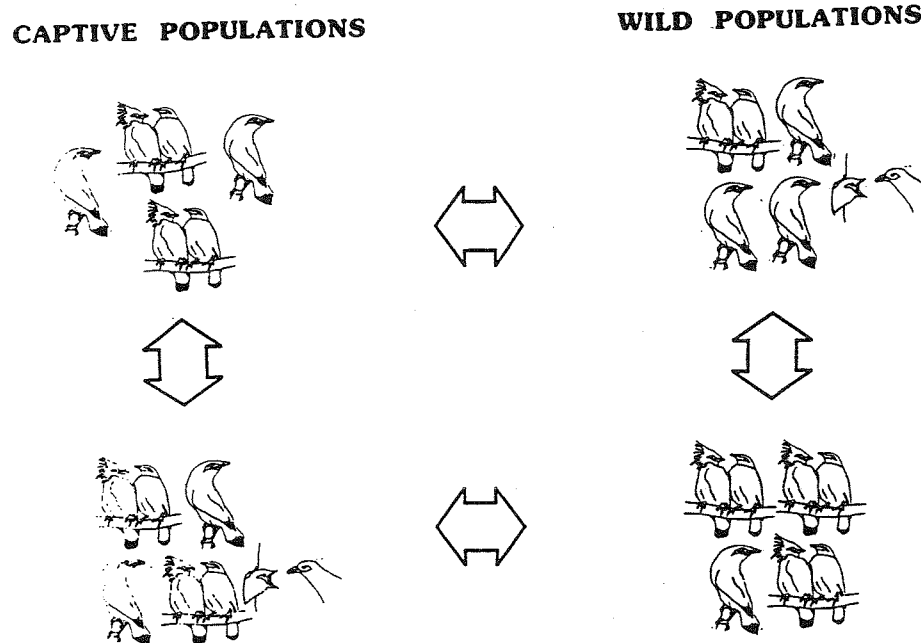


Figure 11. The use of captive populations as part of a metapopulation to expand and protect the gene pool of a species.

The survival of a great and growing number of endangered species will depend on assistance from captive propagation. Indeed, what appears optimal and inevitable are conservation strategies for the species incorporating both captive and wild populations interactively managed for mutual support and survival (Figure 11). The captive population can serve as a vital reservoir of genetic and demographic material; the wild population, if large enough, can continue to subject the species to natural selection. This general strategy has been adopted by the IUCN (the world umbrella conservation organization) which now recommends that captive propagation be invoked anytime a taxon's wild population declines below 1000 (IUCN 1988).

### Species Survival Plans

Zoos in many regions of the world are organizing scientifically managed and highly coordinated programs for captive propagation to reinforce natural populations. In North America, these efforts are being developed under the auspices of the AAZPA, in coordination with the IUCN SSC Captive Breeding Specialist Group (CBSG), and are known as the Species Survival

### Plan (SSP).

Captive propagation can help, but only if the captive populations themselves are based on concepts of viable populations. This will require obtaining as many founders as possible, rapidly expanding the population normally to several hundreds of animals, and managing the population closely genetically and demographically. This is the purpose of SSP Masterplans. Captive programs can also conduct research to facilitate management in the wild as well as in captivity, and for interactions between the two.

A prime examples of such a captive/wild strategy is the combined USFWS Recovery Plan/SSP Masterplan for the red wolf. Much of the captive propagation of red wolves has occurred at a special facility in Washington state, but there is also a growing number of zoos providing captive habitat, especially institutions within the historical range of the red wolf.

Another eminent example of a conservation and recovery strategy incorporating both captive and wild populations is the black-footed ferret. This species now evidently survives only in captivity. Because the decision to establish a captive population was delayed, the situation became so critical that moving all the animals into captivity seemed the only option, circumstances that also applied to the California condor. Another option may have been available if action to establish a captive population had occurred earlier as was done with the Puerto Rican parrot and plain pigeon. Consideration of the survivorship pattern, which exhibited high juvenile mortality for ferrets, as it does for many mammals and birds, suggested that young animals destined to die in the wild might be removed with little or no impact on the population. The AAZPA and CBSG/SSC/IUCN are involved in these kinds of strategies and programs worldwide.

### Population Viability Analysis

R. C. Lacy

Many wildlife populations that were once large, continuous, and diverse have been reduced to small, fragmented isolates in remaining natural areas, nature preserves, or even zoos. For example, black rhinos once numbered in the 100s of thousands, occupying much of Africa south of the Sahara; now a few thousand survive in a handful of parks and reserves, each supporting a few to at most a few hundred animals. Similarly, the Puerto Rican parrot, the only psittacine native to Puerto Rico, was formerly widespread on the island and numbered perhaps a million birds. By 1972 the species was reduced to just 20 birds (4 in captivity). Intensive efforts since have accomplished a steady recovery to 46 captive and 34 wild birds at the end of 1988. In 1989, the Luquillo forest which is home to both the captive and wild flocks of Puerto Rican parrots was severely damaged by a hurricane. Apparently about half of the wild parrots were killed, most of the traditional nest trees were destroyed, the food supply was decimated, and it is unlikely that a viable population remains in the wild.

When populations become small and isolated from any and all other conspecifics, they face a number of demographic and genetic risks to survival: in particular, chance events such as the occurrence and timing of disease outbreaks, random fluctuations in the sex ratio of offspring, and even the randomness of Mendelian gene transmission can become more important than whether the population has sufficient habitat to persist, is well adapted to that habitat, and has an average birth rate that exceeds the mean death rate. Unfortunately, the genetic and demographic processes that come into play when a population becomes small and isolated feed back on each other to create what has been aptly but depressingly described as an "extinction vortex". The genetic problems of inbreeding depression and lack of adaptability can cause a small population to become even smaller --which in turn worsens the uncertainty of finding a mate and reproducing -- leading to further decline in numbers and thus more inbreeding and loss of genetic diversity. The population spirals down toward extinction at an ever accelerated pace. The size below which a population is likely to get sucked into the extinction vortex has been called the Minimum Viable Population size (or MVP).

The final extinction of a population usually is probabilistic, resulting from one or a few years of bad luck, even if the causes of the original decline were quite deterministic processes such as over-hunting and habitat destruction. Recently, techniques have been developed to permit the systematic examination of many of the demographic and genetic processes that put small, isolated populations at risk. By a combination of analytic and simulation techniques, the probability of a population persisting a specified time into the future can be estimated: a process called Population Viability Analysis (PVA) (Soule 1987). Because we still do not incorporate all factors into the analytic and simulation models (and we do not know how important the factors we ignore may be), the results of PVAs almost certainly underestimate the true probabilities of population extinction.

The value of a PVA comes not from the crude estimates of extinction probability, but rather from identification of the relative importance of the factors that put a population at risk and assessment of the value (in terms of increased probability of population persistence) of various possible management actions. That few species recognized as Endangered have recovered adequately to be delisted and some have gone extinct in spite of protection and recovery efforts attests to the acute risks faced by small populations and to the need for a more intensive, systematic approach to recovery planning utilizing whatever human, analytical, biological, and economic resources are available.

### Genetic Processes in Small and Fragmented Populations

Random events dominate genetic and evolutionary change when the size of an interbreeding population is on the order of 10s or 100s (rather than 1000s or more). In the absence of selection, each generation is a random genetic sample of the previous generation. When this sample is small, the frequencies of genetic variants (alleles) can shift markedly from one generation to the next by chance, and variants can be lost entirely from the population -- a process referred to as "genetic drift". Genetic drift is cumulative. There is no tendency for allele frequencies to return to earlier states (though they may do so by chance), and a lost variant cannot be recovered, except by the reintroduction of the variant to the population through mutation or immigration from another population. Mutation is such a rare event (on the order of one in a million for any given gene) that it plays virtually no role in small populations over time scales of human concern (Lacy 1987a). The restoration of variation by immigration is only possible if other populations exist to serve as sources of genetic material.

Genetic drift, being a random process, is also non-adaptive. In populations of less than 100 breeders, drift overwhelms the effects of all but the strongest selection: Adaptive alleles can be lost by drift, with the fixation of deleterious variants (genetic defects) in the population. For example, the prevalence of cryptorchidism (failure of one or both testicles to descend) in the Florida panther (*Felis concolor coryi*) is probably the result of a strongly deleterious allele that has become common, by chance, in the population; and a kinked tail is probably a mildly deleterious (or at best neutral) trait that has become almost fixed within the Florida panther.

A concomitant of genetic drift in small populations is inbreeding -- mating between genetic relatives. When numbers of breeding animals become very low, inbreeding becomes inevitable and common. Inbred animals often have a higher rate of birth defects, slower growth, higher mortality, and lower fecundity ("inbreeding depression"). Inbreeding depression has been well documented in laboratory and domesticated stocks (Falconer 1981), zoo populations (Ralls et al. 1979, Ralls and Ballou 1983, Ralls et al. 1988), and a few wild populations. The male-biased sex ratio of Key deer fawns may be a consequence of inbreeding, as might the low rate of twinning.

Inbreeding depression probably results primarily from the expression of rare, deleterious alleles. Most populations contain a number of recessive deleterious alleles (the "genetic load" of the population) whose effects are usually masked because few individuals in a randomly breeding population would receive two copies of (are "homozygous" for) a harmful allele. Because their parents are related and share genes in common, inbred animals have much higher probabilities of being homozygous for rare alleles. If selection were efficient at removing deleterious traits from small populations, progressively inbred populations would become purged of their genetic load and further inbreeding would be of little consequence. Because random drift is so much stronger than selection in very small populations, even decidedly harmful traits can become common (e.g., cryptorchidism in the Florida panther, biased sex ratio in the Key deer) and inbreeding depression can drive a population to extinction.

The loss of genetic diversity that occurs as variants are lost through genetic drift has other, long-term consequences. As a population becomes increasingly homogeneous, it becomes increasingly susceptible to disease, new predators, changing climate, or any environmental change. Selection cannot favor the more adaptive types when all are identical and none are sufficiently adaptive. Every extinction is, in a sense, the failure of a population to adapt quickly enough to a changing environment.

To avoid the immediate effects of inbreeding and the long-term losses of genetic variability a population must remain large, or at least pass through phases of small numbers ("bottlenecks") in just one or a few generations. Because of the long generation times of the Puerto Rican parrot, the present bottleneck has existed for just one or two generations, and could be exited (successfully, we hope) before another generation passes and further genetic decay occurs. The Florida Key deer has evidently been in a bottleneck for thousands of years, perhaps 2-3 thousand generations. Although we cannot predict which genetic variants will be lost from any given population (that is the nature of random drift), we can specify the expected average rate of loss. Figure 12 shows the mean fate of genetic variation in randomly breeding populations of various sizes. The average rate of loss of genetic variance (when measured by heterozygosity, additive variance in quantitative traits, or the binomial variance in allelic frequencies) declines by drift according to:

$$V_g(t) = V_g(0) \times (1 - 1/(2N_e))^t,$$

in which  $V_g$  is the genetic variance at generation  $t$ , and  $N_e$  is the effective population size (see below) or approximately the number of breeders in a randomly breeding population. As shown in Figure 13, the variance in the rate of loss among genes and among different populations is quite large; some populations may (by chance) do considerably better or worse than the averages shown the Figure 12.

The rate of loss of genetic variation considered acceptable for a population of concern depends on the relationship between fitness and genetic variation in the population, the decrease in fitness considered to be acceptable, and the value placed by humans on the conservation of

natural variation within wildlife populations. Over the short-term, a 1% decrease in genetic variance (or heterozygosity), which corresponds to a 1% increment in the inbreeding coefficient, has been observed to cause about a 1-2% decrease in aspects of fitness (fecundity, survival) measured in a variety of animal populations (Falconer 1981). Appropriately, domesticated animal breeders usually accept inbreeding of less than 1% per generation as unlikely to cause serious detriment. The relationship between fitness and inbreeding is highly variable among species and even among populations of a species, however. A few highly inbred populations survive and reproduce well (e.g., northern elephant seals, Pere David's deer, European bison), while attempts to inbreed many other populations have resulted in the extinction of most or all inbred lines (Falconer 1981).

Concern over the loss of genetic adaptability has led to a recommendation that management programs for endangered taxa aim for the retention of at least 90% of the genetic variance present in ancestral populations (Foose et al. 1986). The adaptive response of a population to selection is proportional to the genetic variance in the traits selected, so the 90% goal would conserve a population capable of adapting at 90% the rate of the ancestral population. Over a timescale of 100 years or more, for a medium-sized vertebrate with a generation time of 5 years such a goal would imply an average loss of 0.5% of the genetic variation per generation, or a randomly breeding population of about 100 breeding age individuals.

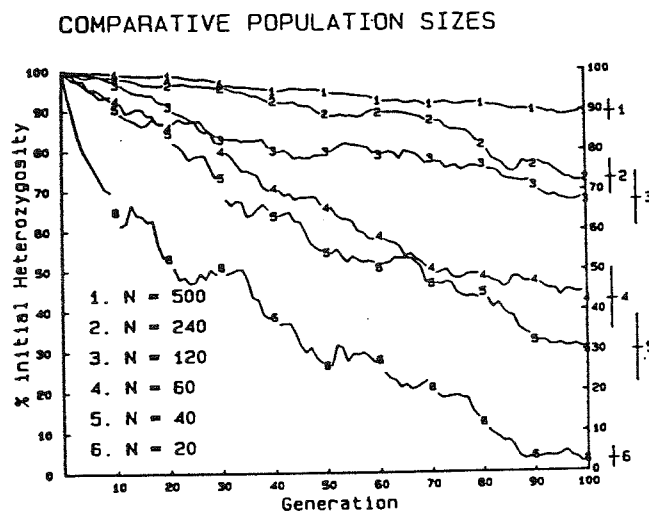


Figure 12. The average losses of genetic variation (measured by heterozygosity or additive genetic variation) due to genetic drift in 25 computer-simulated populations of 20, 50, 100, 250, and 500 randomly breeding individuals. Figure from Lacy 1987a.



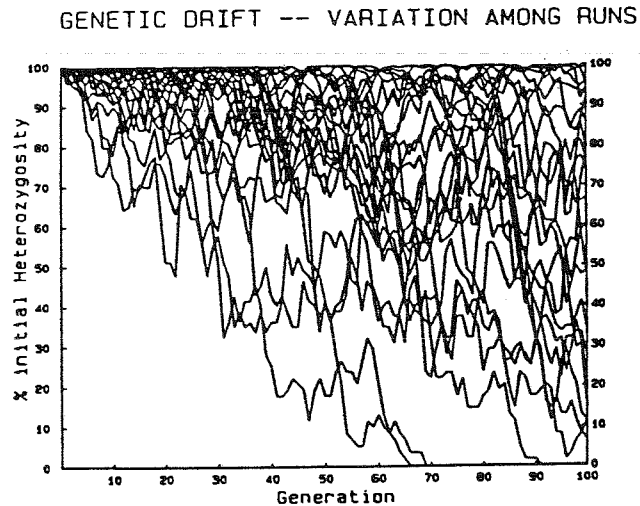


Figure 13. The losses of heterozygosity at a genetic locus in 25 populations of 120 randomly breeding individuals, simulated by computer. Figure from Lacy 1987a.

Most populations, whether natural, reintroduced, or captive, are founded by a small number of individuals, usually many fewer than the ultimate carrying capacity. Genetic drift can be especially rapid during this initial bottleneck (the "founder effect"), as it is whenever a population is at very low size. To minimize the genetic losses from the founder effect, managed populations should be started with 20 to 30 founders, and the population should be expanded to carrying capacity as rapidly as possible (Foose et al. 1986, Lacy 1988, 1989). With twenty reproductive founders, the initial population

would contain approximately 97.5% of the genetic variance present in the source population from which the founders came. The rate of further loss would decline from 2.5% per generation as the population increased in numbers. Because of the rapid losses of variability during the founding bottleneck, the ultimate carrying capacity of a managed population may have to be set substantially higher than the 100 breeding individuals given above in order to keep the total genetic losses below 90% (or whatever goal is chosen).

The above equations, graphs, and calculations all assume that the population is breeding randomly. Yet breeding is random in few if any natural populations. The "effective population size" is defined as that size of a randomly breeding population (one in which gamete union is at random) which would lose genetic variation by drift at the same rate as does the population of concern. An unequal sex ratio of breeding animals, greater than random variance in lifetime reproduction, and fluctuating population sizes all cause more rapid loss of variation than would occur in a randomly breeding population, and thus depress the effective population size. If the appropriate variables can be measured, then the impact of each factor on  $N_e$  can be calculated from standard population genetic formulae (Crow and Kimura 1970, Lande and Barrowclough

1987). For many vertebrates, breeding is approximately at random among those animals that reach reproductive age and enter the breeding population. To a first approximation, therefore, the effective population size can be estimated as the number of breeders each generation. In managed captive populations (with relatively low mortality rates, and stable numbers), effective population sizes are often 1/4 to 1/2 the census population. In wild populations (in which many animals die before they reach reproductive age),  $N_e/N$  probably rarely exceeds this range and often is an order of magnitude less.

The population size required to minimize genetic losses in a medium sized animal, therefore, might be estimated to be on the order of  $N_e = 100$ , as described above, with  $N = 200$  to 400. More precise estimates can and should be determined for any population of management concern from the life history characteristics of the population, the expected losses during the founding bottleneck, the genetic goals of the management plan, and the timescale of management.

Although the fate of any one small population is likely to be extinction within a moderate number of generations, populations are not necessarily completely isolated from conspecifics. Most species distributions can be described as "metapopulations", consisting of a number of partially isolated populations, within each of which mating is nearly random. Dispersal between populations can slow genetic losses due to drift, can augment numbers following population decline, and ultimately can recolonize habitat vacant after local extinction.

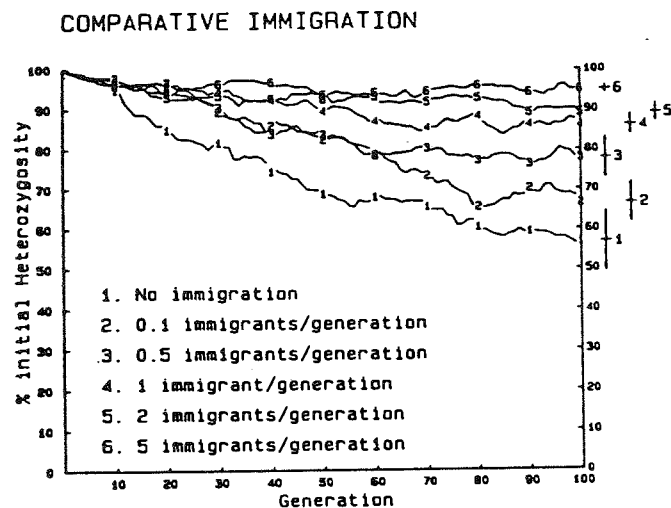


Figure 14. The effect of immigration from a large source population into a population of 120 breeding individuals. Each line represents the mean heterozygosity of 25 computer-simulated populations (or, equivalently, the mean heterozygosity across 25 non-linked genetic loci in a single population). Standard error bars for the final levels of heterozygosity are given at the right. Figure from Lacy 1987a.

If a very large population exists that can serve as a continued source of genetic material for a small isolate, even very occasional immigration (on the order of 1 per generation) can prevent the isolated subpopulation from losing substantial genetic variation (Figure 14). Often no source population exists of sufficient size to escape the effects of drift, but rather the metapopulation is divided into a number of small isolates with each subjected to considerable stochastic forces. Genetic variability is lost from within each subpopulation, but as different variants are lost by chance from different subpopulations the metapopulation can retain much of the initial genetic variability (Figure 15). Even a little genetic interchange between the subpopulations (on the order of 1 migrant per generation) will maintain variability within each subpopulation, by reintroducing genetic variants that are lost by drift (Figure 16). Because of the effectiveness of even low levels of migration at countering the effects of drift, the absolute isolation of a small population would have a very major impact on its genetic viability (and also, likely, its demographic stability). Population genetic theory makes it clear that no small, totally isolated population is likely to persist for long.

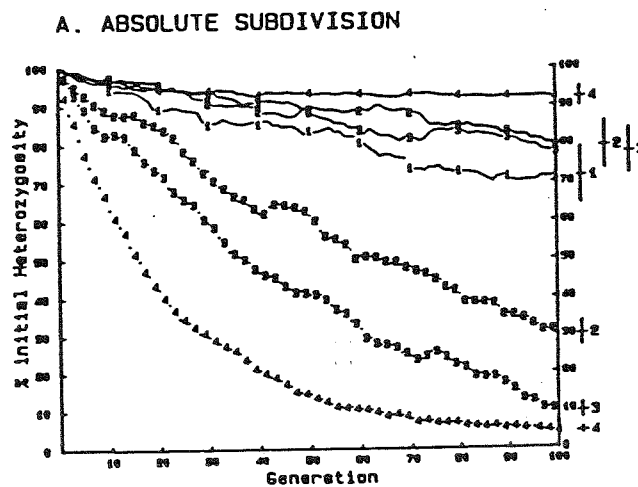


Figure 15. The effect of division of a population of 120 breeders into 1, 3, 5, or 10 isolated subpopulations. Dotted lines (numbers) indicate the mean within-subpopulation heterozygosities from 25 computer simulations. Lines represent the total gene diversity within the simulated metapopulation. Figure from Lacy 1987a.

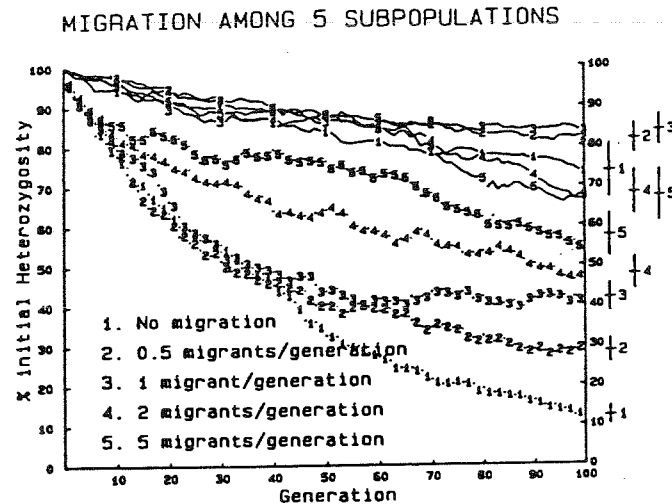


Figure 16. The effect of migration among 5 subpopulations of a population of 120 breeders. Dotted lines (numbers) indicate the mean within-subpopulation heterozygosities from 25 simulations. Lines represent the total gene diversity within the metapopulation. Figure from Lacy 1987a.

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***GRUS AMERICANA***

**WHOOPING CRANE**

**CONSERVATION VIABILITY ASSESSMENT  
WORKSHOP REPORT**

**SECTION 6  
VORTEX**



**VORTEX:**  
**A Computer Simulation Model for  
Population Viability Analysis**

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*Abstract*  
< 1 page  
still to be written

## Introduction

Many wildlife populations that were once widespread, numerous, and occupying contiguous habitat have been reduced to one or more small, isolated populations. The causes of the original decline are often obvious, deterministic forces, such as over-harvest, habitat destruction, or competition or predation from invasive introduced alien species. Even if the original causes of decline are removed, however, once a population becomes small and isolated from any other populations of conspecifics additional forces, intrinsic to the dynamics of small populations, come into play and may drive the population to extinction (Clark and Seebeck 1990). Of particular impact on small populations are stochastic, or random probabilistic, processes. With the exception of aging, virtually all events in the life of an organism are stochastic. Mating, reproduction, gene transmission between generations, migration, disease, and predation can be described by probability distributions, with individual occurrences being sampling from these distributions. Because small samples display high variance around the mean or expectation, the fates of small wildlife populations can be determined more by random luck than by adaptation, or mean birth and death rates.

The stochastic processes impacting small populations have been usefully categorised into demographic stochasticity, environmental variation, catastrophic events, and genetic drift (Shaffer 1981). Demographic stochasticity is the random fluctuation in the observed birth rate, death rate, and sex ratio of a population even if the probabilities of birth and death remain constant. Demographic stochasticity would follow binomial distributions and will be important (the frequency of birth and death events and the sex ratio deviating far from the statistical expectation) only in populations that are smaller than a few tens of animals (ref.). Environmental variation is the fluctuation in the probabilities of birth and death that results from inconstancy of the environment. Weather, the prevalence of enzootic disease, the abundances of prey and of predators, and the availability of nest sites or other required microhabitats can all vary, randomly or cyclically, over time. Catastrophic variation is the extreme of environmental variation, but for both methodological and heuristic reasons rare catastrophic events can be usefully analysed separately from the environmental variation of more typical yearly or seasonal fluctuations. Catastrophes such as epidemic disease, hurricanes or other severe storms, large-scale fires, and floods are outliers in the distributions of environmental variation (see Fig. 1); they have quantitatively and sometimes qualitatively different impacts on wildlife populations (a forest fire is not just a very hot day); and they are often the cause of the final decline of wildlife populations to extinction. One of two populations of whooping cranes (*Grus americana*) was decimated by a hurricane in 1947 and soon after went extinct. The only remaining population of black-footed ferrets (*Mustela nigripes*) was in the process of being eliminated by an outbreak of distemper when the last 18 ferrets were captured. [Good Australian example would be useful.]

Genetic drift, the cumulative, non-adaptive fluctuations in allele frequencies resulting from the random sampling of genes each generation, can impede the recovery or accelerate the decline of wildlife populations for several reasons. Inbreeding, not strictly a component of genetic drift but a correlate of it in small populations, has been documented to cause loss of fitness (decreased survival and fecundity, and increased susceptibility to disease and other environmental stresses) in a wide variety of species, including virtually all sexually

reproducing animals in which the effects of inbreeding have been carefully studied (Wright 1977; Falconer 1981; O'Brien and Evermann 1988; Ralls *et al.* 1988; Lacy *et al. in press*). Even if the immediate loss of fitness of inbred individuals is not large, the loss of genetic variation throughout a population that results from inbreeding and genetic drift will reduce the ability of the population to adapt to future changes in the environment (refs.).

Thus, the effects of genetic drift and consequent loss of genetic variation in individuals (inbreeding) and the population negatively impact demographic rates and also increase susceptibility to environmental perturbations and catastrophes, exacerbating the effects of these stochastic processes on population stability. Reduced population growth and greater fluctuations in numbers in turn accelerates genetic drift (Crow and Kimura 1970). The synergistic destabilising effects of stochastic process on small populations of wildlife has been described as an "extinction vortex" (Gilpin and Soulé 1986). The size below which a population is likely to be drawn into an extinction vortex can be considered one definition of a "minimum viable population" (MVP) (Brussard 1985; Seal *et al.* 1989 \*\*\*\* I need to check this \*\*\*\*; Thomas 1990). The estimation of MVPs or, more generally, the investigation of the probability of extinction of a population constitutes Population Viability Analysis (PVA) (Gilpin and Soulé 1986; Gilpin 1989; Shaffer 1990).

The study of extinction-recolonisation dynamics in natural populations inhabiting patchy environments (Gilpin 1987), the management of small populations (Clark and Seebeck 1990), and the conservation of threatened wildlife (Shaffer 1981, 1990; Soulé 1987; Mace and Lande 1991) all require an understanding of the multiple, interacting forces that contribute to extinction vortices. Because demographic and genetic processes in small populations are inherently unpredictable, the expected fates of wildlife populations will only be describable in terms of probability distributions (of population sizes, times to extinction, and amounts of genetic variation). Because the processes determining the dynamics of small populations are multiple and complex, analytical formulae for describing the probability distributions have been few (e.g., Goodman 1987; Lande 1988; Reed *et al.* 1988; Burgmann and Gerard 1990), and have incorporated only few of the threatening processes. No analytical model exists, for example, to describe the combined effect of demographic stochasticity and loss of genetic variation on the probability of population persistence.

A few studies of wildlife populations have provided empirical data on the relationship between population size and probability of extinction (e.g., Belovsky 1987; Griffith *et al.* 1989; Berger 1990; Thomas 1990), but presently only order of magnitude estimates can be provided for MVPs of vertebrates (Soulé ...), threatened species are by their rarity unavailable and inappropriate for collection of sufficient experimental data to determine MVPs precisely, and it is likely that the function relating extinction probability to population size will differ among species, localities, and times (Lindenmayer *et al. in press*).

Lacking adequate empirical data or theoretical and analytical models to allow prediction of the dynamics of populations of threatened wildlife species, various biologists have turned to computer simulation techniques for Population Viability Analysis. By randomly sampling from defined probability distributions, computer programs can simulate the multiple, interacting events that occur during the lives of organisms and which cumulatively determine the fates of populations. The focus is usually on detailed and explicit modelling of the specific forces impinging on a given population, place, and time of interest,

rather than on delineation of rules (which may not exist) that would apply generally to most wildlife populations. Computer programs available to PVA include: SPGPC (Grier 1980a, 1980b; Grier and Barclay 1988), GAPPS (Harris *et al.* 1986), POPDYN (Cox 1988), RAMAS (Ferson 1990 \*\*\* Check this \*\*\*; Akcakaya and Ferson 1990; Ferson and Akcakaya 1990), FORPOP (Possingham *et al.* 1991), ALEX (Lindenmayer and Possingham *in press*), and SIMPOP (Lacy *et al.* 1989; Lacy and Clark 1990) and its descendant VORTEX.

Lindenmayer *et al.* (*in press*) describe generally the use of computer simulation modelling for PVA, and discuss the strengths and weaknesses of the approach as a tool for wildlife management. In this paper, I present the PVA program VORTEX and describe its structure and capabilities. In an accompanying paper, Lindenmayer *et al.* present a PVA of Leadbeater's Possum (*Gymnobelideus leadbeateri*) using VORTEX. Previously, VORTEX (or SIMPOP) has been used in PVA to help guide conservation and management of the Puerto Rican Parrot (*Amazona vittata*) (Lacy *et al.* 1989), Javan Rhinoceros (*Rhinoceros sondaicus*) (Seal and Foose 1989), Sumatran Rhinoceros (???), Florida Panther (*Felis concolor coryi*) (Seal and Lacy 1989), Florida Key Deer (*Odocoileus virginianus clavium*) (Seal and Lacy 1990), Eastern Barred Bandicoot (*Perameles gunnii*) (Lacy and Clark 1990; Maguire *et al.* 1990), Lion Tamarins (*Leontopithecus rosalia* ssp.) (Ballou *et al.* 1991), Brush-Tailed Rock Wallaby (*Petrogale pencillata pencillata*) (Hill 1991), Red Wolf (*Canis rufus*) (Parker *et al.* 1991), Mountain Pygmy Possum (*Burramys parvus*), Leadbeater's Possum, Long-Footed Potoroo (*Potorous longipes*), Orange-Bellied Parrot (*Neophema chrysogaster*) and Helmeted Honeyeater (*Lichenostomus melanops cassidix*) (Clark *et al.* 1991), Spotted Tree Frog (*Litoria spenceri*), Striped Legless Lizard (*Delma impar*), Red-Tailed Black Cockatoo (*Calyptorhynchus magnificus magnificus*), Malleefowl (*Leipoa ocellata*), Brolga (*Grus rubicundus*), and New Holland Mouse (*Pseudomys novaehollandiae*) (Backhouse *et al. in press*), Whooping Crane (*Grus americana*) (Seal *et al. in press*, a) Tana River Crested Mangabey () and Tana River Red Colobus () (Seal *et al. in press*, b), and Black Rhinoceros () (Seal *et al. in press*, c).

## Description of VORTEX

### Overview

The VORTEX computer simulation model is a Monte Carlo simulation of the effects of deterministic forces as well as demographic, environmental and genetic stochastic events on wildlife populations. Earlier versions of VORTEX were named SIMPOP, and then VORTICES. Many of the algorithms in VORTEX were drawn from the computer simulation program SPGPC (Grier 1980a, 1980b, Grier and Barclay 1988). VORTEX models population dynamics as discrete, sequential events (e.g births, mortality, catastrophes, carrying capacity truncation) that occur according to defined probabilities. The probabilities of events are modelled as constants or as random variables that follow specified distributions.

VORTEX simulates a population by stepping through the series of events that describe the typical life cycle of a sexually reproducing, diploid organism. The program was written originally to model mammalian and avian populations, but it has been used for modelling some species of reptiles and amphibians and could be used for fish, invertebrates and possibly

even plants. VORTEX iterates life events on an annual cycle (although a user could model populations with "years" that are other than 12 months duration). The simulation of the population is then itself iterated to reveal the distribution of fates that the population might experience.

The program models demographic stochasticity by determining the occurrence of probabilistic events (reproduction, litter size, sex determination, death) with a pseudo-random number generator. The probabilities of mortality and reproduction are sex specific and pre-determined for each age class up to the age of breeding, beyond which it is assumed that reproduction and survival probabilities remain constant until a specified upper limit to age is reached. Sex ratio at birth is modelled with a user-specified constant probability (0.50 for most species) of an offspring being male. For each life event, if the random value sampled from a specified probability distribution falls above the mean value, the event is deemed to have occurred, thereby simulating a binomial process.

The source code used to generate random numbers uniformly distributed between 0 and 1 was obtained from Maier (1991), based on the algorithm of Kirkpatrick and Stoll (1981). Random deviates from binomial distributions, with mean  $p$  and standard deviation  $s$ , are obtained by first determining the integral number of binomial trials,  $N$ , that would produce the value of  $s$  closest to the specified value [binomial distributions are discrete and not all values of  $s$  are possible;  $N = p(1-p)/s^2$ ], then conducting  $N$  binomial trials (using sampling from the uniform 0-1 distribution) to obtain the desired result, the frequency or proportion of successes. If the value of  $N$  determined for a desired binomial distribution is larger than 25, a normal approximation is used in place of the binomial distribution. This normal approximation must be truncated at 0 and at 1 to allow use in defining probabilities, although, with such large values of  $N$ ,  $s$  is small relative to  $p$  and the truncation would be invoked only rarely. To avoid introducing any bias with this truncation, the normal approximation to the binomial (when used) is truncated symmetrically around the mean. The algorithm for generating random numbers from a unit normal distribution follows Latour (1986).

VORTEX can model monogamous or polygamous mating systems. In a monogamous system, a relative scarcity of male breeders might limit reproduction by females. In the polygamous model, only one adult male is required to allow breeding by females. In addition, the user can specify the proportion of the adult males in the breeding pool. Males are randomly reassigned to the breeding pool each year of the simulation, and all males in the breeding pool have an equal chance of siring offspring.

The upper limits for population size within a habitat (the "carrying capacity") must be specified by the user. VORTEX imposes the carrying capacity via a probabilistic truncation whenever the population exceeds the carrying capacity. Each animal in the population has an equal probability of being removed during this truncation.

VORTEX can model annual fluctuations in birth and death rates and in carrying capacity as might result from environmental variation. To model environmental variation each demographic parameter (reproductive success, mortality rates, population carrying capacity) is assigned a distribution with a mean and standard deviation that is specified by the user. Annual fluctuations in probabilities of reproduction and mortality are modelled as binomial distributions; environmental variation in carrying capacity is modelled as a normal

distribution. The variance across years in the frequencies of births and deaths resulting from the simulation model (and in real populations) will have two components: the demographic variation resulting from a binomial sampling around the mean for each year, and fluctuations in that mean due to environmental variation.

Data on the annual variation in birth and death rates is important in determining the probability of extinction, as it influences population stability. Unfortunately, this information is rarely available from field data. VORTEX allows a population to be modelled in the absence of any environmental variation, or any plausible range of variation that might be usefully examined. Sensitivity testing, the examination of a range of values when the precise value of a parameter is unknown, can help to identify whether the unknown parameter is likely to be important in the dynamics of a population. This can guide research priorities and indicate where management actions can ameliorate factors that put a population at risk.

Catastrophes are modelled in VORTEX as random events that occur with specified probabilities. A catastrophe will occur if a randomly generated number between zero and one is less than the probability of that occurrence (i.e. a binomial process is simulated). Following a catastrophic event, the chance of survival and successful breeding for that simulated year is multiplied by a severity factor.

Genetic drift is modelled in VORTEX by simulation of the transmission of alleles at a hypothetical locus. At the beginning of the simulation, each animal is assigned two unique alleles. Each offspring created is randomly assigned one of the alleles from each parent. Inbreeding depression which is modelled as a loss of viability during the first year amongst inbred animals.

The impacts of inbreeding on the population are determined by using one of two models available within VORTEX: a Recessive Lethals model and a Heterosis model. In the Recessive Lethals model each founder starts with one unique recessive lethal allele and a unique, dominant non-lethal allele. This model approximates the effect of inbreeding if each individual in the starting population had one recessive lethal allele somewhere in its genome. The fact that the simulation program assumes that all the lethal alleles are at the same locus has a very minor impact on the probability that an individual will die because of homozygosity for one of the lethal alleles. In the model, homozygosity for different lethal alleles are mutually exclusive events, whereas in a multi-locus model an individual could be homozygous for several lethal alleles simultaneously. By virtue of the death of individuals that are homozygous for lethal alleles, the lethal alleles would be removed slowly by natural selection during the generations of a simulation. This would reduce the genetic variation present in the population (relative to the case with no inbreeding depression), but would also lessen the subsequent probability that inbred individuals would be homozygous for a lethal allele. This model gives an optimistic reflection of the impacts of inbreeding on many wildlife species, as the median number of lethal equivalents per diploid genome that is estimated for mammalian populations is approximately three (Ralls *et al.* 1988).

In the Heterosis model, all homozygotes have reduced fitness compared with heterozygotes. Juvenile survival is modelled according to the logarithmic model developed by Morton *et al.* (1955):

$$\ln(S) = A - BF$$

in which S is survival, F is the inbreeding coefficient, A is the logarithm of survival in the



absence of inbreeding, and  $B$  is a measure of the rate at which survival decreases with inbreeding.  $B$  is termed the number of "lethal equivalents" per haploid genome ( $2B$  is the number of lethal equivalents per diploid genome), because it estimates (half) the number of lethal alleles per individual in the population if all deleterious effects of inbreeding were due to recessive lethal alleles. A population with the level of inbreeding depression of one lethal equivalent per diploid genome may have one recessive lethal allele per individual (as in the RECESSIVE LETHAL model, above); it may have two recessive alleles per individual, each of which confer a 50% decrease in survival, or it may have some combination of recessive deleterious alleles which equate in effect with one fully lethal allele per individual.

Inbreeding effects may result not from the expression of fully recessive deleterious alleles in inbred organisms, but rather (or also) because of superior fitness of heterozygotes (heterozygote advantage or "heterosis"). Unlike the situation with fully recessive deleterious alleles, natural selection cannot remove deleterious alleles at heterotic loci, because all alleles are deleterious when homozygous (relative to the heterozygote fitness). Thus the effects of inbreeding are unchanged during the repeated generations of inbreeding.

In addition to simulating the stochastic effects of demographic variation, environmental variation, catastrophes, and genetic drift, VORTEX also can incorporate several deterministic processes. Reproduction can be specified to be density-dependent. The function relating the percent of adult females breeding each year to the total population size is modelled as a fourth-order polynomial (providing a close fit to virtually any plausible density dependence curve). Populations can be supplemented or harvested for any number of years in each simulation. The numbers of additions and removals are specified according to the age and sex of animals. Trends in the carrying capacity can also be modelled in VORTEX. These are specified as an annual percentage change. Thus, a reduction in habitat carrying capacity is incorporated in VORTEX as a linear decrease rather than a geometric decline.

VORTEX can model up to 25 populations, with specification of each pairwise migration rate (probability of an individual moving from one population to another). The probability of an animal migrating between any two populations is independent of the age and sex of the animal. Because of between-population migration and managed supplementation, populations can be recolonised.

In summary, VORTEX is able to simulate many of the processes which influence the size, behaviour and viability of a population. The program tracks the fate of populations and the output contains a summary of: (1) the probability of the extinction during at each specified interval (e.g. every 10 years during a 100 year simulation), (2) the median time to extinction (if at least 50% of the population went extinct in at least 50% of the simulations), (3) the mean time to extinction of those simulated populations that became extinct, and, (4) the mean size of, and genetic variation within, extant populations. Standard deviations across simulations and standard errors of the mean are reported for the probability of extinction [given by  $SE(p) = p \times [1-p]/(\sqrt{n})$ , in which the frequency of extinction was  $p$  over  $n$  simulated populations], population size, and the measures of genetic variation. Demographic and genetic statistics are calculated and reported for each subpopulation and for the metapopulation.

Input can be either from the keyboard or from an input file. In the case of keyboard data entry, an input file with the entered values is created for possible modification and later

use. An example of the output from VORTEX is given in Appendix 1.

VORTEX is written in the C programming language and compiled with the Lattice 80286C Development System (Lattice Inc., Lombard, Illinois, U.S.A.) for use on microcomputers using the MS-DOS (Microsoft Corp.) operating system. The program calls many functions specific to the Lattice compiler, but most have direct counterparts in the function libraries provided with other popular C compilers. Copies of the compiled program, the source code, and a manual for its use are available for nominal distribution costs from the Captive Breeding Specialist Group (Species Survival Commission, IUCN), 12101 Johnny Cake Ridge Road, Apple Valley, MN 55124, USA. The programs have been tested by a variety of workers, but the program cannot be guaranteed to be without errors. Each user retains the responsibility for the assuring that the program does what is intended.

### *Sequence of Program Flow*

(1) The seed for the random number generator is initialised with the number of seconds elapsed since the beginning of the 20<sup>th</sup> century (Lattice function).

(2) The user is prompted for input and output devices, population parameters, duration of simulation, and number of iterations. (See sample output, Appendix 1).

(3) The maximum allowable population size (necessary for preventing memory overflow) is calculated as:

$$N_{\max} = (K + 3s) \times (1 + L)$$

in which  $K$  is the maximum carrying capacity (carrying capacity can be specified to change linearly for a number of years in a simulation, so the maximum carrying capacity can be greater than the initial carrying capacity),  $s$  is the annual environmental variation in the carrying capacity expressed as a standard deviation, and  $L$  is the specified maximum litter size. It is theoretically possible, but very unlikely, that a simulated population will exceed the calculated  $N_{\max}$ . If this occurs then the program will give an error message and abort.

(4) Memory is allocated for data arrays. If insufficient memory is available for data arrays then  $N_{\max}$  is adjusted downward to the size that can be accommodated within the available memory and a warning message is given. In this case it is possible that the analysis may have to be terminated because the simulated population exceeds  $N_{\max}$ . Because  $N_{\max}$  is often several-fold greater than the likely maximum population size in a simulation, a warning that it been adjusted downward because of limiting memory often will not hamper the analyses. Except for limitations imposed by the size of the computer memory (VORTEX can use extended memory, if available), the only limit to the size of the analysis is that no more than 25 populations exchanging migrants can be simulated.

(5) Expected mean growth rate of the population is calculated from mean birth and death rates that have been entered. Algorithms follow standard cohort life-table analyses (ref). Generation time and the expected stable age distribution are also estimated. The life-table estimations assume no limitation by carrying capacity, no limitation of mates, and no loss of fitness due to inbreeding depression, and the estimate of growth rate assumes that the population has already reached the stable age distribution. The effects of catastrophes are incorporated into the life table analysis by using birth and death rates that are weighted averages of the mean values in years with and without catastrophes, weighted by the probability of a catastrophe occurring or not occurring.

(6) Iterative simulation of the population proceeds via steps 7 through 26 below. For exploratory modelling, 100 iterations is usually sufficient to reveal gross trends among sets of simulations with different input parameters. For more precise examination of population behaviour under various scenarios, 1000 or more simulations should be used to minimise standard errors around mean results.

(7) The starting population is assigned an age and sex structure. The user can specify the exact age-sex structure of the starting population, or can specify a total initial population size and request that the population be distributed according to the stable age distribution calculated from the life table. Individuals in the starting population are assumed all to be unrelated. Thus, inbreeding can occur in second and later generations.

(8) Two unique alleles at a hypothetical genetic locus are assigned to each individual in the starting population. The simulation therefore uses an infinite alleles model of genetic variation, with each immigrant individual (due to supplementation of the population by management) bringing in two new alleles. The subsequent fate of genetic variation is tracked by reporting the number of extant alleles each year, the expected heterozygosity or gene diversity, and the observed heterozygosity. The expected heterozygosity, derived from the Hardy-Weinberg equilibrium, is given by  $H_e = 1 - \sum(p_i^2)$ , in which  $p_i$  is the frequency (proportion) of allele  $i$  in the population. The observed heterozygosity is simply the proportion of the individuals in the simulated population that are heterozygous. Because of the starting assumption of two unique alleles per founder, the initial population has a heterozygosity of 1.0 at the hypothetical locus, only inbred animals can become homozygous, and the probability that an individual is homozygous is equal to the inbreeding coefficient of that individual.

(9) The user specifies one of three options for modelling the effect of inbreeding: (a) no effect of inbreeding on fitness, i.e. all alleles are selectively neutral, (b) each founder individual has one unique lethal and one unique non-lethal allele (Recessive Lethals option), or (c) first-year survival of each individual is exponentially related to its inbreeding coefficient (Heterosis option). The first case is clearly an optimistic one, as almost all diploid populations studied intensively have shown deleterious effects of inbreeding on a variety of fitness components (Wright 1977, Falconer 1981). Each of the two methods of modelling inbreeding depression are perhaps still optimistic, in that inbreeding is assumed to impact only first-year survival. The third option allows, however, for the user to specify the severity of inbreeding depression in juvenile survival.

(10) The years of the simulation are iterated via steps 11 through 25 below.

(11) The probabilities of females producing each possible size litter are adjusted to account for density dependence of reproduction (if any).

(12) Birth rate, survival rates, and carrying capacity for the year are adjusted to model environmental variation. Environmental variation is assumed to follow binomial distributions (for birth and death rates) or a normal distribution (for carrying capacity), with mean rates and standard deviations specified by the user. At the outset of each year a random number is drawn from the specified binomial distribution to determine the percent of females producing litters. The distribution of litter sizes among those females that do breed is maintained constant. Another random number is drawn from a specified binomial distribution to model the environmental variation in mortality rates. If environmental variation in reproduction and

mortality are chosen to be correlated, the random number used to specify mortality rates for the year is chosen to be the same percentile of its binomial distribution as was the number used to specify reproductive rate. Otherwise, the new random number is drawn to specify the deviation of age- and sex-specific mortality rates from their means. Environmental variation across years in mortality rates is always forced to be correlated among age and sex classes.

The carrying capacity (**K**) for the year is determined by first incrementing or decrementing the base (year 1) carrying capacity by the amount specified by the user to account for linear changes over time. Environmental variation in **K** is then imposed by drawing a random number from a normal distribution with appropriate mean and standard deviation.

(13) Birth rates and survival rates for the year are adjusted to model catastrophes (if any are determined to have occurred in that year of the simulation).

(14) Breeding males are selected for the year. For each male of breeding age, the male is placed into the pool of potential breeders for that year if a random number drawn for that male is less than the proportion of breeding age males specified to be breeding.

(15) For each female of breeding age, a mate is drawn at random from the pool of breeding males for that year. The size of the litter produced by that pair is determined by comparing the probabilities of each potential litter size (including litter size of 0, no breeding) to a randomly drawn number. The offspring are produced and assigned a sex by comparison of a random number to the specified birth sex ratio. Offspring are assigned, at random, one allele at the hypothetical genetic locus from each parent.

(16) If the Heterosis option is chosen for modelling inbreeding depression, the genetic kinship of each new offspring to each other living animal in the population is determined. The kinship between new animal A, and another existing animal, B, is  $r_{AB} = 0.5 * (r_{MB} + r_{PB})$  in which  $r_{ij}$  is the kinship between animals i and j, M is the mother of A, and P is the father of A. The inbreeding coefficient of each animal is equal to the kinship between its parents,  $F = r_{MP}$ , and the relationship of an animal to itself is  $r_{AA} = 0.5 * (1 + F)$ . (See Ballou 1984 for a detailed description of this method for calculating inbreeding coefficients.)

(17) The survival or death of each animal is determined by comparing a random number to the survival probability for that animal. In the absence of inbreeding depression, the survival probability is given by the age and sex-specific survival rate for that year. If the HETEROSIS model of inbreeding depression is used and an individual is inbred, the survival probability is multiplied by  $e^{-bF}$  in which b is the number of lethal equivalents per haploid genome. If the RECESSIVE LETHALS model is used, all offspring that are homozygous for the lethal allele (half of all founder alleles are recessive lethals) are killed.

(18) The age of each animal is incremented by 1, and any animal exceeding the maximum age is killed.

(19) If more than one population is being modelled, migration among populations is occurs stochastically with specified probabilities.

(20) If population harvest is to occur that year, the number of harvested individuals of each age and sex class are chosen at random from those available and killed. If the number to be harvested do not exist for any age-sex class, the program continues (without completing the harvest) but reports that the harvest was incomplete.

(21) Dead animals are removed from the computer memory to make space for future generations.

(22) If population supplementation is to occur in a particular year, new individuals of the specified age-class are created. Each immigrant is assigned two unique alleles, one of which will be a recessive lethal in the RECESSIVE LETHALS model, and each immigrant is assumed to be genetically unrelated to all other individuals in the population.

(23) The population growth rate is calculated as the ratio of the population size in the previous year to the current size.

(24) If the population size ( $N$ ) exceeds the carrying capacity ( $K$ ) for that year, additional mortality is imposed across all age and sex classes. The probability of each animal dying during this carrying capacity truncation is set to  $(N - K)/N$ , so that the expected population size after the additional mortality is  $K$ .

(25) Summary statistics on population size and genetic variation are tallied and reported. A simulated population is determined to be extinct if either sex has no representatives.

(26) Final population size and genetic variation are determined for the simulation.

(27) Summary statistics on population size, genetic variation, probability of extinction and mean population growth rate are calculated across iterations and output.

#### *Assumptions underpinning VORTEX*

It is impossible to simulate the complete range of complex processes and dynamics typical of a wild populations. As a result there are necessarily a range of mathematical and biological assumptions which underpin any PVA program. Some of the more important assumptions in VORTEX include:

(1) Survival probabilities are density independent when the population size is less than carrying capacity. Additional mortality imposed when the population exceeds  $K$  affects all age and sex classes equally.

(2) The relationship between changes in population size and genetic variability are examined for only one locus. Thus, potentially complex interactions between genes located on the same chromosome are ignored. Such interactions (*e.g.*, linkage disequilibrium) are typically associated with genetic drift in very small populations, but it is unknown if, or how, they would affect population viability.

(3) All animals of reproductive age have an equal probability of breeding. This ignores the likelihood that some animals within a population will have a greater probability of breeding successfully, and breeding more often, than other individuals. If breeding is not at random among those in the breeding pool, then decay of genetic variation and the consequent inbreeding will occur more rapidly than in the model, perhaps further destabilising the population.

(4) The life-history attributes of a population (birth, death, harvesting, supplementation etc) are modelled as a sequence of discrete and therefore seasonal events. However, such events are typically continuous through time and the model therefore ignores the possibility that they may be aseasonal or only partly seasonal.

(5) The genetic effects of inbreeding on a population are determined in VORTEX using one of two possible models: the Recessive Lethals model and the Heterosis model. Both models have attributes likely to be typical of some populations but these will vary between species (Brewer *et al.* 1990). Given this, it is probable that the impacts of inbreeding will fall between the effects of these two models. Inbreeding is assumed to depress only one component of fitness, first-year survival. Effects on reproduction could be incorporated into this component, but longer-term impacts such as increased disease susceptibility or decreased ability to adapt to environmental change are not modelled.

(6) The probabilities of reproduction and mortality are constant from the age of first breeding until an animal reaches the maximum longevity. This assumes that animals continue to breed until they die.

(7) A simulated catastrophe will have an effect on a population only in the year that the event occurs.

(8) Migration rates among populations are independent of age and sex.

(9) Complex, inter-species interactions are not modelled, except in that such community dynamics might contribute to random environmental variation in demographic parameters. For example, cyclical fluctuations caused by predator-prey interactions cannot be modelled by VORTEX.

## Discussion

### *Uses and Abuses of Simulation Modelling for PVA*

Computer simulation modelling is a tool that can allow crude estimation of the probability of population extinction, and the mean population size and amount of genetic diversity, from data on diverse interacting processes that are too complex to be integrated intuitively (mental models) and for which no analytic solutions presently, or are likely to soon, exist. The technique focusses on the specifics of a population, considering the particular habitat, threats, trends, and time frame of interest, and can only be as good as the data and the assumptions fed into the model (Lindenmayer *et al. in press*). Yet the use of even simplified computer models for PVA will provide more accurate predictions about population dynamics than the even more crude techniques available previously, such as calculation of expected population growth rates from life tables. For the purpose of estimating extinction probabilities, methods that assess only deterministic factors are almost certain to be inappropriate, because populations near extinction will commonly be so small that random processes predominate over deterministic ones. The suggestions by Mace and Lande (1991) that population viability be assessed by the application of simple rules (*e.g.*, a taxon be considered Endangered if the total genetically effective population size is below 50 or the total census size below 250) should be followed only if knowledge is insufficient to allow more accurate quantitative analysis. Moreover, such preliminary judgements, while often important in stimulating appropriate corrective measures, should signal, not obviate, the need for more extensive investigation and analysis of population processes, trends, and threats.

At least a handful of good population simulation models are available for PVA (see Introduction). They differ in capabilities, assumptions, and ease of application; ease of application being related to the number of simplifying assumptions and inversely related to the flexibility and power of the model. It is unlikely that a single or even a few simulation models will be appropriate for all PVAs. The VORTEX program has some capabilities not found in many other population simulation programs, but is not as flexible as are a few others (e.g., GAPPs: Harris *et al.* 1986). VORTEX is user-friendly enough to be used by those with relatively little understanding of population biology and extinction processes. This is both an advantage and a disadvantage.

VORTEX, like most other models in use, was designed to represent the life history typical of many larger vertebrates (primarily reptiles, mammals, and birds), with slow reproduction and long lifespans. Although it could and has been used for highly fecund vertebrates and invertebrates, it is awkward to use in such cases (e.g., it requires complete specification of the percent of females producing each possible clutch size), and computer memory limitations often hamper analyses. Unfortunately, it is just such taxa that are the most effected by stochastic processes, show the greatest fluctuations in population numbers, and likely have the greatest minimum viable population sizes.

Because many of the processes being simulated are stochastic, a PVA can never specify what will happen to a population. Rather, PVA can provide estimates of probability distributions describing possible fates of a population. The ultimate fate of a given population may happen to fall at the extreme tail of such a distribution, even if the processes and probabilities are assessed precisely. Therefore, it will be often be impossible to empirically test the accuracy of PVA results by monitoring of one or a few threatened populations of interest. (Presumably, if even a single population followed a course that was well outside of the range of possibilities predicted by a model, that model could be rejected as inadequate. Often, however, the range of plausible fates generated by PVA is quite broad.)

Simulation programs can be checked for internal consistency (e.g., does the simulation model predict the same average long-term growth rate, in the absence of inbreeding depression and other confounding effects, as does a life table calculation? [VORTEX does.]). Beyond this, some confidence in the accuracy of a simulation model can be obtained by comparing observed fluctuations in population numbers to those generated by the model, thereby comparing a data set consisting of perhaps tens to hundreds of data points to model results. For example, from 1938 through 1991, the wild population of whooping cranes had grown at a mean (geometric) rate of 4.1%, with annual fluctuations in the growth rate of  $SD = 13.8\%$  (Seal *et al. in press*). Life table analyses of the whooping crane predict a mean population growth rate of 4.9%. Simulations using VORTEX predicted a mean population growth rate of 4.6% into the future, but just 3.1% annual growth, with an  $SD$  of 11.2%, if the simulations were started with the 18 cranes present in 1938 rather than the 146 cranes in 1991. (The lower predicted growth rate when started from a smaller size reflects the effects of inbreeding and perhaps imbalanced sex ratios among breeders in the simulation, factors that are not considered in the life table calculations.) The closeness of the observed mean population growth rate to the rates in the simulated populations lends support for the accuracy of the estimated birth and death parameters. The simulation model, when started with 18 individuals, slightly under-predicted the mean growth rate and final population size after 52

years ( $108 \pm 91$  SD), but the observed final size of the population (146 at the beginning of 1991) was well within the range observed among simulations. The model also slightly under-predicted the annual fluctuations in population growth (11.2% vs. 13.8% SD). This may reflect a lack of full incorporation of all aspects of stochasticity into the model (e.g., the observed rate of catastrophe years, 14%, was greater than the modelled rate, 10%), or may simply reflect the sampling error inherent in stochastic phenomena. Because the data fed into the model necessarily derive from analysis of past trends, however, such retrospective analysis should be viewed as little more than a check of consistency. As another confirmation of consistency, both deterministic calculations and the simulation model project an over-wintering population consisting of 12% juveniles (less than 1 year old), while the observed frequency of juveniles at the wintering grounds in Texas has averaged 13%.

Convincing evidence of the accuracy, precision, and usefulness of PVA simulation models would require the comparison of the distribution of fates of many replicate populations to model predictions. Such a test probably cannot be conducted on any endangered species, but could and should be examined in experimental non-endangered populations.

#### *Directions for Future Development of PVA Models*

Continuous time models  
Better handling of r-selected life histories  
Cross-validation of programs  
Other?

#### **Appendix 1 - Sample output from VORTEX.**

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# VORTEX

## Simulation model of stochastic population change

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### STOCHASTIC SIMULATION OF POPULATION EXTINCTION

Life table analyses yield average long-term projections of population growth (or decline), but do not reveal the fluctuations in population size that would result from variability in demographic processes. When a population is small and isolated from other populations of conspecifics, these random fluctuations can lead to extinction even of populations that have, on average, positive population growth. The VORTEX program (earlier versions called SIMPOP and VORTICES) is a Monte Carlo simulation of demographic events in the history of a population. Some of the algorithms in VORTEX were taken from a simulation program, SPGPC, written in BASIC by James Grier of North Dakota State University (Grier 1980a, 1980b, Grier and Barclay 1988).

Fluctuations in population size can result from any or all of several levels of stochastic (random) effects. Demographic variation results from the probabilistic nature of birth and death processes. Thus, even if the probability of an animal reproducing or dying is always constant, we expect that the actual proportion reproducing or dying within any time interval to vary according to a binomial distribution with mean equal to the probability of the event ( $p$ ) and variance given by  $V_p = p * (1 - p) / N$ . Demographic variation is thus intrinsic to the population and occurs in the simulation because birth and death events are determined by a random process (with appropriate probabilities).

Environmental variation (EV) is the variation in the probabilities of reproduction and mortality that occur because of changes in the environment on an annual basis (or other timescales). Thus, EV impacts all individuals in the population simultaneously -- changing the probabilities (means of the above binomial distributions) of birth and death. The sources of EV are thus extrinsic to the population itself, due to weather, predator and prey populations, parasite loads, etc.

VORTEX models population processes as discrete, sequential events, with probabilistic outcomes determined by a pseudo-random number generator. VORTEX simulates birth and death processes and the transmission of genes through the generations by generating random numbers to determine whether each animal lives or dies, whether each adult female produces broods of size 0, or 1, or 2, or 3, or 4, or 5 during each year, and which of the two alleles at a genetic locus are transmitted from each parent to each offspring. Mortality and reproduction probabilities are sex-specific. Fecundity is assumed to be independent of age (after an animal reaches reproductive age). Mortality rates are specified for each pre-reproductive age class and for reproductive-age animals. The mating system can be specified to be either monogamous or polygynous. In either case, the user can specify that only a subset of the adult male population is in the breeding pool (the remainder being excluded perhaps by social factors). Those males in the breeding pool all have equal probability of siring offspring.

Each simulation is started with a specified number of males and females of each pre-reproductive age class, and a specified number of male and females of breeding age. Each animal in the initial population is assigned two unique alleles at some hypothetical genetic locus, and the user specifies the severity of inbreeding depression (expressed in the model as a loss of viability in inbred animals). The computer program simulates and tracks the fate of each population, and outputs summary statistics on the probability of population extinction over specified time intervals, the mean time to extinction of those simulated populations that went extinct, the mean size of populations not yet extinct, and the levels of genetic variation remaining in any extant populations.

Extinction of a population (or meta-population) is defined in VORTEX as the absence of either sex. (In some earlier versions of VORTEX, extinction was defined as the absence of both sexes.) Recolonization occurs when a formerly extinct population once again has both sexes. Thus, a population would go "extinct" if all females died, and would be recolonized if a female subsequently migrated into that population of males. Populations lacking both sexes are not considered to be recolonized until at least one male and at least one female have moved in.

A population carrying capacity is imposed by a probabilistic truncation of each age class if the population size after breeding exceeds the specified carrying capacity. The program allows the user to model trends in the carrying capacity, as linear increases or decreases across a specified numbers of years.

The user also has the option of modelling density dependence in reproductive rates, i.e., one can simulate a population that responds to low density with increased (or decreased) breeding, or that decreases breeding as the population approaches the carrying capacity of the habitat. To model density-dependent reproduction, the user must enter the parameters (A, B, C, D, and E) of the following polynomial equation describing the proportion of adult females breeding as a function of population size:

$$\text{Proportion breeding} = A + BN + CN^2 + DN^3 + EN^4$$

in which N is total population size. Note that the parameter A is the proportion of adult females breeding at minimal population sizes. A positive value for B will cause increasing reproduction with increasing population sizes at the low end of the range. Parameters C, D, and E dominate the shape of the density dependence function at increasingly higher population sizes. Any of the values can be set to zero (e.g., to model density dependence as a quadratic equation, set  $D = E = 0$ ). To determine the appropriate values for A through E, a user would estimate the parameters that provide the best fit of the polynomial function to an observed (or hypothetical) data set. Most good statistical packages have the capability of doing this. Although the polynomial equation above may not match a desired density dependence function (e.g., Logistic, Beverton-Holt, or Ricker functions), almost any density dependence function can be closely approximated by a 4th-order polynomial.

After specifying the proportion of adult females breeding, in the form of the polynomial, the user is prompted to input the percent of successfully breeding females that produce litter sizes of 1, 2, etc. It is important to note that with density dependence, percents of females producing each size litter are expressed as percents of those females breeding, and the user does not explicitly enter a percent of females producing no offspring in an average year. (That value is given by the polynomial.) In the absence of density dependence, the user must specify the percent of females failing to breed, and the percents producing each litter size are percents of all breeding age females (as in earlier versions of VORTEX). Read the prompts on the screen carefully as you enter data, and the distinction should become clear.

VORTEX models environmental variation simplistically (that is both the advantage and disadvantage of simulation modelling), by selecting at the beginning of each year the population age-specific birth rates, age-specific death rates, and carrying capacity from distributions with means and standard deviations specified by the user. EV in birth and death rates is simulated by sampling binomial distributions, with the standard deviations specifying the annual fluctuations in probabilities of reproduction and mortality. EV in carrying capacity is modelled by sampling a normal distribution. EV in



reproduction and EV in mortality can be specified to be acting independently or jointly (correlated in so far as is possible for discrete binomial distributions).

Unfortunately, rarely do we have sufficient field data to estimate the fluctuations in birth and death rates, and in carrying capacity, for a wild population. (The population would have to be monitored for long enough to separate, statistically, sampling error, demographic variation in the number of breeders and deaths, and annual variation in the probabilities of these events.) Lacking any data on annual variation, a user can try various values, or simply set  $EV = 0$  to model the fate of the population in the absence of any environmental variation.

VORTEX can model catastrophes, the extreme of environmental variation, as events that occur with some specified probability and reduce survival and reproduction for one year. A catastrophe is determined to occur if a randomly generated number between 0 and 1 is less than the probability of occurrence (i.e., a binomial process is simulated). If a catastrophe occurs, the probability of breeding is multiplied by a severity factor specified by the user. Similarly, the probability of surviving each age class is multiplied by a severity factor specified by the user.

VORTEX also allows the user to supplement or harvest the population for any number of years in each simulation. The numbers of immigrants and removals are specified by age and sex. VORTEX outputs the observed rate of population growth (mean of  $N[t]/N[t-1]$ ) separately for the years of supplementation/harvest and for the years without such management, and allows for reporting of extinction probabilities and population sizes at whatever time interval is desired (e.g., summary statistics can be output at 5-year intervals in a 100-year simulation).

VORTEX can track multiple sub-populations, with user-specified migration among the units. (This version of the program has previously been called VORTICES.) The migration rates are entered for each pair of sub-populations as the proportion of animals in a sub-population that migrate to another sub-population (equivalently, the probability that an animal in one migrates to the other) each year. VORTEX outputs summary statistics on each subpopulation, and also on the meta-population. Because of migration (and, possibly, supplementation), there is the potential for population recolonization after local extinction. VORTEX tracks the time to first extinction, the time to recolonization, and the time to re-extinction.

Overall, the computer program simulates many of the complex levels of stochasticity that can affect a population. Because it is a detailed model of population dynamics, it is not practical to examine all possible factors and all interactions that may affect a population. It is therefore incumbent upon the user to specify those parameters that can be estimated reasonably, to leave out of the model those that are believed not to have a substantial impact on the population of interest, and to explore a range of possible values for parameters that are potentially important but very imprecisely known.

VORTEX is, however, a simplified model of the dynamics of real populations. One of its artificialities is the lack of density dependence of death rates except when the population exceeds the carrying capacity. Another is that inbreeding depression is modelled as an effect on juvenile mortality only; inbreeding is optimistically assumed not to effect adult survival or reproduction.

VORTEX accepts input either from the keyboard or from a data file. Whenever VORTEX is run with keyboard entry of data, it creates a file called VORTEX.BAT that contains the input data, ready for resubmission as a batch file. Thus, the simulation can be instantly rerun by using VORTEX.BAT as the input file. By editing VORTEX.BAT, a few changes could easily be made to the input parameters before rerunning VORTEX. Note that the file VORTEX.BAT is over-written each time that VORTEX is run. Therefore, you should rename the batch file if you wish to save it for later use. By using data file input, multiple simulations can be run while the computer is unattended. (Depending on the computer used, the simulations can be relatively quick -- a few minutes for 100 runs -- or very slow.) Output can be directed to the screen or to a file for later printing. I would recommend that VORTEX only be used on a 80386 (or faster) computer with a math co-processor. It should run on slower machines, but it might be hopelessly slow.

The program can make use of any extended memory available on the computer (note: only extended, not expanded, memory above 1MB will be used), and the extra memory will be necessary to run analyses with the Heterosis inbreeding depression option on populations of greater than about 450 animals. To use VORTEX with expanded memory, first run the program TUNE, which will customize the program EX286 (a Dos Extender) for your computer. If TUNE hangs up DOS, simply re-boot and run it again (as often as is necessary). This behavior of TUNE is normal and will not affect your computer. After TUNEing the Dos Extender, run EX286, and then finally run VORTEX. TUNE needs to be run only once on your computer, EX286 needs to be run (if VORTEX is to be used with extended memory) after each re-booting of the computer. Note that EX286 might take extended memory away from other programs (in fact it is better to

disable any resident programs that use extended memory before running EX286); and it will release that memory only after a re-boot. If you have another extended memory manager on your system (e.g., HIMEM.SYS), you will have to disable it before using EX286.

VORTEX uses lots of files and lots of buffers. Therefore, you may need to modify the CONFIG.SYS file to include the lines

```
FILES=25  
BUFFERS=50
```

in order to get the program to run.

VORTEX is not copyrighted nor copy protected. Use it, distribute it, revise it, expand upon it. I would appreciate hearing of uses to which it is put, and of course I don't mind acknowledgement for my efforts. James Grier should also be acknowledged (for developing the program that was the base for VORTEX) any time that VORTEX is cited.

A final caution: VORTEX is continually under revision. I cannot guarantee that it has no bugs that could lead to erroneous results. It certainly does not model all aspects of population stochasticity, and some of its components are simply and crudely represented. It can be a very useful tool for exploring the effects of random variability on population persistence, but it should be used with due caution and an understanding of its limitations.

## VORPLOTS

Plotting program for use with VORTEX

VORPLOTS creates files from VORTEX output, in HPGL (Hewlett-Packard Graphics Language). These can then be plotted on an HP plotter, or on a printer (e.g., an HP LaserJet with the appropriate font cartridge) that can create plots from HPGL files.

To plot results from VORTEX:

1) Be sure that you specify in the data input that you want data files produced for plotting. VORTEX will then place appropriate summary data into files:

- POPSIZE.VOR -- mean population size (of extant populations) across years
- EXTINCT.VOR -- number of simulation populations going extinct in each time interval
- EXTANT.VOR -- proportion of simulated populations still extant at each year
- HET.VOR -- mean proportion of initial (expected) heterozygosity remaining at each year
- INBREED.VOR -- mean inbreeding coefficient at each year

As you do additional sets of runs (set = one set of input parameters to be simulated), VORTEX appends the plotter data to previously existing files (if any). Thus, the above data can be plotted for several sets of runs on one plot.

If you specified that you wanted plotter files for each run, as well as means across runs, VORTEX will also create:

- NDATA.VOR -- population sizes each year of each run

Note: the above file can be quite large, as it contains data from each year of each simulated population. For the above file, VORTEX will over-write results from previous sets of runs when creating the file. Thus you must rename the file if you want to save results for plotting each run at a later time.

- 2) Edit the above files to produce the subsets that you want to plot.

For POPSIZE.VOR, HET.VOR, INBREED.VOR, EXTANT.VOR, and EXTINCT.VOR, the files will contain data from all the runs you have done. Delete those that you do not want to plot. (Important note: Copy the VOR file to a different name or directory before editing, if you plan to produce plots from various sets of simulations.)

The plotting program, VORPLOTS, scales the x and y axes appropriately for the first data set encountered in the file. Therefore, you should put the data from the largest population, with the longest simulation (in years) at the top of the file. Otherwise, some lines on the plot may go beyond the end of the axes.

- 3) Run program VORPLOTS.

VORPLOTS will create .PLT files from each of the .VOR files. Not all .VOR files need to exist (assuming that you do not want to produce all possible plots).

VORPLOTS tries to pick appropriate axes, labels, etc. for the graphs. Obviously, it cannot anticipate every type of data, and every desire you may have regarding the style of graph. If you know (or are willing to learn) the fairly simple commands of HPGL, you can modify the .PLT files to customize graphs to your taste.

- 4) Send the .PLT files to a Hewlett-Packard plotter, or to any plotter or printer than can use the HPGL code (this includes LaserJet printers with the appropriate font cartridge).



***GRUS AMERICANA***

**WHOOPIING CRANE**

**CONSERVATION VIABILITY ASSESSMENT  
WORKSHOP REPORT**

**SECTION 7  
DISEASE**





# WHOOPING CRANE POPULATION VIABILITY ANALYSIS WORKSHOP

## SUMMARY OF DISEASES AND DISEASE RECOMMENDATIONS IN WHOOPING CRANES

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### GENERAL STATEMENT

Based on wild and captive data, disease appears to be a significant, but insufficiently investigated factor adversely affecting the successful recovery of the whooping crane. Additional information is needed to quantify disease factors, evaluate disease risks, and predict future disease trends and events. However, we can identify the following disease issues, and suggest specific research and management needs to better evaluate and/or control their potential effects. Attachments 1-3 provide more detailed information on diseases in captive and wild whooping cranes.

### DISEASES IN WILD WHOOPING CRANES

During 1976-1989, 25 wild whooping cranes found dead in the field or removed from the wild because of sickness or debility were necropsied. Results of these necropsies provide information on the partitioning of causes of death or debility in wild populations. Two diseases of particular concern were identified. Avian tuberculosis (TB) was diagnosed in 7 (28%) of the carcasses examined, and chronic avian cholera (Pasteurella multocida) was diagnosed in one (4%) crane. Proportional morbidity/mortality from TB was similar between the two extant populations: Five (29%) cases of the 17 examined from Grays Lake - Bosque del Apache and 2 (25%) cases of 8 examined from Wood Buffalo - Aransas.

## Whooping Crane PVA

Extrapolation of proportional mortality rates presented above should be made with extreme caution. Although this sample represents the total population of whooping crane carcasses found in the U.S. since 1976 that were suitable for necropsy, a large proportion of "missing" whooping cranes are not recovered, or remains were unsuitable for examination. Undoubtedly, there are biases in carcass recovery related to the disease process involved. It is likely that chronic disease processes, such as avian tuberculosis, are underrepresented in the sample.

The 28% (7 of 25) proportional mortality from tuberculosis is extremely high compared to the low (<1%) rate found in sandhill cranes, and similarly low rates in other surveys of wild birds. A survey of sandhill cranes and snow geese revealed that the prevalence of TB in these populations was very low (0.3% in sandhill cranes), suggesting that whooping cranes are extremely susceptible to this disease, or that whooping cranes are more frequently exposed to infective levels of the bacteria than other birds.

### OTHER DISEASE RISKS IN THE WILD

Many other disease risks exist for whooping cranes in the wild by virtue of their association with other wild birds and geographic distribution and habitat use in relation to diseases present in the wild. Other diseases of major concern are:

Avian Cholera: Avian cholera in waterfowl has become established, or enzootic, at many geographic locations, and recent patterns suggest that its geographic distribution is increasing. Many of the enzootic areas are also principal areas for migration and wintering of the two whooping crane populations. Most notable are the Rainwater Basin of Nebraska and Alamosa and Monte Vista NWRs in Colorado, and more recently, Bosque del Apache NWR, coastal Texas, and the rice belt of Texas. At these areas, sandhill cranes have died from avian cholera, and whooping cranes have been associated with die-off sites. Other recent avian cholera outbreaks in Idaho, the Dakotas, the prairie provinces, and Northwest Territories raise additional concern about current and future risk to this disease.

Mycotoxicosis: Whooping crane susceptibility to mycotoxins has been demonstrated in captivity. Large-scale sandhill crane epizootics in the wild from aflatoxin and tricothecene fusariotoxin have occurred in coastal, rice-belt, and Playa Lakes areas of Texas, including Aransas NWR. The widespread geographic distribution of mycotoxins in agricultural crops potentially used by whooping cranes, particularly in the prairie states and provinces, Texas, and the southeast, including Florida, thus poses a risk of unknown magnitude. There is evidence of morbidity and mortality in Florida sandhill cranes compatible with mycotoxicosis (6 of 45 examined; unpublished Univ. of Florida Veterinary School data).

## Whooping Crane PVA

Eastern Equine Encephalitis Virus (EEE): Whooping crane susceptibility to this mosquito-borne virus has been demonstrated in captivity. There are no known whooping crane deaths in the wild from EEE. However, EEE antibody is frequently found in wild birds, particularly along the east coast. This disease poses a potential threat of particular concern to the future whooping crane releases in Florida, where EEE virus activity has been demonstrated. However, there is minimal data on the prevalence of the virus in sandhill cranes at the Florida re-introduction site.

Disseminated Visceral Coccidiosis (DVC): DVC has caused mortality in captive whooping and sandhill cranes at the Patuxent Wildlife Research Center (PWRC). Mortality was most pronounced in crane chicks up to several weeks of age. This disease has also been reported in wild sandhill cranes, although mortality has not been reported in the wild. DVC poses a risk of unknown magnitude to wild whooping cranes, particularly chicks.

### DISEASE THREATS TO CAPTIVE POPULATIONS

Major disease threats to captive cranes include, but are not restricted to, the following:

Eastern Equine Encephalitis (EEE): An epizootic in 1984 at PWRC killed 7/39 (18%) whooping cranes.

Disseminated Visceral Coccidiosis (DVC): Epizootics in 1979-80 and 1988 killed approximately 35 sandhill cranes and 5 (6%) whooping cranes at PWRC.

Mycotoxigenesis: An epizootic in 1988 resulted in an 80% morbidity and 15% mortality (3 of 41 [7%] whooping cranes) in approximately 300 captive cranes at PWRC.

Inclusion Body Disease of Cranes: An epizootic in 1978 killed 18 of 100+ (# to be verified) captive cranes at the International Crane Foundation (ICF). Neither of the two whooping cranes present at ICF were involved in the outbreak.

## Whooping Crane PVA

## MANAGEMENT RECOMMENDATIONS

1. Disease and environmental contaminant surveys should be done prior to and during all re-introductions. This could include monitoring wild cranes, other indigenous species, and initially released sandhill cranes.
2. Uniform protocols should be developed and implemented for all whooping crane flocks, including protocols for:
  - a. EEE vaccination of captive birds and birds to be released or transferred. Vaccination of all whooping cranes released into EEE endemic areas should be considered.
  - b. pre-transfer and arrival quarantine
  - c. necropsy data base and collection and storage of blood and tissue samples for banking
  - d. pre-release and pre-transfer health screening (and possible treatment)
  - e. biological sample and data collection during routine handling episodes (e.g. weight, blood, serum, feces)
3. A centralized serum, blood, and tissue bank(s) should be established.
4. A contingency plan for oil (and other toxic) spills in the Aransas area should be developed, including a detailed plan for management of affected whooping cranes.
5. We propose a meeting of individuals involved in the whooping crane disease ecology to:
  - a. compile and analyze all available whooping crane mortality data
  - b. draft the management protocols suggested in #2 above
  - c. develop strategies for identified research needs

## RESEARCH NEEDS

Avian Tuberculosis:

1. Development of technology for identification of infection in wild birds and captive birds, viz., ELISA, tuberculin; development of genetic probes for detection and identification of Mycobacterium avium in tissue and environmental samples.
2. Determine the incidence and prevalence of avian tuberculosis in wild whooping crane populations and associated species. Evaluation of the WBNP-Aransas population should be considered.
3. Conduct epizootiological studies to determine the sources of Mycobacterium avium to whooping cranes.

4. Development of intervention strategies to prevent/control avian tuberculosis in whooping cranes. Develop and evaluate a tuberculosis vaccine for use in whooping cranes.

Eastern Equine Encephalitis (EEE):

1. Determine the prevalence of EEE antibody in Florida sandhill cranes associated with the proposed whooping crane release site, and index virus activity through use of suitable sentinel species.
2. Evaluate virulence and epizootiological factors contributing to epizootic mortality in whooping cranes.
3. Evaluate efficacy of EEE vaccine in whooping cranes or suitable surrogates (quail? non-native crane species?), including protection, duration, significance of antibody titers, and evaluation of anamnestic response to challenge.
4. Monitor the serologic status of whooping cranes re-introduced in Florida.

Avian Cholera:

1. Development and evaluation of an avian cholera vaccine and methods of mass or remote vaccination of cranes.
2. Conduct studies to understand the epizootiology of avian cholera, with emphasis at evaluating risk to whooping cranes and development of intervention strategies to prevent/control avian cholera in whooping cranes.

Mycotoxicosis:

1. Develop a program of surveillance for mycotoxin-associated lesions in sick and dead sandhill and whooping cranes, especially in known areas of risk, such as Florida.
2. Develop more sensitive measures of exposure, e.g. bile acid assays, that could be used to monitor released whooping cranes.
3. Investigate environmental and behavioral factors leading to exposure that might contribute to management control strategies.
4. Determine sublethal effects of mycotoxin exposure in whooping cranes or suitable surrogates, including carcinogenesis, immunodepression, and reproductive suppression.

Inclusion Body Disease of Cranes (IBDC):

1. Determine the status of IBDC in wild cranes in North America.
2. Develop technology to identify latent carriers of IBDC and to fingerprint IBDC virus for epizootiological studies.

General:

1. Evaluate causes of mortality in pre fledging whooping cranes.
2. Evaluate causes of mortality in post fledging whooping cranes.
3. Determine relationships between genetics, immune competence, and resistance to disease in whooping cranes.
4. Investigate effects of sublethal exposure to contaminants on immune function in whooping cranes or suitable surrogates.

Research Priorities:

We recommend that research priorities focus on needs identified to understand and deal with avian tuberculosis and EEE, and evaluation of disease risks for new whooping crane populations. Monitoring of health and causes of mortality in all whooping crane populations and significant associated species should also be a high priority.

WHOOPING CRANE POPULATION VIABILITY ANALYSIS WORKSHOP

SUMMARY OF DISEASES IN WILD WHOOPING CRANES

Christopher J. Brand

U. S. Fish and Wildlife Service  
National Wildlife Health Research Center  
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EXAMINATION OF WHOOPING CRANE CARCASSES

During 1976-89, the U.S. Fish and Wildlife Service, National Wildlife Health Research Center (NWRH) received 25 wild whooping cranes found dead in the field or removed from the wild because of sickness or debility. Necropsy of carcasses and diagnostic examinations of live birds provide information on the partitioning of causes of death or debility in wild populations.

Seventeen of the whooping cranes submitted were from nesting, migration, and wintering areas of the Grays Lake - Bosque del Apache population, and eight were from the migration and wintering areas in the U.S. of the Wood Buffalo - Aransas population.

Impact trauma was the most frequent diagnosis of cause of death or debility, representing 13 (52%) of the cases. Based on collection history, sources of impact trauma included powerline strikes (6), fences (3), suspected auto impact (1), and 3 of unidentified source. Two of these 13 birds also were diagnosed as having avian tuberculosis. It is not clear to what extent this disease debilitated the birds, thus contributing to the cause of death; however, one of the cranes was in advanced stages of tuberculosis. Two of the 13 birds diagnosed as impact trauma were recovered alive. One subsequently died in captivity from a mycotic infection presumably acquired during captivity; the other one survives in captivity. Two (8%) birds died from gunshot wounds. Two birds were depredated; one by a golden eagle, and one by an unidentified predator. The latter bird also suffered from avian tuberculosis; again, it is not clear to what extent this disease may have contributed to its susceptibility to predation.

Avian tuberculosis was diagnosed in 7 (28%) of the 25 cranes examined, including the three previously discussed cases involving impact trauma and predation cases. Of the other four tuberculosis cases, the disease was the direct cause of death in three; in the remaining case, tuberculosis likely set the stage for an overwhelming salmonella septicemia (*Salmonella enteritides*). Five of the seven tuberculosis cases were from the Grays Lake-Bosque del Apache population, and were collected in nesting, migration, and wintering areas. The two cases from the Wood Buffalo - Aransas population were found at Aransas NWR. The proportion of tuberculosis cases in carcasses and debilitated cranes examined was similar between the two populations: 29% for Grays Lake - Bosque del Apache, and 25% for Wood Buffalo - Aransas. Year of recovery for tuberculosis cases spanned from 1982-89. The sex ratio of cases was 5 males:2 females. Of particular interest and significance is the age ratio of tuberculosis cases, which includes 2 young-of-year birds (one from each population): 1 immature; 4 adults.

Lead poisoning was diagnosed as cause of death in a whooping crane recovered alive at Bosque del Apache NWR and unsuccessfully treated at the Rio Grande Zoo (necropsy of this bird was done at the Rio Grande Zoo; lead concentrations were determined at the NWR). The source of the particulate lead recovered from the gizzard is not known, but was not from spent shotgun pellets.

A moribund crane was recovered alive at Bosque del Apache NWR, and diagnosed as having an otitis media and air sacculitis. *Pasteurella multocida* was recovered from the ear of this bird. The bird was treated for pasteurellosis in captivity at the Rio Grande Zoo, but died of complications resulting from surgery for a fracture obtained in captivity. *Pasteurella multocida* was not recovered from the bird at necropsy. We consider this case to represent a chronic infection by *P. multocida*, not to be confused with the acute septicemic form of avian cholera responsible for mass epizootics in waterfowl caused by the same microorganism.

A crane was observed to die by a group of hunters near Grays Lake NWR. Necropsy indicated this bird died from heart failure as a result of cardiac decompensation due to a congenital AV malformation in the heart.

Other diseases, parasites, and pathological conditions were noted at necropsy, but were judged as incidental findings or non-contributing to mortality or debilitation. These include *Salmonella cerro*, louse infestations (*Gruimenopon canadense*, *Helonomus* sp., *Esthropterum* sp.), *Tetrameres grusi*, and an enteritis and esophagitis of unknown etiology.

Extrapolation of proportional mortality rates presented above should be made with extreme caution. Although this sample represents the total population of whooping crane carcasses found in the U.S. since 1976 that were suitable for necropsy, a large proportion of "missing" whooping cranes are not recovered, or remains are unsuitable for examination. Undoubtedly, there are biases in carcasses recovered related to the likelihood of finding suitable remains. It is likely that chronic disease processes, such as avian tuberculosis, are underrepresented in our sample. In waterfowl, birds with chronic diseases often seek seclusion and are less likely to be found, and if found, the remains are often too scavenged or decomposed for necropsy. In addition, progressive debilitation from chronic disease likely predisposes individuals to predation, thus making carcasses unavailable or unsuitable, or masking the primary cause.

We feel the 28% proportional mortality from tuberculosis is extremely high, and is probably underrepresented in our sample. In sandhill cranes, we found a proportional mortality from tuberculosis of < 1% of 107 carcasses submitted to the NWR (Windingstad 1988), and similarly low prevalence in other avian carcasses submitted. Surveys of wild birds generally report tuberculosis prevalence of 0.3-1.0%.

In an initial effort to understand more about the high incidence of tuberculosis in whooping cranes, we conducted a survey of potential sources or reservoirs of infection to determine the prevalence of tuberculosis in two species that are closely associated with whooping cranes: sandhill cranes and snow geese. In 1986-87, 220 greater sandhill cranes, 111 lesser sandhill



cranes, and 81 snow geese were collected from hunters in Wyoming and New Mexico. In addition, 17 lesser sandhill cranes from a mycotoxin die-off in New Mexico were tested for tuberculosis. A total of 1,144 tissues, including livers, spleens, and intestines were cultured using a variety of tissue preparation and culture methods to maximize recovery of the organism.

*Mycobacterium avium* was isolated from one (0.3%) of the sandhill cranes; this crane from New Mexico had gross lesions of tuberculosis in the liver and small intestine. The organism was not isolated from any of the snow geese. More than six other mycobacteriae were isolated from both sandhill cranes and snow geese, including *M. chelonae*, *fortuitum*, *gordonae*, *intracellulare*, *scrofulaceum*, *terrae*, and other untypable species.

The low prevalence of tuberculosis in sandhill cranes and snow geese is similar to that reported in other wild bird populations. The high incidence of tuberculosis in whooping cranes suggests that this species may be extremely susceptible to this disease, or that whooping cranes are more frequently exposed to infective levels of the bacteria than other birds. Fecal contamination of the environment is a major source of dissemination and persistence of the disease in poultry, and organisms shed into the environment can remain viable for many years. Avian tuberculosis is usually a chronic disease affecting adult birds. The loss of two young-of-year birds to tuberculosis suggests that they were exposed to many virulent organisms either through the food chain, from the environment, or from infective parents. Tuberculosis in chickens can be transmitted through the egg, suggesting another possible source of early infection in whooping cranes.

#### OTHER DISEASE RISKS IN THE WILD

Many other disease risks exist for whooping cranes in the wild by virtue of their association with other wild birds and geographic distribution and habitat use in relation to diseases present in the wild. Diseases and parasites of sandhill cranes are of particular concern. Windingstad (1988) reported on causes of mortality and epizootics reported to the NWHR in sandhill cranes, including avian cholera, avian botulism (type C), tuberculosis, aspergillosis, aflatoxicosis (B1), and lead poisoning. Windingstad et al. (1989) further describe an epizootic in sandhill cranes attributed to tricothecene, a *Fusarium* mycotoxin. Thomas (unpublished) prepared a further list of diseases and disease agents of sandhill cranes from NWHR records and the literature; the significance of many of these bacterial and parasitic agents in causing disease is unknown.

Among the many potential disease problems faced by whooping cranes in the wild, we identify four diseases of major concern. Avian tuberculosis has already been briefly discussed.

**Avian Cholera:** Avian cholera in waterfowl has become established, or enzootic, at many geographic locations, and recent patterns suggest that its geographic distribution is increasing. Mortality among waterfowl during a single outbreak can range from several hundred to one hundred thousand. Many of the enzootic areas are also principal areas for migration and wintering of

the two whooping crane populations. Most notable are the Rainwater Basin of Nebraska and Alamosa and Monte Vista NWRs in Colorado, and more recently, Bosque del Apache NWR; at these areas, sandhill cranes have died from avian cholera, and whooping cranes have been associated with die-off sites. Coastal Texas, including Aransas NWR, has experienced periodic outbreaks since 1979, and the rice belt of Texas has had a major avian cholera outbreak in each of the past three years. Other recent avian cholera outbreaks in Idaho, the Dakotas, the prairie provinces, and Northwest Territories raise additional concern about current and future risk to this disease.

*Mycotoxicosis:* There are many types of mycotoxins produced by molds or fungi growing on various agricultural crops, including corn, peanuts, wheat, nuts, and others. Species susceptibility to the various mycotoxins can vary considerably. Mycotoxins may cause acute mortality, but have also been shown to be immunosuppressive and carcinogenic and to suppress reproduction in domestic poultry and other animals. Deaths of whooping cranes in captivity have been attributed to a mycotoxicosis. Large-scale sandhill cranes in captivity have been attributed to a mycotoxicosis. Large-scale sandhill crane epizootics in the wild from aflatoxin and tricothecene fusariotoxin demonstrate this species' susceptibility to mycotoxins produced in the environment. Mycotoxins are also being considered as a potential cause of a high incidence of tumors in Mississippi sandhill cranes, and have been speculated as contributing to the occurrence of avian cholera in waterfowl as a result of immunosuppression. Aflatoxin outbreaks in sandhill cranes and snow geese have occurred at Aransas NWR, as well as waterfowl and cranes in the Playa Lakes, west-central, and north Texas. The wide geographic distribution of mycotoxins in agricultural crops potentially used by whooping cranes, particularly in agricultural areas of the prairie states and provinces, Texas, and the southeast, including Florida, thus poses a risk of unknown magnitude.

*Eastern Equine Encephalitis Virus (EEE):* Whooping crane susceptibility to this mosquito-borne virus has been demonstrated in an epizootic in 1984 in captive birds at Patuxent Wildlife Research Center (PWRC) (Dein et al. 1986). During this epizootic, none of 240 sandhill cranes present died, although 13 of 32 tested seroconverted. It is not clear why mortality occurred during 1984 and not other years, since EEE activity in birds at PWRC has been demonstrated in 1960 and 1974, and is presumed to have been present in other years. It is also not clear why the sandhill cranes suffered not mortality, but it is suggested that they are not susceptible to this disease. EEE is commonly found circulating in birds, particularly along the east coast, although foci of activity have been found as far west as the Houston area. This disease poses a potential threat of particular concern to the future whooping crane released in Florida, where EEE activity has been demonstrated.

*Other Disease Concerns:* Numerous other diseases have been voiced as being of potential concern, but little information is available to evaluate their risk to wild whooping cranes. Some of these include: coccidiosis, Leucocytozoon, *Tetrameres*, avian botulism, salmonellosis, Newcastle disease, red tide, and Inclusion Body Disease of Cranes (crane herpes virus). In addition, potential exposure of whooping cranes to contaminants such as agricultural and industrial chemicals, petroleum pollutants, and heavy metals poses a risk of

unknown magnitude from both acute mortality and sublethal effects such as reproductive and behavioral impairment and immunosuppression.

#### **DISEASE IMPLICATIONS OF RELEASE OF CAPTIVE-PROPAGATED CRANES**

The captive propagation and release of whooping cranes poses an additional disease potential to wild whooping cranes. In captivity, whooping cranes are prone to specific disease of captivity (presented separately). Some of these diseases are common to both wild and captive whooping cranes, but may be manifested differently in captivity. Disseminated visceral coccidiosis may be an example of such a disease (Carpenter et al. 1980). Other diseases may not be present in the wild, but may circulate in captive crane populations, potentially exposing whooping cranes having direct or indirect contact with affected species. Inclusion body disease of cranes is such a disease of potential concern (Docherty and Henning 1980, Dein and Docherty 1988). Health Management, including antibiotics and vaccination, may help to control certain diseases in captive whooping cranes; however, controlling disease does not always mean elimination of the disease agent. Release of birds that are latent carriers of disease or those with subclinical infections poses an obvious risk to not only the individual released, but also to the wild population. Screening for disease agents or for antibody to specific diseases may reduce the risk of release of infected cranes, provided the testing methods and diagnostic technology is sufficient to identify carriers or subclinical infections. Effects of antibiotics and some vaccines are short-lived, and released cranes are subject to new infections in the wild or reinfection if the therapy controlled, but did not eliminate, the pathogen.

#### **RESEARCH NEEDS**

We identify the following general research needs. Specific research priorities can be further developed in the disease working group.

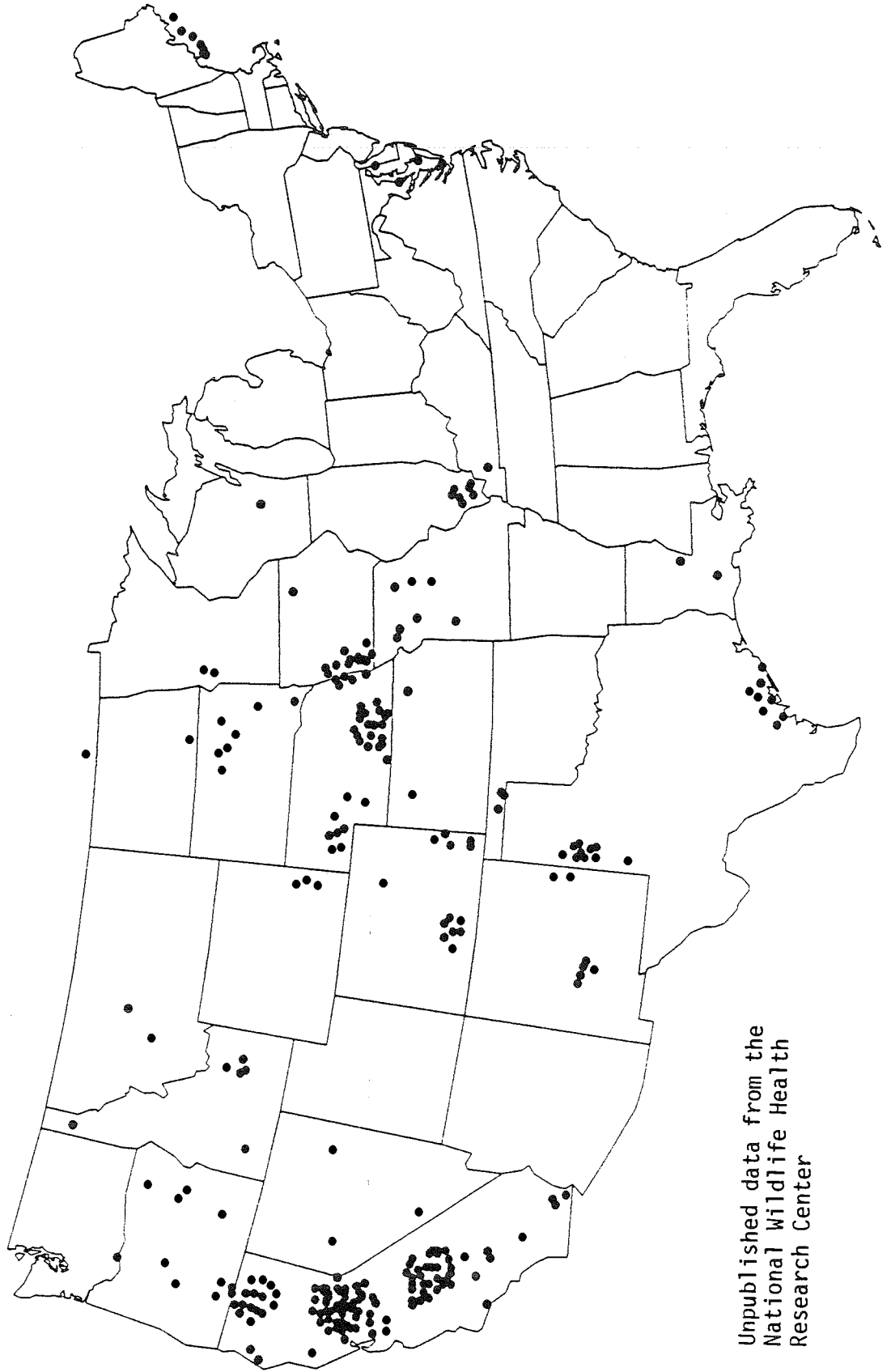
1. Identify and understand the epizootiology of specific diseases in wild whooping crane populations and other wildlife posing risk to whooping cranes, particularly avian tuberculosis. Includes development of technologies where needed to evaluate populations and the environment.
2. Develop and evaluate methods for prevention and control of disease in wild whooping cranes, including vaccination. Specific emphasis on avian tuberculosis, avian cholera, and EEE.
3. Identify and understand the epizootiology of specific diseases in captive whooping cranes and associated species.
4. Develop and evaluate methods for prevention and control of disease in captive whooping cranes.
5. Evaluate disease risk to whooping cranes for all potential areas of release and subsequent use.
6. Monitor disease occurrence and status in newly-established populations and associated species.

7. Develop an understanding of relationships between genetics, immune function, and disease in the whooping crane.

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# Avian Cholera Die-off Sites, 1970-1990



Unpublished data from the  
National Wildlife Health  
Research Center

Attachment 5

SUGGESTIONS FOR WHOOPING CRANE  
DISEASE AND DISEASE MANAGEMENT MEETING

Suggested Participants

National Wildlife Health Research Center:

Nancy Thomas  
Ron Windingstad  
Josh Dein  
Christopher Brand  
Jessie Price  
Linda Benjamin

Florida:

Marilyn Spaulding  
George Kollias

International Crane Foundation:

Julie Langenberg

Patuxent Wildlife Research Center:

Pat Klein  
Glen Olsen

Kansas State University:

Jim Carpenter

Calgary Zoo:

B. Cooper

San Antonio Zoo:

M. Richardson

Others:

Gary Wobeser  
B. Snyder

Logistics

2-3 day meeting at NWHRC  
NWHRC/ICF sponsored

Suggested Agenda

Compilation/analysis of mortality data from captive and wild

Development of management protocols:

-health screening

-quarantine

-necropsy and sample banking

-EEE vaccination

Discussion/prioritization of research needs

Discussion/identification of contingency plan needs

**DISEASE AND CONSERVATION OF  
THREATENED SPECIES**

Report of A Working Group Meeting

28-29 May 1991

National Zoo, Washington, D.C.

Arranged by CBSG/SSC/IUCN in collaboration with AAZPA, AAZV and VSG.

Supported, in part, by a grant from AAZPA

8 October 1991



## Introduction

There has arisen, in the captive breeding and the conservation communities, a concern about the risk of diseases acquired in captivity being introduced into wild populations with the release or reintroduction of captive held, and captive-bred wild animals. There is also concern that diseases endemic in wild populations may adversely affect released animals, jeopardizing the entire effort. Disease risks need to be addressed in the planning of any captive breeding - release/translocation program so that appropriate pre- and post-release health monitoring procedures can be developed, thereby reducing the potential on the released and native populations.

Disease, whether induced by viruses, procaryotes, or eucaryotes has long been recognized as an important selective factor in the evolution of all organisms. Mechanisms for recognition and defense against invasion by foreign organisms and mechanisms for the repair of damage are prominent in vertebrates and present in all eucaryotes. The challenges of disease may sometimes be the most powerful evolutionary selection forces acting on all life forms.

A general lack of data or information on (1) the incidence, distribution and risks of disease in captive populations, (2) the distribution and incidence of disease in wild populations, (3) effective quarantine requirements, and (4) detection and monitoring of disease, has resulted in a lack of a working database for informed risk assessment.

In an attempt to clarify the scope of the problem, a disease working group was formed, comprised of representatives from the following affiliations or institutions: American Association of Zoo Veterinarians, Association of Avian Veterinarians, American College of Zoological Medicine, American Association of Zoological Parks and Aquariums, Captive Breeding Specialist Group SSC/IUCN, Center for Reproduction of Endangered Species, Desert Tortoise Recovery Team, IUCN Veterinary Specialist Group, Pathologists, USFWS National Wildlife Health Research Center, University of Washington Veterinary College, Wildlife Disease Association, Zoological Society of London.

This working group meeting defined the following issues and recommended that:

- A. Events be defined that may lead to potential situations for disease spread and instances described where disease transmission has occurred between populations. There is a need to fund a short-term project to assemble the literature and anecdotal information on such events
- B. Information on disease processes in captive collections needs to be collected in a central location. There is an immediate need to fund the further development of MEDARKS for use by zoos as a standard record system and for a central database
- C. Information on disease processes in wild populations needs to be collected on a current basis, assessed and monitored, and maintained in a central location. An agency and mechanisms to accomplish this task need to be identified.

D. Disease diagnosis has a central role in monitoring and assessment. Needs, limitations, current capabilities and future directions of disease diagnosis were outlined. Specific research and development needs were identified to utilize current technology to enhance our diagnostic capabilities

E. Effective quarantine procedures to prevent the spread of diseases between populations is essential. Protocols will need to be developed on a taxon, project, and geographic basis

F. Research resources available to further study disease processes and transmission in exotic species are limited. More resources are needed for targeted research to enhance our knowledge

G. The working group recommended that an international symposium be held to further discuss and explore the issues at hand and to begin drafting preliminary guidelines for the recognition, assessment and long-term monitoring of infectious disease processes and their impact on the conservation of captive and wild populations.

#### **A. Disease Event Categories, Potential Problems, and Examples**

1. Zoo to zoo animal movements (local and global) and zoo to private sector and private sector to zoo animal movements
  - a. Regulatory inconsistencies of diagnostic screening (e.g. tuberculosis in non-domestic hoofstock)
  - b. Lack of uniformity of preshipment procedures and quarantine (e.g. screening for chlamydia, salmonella, parasites; vaccinations and other preventative procedures, etc.)
  - c. Lack of adequate transfer of medical records with animal movements (e.g., health certificate and medical history do not always accompany animal)
  - d. Disease exposure during transportation (e.g., canids contracting viral diseases during transport; potential exposure during off-loading or zoonotic exposure)
  - e. Lack of recognition of specific transmissible diseases in a collection prior to designated SSP moves (e.g., Herpes in many species, FIP, TB, etc.)
  - f. Permanent identification of each animal (tattoos, bands or transponders)
  - g. Lack of awareness and routine screening for potential hereditary defects and diseases
2. Translocations
  - a. Contamination of naive population by infected animals and vice versus. (e.g., Leptospirosis in black rhino)
  - b. Lack of recognition of specific transmissible diseases in the old and new environment prior to designated moves (e.g., parasites, canine distemper in black footed ferrets)

- c. Appropriate long term monitoring of the health status of both populations
  - d. See 1a, 1b, 1d, 1f, 1g
3. Supplementation of Wild Populations by translocation of individual animals.
    - a. 1f, 1g, 2a, 2b, 2c, 2d.
  4. Supplementation of wild populations by utilizing artificial breeding techniques to enhance genetic diversity
    - a. Determine health status of gamete donors and recipient
    - b. Determine possible diseases transferred by genetic material (e.g., FMD, Brucella, viruses.)
    - c. 1f, 1g, 2d
  5. Supplementation of wild populations with captive animals
    - a. Prior to release, determine health status of the captive animals and the receiving population, and other species (including domestic animals and humans) in the ecosystem (e.g., TB, Pasteurella, lung worms in Arabian Oryx)
    - b. 1a, 1d, 1f, 1g, 2a, 2d.
  6. Supplementation of captive population with wild populations by utilizing artificial breeding techniques and/or through individual animals
    - a. 1f, 1g, 4a, 4b, 5a, 5b, 2d.
  7. Introducing captive animals into suitable ecosystems
    - a. Predict the disease impact of the animal on the existing resident species (including domestic and humans) and the reverse
    - b. 1a, 1b, 1d, 1f, 1g, 2d.
  8. Introduction of captive animals to repopulate an historic ecosystem
    - a. Prior to release, determine health status of the captive animals and the receiving population, and other species (including domestic animals and humans) in the ecosystem (e.g., meningeal worm in cervids)
    - b. 1a, 1b, 1d, 1e, 1f, 1g, 2a, 2c, 2d,
  9. Rehabilitation of wild and confiscated individuals with return to the wild habitat, be it at or distant from the original collection point. (Pancake Tortoises, Monk Seals)
    - a. 1a, 1b, 1d, 1f, 2a, 5a (e.g. confiscated Pancake Tortoises, Monk Seals)

10. Private sector and agency animal release programs and/or escapes, (including native and non-native species) in their home range or an appropriate or inappropriate ecosystem, (e.g., Desert Tortoises)
  - a. acknowledgment of our inability to always control and monitor the impact of these events.
11. Research Resources
  - a. Identify key personnel who have expertise with particular species and/or disease problems.
  - b. Obtain overviews of research resources from other organizations(e.g. AAZV, ACZM, WDA, AAV, etc.)

#### **B. Lack of Biomedical Data Collection Across Captive Collections**

**Problem:** Critical medical information affecting decisions that concern the movement of animals is currently limited.

1. There are no universally used standardized programs of biomedical data collection (clinical and pathology records) in captive collections. Existing Programs: a. medARKS; b. Individual zoo computerized record keeping system; c. Individual zoo handwritten record keeping systems; d. No medical records or scanty medical records
2. Within existing programs there is limited centralized processing of collected data between institutions. Existing Programs: a. ISIS (clinical pathology, pathology codes); b. Studbooks, SSPs and TAGs; c. AAZV (infectious disease committee.); d. Surveys performed by an individual with a particular disease or species interest
3. Priorities: a. Identification and incidence of infectious diseases that are affecting the living collection; b. Identification and incidence of infectious diseases that are causing mortality in captive collections; c. Standardization of data collection between institutions; d. Centralization of collected data; e. Methods of data availability
4. Recommendations
  - a. SSPs and TAGs should have veterinary advisors (medical, pathology)
  - b. Gathering of biomedical information should begin with species that have studbooks, SSPs or TAGs
  - c. Develop a task force comprised of veterinary advisors, ISIS and medARKS representatives, other knowledgeable groups and individuals to develop a standardized format for data collection, centralization and distribution. This task force should be sanctioned and given high priority and funding by AAZPA in concert with other groups.

### C. Collection of Information on the Health of Captive Species

For most endangered species, a centralized medical comparative data base does not exist. Developing an epidemiological data base is the foundation for comparison of disease risks in captive and wild populations, and translocations between and within each. Within the captive community, generation of such a data base should be given top priority and instituted via the following steps:

1. A veterinary advisor should be appointed to each regional captive management plan (e.g., SSPs, EEPs, etc.). Such advisors should review all mortalities annually, evaluate the incidence of disease in the living population, and make recommendations regarding anesthesia, the prevention and monitoring of disease. Data collection should be standardized. An advisor should identify areas that require further research and assist in the identification of interested researchers and centralized facilities. Cooperation of regional management program veterinary advisors should take place through the auspices of the CBSG, including the distribution of annual regional reports for each species.
  - a. CBSG should petition SSP through this report and other means to effect the addition of veterinary advisors to all SSP Committees.
  - b. AAZV should also effect a similar petition and assist in the identification of interested veterinarians.
2. For each species, the Veterinary Advisor should supervise the establishment of centralized biomaterial (sera/tissue) banks to aid present and future research. These banks should be established in cooperation with ongoing projects.
  - a. Letters of support from CBSG and AAZV as above.
  - b. Identification of central funding resources.
  - c. Commitment of directors of SSP institutions to make not only funding commitments (e.g., shipment costs of materials to the central banks), but also the manpower commitments for increased participation in such programs on the individual and supervisory levels (e.g., time for veterinarians to coordinate these activities and attend related meetings).
3. Centralized data banks, such as MedARKS should be encouraged, and further effort should be made to design appropriate software for these programs (such as was done with the orangutan medical management survey - similar studies with black lemurs and elephants are in progress).
  - a. Encourage more rapid development of MedARKS, in particular, rapid development of the text medical record keeping system that would allow for the evaluation of medical problems in the living population.
  - b. request that all medical data be submitted to the regional program Veterinary Advisor in MedARKS format, if not in the program itself.

4. Regional program veterinary coordinators should be included in any review evaluating disease risks in the reintroduction of captive species.
5. Additional contact and cooperation with the private community holding endangered species should be encouraged by:
  - a. Identifying private holders that are listed in studbooks.
  - b. Veterinary contact with holders of key species.
  - c. Contact with private interest groups.
  - d. Dissemination of information through lay publications.

#### **D. Wild Population Concerns**

All "translocation" activities have the potential to adversely impact wild populations. Generally, there is a paucity of information pertaining to the existence of diseases in a habitat, and if the data does exist it is difficult to assemble. Therefore, before any translocations occur, the following should be considered:

1. There are no universally used standardized programs of biomedical data collection (clinical and pathology records) for wild populations. Existing Programs: a. USFWS National Health Wildlife Laboratory; b. Individual national record keeping system; c. Individual regional, state and local record keeping systems; d. No international databases or systems except for diseases of domestic animals (FAO).
2. Translocation guidelines should apply to all species as resources are available.
3. Governments should identify or assign an agency or individual to serve as a central information source and central repository for disease related information. This office should be responsible for promoting public awareness and distribution of the guidelines.
4. During the planning of a translocation project, all interested parties should be assembled to discuss disease concerns, in relation to the entire project.
5. Disease related questions (handout) should be answered with regard to the prevalence of agents of concern in a habitat and potential impact on endemic species. a. This should be done after review of pertinent literature and diagnostic databases; b. Consideration should be given to undertaking significant specific surveys or monitoring efforts to address unanswered questions.
6. The benefits to the species should be considered with respect to the potential uncontrollable disease risks: a. An individual or agency should be designated to make the final decision.

7. If a decision is made for a translocation, consideration should be given to establish a monitoring program for both the introduced animals, the endemic population and other ecosystem components.

**E. Quarantine Considerations for Reintroduction Programs as a Component of an Overall Health Screening Procedure**

There is a recognized need and obligation to develop a Model Procedures Manual/Guidebook to address infectious disease-related issues in the release of captive wildlife. This document should include advice on a number of basic procedures including general standards for quarantine and diagnostic test which will probably be applicable at the taxon level, such a document has been started by the AAZPA (attached). It is understood that quarantine is one of several components of an overall health screening procedure to prevent the transfer of infectious diseases to various animals in the ecosystem where the reintroduced animals are released. It should be also recognized that the type and length of a quarantine is dependant upon: 1- species 2- disease concerns 3- facilities available. There are documented situations where a quarantine had a negative effect on the animals (e.g. introduction of Gould's Wild Turkey from Mexico to Arizona where the USDA required quarantine resulted in self-destruction of the bird).

For an effective quarantine the medical advisors must be aware of the infectious diseases of concern for this species and /or diseases that the animals may have been exposed to while in captivity. This information must be derived from a systematic gathering and review of medical and pathology data generated on the species while in captivity. The regulatory and unofficial concerns of the country receiving the animals must also be known and addressed.

The quarantine period will serve as a time to collect and process the necessary samples from these animal to assure their health status and hopefully detect animals who may be incubating or carriers of infectious diseases of concern. The reliability of the testing procedures is a concern of medical advisors and has been addressed elsewhere.

The quarantine process will occur on several levels and may have varied functions at each level. The first level of quarantine occurs at the captive animal's home institution. It may also be necessary to collect the animal at a central location prior to shipment to their final destination and it will be necessary to continue and possibly augment the quarantine procedure. The final area of quarantine will occur in the area of reintroduction where appropriate testing will also occur.

The standards of the quarantine should be guided by the following concepts:

1. Decisions should be made on pre-entry vs post-entry quarantines. Usually both are needed.
2. Quarantines by definition should be all-in/all-out.
3. Quarantines by definition should isolate the animals from known routes of exposure for the primary diseases and parasites of concern, and/or treatments of animals in quarantine should be conducted to remove diseases or parasites.
4. Quarantines must be both general and specific . During the quarantine period, any abnormal health condition must be investigated and documented. In addition, specific testing required to document freedom of disease or parasites in question should be conducted (serology, culture, blood smears, fecals, ectoparasite infections, etc.)
5. Whenever possible, length of pre-entry and post-entry quarantine should be longer than incubation periods of any of the acute infectious diseases or parasites in question.
6. Freedom from a specific disease or parasites in the source population, when adequately documented, should be considered as an acceptable alternative to testing of animals in quarantine when such testing may be overly harmful to the animal or if no testing methods are available.
7. Quarantine standards for translocation of wild species should be formulated with consideration of current standards for the same potential disease problems in domestic animals so that wildlife restoration programs are not burdened with unreasonable restriction.
8. Prior to initiating a quarantine, a decision must be reached regarding the disposition of animals that test positive. In particular, whether entire groups of animals will be disqualified if one animal is positive.

**F. Diagnostic Capabilities**

1. Summary of the Problem  
Limited resources available to evaluate samples and interpretation of the data.
  - a. Limited facilities;



- b. Lack of a priority list of high risk, low risk and undefined diseases. Define list of realistic goals in terms of disease diagnosis and captive management.
- c. Limited diagnostic reagents available for making disease diagnosis.
- d. Lack of quality assurance programs at the laboratory level.

## 2. Solutions

- a. For limited facilities
  - 1) List of currently available labs to do wildlife diagnosis
  - 2) Support the development of wildlife disease centers with specialty areas.
    - a) Reptiles - Florida
    - b) Avian - Wisconsin
    - c) Cooperation between universities and zoological parks and aquariums - San Diego and Washington State University
  - 3) Support quality control programs
- b. Prepare a priority list through the various SSP groups
- c. Improve the quality of diagnostic reagents via biotechnology
- d. Standardized list of sample selection via handouts and workshops.
- e. Increase the validity of laboratory interpretation by increasing sensitivity and specificity. This increased validity will increase compliance of veterinarians and biologists working with SSP groups.

## 3. Implementation and Interactions with Other Working Groups

- a. Prepare directory of currently available diagnostic laboratories.
- b. Recommend use of a letter to be sent to Colleges of Veterinary Medicine inquiring about interest in developing centers for wildlife disease management. Letter also to biotechnology centers stating our needs. Request listing of contact individuals within each institution interested in wildlife disease. Also need to send letter to AVMA.
- c. Request the top 5 diseases from each SSP group. Request a report on causes of mortality and morbidity from each SSP group.
- d. Bring together individuals involved in wildlife disease/conservation with researchers in biotechnology. This would be best achieved through a meeting.
- e. Need to identify a person or persons within each SSP group to develop a handout for collection and handling of biologic specimens for evaluation. This should be done in consultation with a contact person in the lab receiving the samples.

Essentially there would be a brochure for each of the SSP programs developed.

- f. Put together a list of papers in the literature that are relevant to the diseases of concern to the SSP groups. Need to keep this file up to date. Needs to be a centralized repository - possibly Minnesota. Needs to be an active computerized file. This file would center on diagnostic tests and infectious diseases.
- g. Quality assurance - routine test checks between various laboratories. Need to establish serum and tissue banks for various specimens.
- h. Need to send out letter to universities inquiring about existence of various tissue/serum banks.

#### **G. International Symposium**

The working group recommended that an International Symposium be held to assemble current and state-of-the-art information on the past, present and future impact of infectious diseases as they relate to the captive management, introduction, reintroduction and supplementation of populations of captive and free-roaming species. There has not been a symposium on these topics for 10 years. One goal of the symposium is to generate guidelines to be used by captive and free ranging wildlife managers in an attempt to minimize the spread of human and captivity induced disease events.

**Title: Implications of Infectious Diseases for Captive Propagation and Reintroduction Programs of Threatened Species.**

#### Outline of Sessions

- 0. Introduction to Problem
- 1. Review of translocations: rationale and types; reintroductions; translocations
- 2. Historical survey of disease problems associated with releases; Sections on mammals, birds, reptiles, amphibians, freshwater fish, marine vertebrates (fish, reptiles, mammals).
- 3. Investigation, monitoring and surveillance of disease in captive animals
- 4. Investigation, monitoring and surveillance of disease in free-ranging animals
- 5. Interspecies transmission of infectious agents
- 6. Emerging infectious diseases
- 7. Future thrusts in diagnostic technology
- 8. Information and data collection systems
- 9. Impact of infectious disease on population dynamics

10. Predisposing factors to infectious diseases: genetic, immunologic, nutritional
11. Economic considerations of monitoring and screening programs
12. Vaccination and prevention
13. Government and international interactions
14. Planning and risk assessment for release programs

We have suggestions for session leaders (chair persons). Each session would include a few papers and a discussion period. There would be poster displays and workshops (e.g., informatics, diagnostics).

The suggested symposium sessions originated from the issues identified during the working group. Sessions will expand on these issues by drawing on international experts in a particular field. Proceedings from the symposium will be published in such a manner so that they are universally available to those most in need of the information. This will be accomplished by publishing the proceedings in an internationally recognized journal.

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***GRUS AMERICANA***

**WHOOPING CRANE**

**CONSERVATION VIABILITY ASSESSMENT  
WORKSHOP REPORT**

**SECTION 8  
REINTRODUCTION**





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RH: Whooping Crane Recovery · Ellis et al.

POPULATION RECOVERY OF THE WHOOPING CRANE WITH EMPHASIS ON  
REINTRODUCTION EFFORTS: PAST AND FUTURE

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Abstract: All 15 species of cranes have been successfully bred in captivity. The U.S. Fish and Wildlife Service began building a captive whooping crane (Grus americana) colony at the Patuxent Wildlife Research Center (Patuxent) in Maryland in 1966. This colony first produced eggs in 1975. The first chick fledged in 1976. From 1976 to 1984, 73 eggs (61 known to be fertile) from this colony were sent to Grays Lake, Idaho, the site of the first whooping crane reintroduction attempt. Canada also provided 216 eggs (1976-1988) from the wild population. All eggs were placed in sandhill crane nests. Although 84 chicks fledged from the 289 eggs, the egg transfer program has been discontinued because of inordinately high mortality and lack of breeding.

In recent decades, new methods have emerged for introducing captive-produced offspring to the wild. Surrogate studies with sandhill cranes (G. canadensis) will eventually provide techniques useful for the recovery of the whooping crane. The largest sandhill crane introduction effort involves the rearing

of Mississippi sandhill cranes (G.c. pulla), either by captive sandhill crane foster parents, or by costumed humans in close association with live cranes and with lifelike taxidermy crane heads (feeding models) and whole birds (brooder models). These two techniques have resulted in high post-release survival rates and will likely be used in future whooping crane reintroduction programs.

Current recovery objectives for the whooping crane include the establishment of a third captive colony in Canada and the building of two other wild populations. The Kissimmee Prairie in central Florida has been selected for the next release experiment. Evaluation of this site began in 1984.

Environmental assessments and other risk surveys commenced in 1988. A critical risk assessment will commence in 1991 or 1992 with the transfer and monitoring of a group of juvenile whooping cranes reared at Patuxent and ICF in 1991. These "tests of the environment" will, if results are favorable, be followed by a full-scale reintroduction effort (at least 20 birds/year) beginning in 1994 or 1995.

Key Words: whooping crane, Grus americana, recovery, captive breeding.

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Of the 15 species of cranes worldwide, 6 species and 2 subspecies are listed as endangered (U.S. Fish and Wildlife Service 1988). All 15 species have been bred in captivity, and during the last 20 years, several reintroduction projects have

been initiated. Herein, we relate these efforts to past and potential recovery actions for the whooping crane.

### **Whooping Crane population decline**

Historically, the breeding range of the whooping crane extended from Iowa northwest through Minnesota and the Dakotas into Alberta, Saskatchewan, and southern Manitoba (Allen 1952). In 1939, a small, widely disjunct population was also found breeding in the marshes north of White Lake, Louisiana (Lynch 1984). Breeding may have also occurred at other locations, but information is limited. Wintering populations ranged from the Rio Grande delta eastward along the coast of Texas and Louisiana to Florida and as far north as New Jersey on the Atlantic coast (Allen 1952). In the 1800's, a combination of habitat destruction, human disturbance, hunting, and egg and specimen collection for museums and private collectors contributed to a rapid population decline. By 1870, fewer than 1400 individuals remained (Allen 1952). In 1945, the population consisted of two disjunct flocks totaling about 21 birds (Figure 1) (U.S. Fish and Wildlife Service 1986); only three birds remained of the small (soon to be extinct) sedentary flock in Louisiana. The remaining 18 birds comprised a flock that wintered at Aransas National Wildlife Refuge (Aransas) along the Texas gulf coast and nested in Wood Buffalo National Park (Wood Buffalo), Northwest Territories, Canada (Allen 1956) (Figure 1). Following this nadir, the whooping crane population began its slow increase.

Ellis et al.

4

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#### PATUXENT'S CAPTIVE COLONY

The ponderous expansion of the whooping crane population in the 1940's and 1950's prompted a search for management schemes to bolster the wild population. Captive breeding was attempted for many years with isolated pairs at Audubon Park Zoo in New Orleans (1948 to 1966), in confinement at Aransas (1948 to 1951), and at the San Antonio Zoo (1967 to present) (McNulty 1966 and unpubl. data). The idea that a sizeable captive flock be established by removing young whooping cranes from the Aransas-Wood Buffalo population was first proposed by Lynch (1956). Theoretically, whooping cranes produced by the captive flock could be released to augment the wild population and serve as a hedge against catastrophic loss of the wild population. Hyde (1957) was apparently the first to note that sandhill cranes and whooping cranes usually laid two eggs but rarely raised two young. He suggested that a captive flock could be established without detriment to the wild population by removing one egg from each clutch. Erickson (1968) recommended first developing a surrogate flock of nonendangered sandhill cranes. In 1961, the U.S. Fish and Wildlife Service (USFWS) established a captive flock of sandhill cranes at Monte Vista National Wildlife Refuge in

Colorado to develop crane husbandry and propagation techniques. In 1966, the surrogate flock and Canus, a flightless male whooping crane recovered in Canada in 1964, were moved to Patuxent Wildlife Research Center (Patuxent) in Laurel, Maryland. In 1967, the second eggs from six nests in Wood Buffalo were taken to Patuxent. Egg taking has continued sporadically ever since (Table 1), with eggs going either to Patuxent, or to Grays Lake National Wildlife Refuge (Grays Lake), Idaho, or, more recently, to the International Crane Foundation (ICF), Baraboo, Wisconsin. Management agencies and researchers generally believe that this egg harvest has not adversely affected, and may have actually increased, the number of chicks fledged each fall in Canada (F. G. Cooch, \_\_\_\_\_ N.M., pers. commun.).

During the colony's first decade at Patuxent, disease and nutritional problems that initially impaired survival of whooping cranes in captivity were resolved (Carpenter 1977, Carpenter and Derrickson 1981, Erickson 1975, Serafin 1981). It then became possible to address more subtle problems such as failure of neonatal young to feed, failure of pairs to bond and breed, sexual imprinting of chicks on human caretakers, etc. (Kepler 1977). In 1975, the first eggs were produced by captive females at Patuxent. Next, problems with artificial insemination, incubation, and chick rearing were identified and solved, and annual productivity increased accordingly (Kepler 1977, Gee 1978, Archibald 1974). Between 1975 and 1990, the Patuxent flock produced 234 eggs, of which 73 were transferred in an attempt to

establish a second wild flock at Grays Lake. The captive population slowly expanded (Figure 2), then in 1984, a major epizootic, Eastern Equine Encephalitis (EEE), claimed two males and five females. This outbreak and two other epizootics led to a decision to establish a second captive breeding flock at a site remote from Patuxent. In November 1989, 22 birds, representing all families in the captive flock, were transferred to the ICF. A third captive flock is also being planned for the Calgary Zoo in western Canada (Cooch et al. 1988).

The following factors compound the difficulty of propagating whooping cranes in numbers sufficient to build three captive colonies while supporting the Florida reintroduction project:

- (1) delayed sexual maturity (i.e., only two-thirds of the captive females have laid eggs by 8 years of age),
- (2) moderate fertility levels (only three-fourths of captive produced eggs are fertile),
- (3) moderate hatchability rates (only three-fourths of fertile eggs hatch),
- (4) low fledging success (only three-fifths of chicks fledge), and
- (5) demographic anomalies characteristic of small populations (e.g., unequal sex ratios and differential mortality).

Based on these demographic factors, we projected future population size (Figure 3). Recognize, however, that infusions of eggs from Canada and/or drains (e.g., major mortality or providing many birds for release) can drastically affect these predictions.

## REINTRODUCTION ATTEMPTS

### The First Attempt, Translocation of a Single Bird

By 1947, only one wild bird remained in the marshes near White Lake, Louisiana (Figure 1) (McNulty 1966, Doughty 1989). On 11 March 1950, this crane was captured by helicopter and translocated by truck to join the Aransas-Wood Buffalo flock. On arrival, the dangerously weakened crane was penned and force fed for 2 days, then released into a freshwater marsh; later, it was attacked by two wild cranes. The transplanted crane was recaptured, fed, and released at a freshwater lake some distance from other whooping cranes. The crane survived through the spring and summer but was found dead in September. This first experiment ended in failure, but it demonstrated some of the problems inherent in translocating adult cranes.

### The Grays Lake Experiment

The only reintroduction effort, so far attempted, consisted of placing nearly 300 whooping crane eggs in greater sandhill crane (*G. c. tabida*) nests at Grays Lake. This experiment was designed to create a disjunct population of whooping cranes that, like their sandhill crane foster parents, would nest in Idaho and winter along the Rio Grande in west-central New Mexico (Drewien and Bizeau 1978). Beginning in 1975, eggs from Patuxent and Wood Buffalo were placed singly in nests of greater sandhill cranes.

According to plan, the sandhill crane foster parents incubated the eggs and reared the young whooping cranes that hatched. The chicks also accepted their foster parents and

followed them on migration. However, only 209 (72%) of the 289 whooping crane eggs transferred to Grays Lake hatched, and only 84 (40% of the 209 that hatched or 29% of the original 289 eggs) fledged. High egg and chick mortality rates were associated with inclement weather and coyote (Canis latrans) predation (Drewien and Bizeau 1978, Drewien et al. 1985). Most young that managed to fledge died from powerline strikes (Brown et al. 1987) or avian tuberculosis (Doughty 1989). Recruitment has not kept pace with mortality, and the Grays Lake whooping crane flock has declined from a high of 33 birds in 1984-85 to 13 birds in 1991 (Lewis 1990 and unpubl. data).

Low survival rates in young birds at Grays Lake was compounded by the failure of surviving whooping cranes to form pair bonds and breed. Unequal sex ratios among the breeding-age birds caused by differences in male and female mortality contributed to this failure. More importantly, the few females that reached breeding age failed to pair with males on the wintering ground and scattered on northward migration, thereby further diminishing their chances of finding mates. Yearly attempts were made to capture these wandering females and transport them back to pair with wild males at Grays Lake. Because no pairing occurred naturally, two Patuxent-reared females were introduced to males at Grays Lake in 1981 and 1989. Both females seemed to form temporary pair bonds with wild males, but neither experiment resulted in eggs, or in pairs that migrated south together (Drewien et al. 1989).



Due to unfavorable demographic trends, the Grays Lake experiment is being phased out. The last egg transfer was in 1988, and no further transfers of captive-reared females are anticipated. Because of fear of transmitting avian tuberculosis to other flocks, captive or wild, there is little likelihood that any of the surviving birds in the Grays Lake flock will be captured or translocated. The 13 birds are still under study in hopes of learning as much as possible for future experiments, but the population is expected to languish, then disappear.

#### CHOOSING FUTURE REINTRODUCTION SITES

All factors (i.e., mortality rates during migration, disease hazards, and demographics) recommend that preferred reintroduction sites should: (1) provide extensive suitable habitat, (2) be at a considerable distance from other wild populations, (3) be at a latitude and location that would not require introduced birds to migrate, and (4) be within the historic range of the species. For biological reasons, the marshes north of White Lake in southern Louisiana are a favored choice for reintroduction of a sedentary population. It seems logical to return the birds to the wild where they most recently lived. The creation of a nonmigratory population is also preferred because of experience gained from the Grays Lake experiment and the increased risks during migration, wherever it occurs.

During the last decade, White Lake appeared to be unavailable as a reintroduction site because the state wildlife management

agency disfavored the idea, fearing that waterfowl hunting would be impaired (Lewis pers. commun.) As a consequence, three other sites were considered: the Kissimmee Prairie in central Florida, the Okefenokee Swamp in southeastern Georgia, and the Seney National Wildlife Refuge on the Upper Peninsula of Michigan. Habitat is believed to be favorable at all three sites. All areas have extensive wetland, are somewhat removed from urban areas, and support sizeable sandhill crane populations. Whooping crane breeding, however, has never been documented for any of the three areas. Allen (1952) and Nesbitt (1981, 1989 Unpubl.) reviewed and evaluated whooping crane records for Florida and found evidence that the species occurred and perhaps was even resident in that state in the last century.

In 1988, the USFWS decided to proceed with a whooping crane introduction experiment in Florida. The Kissimmee Prairie was chosen largely because of sandhill crane demography (e.g., low mortality rates in young birds). Unfortunately, the region poses considerable risk of EEE and Venezuelan Equine Encephalitis. Although EEE outbreaks have also been reported for southwestern Michigan, Carpenter et al. (1989) concluded that the risk of contact with EEE was least likely for birds breeding in northern Michigan. Birds introduced there would probably visit southern regions, where EEE was common, only in winter, when EEE transmission is less likely because of reduced activity of the mosquito vector.

**REINTRODUCTION TECHNIQUES**

Reintroduction techniques for fledged cranes were described by Derrickson and Carpenter (1983), Konrad (1976), Nagendran and Urbanek (In prep.), and Ellis et al. (In prep.). The techniques most likely to be employed in future whooping crane introduction attempts are listed below.

**Gentle Releases of Parent-reared Cranes**

High survival rates have been achieved in releasing parent-reared Mississippi sandhill cranes. Two-thirds of the birds released from 1981 through 1989 survived for at least 1 year (McMillen et al. 1987, Zwank and Wilson 1987, and Ellis et al., In prep.). During the last 5 years, at least 13 captive-reared Mississippi sandhill cranes have paired or bred in the wild.

Although various attempts have been made to release hand-reared birds, until the mid-1980's hand-reared birds generally proved unsuitable. For example, none of 13 hand-reared birds released without acclimation near Lake Okeechobee, Florida integrated into the wild flock, and within a few months all had died (Nesbitt 1978). In recent experiments, sandhill crane chicks have been reared in relative isolation from humans. In addition, some chicks are penned in visual and auditory (but not physical) contact with adult cranes. Fledged birds from releases in Wisconsin, Michigan, and Mississippi have survived well and at least two birds have paired with wild cranes (Archibald and Archibald, In Press, Urbanek 1989a Unpubl., Urbanek and Bookhout 1987 Unpubl., G.A. Archibald Int. Crane Found., pers. commun.).

Unfortunately, some cranes released at northern latitudes have required intensive assistance after they failed to migrate unaided (R.H. Horwich Gays Mills WI, pers. commun.; Urbanek 1989b Unpubl.). In general, captive-reared cranes, hand-reared or parent-reared, have had lower survival rates and dispersed more widely when released in migratory situations, whereas releases in nonmigratory situations have resulted in a large proportion of the release birds surviving more than 1 year and remaining near the release site. } see  
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#### **FUTURE RECOVERY GOALS AND SCHEDULE**

The USFWS and Canadian Wildlife Service (CWS) have separately published recovery plans for the whooping crane (U.S. Fish and Wildlife Service 1986, Cooch et al. 1988). Common goals in the recovery plans are increases in the size of current wild and captive flocks and establishment of two additional, disjunct wild flocks. The two agencies also operate under a 1990 Memorandum of Understanding that dictates cooperative decision-making in the day-to-day management of captive and wild whooping crane populations.

#### **Increasing the size of the Aransas-Wood Buffalo flock**

Both USFWS and CWS recovery plans agree on the need to increase the wild whooping crane flock. Because increases in the wild flock depend primarily on natural recruitment, recovery plans stress the need to reduce mortality. Specific concerns include identifying and evaluating disturbances, and developing contingency plans for rapid containment of hazards such as oil

spills, disease, and human or "pest" disturbances. Plans also call for identifying and preserving essential habitat for use in winter, during migration, and during the breeding season.

Although extraordinary efforts have been made to build captive whooping crane colonies and to create a wild flock at Grays Lake, we emphasize that the expansion of the Arkansas-Wood Buffalo flock (Figure 1) has been due entirely to endogenous production. Not one egg or crane has come from captivity. This statement is not meant to demean human efforts in the crane's behalf: for surely, without intensive efforts to create refuges and to educate hunters along the flyway, the population would not have grown to its present number (about 146 birds) (Figure 1). Furthermore, beginning in 1984, the second fertile eggs in some nests in Canada have been moved to nests where pairs were incubating infertile eggs. This type of manipulation has resulted in more pairs fledging chicks than would have occurred naturally (F.G. Cooch \_\_\_\_\_ N.M., pers. commun.).

#### **Captive Populations**

Recovery goals to be achieved by 1995 include increasing the size of captive breeding flocks to 15 breeding pairs at Patuxent and 10 breeding pairs at the ICF and establishing an additional captive flock with 10 pairs at the Calgary Zoo in Alberta, Canada. Pen construction will begin at Calgary in summer 1991, with surrogate sandhill cranes arriving the same year. Beginning in 1992, young whooping cranes reared in captivity at Patuxent and ICF are to be transferred to Calgary.

Recovery plans also emphasize maximizing genetic diversity in the captive flocks by selectively harvesting eggs from the Wood Buffalo flock and utilizing other genetic management tools. The plans also call for research to enhance captive reproduction by further refining incubation, hatching, and rearing procedures, and by behavioral management of pairs.

#### **Establishing Additional Wild Flocks**

Long-term survival of whooping cranes can be ensured by establishing disjunct captive and wild populations. The USFWS recovery plan calls for at least two additional wild flocks. By 2020, each flock is to have a minimum of 25 nesting pairs (U.S. Fish and Wildlife Service 1986).

From projections of conservative values for age-specific mortality rates at Grays Lake, Garton et al. (1989) concluded that at best only six pairs of whooping cranes would be breeding after infusions of 30 eggs per year for 50 years. The future of the project had been under question since the mid 1980's, but egg transfers continued until 1988. Then, in March 1990, a decision was made to deemphasize the Grays Lake experiment. Thereafter, it became urgent to choose alternate destinations for the eggs from Wood Buffalo. In 1989 and 1990, most of the second eggs in each clutch came to the captive colonies although a few clutches were left at 2 eggs. Another likely use of these eggs was to begin another wild flock. In preparation for this eventuality, sandhill crane demography had been under study at three likely sites from 1984-87 (McMillen et al. In press): (1) the Upper

Peninsula of Michigan (McMillen 1988 Unpubl.), (2) Okefenokee Swamp in southern Georgia (Bennett In press, Bennett and Bennett In press), and (3) the Kissimmee Prairie region in central Florida (Bishop In Press). Another Florida sandhill crane population on Payne's Prairie in northern Florida, had been under study for a decade (Nesbitt 1988). Unfortunately, none of these sites are within the confirmed historic whooping crane breeding range. However, in 1988, the USFWS, with the concurrence of the CWS agreed on the Kissimmee Prairie for the next whooping crane reintroduction experiment.

Long-term survival of any reintroduced wild flock depends on the same factors that Griffith et al. (1989) associated with successful translocations of other avian groups: (1) large founder populations, (2) suitable habitat, and (3) high fecundity. These conditions can be only partially met in any whooping crane release.

#### PROJECTIONS AND CONCLUSIONS

With the expansion of the Aransas-Wood Buffalo population to 140-plus birds, the growth of the Patuxent flock to 30-plus birds, and the establishment of the ICF flock with 30 birds, we are optimistic about whooping crane recovery. This optimism is reflected in the MOU signed in April 1990 by the USFWS and the CWS calling for joint cooperation in (1) enhancing and preserving habitat, (2) increasing bird survival rate, (3) improving bird and egg transfer practices, (4) establishing new captive flocks and wild populations, (5) determining disposition of specimens

and handicapped birds, and (6) deciding on the best uses for wild and captive-produced birds and eggs.

### Goals

The USFWS recovery plan (U.S. Fish and Wildlife Service 1986) calls for expansion of the Aransas-Wood Buffalo population to 40 breeding pairs by the turn of the century and the establishment of two additional wild populations by 2020. The CWS (Cooch et al. 1988) calls for a separate population of 25 pairs in the United States and another population of at least 5 pairs in Canada by 2010.

A recent draft appendix to the CWS plan (Cooch, pers. commun.) provides an action plan governing the fate of eggs from Canada and the captive flocks. According to this plan, 15 eggs are to be harvested in Canada in 1991, and the young are to be reared in captivity. Also in 1991, nine young are to be reared at Patuxent and ICF for transfer to Florida to begin reintroduction experiments. The 1992 eggs (20) from Canada are to provide young (12) for all captive flocks and to establish a captive flock in Canada (probably at the Calgary Zoo). Eggs from 1993 and 1994 are to provide young to further build captive flocks, and beginning in 1994, captive colonies are to provide 20 young each year for 10 years to establish a wild flock in Florida. Some eggs from Canada may provide chicks to supplement the early Florida releases, and if all proceeds satisfactorily, another release may begin in Canada in the late 1990's while the Florida release is still underway.



As in the past, all increases in the Aransas-Wood Buffalo population will be from natural reproduction and recruitment. Although no eggs or birds are to come from captive flocks, fertile eggs in the nests in Wood Buffalo will be distributed so that nesting pairs have at least one viable egg.

In the 1940's, the whooping crane teetered on the brink of extinction; fewer than 30 birds remained in the world. In the intervening 5 decades, the wild population has expanded seven fold, while sustaining a massive effusion of 333 eggs to build the Grays Lake flock and captive flocks. The recovery of the whooping crane, although not yet complete, stands as a singular marvel in the annals of wildlife management.

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Ellis et al.

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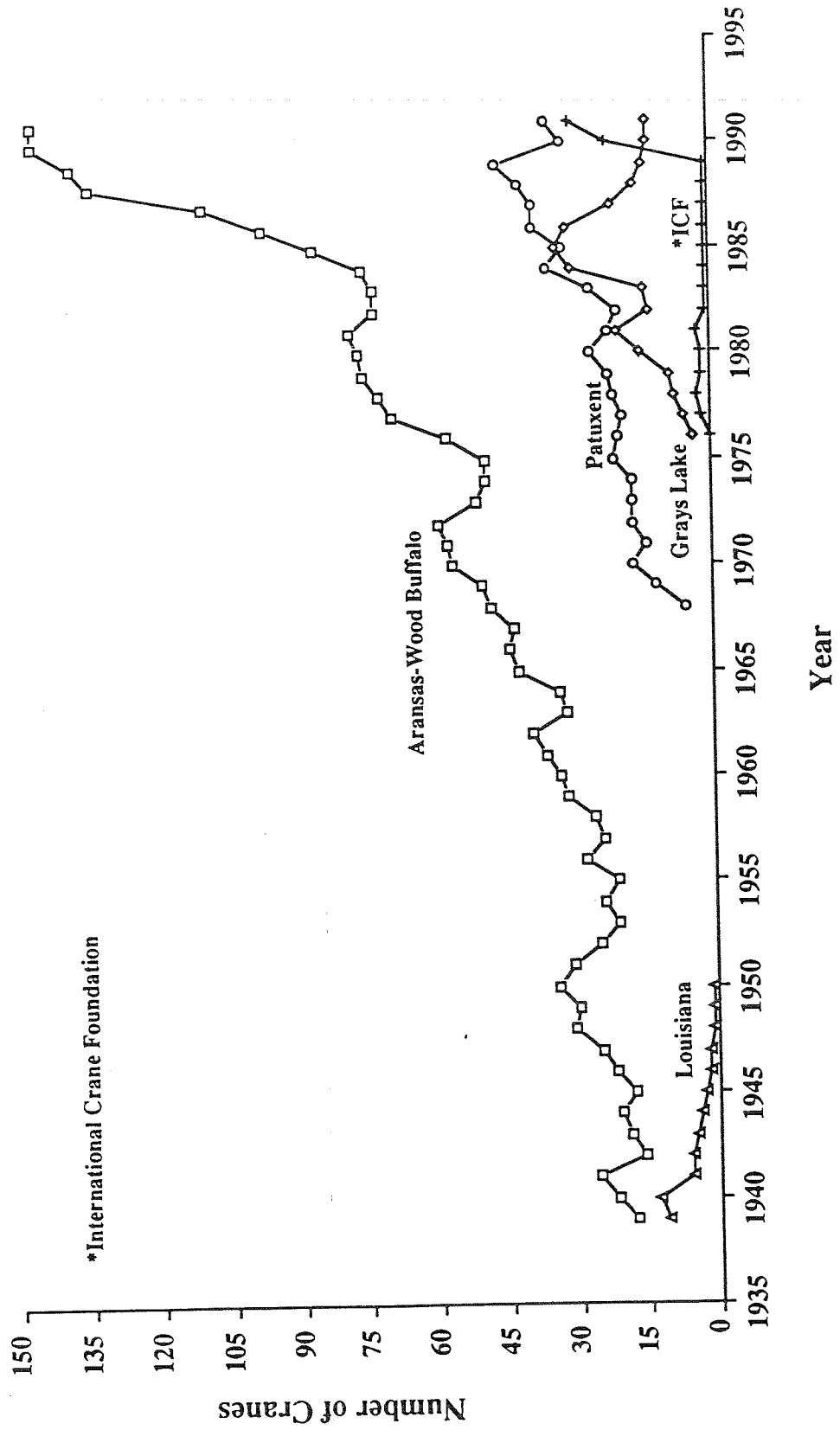
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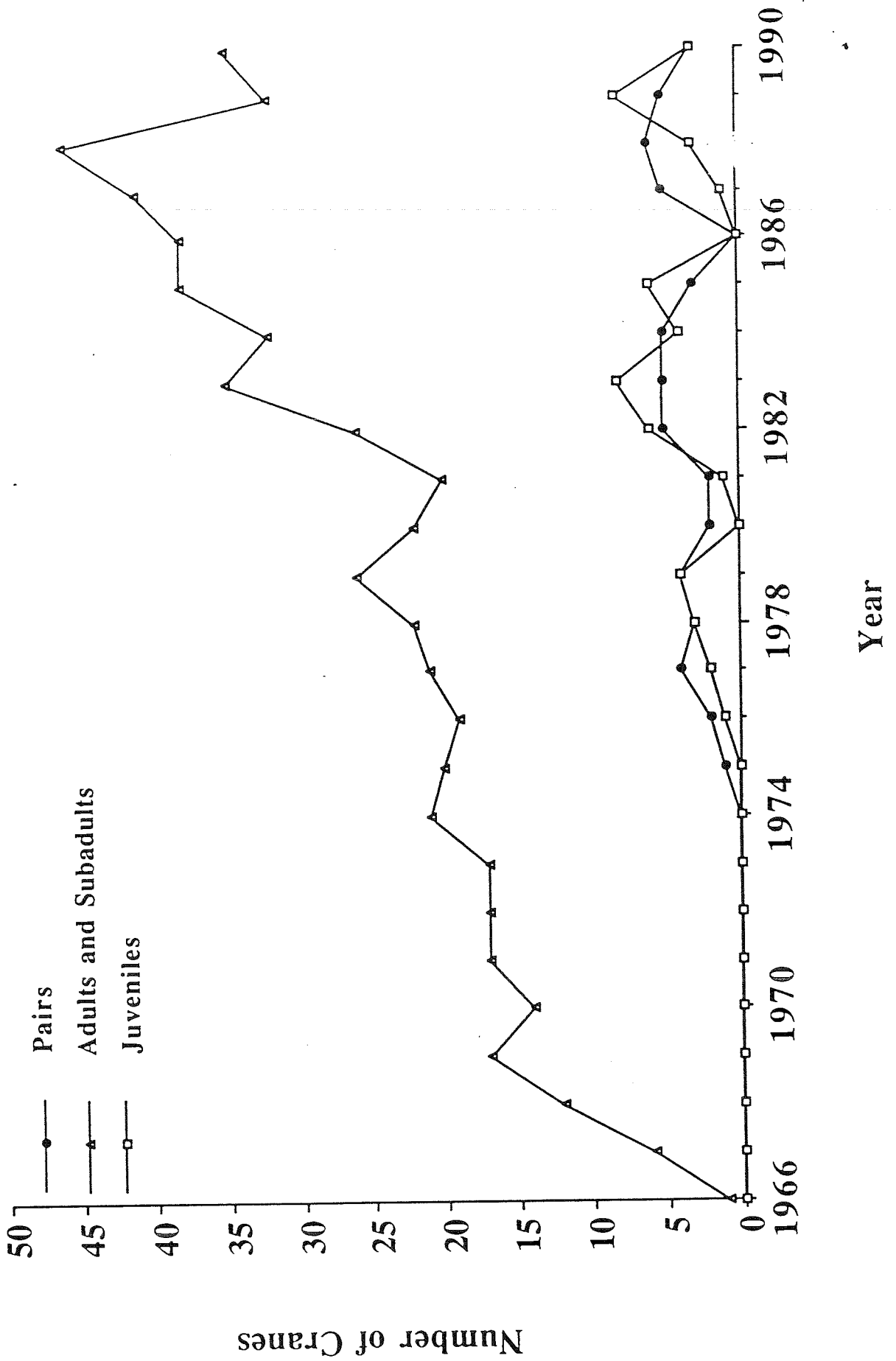
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**FIGURE 1**  
**Whooping Crane Populations**  
**Winter Counts**



**FIGURE 2**  
**Patuxent Wildlife Research Center**  
**Whooping Crane Captive Flock,**  
**January Flock Size**



**FIGURE 3**  
**PROJECTED WHOOPING CRANE CAPTIVE**  
**COLONIES**

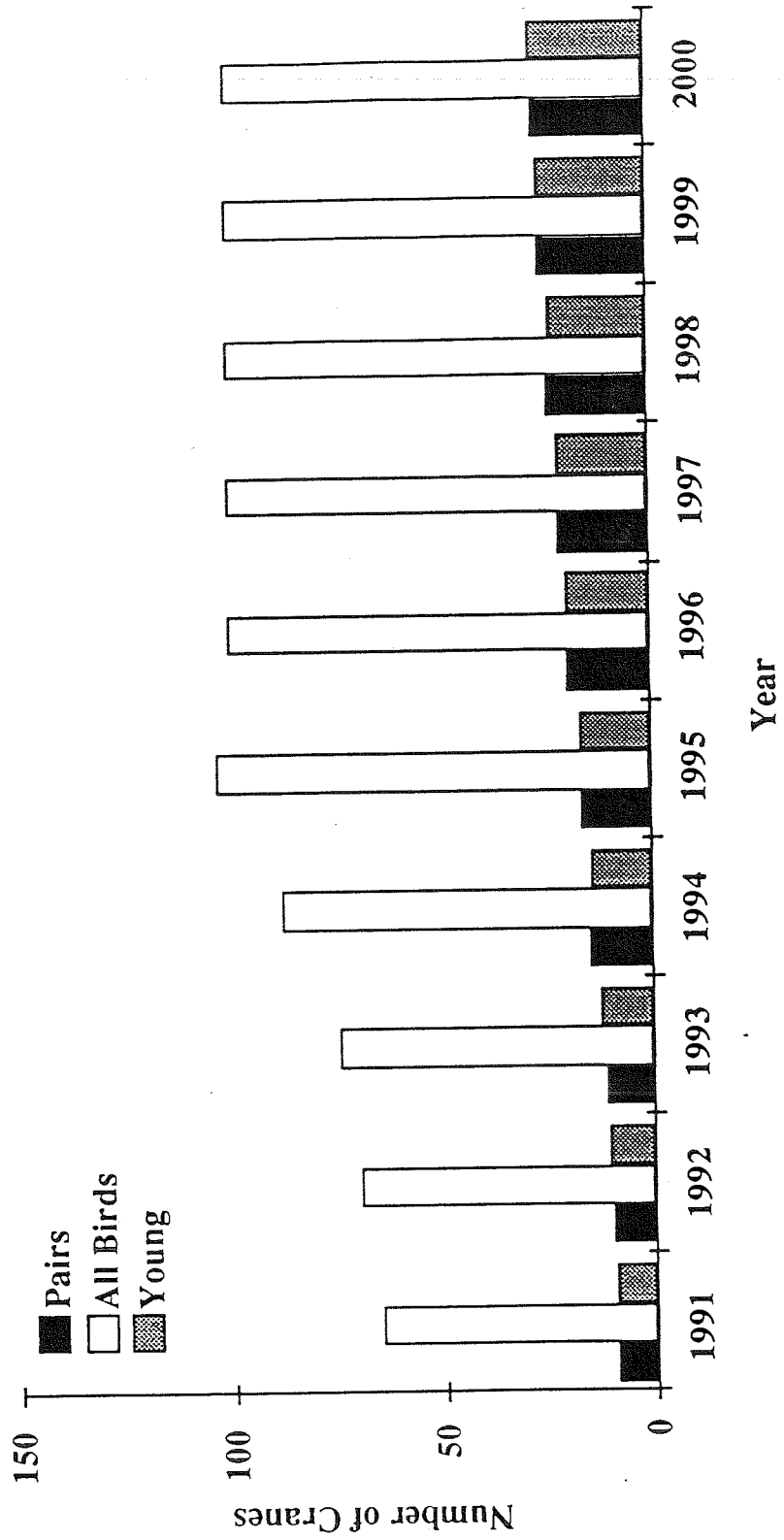


TABLE 1. Destination and Fate of Whooping Crane Eggs Taken From Wood Buffalo National Park.

YEAR	No. Eggs Collected	Patuxent Wildlife Research Center		Grays Lake National Wildlife Refuge	
		No. Eggs Received	No. Young Fledged	No. Eggs Received <sup>a</sup>	No. Young Fledged
1967	6	6	4	0	0
68	11	11	6	0	0
69	14	14	6	0	0
70	7 (2 known infertile)	5	0	0	0
71	10	10	2	0	0
72	0	0	0	0	0
73	0	0	0	0	0
74	13 (2 known infertile)	11	4	0	0
75	14	0	0	14	5
76	15	0	0	15	4
77	16	0	0	16	4
78	13	0	0	13	3
79	19	0	0	19	6
80	13	0	0	13	4
81	12	0	0	12	0
82	16	2	1	14	3
83	18	2	2	16	11
84	25	3	1	22	10
85	25 (2 known infertile)	2	1	23	11
86	24 (1 known infertile)	9	2	15	2
87	7	7	5	12	2
88	26	14	7	12	2
89	9 (6 known infertile)	9	3	0	0
90	12 <sup>b</sup>	0	0	0	0

<sup>a</sup> An additional 73 eggs (61 fertile from which 17 young fledged) from Patuxent were transferred to Grays Lake National Wildlife Refuge from 1976 to 1984.

<sup>b</sup> All 12 eggs were sent to the International Crane Foundation. Eight chicks fledged.

LEGENDS FOR FIGURES

FIGURE 1 - Whooping Crane Populations, Captive Colony counts are for January 1. All others are Winter Counts  
Each peak winter count (e.g. 1978-79) reported for January of the latter year (e.g. 1979).

FIGURE 2 - Patuxent Wildlife Research Center Whooping Crane Captive Flock, January Flock Size

FIGURE 3 - Projected Whooping Crane Captive Colonies

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## Translocation as a Species Conservation Tool: Status and Strategy

BRAD GRIFFITH, J. MICHAEL SCOTT, JAMES W. CARPENTER, AND CHRISTINE REED

# Translocation as a Species Conservation Tool: Status and Strategy

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Surveys of recent (1973 to 1986) intentional releases of native birds and mammals to the wild in Australia, Canada, Hawaii, New Zealand, and the United States were conducted to document current activities, identify factors associated with success, and suggest guidelines for enhancing future work. Nearly 700 translocations were conducted each year. Native game species constituted 90 percent of translocations and were more successful (86 percent) than were translocations of threatened, endangered, or sensitive species (46 percent). Knowledge of habitat quality, location of release area within the species range, number of animals released, program length, and reproductive traits allowed correct classification of 81 percent of observed translocations as successful or not.

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**A** TRANSLOCATION IS THE INTENTIONAL RELEASE OF ANIMALS to the wild in an attempt to establish, reestablish, or augment a population (1) and may consist of more than one release. To date, translocations have been used to establish populations of nonnative species and restore native species extirpated by hunting. An increasing perception of the value of biological diversity has focused attention on translocations of rare native species. These latter translocations are expensive (2, 3) and are subject to intense public scrutiny (4). They have varied goals (3) that include bolstering genetic heterogeneity of small populations (5-7), establishing satellite populations to reduce the risk of species loss due to catastrophes (8, 9), and speeding recovery of species after their habitats have been restored or recovered from the negative effects of environmental toxicants (2) or other limiting factors.

In the face of increasing species extinction rates (10-12) and impending reduction in overall biological diversity (12), translocation of rare species may become an increasingly important conservation technique. If current patterns of habitat loss continue, natural communities may become restricted to disjunct habitat fragments and intervening development may disrupt dispersal and interchange mechanisms (2). Increased rates of extinction may be expected in small fragmented habitats (13) and translocation may be required to maintain community composition, especially for species with limited dispersal abilities.

The immediacy of reduction in biodiversity (14) demands a rigorous analysis of translocation methodology, results, and strategy. We need to know how well it works, what factors are associated with success, and what strategies suggest greatest potential success.

We conducted three surveys of contemporary (1973 to 1986) translocations of native birds and mammals in Australia, Canada, Hawaii, New Zealand, and the United States (15). In the first

survey, we obtained general information on the number of programs completed by various organizations. In the later surveys, we sought detailed information on translocations of (i) threatened, endangered, or sensitive species and (ii) native game birds and mammals.

## Current Status

At least 93 species of native birds and mammals were translocated between 1973, the year the Endangered Species Act became law, and 1986. Most (90%) translocations were of game species; threatened, endangered, or sensitive species accounted for 7%. Ungulates (39%), gallinaceous birds (43%), and waterfowl (12%) dominated translocations of game species; raptors (28%) and marsupials (22%) dominated threatened, endangered, or sensitive species translocations.

A typical translocation consisted of six releases over the course of 3 years. Many (46%) released 30 or fewer animals and most (72%) released 75 or fewer animals.

The average number of translocations per reporting organization doubled from 1974 (5.5) to 1981 (10.6) suggesting contemporary totals of 700 translocations per year. Most (98%) of these were conducted in the United States and Canada. Effort was not uniformly distributed; 21% of North American agencies conducted 71% of North American translocations. Only 27% of reporting organizations had protocols that specified the types of information to be recorded during translocation programs.

## Theoretical Considerations

A translocation is a success if it results in a self-sustaining population; conversely, the founder group may become extinct. Theoretical considerations predict that population persistence is more likely when the number of founders is large, the rate of population increase is high, and the effect of competition is low (13). Low variance in rate of increase (16), presence of refugia (9), reduced environmental variation (16), herbivorous food habits (17), and high genetic diversity among founders (18) may also enhance persistence. Suitable, protected, and maintained habitat, control of limiting factors, and proper care and training of captive reared

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animals (3, 19) are also considered prerequisites of a successful translocation.

We found that several factors were associated with success of translocations (Table 1). Native game species were more likely to be successfully translocated than were threatened, endangered, or sensitive species. Increased habitat quality was associated with greater success. Translocations into the core of species historical ranges were more successful than were those on the periphery of or outside historical ranges. Herbivores were more likely to be successfully translocated than either carnivores or omnivores. Translocations into areas with potential competitors of similar life form were less successful than translocations into areas without competitors or areas with a congeneric potential competitor. Early breeders with large clutches were slightly more likely to be successfully translocated than were species that bred late and had small clutches.

Translocations of exclusively wild-caught animals were more likely to succeed than were those of exclusively captive-reared animals (Table 1). Among translocations of exclusively wild-caught animals, success depended ( $P \leq 0.10$ ) on whether the source population density was high (77% success,  $n = 109$ ), medium (78%,  $n = 37$ ), or low (37%,  $n = 8$ ). Success of translocations of wild-caught animals was also associated ( $P \leq 0.10$ ) with whether the source population was increasing (83% success,  $n = 93$ ), stable (63%,  $n = 49$ ), or declining (44%,  $n = 9$ ). Successful translocations released more animals than unsuccessful translocations (160 compared to 54, respectively;  $P = 0.024$ ).

Our results are consistent with analyses of naturally invading or colonizing species that show (i) larger founder populations are more successful (20, 21), (ii) that habitat suitability is important (21), and (iii) increased number and size of clutches enhances successful invasion (22). Our data also support the hypothesis that herbivores

**Table 1.** Percentage success of intentional introductions or reintroductions (translocations) of native birds and mammals to the wild in Australia, Canada, Hawaii, New Zealand, and the United States between 1973 and 1986. Data were obtained from a survey conducted in 1987 (15). The data include 134 translocations of birds and 64 translocations of mammals. For all variables listed,  $\chi^2$  was statistically significant ( $P \leq 0.10$ ), implying true differences in the percentages of successful translocations among the categories. Animals that first give birth at age 2 or less with average clutch size of three or more are considered early breeders with large clutches; all others are late breeders with small clutches.

Variable	Trans- locations (n)	Success (%)
Threatened, endangered, or sensitive species	80	44
Native game	118	86
Release area habitat		
Excellent	63	84
Good	98	69
Fair or poor	32	38
Location of release		
Core of historic range	133	76
Periphery or outside	54	48
Wild-caught	163	75
Captive-reared	34	38
Adult food habit		
Carnivore	40	48
Herbivore	145	77
Omnivore	13	38
Early breeder, large clutch	102	75
Late breeder, small clutch	96	62
Potential competitors		
Congeneric	39	72
Similar	48	52
Neither	105	75

are more successful invaders than carnivores (17) and the conclusion that, for birds, morphologically similar species have a greater depressing effect on successful invasion than do congeneric species (23).

We found no consistent association of translocation success with number of releases, habitat improvement, whether the release was hard (no food and shelter provided on site) or soft, immediate or delayed release on site, or average physical condition of animals at release. We were unable to directly evaluate genetic heterogeneity, sex and age composition, or specific rearing and handling procedures for released animals because of inadequate response to survey questions.

## Evaluating Alternative Strategies

Analyses of individual factors associated with translocation success do not adequately reflect the multivariate nature of actual translocations. To overcome this problem, we used stepwise logistic regression (24, 25) to develop preliminary predictive equations for estimating the success of translocations (Table 2). An expanded data set or independent sample would probably yield different regression coefficients and estimates of success than we report. As a result, extrapolation to conditions much different than those represented by our data and applications to individual species are discouraged.

The coefficients from Table 2 can be used to plot predicted success of different kinds of translocations as a function of continuous variables such as the number released. We present an example for a threatened, endangered, or sensitive bird (Fig. 1).

This exercise (Fig. 1) illustrates that the increase in success associated with releasing larger numbers of organisms quickly becomes asymptotic. Releases larger than 80 to 120 birds do little to increase the chances that a translocation will be successful for this particular set of conditions. The asymptotic property is consistent across other classifications of the data but the inflection point varies. For large native game mammals the asymptote is reached at releases of 20 to 40 animals with a concurrently higher predicted success.

The asymptotic property of the association of translocation success and number released (Fig. 1) is consistent with theoretical predictions (13) and analytical treatments (26) that suggest a threshold population size below which extinction is likely, primarily due to chance events affecting birth and death of individuals. The existence of the inflection (Fig. 1) is also consistent with the prediction of a threshold density below which population social interactions and mating success are disrupted (27), again leading to diminished population viability.

The coefficients from Table 2 and relationships presented in Fig. 1 can be used to assess alternative strategies. Suppose 300 threatened and endangered birds are available for a translocation program and they must be released during a 3-year time frame. Further suppose that two potential translocation areas are available within the core of the species historical range. If the goal of the translocation is to establish at least one geographically disjunct population to reduce the risk of catastrophic loss of the species, how should the birds be distributed between the two potential translocation areas to minimize the probability that both translocations will fail?

If both release areas have excellent habitat quality, and the areas are independent, the answer is obvious. The birds should be divided between the areas. The coefficients from Table 2 allow us to estimate the probability that a single release of 300 birds will fail (1.0 minus probability of success) is 0.257. Two releases of 150 birds each have individual probabilities of failure of 0.312. The probability that both will fail is  $0.312 \times 0.312 = 0.097$ ; substantial gain is achieved by splitting the birds between areas.



If we complicate the picture and say that one potential area has excellent habitat quality and the other has only good habitat quality, we see that it remains slightly advantageous to split the birds between areas. Predicted probabilities of failure are 0.312 for excellent and 0.698 for good habitat, respectively. The probability that both translocations will fail is  $0.312 \times 0.698 = 0.218$  compared to 0.257 for putting all birds in a single excellent habitat quality area. In this example, slight advantage to splitting the translocated birds between areas is maintained down to a total release of 40 birds. However, with so few birds released the probability that both translocations will fail is increased to about 0.42.

The model coefficients in Table 2 may be used to evaluate other scenarios. For example, given two alternatives, should a given number of birds be released in good habitat quality in the core of the historical species range or in excellent habitat quality on the periphery or outside the historical range? Good habitat quality in the core of the range is the better choice regardless of the number of birds released. This suggests that the physiological amplitude of a species may influence local population viability.

### Enhancing the Chances of Success

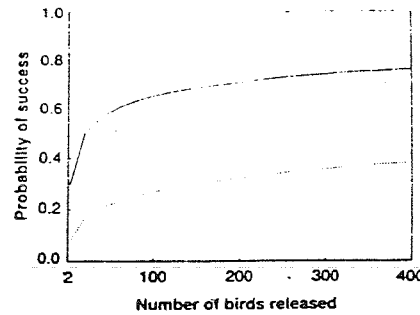
Without high habitat quality, translocations have low chances of success regardless of how many organisms are released or how well they are prepared for the release. Active management is required. Limiting factors must be identified and controlled and assurances of maintenance of habitat quality obtained prior to translocation.

Identification and retention of adequate habitat will require a combined species and ecosystem approach. Ecological information will be necessary to identify critical life history traits, factors determining habitat quality, species interactions, and minimum

**Table 2.** Stepwise logistic regression (24) model coefficients for predicting probability [ $P = 1/(1 + e^{-x})$ ] of success of intentional introductions or reintroductions (translocations) of native birds and mammals in Australia, Canada, Hawaii, New Zealand, and the United States between 1973 and 1986;  $x$  is the sum of applicable coefficients for categorical variables plus the applicable coefficient times the value of continuous variables. The model is based on 155 translocations; 100 were of birds and 55 were of mammals. Data were obtained from a survey conducted in 1987 (15). The stepwise procedure was run at the  $\alpha = 0.10$  level for entry of terms and the  $\alpha = 0.15$  level for removal of terms. Probability of larger test statistics for the model were  $\chi^2$ ,  $P = 0.90$  (24); Hosmer-Lemeshow  $\chi^2$ ,  $P = 0.121$  (24); Brown's  $\chi^2$ ,  $P = 0.537$  (24). The model correctly classified 81.3% of observed translocations based on a cutoff point of 0.50 in predicted probability of success.

Variable	Coefficient (SE)
Threatened, endangered, or sensitive species	-1.418 (0.738)
Native game	-0.972 (0.253)[1]*
Birds	0.972 (0.253)[1]
Mammals	-0.919 (0.374)[6]
Release area habitat	0.919 (0.374)[6]
Excellent	1.681 (0.438)[2]
Good	0.053 (0.314)[2]
Fair or poor	-1.734 (0.450)[2]
Release area	
Core of historic range	1.028 (0.267)[3]
Periphery or outside	-1.028 (0.267)[3]
Early breeder, large clutch	1.080 (0.355)[5]
Late breeder, large clutch	-1.080 (0.355)[5]
Log(number released)	0.887 (0.405)[7]
Program length (years)	0.181 (0.074)[4]

\*Numbers in brackets represent order of entry.



**Fig. 1.** Predicted probability of successful translocation as a function of the number of animals released during a 3-year period in the core of the historic species range in either excellent (solid line) or good (dashed line) habitat quality for a threatened, endangered, or sensitive bird species that first breeds at 2 years of age or more with average clutch size

of three or less. Probabilities are based on stepwise logistic regression model coefficients (Table 2).

habitat fragment size (28). Regional approaches to maintaining diversity (29) will be essential to ensure that existing species and habitat assemblages are identified, their interactions are understood, and remnant habitats are protected. The latter approach may ultimately reduce the number of species that require translocation if it enhances understanding of the effects of habitat fragmentation on persistence of multiple disjunct populations.

We may reduce the need for and increase the success of translocations if we can improve our ability to identify potentially tenuous situations and act before we are faced with a rescue. Simulation modeling (28, 32) of the behavior of small populations of species or of groups of species with similar reproductive strategies can provide guidance for establishing minimum population and vital rate goals. Simulations will be most productive if set in a regional context that addresses the interaction among metapopulations and the spatial relation among reserves or potential release sites (28).

The asymptotic nature of the relation between translocation success and number of animals released emphasizes the point that releasing large numbers of animals does little to increase the success of translocations. Lack of demonstrated success after translocating large numbers of animals is cause for reevaluating other variables associated with success.

The asymptotic levels do suggest that there is a minimum number of animals that should be released. Because longer translocation programs are more successful (Table 2), the minimum number may be released over several years if insufficient animals are available for a single release. Captive rearing programs that are focused on translocation should have the goal of establishing multiple self-sustaining populations so they can provide sufficient animals over a number of years and increase the success of these expensive (2, 3) programs.

Those planning translocations should adopt rigorous data recording procedures (19, 30). Details of translocation attempts should be assembled in a database. It is critical that both failures and successes be adequately documented. Permit-granting agencies may need to assume the role of ensuring that adequate records are kept so the database can be increased and predictability of success enhanced.

Because of the low success of translocations of small numbers of endangered, threatened, or sensitive species, even in excellent habitat quality, it is clear that translocation must be considered long before it becomes a last resort for these species—before density has become low and populations are in decline. Both these traits are associated with low chances of successful translocation. In addition, obtaining sufficient numbers of animals to achieve reasonable chances of success may be impossible. The greatest potential for establishing satellite populations may occur when a candidate population is expanding and numbers are moderate to high. These conditions are the ones that tend to make endangered species biologists relax; our analysis suggests that these conditions may point out the time for action.

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***GRUS AMERICANA***

**WHOOPING CRANE**

**CONSERVATION VIABILITY ASSESSMENT  
WORKSHOP REPORT**

**SECTION 9  
GENETICS**



# WHOOPING CRANE POPULATION VIABILITY ANALYSIS WORKSHOP

## GENETICS WORKING GROUP REPORT

### Participants

George Gee, John Longmire, Claire Mirande, (George, please complete this list).

### Questions Addressed

1. What do we know about diversity and heterozygosity in the Whooping Crane population, especially as it relates to other crane populations?
2. Some paternity questions are still unanswered. How can we best determine paternity in those unknowns?
3. How should we use the histocompatibility complex information in our breeding programs?
4. How do we use band sharing information from the DNA fingerprinting data?
5. What do we know about potential inbreeding effects? What do we do with inbreeding effects and genetic defects which occur within the population?
6. What future studies should we conduct and how?

### Diversity and Heterozygosity

We have two major estimates of genetic diversity at this time. These are allozyme and DNA fingerprinting data. The allozyme data indicate about average heterozygosity (Hz) in the Whooping Crane population as compared to other populations of cranes. The fingerprinting data indicate Hz is lower than average when compared to other species. The degree of DNA fingerprint band sharing, an indication of HZ in the Whooping Crane population, is 0.42. The Fiji Peregrine population has band sharing greater than 0.8, Mauritius Kestrel 0.44, Puerto Rican Parrot .42, and Peregrine Falcon .12 (which is approximately what we observe in humans).

### Paternity Determinations

We should look for agreement between the molecular and pedigree information. Molecular data currently include allozyme analysis and fingerprinting data. Dr. Jarvi is conducting additional work at the Major Histocompatibility Complex (MHC) locus including blood typing and chromosomal DNA (cDNA) probes. Dr. Krajewski studies of nuclear and mitochondrial DNA (mDNA) may also help resolve some issues.

We should attempt to recover skin, tissue, feathers, anything available from the possible sire from which we currently do not have DNA. We may need to make PCR probes to reconstruct the profiles and make the comparisons.

**POLYMORPHISM AND DIVERSITY IN THE SANDHILL, SARUS,  
WHOOPING  
AND SIBERIAN CRANES**

<u>Isozyme</u>	<u>Sandhill (58) Alleles %</u>		<u>Sarus (9) Alleles %</u>		<u>Siberian (23) Alleles %</u>		<u>Whooper (33) Alleles %</u>	
IDHP	c	98	c	100	c	10	c	98
	<b>b</b>	02					b	02
GK	f	93	e	83	d	100	c	92
	e	05	f	11			b	05
	<b>c</b>	02	d	06			d	03
Est-1	c	72	c	56	b	91	a	100
	b	28	b	44	c	09		
PEP-B	c	62	c	100	c	100	c	100
	<b>b</b>	36						
	<b>a</b>	02						
	<b>d</b>	01						
PEP-C	b	72	c	100	b	83	d	100
	a	28			a	17		
PGM-1	c	98	c	100	c	89	c	95
	d	02			d	11	d	05

( ) Number of cranes  
 Unique alleles bolded large  
 IDHP = Isocitrate dehydrogeuase  
 GK = Glukokinase  
 EST - 1 = Estrase - 1  
 PEP - B = Tripeptiduse - B  
 PEP - C = Dipeptiduse -C  
 MPI = Mannose -G- phosphate Isomerate  
 PGM -1 = Phosphoglucomutase -1

### **Use of New Molecular Data in Breeding Program**

After a great deal of discussion, the consensus of the group was that the pedigree information should be used to maximize outcrossing among the pairs. Molecular data should be used as a secondary criteria for mate selection. We do not believe that we should try to conserve rare alleles at the expense of losing overall Hz.

### **Potential Inbreeding Effects**

We felt that we should not select against any potential inbreeding effects since we felt that natural selection would take care of them. We believe it is more important to retain diversity from all lines than it is to run the risk of losing some of these lines in selecting against a rare allele.

### **Future Research**

- 1- Conduct pedigree analysis of the captive and wild populations for the existence of scoliosis as a genetic defect.
- 2- Develop single locus fingerprinting probes and build recombinant DNA libraries using vectors and host systems which will maximize preservation of sequences present in the WC genome.
- 3- Continue development of the MHC reagents and probes.
- 4- Compare levels of Hz between captive and wild populations using molecular analyses.
- 5- Continue paternity analysis using molecular and blood typing techniques.
- 6- Compare mini satellite fingerprinting diversity of other crane species to WC.
- 7- Compare the band sharing obtained through DNA fingerprinting to productivity.
- 8- The Captive Propagation Group should develop plans for expanding the frozen gene pool.
- 9- Expand analyses comparing the levels of Hz in the Whooping Crane to other species.

INDICES OF DIVERSITY IN POPULATION SAMPLES  
OF CRANES FROM THE WILD

<u>Taxon &amp; Number</u>	<u>Heterozygosity</u>		<u>Alleles/ Locus*</u>	<u>Polymorphism Percent</u>
	<u>Direct Count *</u>	<u>Estimates **</u>		
AME 15	0.036+0.018	0.042+0.029	1.14+0.07	14.3
CAM 17	0.028+0.012	0.032+0.023	1.14+0.08	10.7
CAG 17	0.056+0.025	0.059+0.027	1.29+0.11	21.4
CAO 11	0.024+0.013	0.032+0.019	1.11+0.06	10.7
CAF 14	0.031+0.022	0.042+0.029	1.07+0.05	07.1
LEU 24	0.028+0.015	0.025+0.013	1.14+0.07	14.3
ANT 09	0.024+0.017	0.026+0.020	1.11+0.08	07.1

\* Means  $\pm$  standard error

\*\* Calculated from gene frequencies using Hardy-Weinberg assumption



POLYMORPHISM IN CRANES

LOCUS	TRUMPETER CRANES	CROWNED CRANES	SANDHILL GROUP 1	SANDHILL GROUP 2	WHOOPER GROUP	
LDH-1	a	b				
LDH-2	a	b				
sMDH	a	a				
mMDH	a	a				
sIDHP	a,d		b>a	b	b	b>a
PGDH	a	b				
GPDHP-1	a		a	b	a	a
GPDHP-2	a	a				
SOD	a		c	b	b	b
sAAT	a		b	b	a,b	b
PGM-1	e		b>c	c>d	b>c	c>b
PGM-2	a	a	a	a	a	a
GK	f	f,a	a>b	f>e	e>d,b>c	g,c
AK	a	a				
ACP	b	b				
EST-1	a		c>b	b>c	a	a
EST-2	d		a	c	c	b
EST-3	a	a				
ESTD	d	b				
PEPA	c		a	b	b	b
PEPB	d		e	c>b	c	c
PEPC	d		c	b>a	b>c>a	d,c
PEPD	a		b	a	b,a	a
ADA	a	a				
GPI	d		b	c	c	c,d
HB-1	a	b	c	b	b	b
HB-2	b	a				

Trumpter; Crowned Cranes = Black-crowned, Gray-crowned;  
 Sandhill Group 1 = Siberian, Sarus, and Sandhills  
 Sandhills Group 2 = Brolga, Wattled, Demoiselle, and Stanley;  
 Whooper Group- Whooping, Common, Hooded, Black-necked,  
 White-naped, and Red-crowned.

**POLYMORPHISM AND DIVERSITY IN SANDHILL CRANE**

<u>Isozyme</u>	Mississippi (17) <u>Allele %</u>		Florida (10) <u>Allele %</u>		Okfenokee (14) <u>Allele %</u>		Greater (17) <u>Allele %</u>	
IDHP	c	100	c	100	c	96	c	97
			b	04	<b>b</b>	03		
GK	f	94	f	88	f	85	f	100
	<b>c</b>	06	e	12	e	15		
Est-1	c	94	c	100	c	100	b	88
	b	06					c	12
PEP-B	c	85	<del>b</del>	89	c	77	c	59
	<b>b</b>	15	a	11	a	23	b	38
						d	03	
PEP-C	b	97	b	70	b	57	b	62
	a	03	a	30	a	43	a	38
MPI	<b>b</b>	44	d	59	d	100	b	88
	d	38	e	41			d	06
	e	12					e	06
	<b>c</b>	06						
PGM-1	c	100	c	100	c	100	c	94
							d	06

( ) Number of cranes

Unique alleles bolded large

IDHP = Isocitrate dehydrogeuase

GK = Glucokinase

EST -1 = Estrase-1

PEP-B = Tripeptidase-B

PEP-C = Dipeptiduse-C

MPI = Mannose-G-phosphate Isomerate

PGM-1 = Phosphglucomutase-1

### EVOLUTIONARY DISTANCE AMONG CRANES

<u>Species</u>	<u>Nei</u>	<u>Rogers</u>	<u>Comments</u>
Trumpeter/Crane	0.95	0.61	11 unique alleles
Crowned Cranes/Others	0.485	0.39	07 unique alleles
Among Others	0.22	0.21	
Whooper Species Group	0.15	0.18	
Sandhill/Brolga	0.18	0.19	
Sandhill/Sarus/Sibe	0.08	0.1	
Sandhills	0.04	0.21	02 unique alleles
Mississippi/Florida	0.02	0.05	05 differet alleles
Hooded/Black-necked	0.02	0.04	
Crowned Cranes	0.01	0.04	

1. Uses all 27 loci examined in calculation.
2. Trumpeter out group for analysis.
3. Distance between Crowned cranes (Gray and Black species) between Hooded and Black-necked - similar as between MC and FC.

EVOLUTIONARY DISTANCE - R.F.L.P. WHOOPER PROBE  
J. Love - 1990

CLOSEST RELATIONSHIP

Whooping Crane	<i>Grus americana</i>
Common Cranes	<i>Grus grus</i>
Black-necked Crane	<i>Grus nigricollis</i>
Hooded Crane	<i>Grus monachus</i>
Red-crowned Crane	<i>Grus japonensis</i>
Sandhill Cranes	<i>Grus canadensis</i>
White-naped Cranes	<i>Grus vipio</i>
Sarus Cranes	<i>Grus antigone</i>
Brolga Cranes	<i>Grus rubicundus</i>
Siberian Crane	<i>Bulgeranus leucogeranus</i>
Wattled Crane	<i>Bulgeranus carunculatus</i>
Demoiselli Crane	<i>Anthropoides virago</i>
Stanley Crane	<i>Anthropoides paradisea</i>
Crowned Cranes	<i>Balearica pavonina</i>

MOST DISTANT RELATIONSHIP

***GRUS AMERICANA***

**WHOOPING CRANE**

**CONSERVATION VIABILITY ASSESSMENT  
WORKSHOP REPORT**

**SECTION 10  
STUDBOOKS**

# **The Genealogy of Wood Buffalo National Park Whooping Cranes (*Grus Americana*)**

**Data collected by:**

**Ernie Kuyt**

**Tom Stehn**

**Compiled by:**

**Sheri Snowbank**

**Claire Mirande**

**Current through:**

**31 December 1988**

The information herein is based on data collected by Ernie Kuyt of the Canadian Wildlife Service and Tom Stehn, Aransas National Wildlife Refuge. Information compiled by Sheri Snowbank and Claire Mirande, International Crane Foundation.

These are preliminary analyses. Data should not be used or reproduced without the permission of Ernie Kuyt and Tom Stehn.

Survival of Color-banded Whooping Cranes (1 November to 1 November).

Hatching Year	Age (years)												
	1	2	3	4	5	6	7	8	9	10	11	12	13
1977	9/10	9/9	8/9	7/8	6/7	6/6	5/6	3/5	3/3	2/3	2/2	2/2	2/2
1978	7/8	5/7	5/5	5/5	5/5	5/5	4/5	4/4	4/4	4/4	3/4	3/3	3/3
1979	5/6	5/5	5/5	5/5	4/5	4/5	4/4	4/4	4/4	4/4	3/4	2/3	
1980	4/6	3/4	3/3	3/3	3/3	2/3	2/2	2/2	2/2	2/2	2/2		
1981	2/3	1/2	1/1	1/1	1/1	1/1	1/1	1/1	1/1	1/1			
1982	5/7	3/5	3/3	1/3	1/1	1/1	1/1	1/1	1/1				
1983	6/10	6/6	5/6	4/5	4/4	4/4	4/4	4/4					
1984	10/13	8/10	6/8	6/6	4/6	3/3	3/3						
1985	16/16	16/16	16/16	12/16	12/12	11/12							
1986	18/18	17/18	15/17	11/15	10/11								
1987	21/21	18/21	16/18	16/16									
1988	14/17	12/13	9/12										
TOTAL:	117/135	103/116	92/103	71/83	51/55	38/40	24/26	19/21	15/15	13/14	10/12	7/8	5/5
SURVIVAL													
RATE%: 86.6    88.8    89.3    85.5    92.7    95    92.3    90.5    100    92.86    83.3    87.5    100    100													

a Period between banding (late July to mid-August and first arrival at ANWR  
 These enteries are from a combined effort of Ernie Kuyt's WBNP breeding surveys and Tom Stehn's Arkansas  
 winter census compiled during the 1991 WC PVA meeting.



**EGG SWITCHES**

**1977**

11/77 (S-4) TO 3/77 (S-3)

**1978**

4/78 (S-4) TO 5/78 (S-3)

8/78 (K-1) TO 3/78 (K-7)

**1979**

**1980**

**1981**

**1982**

**1983**

**1984**

**1985**

7/85 (ALTA) TO 27/85 (K-15)

12/85 (S-4) TO 6/85 (K-7)

9/85 (K-1) TO 14/85 (K-3)

**1986**

12/86 (K-3) TO 23/86 (K-14)

2/86 (K-7) TO 23/86 (K-1)

10/86 (K-1) TO 26/86 (S-13)

8/86 (LOB) TO 27/86 (S-4)

**1987**

1/87 (LOB) TO 9/87 (SK-2)

2/87 (S-8) TO 25/87 (S-9)

**1988**

5/88 (LOB) TO 18/88 (S-11 ?4)

6/88 (S-2) TO 28/88 (S-14)

7/88 (S-3) TO 8/88 (S-12)

9/88 (S-1) TO 27/88 (S-15)

3/88 (K-12) TO 29/88 (K-16)

10/88 (K-5) TO 30/88 (K-6)

11/88 (K-2) TO 14/88 (K-3)

**1989**

20/89 (N-1) TO 28/89 (N-3)

21/89 (K-10) TO 27/89 (SK-5)

13/89 (S-1) TO 22/89 (S-16)

**1990**

3/90 (S-11) TO 24/90 (S-1)

13/90 (S-2) TO 23/90 (S-NEW)

7/90 (K-10) TO 17/90 (K-3)

WOOD BUFFALO WHOOPING CRANES Studbook  
(Grus americana)

Stud #	Sex	Hatch Date	Sire	Dam	Location	Date	Local ID	Event	Tag/Band	ORIGIN/PAIR	/BAND	/
1000	M	????	WILD	WILD	WBNP	????	UNK	Hatch		UNK	K-U	UNBANDED
1001	F	????	WILD	WILD	WBNP	????	UNK	Hatch		UNK	K-U	UNBANDED
1002	M	????	WILD	WILD	WBNP	????	UNK	Hatch		UNK	S-1	UNBANDED
1003	F	????	WILD	WILD	WBNP	????	UNK	Hatch		UNK	S-1	UNBANDED
1004	M	????	WILD	WILD	WBNP	????	UNK	Hatch		UNK	S-6	UNBANDED
					N.AMERICA	????		Death				
1005	F	????	WILD	WILD	WBNP	????	UNK	Hatch		UNK	S-6	UNBANDED
					N.AMERICA	????		Death				
1006	M	????	WILD	WILD	WBNP	????	UNK	Hatch		UNK	K-1	UNBANDED
					N.AMERICA	- 1988		Death				
1007	F	????	WILD	WILD	WBNP	????	UNK	Hatch		UNK	K-1	UNBANDED
1008	M	????	WILD	WILD	WBNP	- 1986	UNK	Hatch		UNK	S-2	UNBANDED
1009	F	????	WILD	WILD	WBNP	????	UNK	Hatch		UNK	S-2	UNBANDED
1010	M	????	WILD	WILD	WBNP	????	UNK	Hatch		UNK	S-4	UNBANDED
1011	F	????	WILD	WILD	WBNP	????	UNK	Hatch		UNK	S-4	UNBANDED
1012	M	????	WILD	WILD	WBNP	????	UNK	Hatch		UNK	K-2	UNBANDED
1013	F	????	WILD	WILD	WBNP	????	UNK	Hatch		UNK	K-2	UNBANDED
1014	M	????	WILD	WILD	WBNP	????	UNK	Hatch		UNK	S-3	UNBANDED
1015	F	????	WILD	WILD	WBNP	????	UNK	Hatch		UNK	S-3	UNBANDED
1016	M	????	WILD	WILD	WBNP	????	UNK	Hatch		UNK	S-5	UNBANDED
1017	F	????	WILD	WILD	WBNP	????	UNK	Hatch		UNK	S-5	UNBANDED
1018	M	????	WILD	WILD	WBNP	????	UNK	Hatch		UNK	K-5	UNBANDED
1019	F	????	WILD	WILD	WBNP	????	UNK	Hatch		UNK	K-5	UNBANDED
1020	M	????	WILD	WILD	WBNP	????	UNK	Hatch		UNK	K-3	UNBANDED
1021	F	????	WILD	WILD	WBNP	????	UNK	Hatch		UNK	K-3	UNBANDED
1022	M	????	WILD	WILD	WBNP	????	UNK	Hatch		UNK	K-7	UNBANDED
1023	F	????	WILD	WILD	WBNP	????	UNK	Hatch		UNK	K-7	UNBANDED

WOOD BUFFALO WHOOPING CRANES Studbook  
(Grus americana)

Stud #	Sex	Hatch Date	Sire	Dam	Location	Date	Local ID	Event	Tag/Band	ORIGIN/PAIR	BAND	/
1024	M	????	WILD	WILD	WBNP	????	UNK	Hatch		UNK K-4	UNBANDED	
1025	F	????	WILD	WILD	WBNP	????	UNK	Hatch		UNK K-4	UNBANDED	
1026	F	????	WILD	WILD	WBNP	????	UNK	Hatch		UNK N-1	UNBANDED	
1027	M	????	WILD	WILD	WBNP	????	UNK	Hatch		UNK N-1	UNBANDED	
1028	M	????	WILD	WILD	WBNP	????	UNK	Hatch		UNK S-8	UNBANDED	
1029	F	????	WILD	WILD	WBNP	????	UNK	Hatch		UNK S-8	UNBANDED	
1030	M	????	WILD	WILD	WBNP	????	UNK	Hatch		UNK S-7	UNBANDED	
					N.AMERICA	????		Death				
1031	F	????	WILD	WILD	WBNP	????	UNK	Hatch		UNK S-7	UNBANDED	
					N.AMERICA	????		Death				
1032	M	????	WILD	WILD	WBNP	????	UNK	Hatch		UNK K-6	UNBANDED	
1033	F	????	WILD	WILD	WBNP	????	UNK	Hatch		UNK K-6	UNBANDED	
					N.AMERICA	- 1985		Death				
1034	M	????	WILD	WILD	WBNP	????	UNK	Hatch		UNK ALTA	UNBANDED	
1035	F	????	WILD	WILD	WBNP	????	UNK	Hatch		UNK ALTA	UNBANDED	
1036	M	????	WILD	WILD	WBNP	- 1987	UNK	Hatch		UNK K-8	UNBANDED	
1037	F	????	WILD	WILD	WBNP	????	UNK	Hatch		UNK K-8	UNBANDED	
1038	M	????	WILD	WILD	WBNP	????	UNK	Hatch		UNK SK-1	UNBANDED	
1039	F	????	WILD	WILD	WBNP	????	UNK	Hatch		UNK SK-1	UNBANDED	
					N.AMERICA	- 1987		Death				
1040	F	????	WILD	WILD	WBNP	????	UNK	Hatch		UNK S-9	UNBANDED	
1041	M	????	WILD	WILD	WBNP	????	UNK	Hatch		UNK K-10	UNBANDED	
1042	F	????	WILD	WILD	WBNP	????	UNK	Hatch		UNK K-10	UNBANDED	
1043	F	- 1977	1027	1026	WBNP	- 1977	10/77	Hatch	599-09801	N-1 K-5	GREEN-RED	
1044	F	- 1977	1006	1007	WBNP	- 1977	8/77	Hatch	599-09802	K-1 S-10	RED-GREEN	
1045	M	- 1977	1002	1003	WBNP	- 1977	12/77	Hatch	599-09803	S-1 K-9	RED-WHITE	
					N.AMERICA	- 1984		Death				
1046	M	- 1977	1008	1009	WBNP	- 1977	5/77	Hatch	599-09804	S-2	WHITE-RED	
					N.AMERICA	- Oct 1981		Death				

WOOD BUFFALO WHOOPING CRANES Studbook  
(Grus americana)

Stud #	Sex	Hatch Date	Sire	Dam	Location	Date	Local ID	Event	Tag/Band	ORIGIN/PAIR	BAND	/
1047	F	- 1977	1010	1011	WBNP N.AMERICA	- 1977 - 1984	11/77	Hatch Death	599-09805	S-4	S-11	RED-RED
1048	M	- 1977	1016	1017	WBNP N.AMERICA	- 1977 - 1980	1/77	Hatch Death	599-09806	S-5	S-11	RED-BLUE
1049	?	- 1977	1024	1025	WBNP N.AMERICA	- 1977 27 Jun 1979	2/77	Hatch Death	599-09807	K-4		NIL-RED
1050	M	- 1977	1032	1033	WBNP N.AMERICA	- 1977 - 1986	7/77	Hatch Death	599-09808	K-6	SK-2	BLUE-RED
1051	M	- 1977	1018	1019	WBNP	- 1977	6/77	Hatch	599-09809	K-5	S-1	RED-NIL
1052	F	- 1977	1034	1035	WBNP	- 1977 -30 Jul 1977	17/77	Hatch Death	NO BANDS	ALTA		UNBANDED
1053	F	????	WILD	WILD	WBNP	????	UNK	Hatch	UNK	K-9		UNBANDED
1054	F	????	WILD	WILD	WBNP	????	UNK	Hatch	UNK	LOB		UNBANDED
1055	M	- 1978	1027	1026	WBNP	- 1978	12/78	Hatch	NIL-SILVERN-1	S-9		RwR-NIL
1056	?	- 1978	1006	1007	WBNP N.AMERICA	- 1978 - 1984	8/78	Hatch Death	599-09811	K-1		NIL-RwR
1057	M	- 1978	1012	1013	WBNP ARANSAS	- 1978 - 1988	7/78	Hatch Death	599-09812	K-2	K-12	RWR-WHITE
1058	?	- 1978	1020	1021	WBNP N.AMERICA	- 1978 - 1978	13/78	Hatch Death	599-09813	K-3		WHITE-RWR
1059	M	- 1978	1032	1033	WBNP	- 1978	10/78	Hatch	599-09814	K-6	LOB	RWR-BLUE
1060	?	- 1978	1002	1003	WBNP N.AMERICA	- 1978 - 1980	6/78	Hatch Death	599-09815	S-1		BLUE-RWR
1061	M	- 1978	1010	1011	WBNP	- 1978	4/78	Hatch	599-09816	S-4	S-12	RWR-ORANGE
1062	?	- 1978	1028	1029	WBNP N.AMERICA	- 1978 - 1979	1/78	Hatch Death	599-09817	S-8		ORANGE-RWR
1063	F	????	WILD	WILD	WBNP	????	UNK	Hatch	UNK	K-12		UNBANDED
1064	M	????	WILD	WILD	WBNP	????	UNK	Hatch	UNK	K-11		UNBANDED
1065	F	????	WILD	WILD	WBNP N.AMERICA	???? - 1987	UNK	Hatch Death	UNK	K-11		UNBANDED
1066	F	- 1979	1032	1033	WBNP N.AMERICA	- 1979 - 1990	2/79	Hatch Death	599-09823	K-6	SK-4	BWB-RED

WOOD BUFFALO WHOOPING CRANES Studbook  
(Grus americana)

Stud #	Sex	Hatch Date	Sire	Dam	Location	Date	Local ID	Event	Tag/Band	ORIGIN/PAIR	BAND	/
1067	M	- 1979	1018	1019	WBNP N.AMERICA	- 1979 - 1989	8/79	Hatch Death	599-09824	K-5	SK-3	RED-BWB
1068	F	- 1979	1036	1037	WBNP	- 1979	17/79	Hatch	599-09825	K-8	S-12	BWB-R/W
1069	M	- 1979	1006	1007	WBNP	- 1979	9/79	Hatch	599-09826	K-1	K-14	r/w-BWB
1070	?	- 1979	1014	1015	WBNP N.AMERICA	- 1979 - 1979	7/79	Hatch Death	599-09827	S-3		BWB-R/G
1071	M	- 1979	1010	1011	WBNP N.AMERICA	- 1979 - 1981	6/79	Hatch Death	599-09828	S-4	S-10	BWB-g/r
1072	M	????	WILD	WILD	WBNP	????	UNK	Hatch		UNK	K-13	UNBANDED
1073	F	????	WILD	WILD	WBNP	????	UNK	Hatch		UNK	K-13	UNBANDED
1074	F	????	WILD	WILD	WBNP	????	UNK	Hatch		UNK	SK-3	UNBANDED?
1075	F	????	WILD	WILD	WBNP N.AMERICA	???? - 1988	UNK	Hatch Death		UNK	K-14	UNBANDED
1076	M	????	WILD	WILD	WBNP N.AMERICA	???? - 1984	UNK	Hatch Death		UNK	SK-4	UNBANDED
1077	M	- 1980	1028	1029	WBNP	- 1980	2/80	Hatch	599-01801	S-8	S-11?	RED-r/b
1078	F	- 1980	1018	1019	WBNP	- 1980	8/80	Hatch	599-01802	K-5		RED-B/R
1079	F	- 1980	1032	1033	WBNP	- 1980	9/80	Hatch	599-01803	K-6		B/R-RED
1080	M	- 1980	1024	1025	WBNP	- 1980	6/80	Hatch	599-01804	K-4	K-5	RED-r/w
1081	F	- 1980	1006	1007	WBNP N.AMERICA	- 1980 - 1986	11/80	Hatch Death	599-01805	K-1	S-11?	r/b-RED
1082	M	- 1980	1036	1037	WBNP N.AMERICA	- 1980 - 1981	15/80	Hatch Death	599-01806	K-8		R/W-RED
1083	F	????	WILD	WILD	WBNP	????	UNK	Hatch		UNK	K-15	UNBANDED
1084	F	????	WILD	WILD	WBNP N.AMERICA	???? - Jan 1990	UNK	Hatch Death		UNK	SK-2	UNBANDED
1085	F	- 1981	1027	1026	WBNP TEXAS	- 1981 16 Oct 1982	7/81	Hatch Death	599-01807	N-1		WHITE-R/W
1086	M	- 1981	1006	1007	WBNP SASKATCHE	- 1981 18 Oct 1981	2/81	Hatch Death	599-01808	K-1		R/W-GREEN

WOOD BUFFALO WHOOPING CRANES Studbook  
(Grus americana)

Stud #	Sex	Hatch Date	Sire	Dam	Location	Date	Local ID	Event	Tag/Band	ORIGIN/PAIR	BAND
1087	M	- 1981	1034	1035	WBNP	- 1981	3/81	Hatch	599-01809	ALTA	K-15 GREEN-R/W
1088	F	????	WILD	WILD	WBNP	????	UNK	Hatch		UNK	K-16 UNBANDED
1089	M	????	WILD	WILD	WBNP	????	UNK	Hatch		UNK	S-14 UNBANDED
1090	M	- 1982	1059	1054	WBNP	- 1982	10/82	Hatch	599-01810	LOB	S-13 WHITE-RED
1091	?	- 1982	1010	1011	WBNP	- 1982	1/82	Hatch	599-01811	S-4	W/R-GREEN
					ARANSAS	2 Feb 1983		Death			
1092	F	- 1982	1028	1029	WBNP	- 1982	2/82	Hatch	599-01812	S-8	GREEN-W/R
					ARANSAS	15 Nov 1984		Death			
1093	?	- 1982	1014	1015	WBNP	- 1982	3/82	Hatch	599-01813	S-3	WHITE-R/R
						15 Nov 1982		Death			
1094	?	- 1982	1008	1009	WBNP	- 1982	4/82	Hatch	599-01814	S-2	RED-B/W
						19 Aug 1982		Death			
1095	?	- 1982	1024	1025	WBNP	- 1982	6/82	Hatch	599-01815	K-4	B/W-RED
					ARANSAS	4 Jan 1983		Death			
1096	?	- 1982	1038	1039	WBNP	- 1982	16/82	Hatch	599-01816	SK-1	R/R-BLUE
					N.AMERICA	- 1984		Death			
1097	?	- 1982	WILD	WILD	WBNP	- 1982	7/82	Hatch	NO BANDS	UNK	UNBANDED
					SASKATCHE	14 May 1983		Death			
1098	M	????	WILD	WILD	WBNP	????	UNK	Hatch		UNK	SK-2 UNBANDED
1099	M	????	WILD	WILD	WBNP	????	UNK	Hatch		UNK	SK-4 UNBANDED
1100	M	- 1983	1018	1019	WBNP	- 1983	18/83	Hatch	599-09818	K-5	AB-2 B/B-YELLOW
1101	M	- 1983	1012	1013	WBNP	- 1983	15/83	Hatch	599-09819	K-2	K-16 YELLOW-B/B
1102	M	- 1983	1036	1037	WBNP	- 1983	6/83	Hatch	599-09820	K-8	S-167 B/W-R/B
					ARANSAS	- 1989		Death			
1103	?	- 1983	1022	1023	WBNP	- 1983	6/83	Hatch	599-09821	K-7	WHITE-R/Y
						15 Sep 1983		Death			
1104	F	- 1983	1041	1042	WBNP	- 1983	19/83	Hatch	599-09822	K-10	S-13 R-YELLOW
1105	?	- 1983	1038	1039	WBNP	- 1983	21/83	Hatch	599-09829	SK-1	Y/R-GREEN
						16 Sep 1983		Death			
1106	?	- 1983	1002	1003	WBNP	- 1983	3/83	Hatch	599-09830	S-1	WHITE-GREEN
						16 Sep 1983		Death			

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Data current thru: 31 Dec 1988

ISIS/SPARKS  
22 Jan 1992

WOOD BUFFALO WHOOPING CRANES Studbook  
(Grus americana)

Stud #	Sex	Hatch Date	Sire	Dam	Location	Date	Local ID	Event	Tag/Band	ORIGIN/PAIR	BAND	/
1107	?	- 1983	1008	1009	WBNP	- 1983 16 Sep 1983	2/83	Hatch Death	599-09831	S-2	B/R-WHITE	
1108	?	- 1983	1014	1015	WBNP N.AMERICA	- 1983 21 Nov 1984	9/83	Hatch Death	599-09832	S-3	YELLOW-Y/R	
1109	?	- 1983	1014	1015	WBNP N.AMERICA	- 1983 - 1986	20/83	Hatch Death	599-09833	S-3	BWSP-RED	
1110	F	????	WILD	WILD	WBNP	????	UNK	Hatch		UNK	K-14	UNBANDED
1111	F	????	WILD	WILD	WBNP	????	UNK	Hatch		UNK	SK-5	UNBANDED
1112	M	- 1984	1055	1040	WBNP	- 1984	16/84	Hatch	629-01817	S-9	S-15	YELLOW-BWSP
1113	M	- 1984	1014	1015	WBNP N.AMERICA	- 1984 - 1986	21/84	Hatch Death	629-01818	S-3	BWSP-WHITE	
1114	M	- 1984	1002	1003	WBNP ARANSAS	- 1984 - 1986	4/84	Hatch Death	629-01819	S-1	BWSP-YELLOW	
1115	F	- 1984	1057	1063	WBNP ARANSAS	- 1984 - 1989	19/84	Hatch Death	629-01820	K-12	AB-2	BWSP-BWSP
1116	M	- 1984	1024	1025	WBNP	- 1984	7/84	Hatch	629-01821	K-4	YELLOW-WHITE	
1117	F	- 1984	1067	1074	WBNP	- 1984	24/84	Hatch	629-01822	SK-3	S-NEW	YELLOW-YELLOW
1118	F	- 1984	WILD	WILD	WBNP N.AMERICA	- 1984 - 1989	26/84	Hatch Death	629-01823	K-?	S-16	WHITE-BLUE
1119	F	- 1984	1006	1007	WBNP	- 1984	11/84	Hatch	629-01824	K-8	R/R-W	BLACK W
1120	F	- 1984	1036	1037	WBNP	- 1984	23/84	Hatch	629-01825	K-2	B/Y-B/Y	
1121	M	- 1984	1018	1019	WBNP N.AMERICA	- 1984 - 1985	25/84	Hatch Death	629-01826	K-5	W Bk	W-Y
1122	F	- 1984	1032	1033	WBNP N.AMERICA	- 1984 - 1988	6/84	Hatch Death	629-01827	K-6	Y-W Bk	W
1123	F	- 1984	1008	1053	WBNP N.AMERICA	- 1984 - 1986	3/84	Hatch Death	629-01828	S-2	W Bk	W-R
1124	F	- 1984	1028	1029	WBNP	- 1984	2/84	Hatch	629-01829	S-8	S-14	BLUE-WHITE
1125	?	- 1984	1027	1026	WBNP N.AMERICA	- 1984 ????	19/84	Hatch Death		N-1	UNBANDED	
1126	?	- 1984	1034	1035	WBNP N.AMERICA	- 1984 ????	14/84	Hatch Death		ALTA	UNBANDED	

WOOD BUFFALO WHOOPING CRANES Studbook  
(Grus americana)

Stud #	Sex	Hatch Date	Sire	Dam	Location	Date	Local ID	Event	Tag/Band	ORIGIN/PAIR	BAND	/
1127	F	????	WILD	WILD	WBNP N.AMERICA	???? - 1987	UNK	Hatch Death		UNK S-15	UNBANDED	
1128	M	- 1985	1059	1054	WBNP N.AMERICA	- 1985 - 1988	18/85	Hatch Death	629-01830	LOB S-16	GREEN-YELLOW	
1129	M	- 1985	1010	1011	WBNP N.AMERICA	- 1985 - 1990	12/85	Hatch Death	629-01831	S-4	GREEN-GREEN	
1130	F	- 1985	1014	1144	WBNP	- 1985	2/85	Hatch	629-01832	S-3 AB-2	YELLOW-RED	
1131	F	- 1985	1055	1040	WBNP	- 1985	20/85	Hatch	629-01833	S-9 S-16	YELLOW-GREEN	
1132	F	- 1985	1038	1039	WBNP	- 1985	8/85	Hatch	629-01834	SK-1	BYB-BYB	
1133	M	- 1985	1008	1053	WBNP	- 1985	3/85	Hatch	629-01835	S-2	W-RWR	
1134	F	- 1985	1028	1029	WBNP N.AMERICA	- 1985 - 1988	1/85	Hatch Death	629-01836	S-8	WHITE-RED	
1135	M	- 1985	1072	1073	WBNP	- 1985	17/85	Hatch	629-01837	K-13	BLUE-R/W/R	
1136	F	- 1985	1057	1063	WBNP	- 1985	10/85	Hatch	629-01838	K-12	WHITE-GREEN	
1137	M	- 1985	1067	1074	WBNP N.AMERICA	- 1985 - 1988	22/85	Hatch Death	629-01839	SK-3	WHITE-WHITE	
1138	M	- 1985	1041	1042	WBNP	- 1985	15/85	Hatch	629-01840	K-10	RWR-ORANGE	
1139	M	- 1985	1036	1037	WBNP	- 1985	23/85	Hatch	629-01841	K-8 S-NEW	BYB-WBW	
1140	F	- 1985	1064	1065	WBNP	- 1985	16/85	Hatch	629-01842	K-11 SK-3?	BWB-GWG	
1141	F	- 1985	1024	1025	WBNP	- 1985	13/85	Hatch	629-01843	K-4	W Bk W-BYB	
1142	F	- 1985	1006	1007	WBNP	- 1985	9/85	Hatch	629-01844	K-1 S-15	WBkW-WBkW	
1143	?	- 1985	1018	1019	WBNP N.AMERICA	- 1985 - 1988	28/85	Hatch Death	629-01845	K-5	GWG-GWG	
1144	?	????	WILD	WILD	WBNP	????	UNK	Hatch		UNK S-N2	UNBANDED	
1145	M	- 1986	1059	1054	WBNP N.AMERICA	- 1986 - 1988	8/86	Hatch Death	629-01846	LOB	ORANGE-WBW	
1146	F	- 1986	1057	1063	WBNP	- 1986 - Jun 1989	19/86	Hatch Death	629-01847	K-12	ORANGE-RED	
1147	F	- 1986	1101	1088	WBNP N.AMERICA	- 1986 - 1989	28/86	Hatch Death	629-01848	K-16	W Bk W-O	



WOOD BUFFALO WHOOPING CRANES Studbook  
(Grus americana)

Stud #	Sex	Hatch Date	Sire	Dam	Location	Date	Local ID	Event	Tag/Band	ORIGIN/PAIR /BAND
1148	M	- 1986	1080	1043	WBNP	- 1986	20/86	Hatch	629-01849 K-5	NIL-YELLOW
1149	M	- 1986	1012	1013	WBNP N.AMERICA	- 1986 - 1986	13/86	Hatch Death	629-01850 K-2	WHITE-ORANGE
1150	F	- 1986	1027	1026	WBNP	- 1986	17/86	Hatch	629-01851 N-1	ORANGE-WHITE
1151	F	- 1986	1087	1083	WBNP N.AMERICA	- 1986 - 1988	16/86	Hatch Death	629-01852 K-15	YELLOW-ORANGE
1152	M	- 1986	1022	1023	WBNP N.AMERICA	- 1986 - 1987	2/86	Hatch Death	629-01853 K-7	W Bk W-BLUE
1153	F	- 1986	1006	1007	WBNP	- 1986	10/86	Hatch	629-01854 K-1	O-Y/BLUE
1154	F	- 1986	1036	1037	WBNP	- 1986	3/86	Hatch	629-01855 K-8	SK-2 RED-YELLOW
1155	M	- 1986	1038	1039	WBNP N.AMERICA	- 1986 - 1988	4/86	Hatch Death	629-01856 SK-1	B-W Bk W
1156	F	- 1986	1051	1003	WBNP	- 1986	9/86	Hatch	629-01857 S-1	K-11? BLUE-o/y
1157	F	- 1986	1008	1009	WBNP	- 1986	5/86	Hatch	629-01858 S-2	K-11? y-blue/o
1158	M	- 1986	1014	1015	WBNP	- 1986	1/86	Hatch	629-01859 S-3	YELLOW-RED
1159	?	- 1986	1028	1029	WBNP N.AMERICA	- 1986 - 1987	6/86	Hatch Death	629-01860 S-8	BWSP-O/W
1160	F	- 1986	1067	1074	WBNP	- 1986	22/86	Hatch	629-01861 SK-3	r/b-o
1161	F	- 1986	1022	1023	WBNP	- 1986	2/86	Hatch	629-01862 K-7	N-3 o-r/b
1162	?	- 1986	1064	1065	WBNP	- 1986	11/86	Hatch	629-01863 K-11	S-N 2 o/w-BWSP
1163	?	- 1986	1032	W1165	WBNP N.AMERICA	- 1986 ????	14/86	Hatch Death	K-6	UNBANDED
1164	?	- 1986	1072	1073	WBNP N.AMERICA	- 1986 ????	15/86	Hatch Death	K-13	UNBANDED
1165	M	????	WILD	WILD	WBNP	????	UNK	Hatch	UNK N-3	UNBANDED
1166	?	- 1987	1059	1054	WBNP	- 1987	1/87	Hatch	629-01864 LOB	Y Bk Y-Y
1167	?	- 1987	1034	1035	WBNP	- 1987	17/87	Hatch	629-01865 ALTA	GWG-Y Bk B
1168	?	- 1987	1028	1029	WBNP	- 1987	2/87	Hatch	629-01866 S-8	Y Bk Y-GWG
1169	?	- 1987	1014	1015	WBNP	- 1987	12/87	Hatch	629-01867 S-3	Y Bk Y-RWR

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Data current thru: 31 Dec 1988

ISIS/SPARKS  
22 Jan 1992

## ASSUMPTIONS

1. IF OBSERVATIONS INDICATED DEFINITELY THAT ONE OR BOTH MEMBERS OF A PAIR ON A TERRITORY CHANGED BETWEEN YEARS, THE FOLLOWING ASSUMPTIONS WERE MADE:
  - A. IT WAS ASSUMED THAT ONLY 1 BIRD CHANGED IN ORDER NOT TO OVERESTIMATE GENETIC DIVERSITY. AT PRESENT "NEW" BIRDS ARE HANDLED AS FOUNDERS SINCE WE ARE UNABLE TO DETERMINE THEIR RELATEDNESS TO THE REST OF THE POPULATION.
  - B. IT WAS ASSUMED THAT THE FEMALE CHANGED AND THE ORIGINAL FEMALES WERE TERMINATED.
2. THE BIRTHDATES OF THE FOUNDERS WERE PUT AS UNKNOWN, BUT IN THE PROGRAM TO KEEP THE CORRECT ORDER THEY HAVE A HATCH DATE OF 5 YEARS BEFORE THEIR FIRST NESTING.
3. 1074 UNBANDED? - REFERS TO THE FACT THIS COULD BE NIL-RW WHO LOST BANDS OR A NEW FEMALE.
4. 1118 K-? - "ROUGE PAIR" THAT LAID AND HATCHED A CHICK IN THE KLEWI AREA, BUT NEVER RETURNED TO ESTABLISH A TERRITORY.
5. UNBANDED BIRDS WERE ENTERED ONLY IF A BIRTH AND DEATH DATE WERE KNOWN.
6. WHEN THERE WERE EGGS SWITCHED BETWEEN NESTS, THE SIRES AND DAMS LISTED IN THE STUDBOOK ARE THE GENETIC PARENTS. "ORIGIN" REFERS TO THE TERRITORY AT WHICH THEY WERE LAID. THE FOSTER PARENTS AND REARING TERRITORY ARE LISTED UNDER "SPECIAL DATA".

WOOD BUFFALO WHOOPING CRANES Studbook  
(Grus americana)

Stud #	Sex	Hatch Date	Sire	Dam	Location	Date	Local ID	Event	Tag/Band	ORIGIN/PAIR	/BAND	/
1170	M	- 1987	1010	1011	WBNP	- 1987	10/87	Hatch	629-01868 S-4	AB-1	Y-Y Bk Y	
1171	?	- 1987	1112	1142	WBNP	- 1987	32/87	Hatch	629-01869 S-15	S-16?	RWR-Y Bk Y	
1172	?	- 1987	1028	1029	WBNP	- 1987	2/87	Hatch	629-01870 S-8		R-Y Bk Y	
1173	?	- 1987	1090	1104	WBNP	- 1987	26/87	Hatch	629-01871 S-13		BWB-Y Bk Y	
1174	?	- 1987	1038	1039	WBNP	- 1987	20/87	Hatch	629-01872 SK-1		Y Bk Y-R	
					N.AMERICA	- 1988		Death				
1175	?	- 1987	1067	1074	WBNP	- 1987	21/87	Hatch	629-01873 SK-3	AB-1	W-Y Bk Y	
1176	?	- 1987	1087	1083	WBNP	- 1987	13/87	Hatch	629-01874 K-15		Y Bk Y-G	
					N.AMERICA	- 1989		Death				
1177	?	- 1987	1022	1023	WBNP	- 1987	3/87	Hatch	629-01875 K-7		Y BK Y-BWB	
					N.AMERICA	- 1989		Death				
1178	?	- 1987	1057	1063	WBNP	- 1987	8/87	Hatch	629-01876 K-12		G-Y Bk Y	
1179	?	- 1987	1012	1013	WBNP	- 1987	7/87	Hatch	629-01877 K-2		YBkY-YBkY	
1180	?	- 1987	1080	1043	WBNP	- 1987	16/87	Hatch	629-01878 K-5		Y Bk Y-W	
1181	?	- 1987	1101	1088	WBNP	- 1987	30/87	Hatch	629-01880 K-16		Y/B-Y Bk Y	
					N.AMERICA	- 1988		Death				
1182	?	- 1987	1099	1066	WBNP	- 1987	27/87	Hatch	629-01881 SK-4		Y/B-Y Bk Y	
1183	?	- 1987	1006	1007	WBNP	- 1987	6/87	Hatch	629-01882 K-1		YBkY-Y/G	
1184	?	- 1987	1032	W1165	WBNP	- 1987	28/87	Hatch	629-01883 K-6		Y Bk Y-O	
1185	?	- 1987	1072	1073	WBNP	- 1987	29/87	Hatch	629-01884 K-13		Y/G-YELLOW	
1186	?	- 1987	1064	1065	WBNP	- 1987	23/87	Hatch	629-01885 K-11		R/G-BWB	
					N.AMERICA	- 1988		Death				
1187	?	- 1987	1008	1053	WBNP	- 1987	11/87	Hatch	UNBANDED S-2		UNBANDED	
						8 Aug 1987		Death				
1188	?	- 1987	1027	1026	WBNP	- 1987	24/87	Hatch	UNBANDED N-1		UNBANDED	
					N.AMERICA	????		Death				
1189	?	- 1988	1099	1066	WBNP	- 1988	21/88	Hatch	629-01886 SK-4		RWR-GWG	
1190	?	- 1988	1087	1083	WBNP	- 1988	22/88	Hatch	629-01887 K-15		RWR-BWB	
1191	?	- 1988	1067	1074	WBNP	- 1988	20/88	Hatch	629-01888 SK-3		YELLOW-GWG	
					ARANSAS	- 1988		Death				

Compiled by: Sheri Snowbank thru International Crane Foundation  
Data current thru: 31 Dec 1988

WOOD BUFFALO WHOOPING CRANES Studbook  
(Grus americana)

Stud #	Sex	Hatch Date	Sire	Dam	Location	Date	Local ID	Event	Tag/Band	ORIGIN/PAIR	BAND	/
1192	?	- 1988	1022	1023	WBNP	- 1988	2/88	Hatch	629-01889	K-7	RED-WHITE	
1193	?	- 1988	1006	1007	WBNP	- 1988	4/88	Hatch	629-01890	K-1	WBW-GWG	
					N.AMERICA	- 1990		Death				
1194	?	- 1988	1032	W1165	WBNP	- 1988	10/88	Hatch	629-01891	K-5	GWG-RED	
					ARANSAS	- 1988		Death				
1195	?	- 1988	1041	1042	WBNP	- 1988	16/88	Hatch	629-01892	K-10	RED-GREEN	
					N.AMERICA	- 1990		Death				
1196	?	- 1988	1024	1025	WBNP	- 1988	13/88	Hatch	629-01893	K-4	GREEN-WHITE	
					N.AMERICA	-30 Oct 1989		Death				
1197	?	- 1988	1080	1043	WBNP	- 1988	10/88	Hatch	629-01894	K-5	GWG-BWB	
1198	?	- 1988	1101	1088	WBNP	- 1988	3/88	Hatch	629-01895	K-12	GWG-RWR	
					N.AMERICA	- 1988		Death				
1199	?	- 1988	1008	1009	WBNP	- 1988	6/88	Hatch	629-01896	S-2	RED-GWG	
1200	?	- 1988	1051	1003	WBNP	- 1988	9/88	Hatch	629-01897	S-1	GWG-WHITE	
1201	?	- 1988	1014	1015	WBNP	- 1988	7/88	Hatch	629-01898	S-3	GWG-WBW	
					N.AMERICA	- 1989		Death				
1202	?	- 1988	1014	1015	WBNP	- 1988	7/88	Hatch	629-01899	S-3	GWG-YELLOW	
					N.AMERICA	- 1988		Death				
1203	?	- 1988	1028	1029	WBNP	- 1988	1/88	Hatch	629-01900	S-8	RED-RED	
1204	?	- 1988	1034	1035	WBNP	- 1988	17/88	Hatch	629-09834	ALTA	GREEN-GWG	
1205	?	- 1988	1059	1054	WBNP	- 1988	5/88	Hatch	629-09835	LOB	GWG-GREEN	
1206	?	- 1988	1027	1026	WBNP	- 1988	24/88	Hatch		N-1	UNBANDED	
					N.AMERICA	????		Death				
1207	?	- 1988	1069	1075	WBNP	- 1988	15/88	Hatch		K-14	UNBANDED	
					N.AMERICA	????		Death				
1208	?	- 1988	WILD	WILD	WBNP	- 1988	UNK	Hatch		UNK	UNBANDED	
					N.AMERICA	????		Death				
1209	?	- 1988	1057	1063	WBNP	- 1988	3/88	Hatch		K-12	UNBANDED	
					N.AMERICA	????		Death				
1210	?	- 1988	1008	1009	WBNP	- 1988	6/88	Hatch		S-2	UNBANDED	
					N.AMERICA	????		Death				

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**TOTALS: 68.73.70 (211)**

Compiled by: Sheri Snowbank thru International Crane Foundation

Data current thru: 31 Dec 1988

**ISIS/SPARKS**  
22 Jan 1992

WOOD BUFFALO NATIONAL PARK WHOOPING CRANE  
COMPOSITE NESTING AREA (CNA) HISTORIES

This summary is completed to the best of our knowledge at this time. Due to the difficulties in observing the wild populations there are bound to be discrepancies in data.

Glossary of Terms:

**KLEWI:** Main breeding area which is broken down into smaller composite nesting areas-CNA.

**K-1:** Name of the CNA a particular pair inhabits. Letter indicates breeding area and number the indicates its historical appearance.

**Winter Territory:** The annual wintering grounds held by the pair according to Aransas National Wildlife Refuge (ANWR) records.

**Pair Observations:** The year and any observation made of the pair and reference. SP refers to same pair as previous year.

**Banded Chicks:** Chicks banded by the Canadian Wildlife Service (CWS) team.

8/77

Nest #/Year the egg was originally found. **Bold** indicates living bird.

(F)

Sex of Chick: F=Female, M=Male, U=Unknown.

09802

Last 5 digits of the metal CWS band placed on the chick.

**Red-Green** Color ID leg bands. Color/color is division of colors on one leg. Color-color is the separation between left and right leg.

**Unbanded Chicks:** The year(s) the pair had chicks that weren't banded.

**Egg Switch:** Year and location of each egg switch between nests relevant to this CNA.

in out

'71 (K-7)

In 1971 one of K-7's eggs went out to replace K-3's eggs.

'85 (K-3)

In 1985 one of K-3's eggs was brought in to replace K-s eggs.

**Gray's Lake:** ID# of eggs taken for the Gray's Lake Experiment which are still alive.

**Captive Offspring:** Year, name if known, ID # and life (live, dead, or dead with living young) of birds brought into captivity through capture or as eggs.

\*: An asterisk denotes discrepancies between ANWR and Kuyt (CWS) Data.

CNA SUMMARIES

KLEWI

K-1

Winter Territory:  
N. Sundown Bay

Pair Observations:

Same unbanded pair 1967-1988.  
1984 unbanded, same pair(SP) - Kuyt '87  
1986 SP  
1988 male(?) died at ANWR - ANWR  
1989 No birds seen in summer

Banded Chicks:

8/77	8/78	9/79	11/80	2/81	9/85
(F)	(U)	(M)	(F)	(M)	(F)
09802	09811	09826	01805	01808	01844
Red-Green	Nil-RWR	r/w-BWB	r/b-red	r/w-Green	WBW-WBW
					Foster K-3
10/86	6/87	4/88			
(F)	(U)	(U)			
01854	01882	01890			
o/y-B	YBY-y/g	WbW-GwG			

Unbanded Chicks:

1984

Egg Switch: in out  
'78 (K-7)  
'85 (K-3)  
'86 (S-13)

Captive Offspring:

1968, Rattler, 68-002 live  
1969, Klewi, R6/221 live  
1971, Mrs. C, 71-001 live

K-2

Winter Territory:  
Middle Sundown Bay

Pair Observations:

Possibly same unbanded pair 1967-90  
1984 unbanded - Kuyt '87  
1986 SP  
1990 SP - Kuyt Data

Banded Chicks:

7/78	15/83	23/84	13/86	7/87
(M)	(U)	(F)	(M)	(U)
09812	09819	01825	01850	01877
RWR-White	Yellow-b/b	b/y-b/y	White/o	YBY-YBY

**Unbanded Chicks:**  
1989, 1990

**Egg Switch:** in out  
\*'88(K-4) '88 (K-3)

**Captive Offspring:**  
1968, Ursula, 13-016 live  
1990, Baratux, 130031 live

\*ANWR data supports '88(K-4) chick raised in K-2 winter territory.

**K-3 (Pistol Island)**  
**Winter Territory:**  
Cottonwood Bayou

**Pair Observations:**  
Probably same unbanded pair 69-90. Pair has a history  
of eggs not hatching.  
1976 unbanded  
1980 nest abandoned then renested after pick-up - Kuyt '81a  
1983 unbanded  
1984 unbanded pair - Kuyt '87  
1985 definitely one unbanded of pair  
1986 SP  
1990 SP - Kuyt data

**Banded Chicks:**  
13/78  
(U)  
09813  
White-RWR

**Unbanded Chicks:**  
1980, 1982

**Egg Switch:** in out  
'85 (K-1) '86 (K-14)  
'88 (K-2)  
'90 (K-10)

**Captive Offspring:**  
1971, WB 430 Dead  
1974, 254/B2 Dead-Possible chick  
1990, Milt, 130032 Live



K-4

**Winter Territory:**

North Cottonwood Bayou

**Pair Observations:**

- Unbanded 70-90
- 1976 unbanded
- 1981 nest abandoned - Kuyt data
- 1983 nest abandoned - Kuyt data
- 1984 Unbanded - Kuyt '87
- 1987 nest destroyed and abandoned - Kuyt data
- 1988 at least one bird unbanded (nested)
- 1990 SP - Kuyt data

**Banded Chicks:**

2/77	6/80	6/82	7/84	13/85	13/88
(U)	(M)	(U)	(M)	(F)	(U)
09807	01804	01815	01821	01843	01893
Nil-Red	Red-R/W	B/W-Red	Y-W	WBW-BYB	Green-White
					*Foster K-2

**Unbanded Chicks:**

1979, 1987, 1989

**Captive Offspring:**

1974, WB 249	Dead
1984, 84-002	Live

\*ANWR data shows 13/88 wintering on K-2 territory

K-5

**Winter Territory:**

None mentioned by ANWR

**Pair Observations:**

- 1976 unbanded
- 1980 unbanded
- 1981 unbanded
- 1983 one unbanded
- 1984 unbanded - Kuyt '87
- Chick WbW-Y in fall was with R-r/w and nil-high silver - ANWR
- 1986 Red-Red/White and ?Green-Red 09801(now Nil-Silver) - Kuyt data
- 1987 Red/White (now) metal low - Kuyt data
- 1988 R-R/W now Red-Silver (6\80) - Kuyt data
- 1989 male faded Red-red, female metal band on left leg- Kuyt data
- 1990 SP - Kuyt data

**Banded Chicks:**

6/77	8/79	8/80	18/83	25/84	28/85
(U)	(U)	(F)	(M)	(M)	(U)
09809	Red-BWB	01802	09818	01826	01845
Red-Nil	Nil-BWB	R-B/R	B/B-yellow	W Black W-Yellow	GWG-GWG

20/86	16/87	10/88	10/88
(M)	(U)	(U)	(U)
01849	01878	01894	01891
Nil-Yellow	YBY-White	GWG-BWB	GWG-R
			Foster K-6

**Unbanded Chicks:**

1991

**Egg Switch:** in out  
'88 (K-6)

**Captive Offspring:**

1969, Pax, R13/218	Live
1974, WB243	Dead
1987, 870035	Dead
1989, 89079	Dead
1990, Kohler, 130029	Live

**K-6**

**Winter Territory:**

East Dunham Bay

**Pair Observations:**

Possible switch 84-85, female died, new pair or female  
- Kuyt data  
1970-1982 SP - Kuyt data  
1983 unbanded  
1984 unbanded - Kuyt '87  
1985 unbanded pair  
1990 SP - Kuyt data

**Banded Chicks:**

7/77	10/78	2/79	9/80	6/84	28/87
(M)	(M)	(F)	(F)	(F)	(U)
09808	09814	09823	01803	01827	01883
Blue Red	RWR-Blue	BWB-Red	B/R-Red	Yellow-W Black W	YBY-O

**Unbanded Chicks:**

1986, 1989

**Egg Switch:** in out  
'88 (K-5)

**Gray's Lake:**

GL-76/7 & 78/10

**Captive Offspring:**

1967, 271/14	Dead
1968, Killer 68001	Dead, living chicks
1969, R12/219	Dead
1971, WB431	Dead
1987, 87-042	Live
1988, 88-058	Live
1990, Ole' 13-036	Dead

**K-7**

**Winter Territory:**

W. Welder Point

**Pair Observations:**

Unbanded birds from 69-78. Eggs didn't hatch. - Kuyt '81b

1976 nest abandoned, reneest failed - Kuyt '87 & '81a

1977 no nest - Kuyt '81b

1978 considered to have poor reproduction rate - Kuyt '81b

1979 hatch died - Kuyt '81b

1980 Low reproductive rate - Kuyt data

1984 considered to have poor reproduction rate, unbanded - Kuyt '87

1989 R-BWB and unbanded - Kuyt data

Winter territory still has unbanded pair - ANWR

1990 SP - Kuyt data

Winter territory still has unbanded pair - ANWR

**Banded Chicks:**

6/83	2/86	2/86	3/87	2/88
(U)	(M)	(U)	(U)	(U)
09821	01853	01862	01875	01889
White-R/Y	WBW-Blue	o-r/b	YBY-BWB	R-W

Foster K-10

**Unbanded Chicks:**

1980, 1991

**Egg Switch:**

in	out
'85 (S-4)	'86 (K-10)
'78 (K-1)	

**K-8**

**Winter Territory:**

East Welder Point

**Pair Observations:**

Unbanded pair 79-90  
1981 No nest - ANWR  
1983 unbanded  
1984 unbanded - Kuyt '87  
1985 definitely one unbanded in pair  
1986 unbanded  
1988 early nesters - Kuyt data  
1990 SP - Kuyt data

**Banded Chicks:**

17/79	15/80	7/83	*11/84	23/85	3/86
(U)	(M)	(U)	(F)	(M)	(F)
09825	01806	09820	01824	01841	01855
BWB-r/w	r/w-R	b/w-r/b	R/R-WBW	BYB-WBW	Red-Yellow

**Unbanded Chicks:**

1987, 1989, 1990, 1991?

**Captive Offspring:**

1983, Kate 83-004           Live  
1990, Kubley 13-030       Dead

\*ANWR has 3/84 as 1984 chick instead of 11/84.

**K-9**

**Winter Territory:**

South San Jose

**Pair Observations:**

Could be the forerunner to K-15 based on winter use area.  
Red-White and unbanded bird 80-83  
1980 3 year old Red-White (12/77) parents S-1 nest with  
unbanded bird - nest was destroyed and abandoned  
- Kuyt '87  
1981 4 year old Red-White, same as above - Kuyt data  
1982 5 year old Red-White, same as above - Kuyt data  
1983 6 year old Red-White, same as above - Kuyt data  
1984 did not return - Kuyt '87

**K-10**

**Winter Territory:**

Ayres Island

**Pair Observations:**

Unbanded pair 81-90  
1981 unbanded first nest  
1982 no nest  
1983 same pair as 1981  
1984 unbanded - Kuyt '87  
1985 Red/Red-Blue(16/82) not nesting (ANWR doesn't mention)  
(Could have been bird wandering around nest site)  
1990 SP - Kuyt data

**Banded Chicks:**

19/83	15/85	16/88
(F)	(M)	(U)
09822	01840	01892
r-Yellow	RWR-Orange	Red-Green

**Unbanded Chicks:**

1987, 1989, 1990

**Egg Switch: in**

out

'89 (SK-5)

'90 (K-3)

**Captive Offspring:**

1986, Jack 86-033                      Live

**K-11(Snoopy Lake)**

**Winter Territory:**

Blackjack Point

**Pair Observations:**

Unbanded pair 83-90.    ANWR reports unbanded pair on  
Point 1977-1985  
1984 unbanded - Kuyt '87  
1985 SP  
1987 unbanded pair, female lost '87 - Kuyt data  
1988 y/b-o female and unbanded male 9/86 - ANWR data  
1989 Blue-Orange and unbanded male - Kuyt data  
1990 SP - Kuyt data

**Banded Chicks:**

16/85	*11/86	23/87
(F)	(U)	(U)
01842	01863	01885
BWB-GWG	o/w-BWSP	r/g-BWB

**Unbanded Chicks:**

1983, 1990

**Captive Offspring:**  
1987, Saddleback 87-033 Live

\*ANWR has 11/86 as having BWsp-o/w band.

**K-12**

**Winter Territory:**  
North Sundown Island

**Pair Observations:**

83-88 One banded Bird  
1983 first year Nil White orig. RWR-White (7/78)(M)  
Parents K-2. - Kuyt data  
1984 Nil White and wounded bird, one banded - Kuyt '87  
1985 same as above - Kuyt data  
1986 same as above  
1988 Pair failed to arrive in ANWR - ANWR data  
1989 No pair present - ANWR data

**Banded Chicks:**

19/84	10/85	19/86	8/87	3/88
(F)	(U)	(F)	(U)	(U)
01820	01838	01847	01876	01895
BWSP-BWSP	W-G	o-Red	Green-YBY	GwG-RwR
				Foster K-16

**Egg Switch:** in out  
'88 (K-16)

**K-13**

**Winter Territory:**  
Cottonwood Bayou A

**Pair Observations:**

Possibly unbanded pair from K-5 - ANWR  
1984 unbanded - Kuyt '87  
1986 SP  
1988 SP  
1989 unbanded - Kuyt data  
1990 SP - Kuyt data

**Banded Chicks:**

17/85	29/87
(M)	(U)
01837	01884
Blue-RWR	Y/G-Yellow

**Unbanded Chicks:**  
1984, 1986, 1989

**Gray's Lake:**  
GL-15/86

**Captive Offspring:**

1985, Woody 13-012            Live  
1989, 89-089                 Dead

If pair confirmed as unbanded K-5 pair captive and banded young prior to 1984 should move to K-13 notes.

**K-14**

**Winter Territory:**

S.Redfish Slough

**Pair Observations:**

1984 r/w-BwB (9/79(M) Parents K-1 and unbanded bird, infertile eggs. One banded - Kuyt '87  
1985 Red/White-BWB and unbanded bird, infertile eggs. - Kuyt data  
1986 one banded  
1987 Red/White-Nil - Kuyt data  
1988 Red/White-BWB(Red/White-Nil) and 1984 bird, female died at ANWR in fall. - Kuyt data  
1989 Red/White-Nil and new unbanded female - Kuyt data  
1990 r/w-nil single in fall - ANWR data

**Unbanded Chicks:**

1988, 1989

**Egg Switch:**    in            out  
                  '86 (K-3)

**Captive Offspring:**

1987, Andre' 82-027            Live  
1991, 91-077                    Dead

**K-15**

**Winter Territory:**

Jay Bird Point

**Pair Observations:**

Once called K-U, but became vacant in 1970.  
85-90 new pair. An Alberta bird (one banded) and unbanded bird.  
1985 Green-Red/White (3/81)(M) parents Alta - Kuyt data  
1986 G-R/W - Kuyt data  
1987 one banded White/Red - Kuyt data  
1988 (?)G-R/W and R/W-BWB - Kuyt data  
1989 one banded White/Red and unbanded bird - Kuyt data  
1990 SP - Kuyt data

**Banded Chicks:**

16/86	13/87	22/88
(F)	(U)	(U)
01852	01874	01887
Yellow-o	Y Black Y-Green	RwR-BwB

**Unbanded Chicks:**  
1989?

**Egg Switch:** in out  
'85 (Alta)

**Captive Offspring:**

1968, "259" R8/259	Dead, living chicks
1969, Ulysses 13-017	Live
1989, Mousse 13-026	Live

**K-16**

**Winter Territory:**  
Third Chain

**Pair Observations:**

1986 Yellow-b/b (15/83) and nil-nil - Kuyt data  
1987 Y-b/b - Kuyt data  
1989 female unbanded  
1990 SP - Kuyt data

**Banded Chicks:**

28/86	30/87
(F)	(U)
01848	01880
WBW-o	y/b-YBY

**Unbanded Chicks:**  
1989, 1990

**Egg Switch:** in out  
'88 (K-13)

**Captive Offspring:**

1988, 1425 88-055	Live
1989, Bosque 13-028	Live
1990, Herfy 13-033	Live

**SASS**

**S-1**

**Winter Territory:**  
Cedar Bayou

**Pair Observations:**

Unbanded 66-81 one had neck growth. - Kuyt '81b  
83-90 (?)RWR-Nil(12178(M) or R-Nil, Now Nil Silver &  
female most likely from old pair.  
1977 one of pair died - Kuyt '81b  
1984 Unbanded pair - Kuyt '87  
1985 Metal band first noticed in summer - ANWR data  
1989 definitely one banded  
1990 SP - Kuyt data



**Banded Chicks:**

12/77	6/78	3/83	4/84	9/86
(M)	(U)	(U)	(M)	(F)
09803	09815	09830	01819	01857
Red-White	Blue-RWR	White-Green	BWSP-Y	Blue-O/Y

**9/88**

(U)  
01897  
GWG-White

**Unbanded Chicks:**

1989, 1990

**Egg Switch:**    in                    out  
    '88 (S-15)  
    '89 (S-16)  
                              '90 (S-11)

**Gray's Lake:**

GL-3/83

**Captive Offspring:**

1967, Ektu R18/268	Dead, live chick
1968, ID UNK	Dead
1971, Mrs. Screwbill	Dead, live chick
1990, Franson 13-038	Dead

**S-2**

**Winter Territory:**

Redfish Slough

**Pair Observations:**

Possibly most consecutive years(22+) of nesting.  
1976 wildbird  
1978 no nest - Kuyt '81b  
1979 Possible new breeding pair or replacement of one of the old pair. - Kuyt '81b  
1984 unbanded pair - Kuyt '87  
1986 at least one unbanded - Kuyt data  
1988 unbanded pair - Kuyt data  
1990 SP - Kuyt data

**Banded Chicks:**

*5/77	4/82	2/83	* 3/84	3/85
(M)	(U)	(U)	(F)	(M)
09804	01814	09831	01828	01835
White-Red	Red-B/W	B/R-White	W Black W-Red	White-RWR

**\*5/86**

(F)	(U)
01858	01896
Yellow-B/O	Red-GWG
	Foster S-14

Unbanded Chicks:  
1987, 1989

Egg Switch: in out  
'88 (S-14)  
'90 (S-New 23/90)

Captive Offspring:  
1967, Screwbill 270/R19 Dead, live chick  
1968, WB266 Dead  
1969, Leg1 Dead  
1971, Patuxent WB425 Dead, possible chick  
1974, 252/B3 Dead

\*ANWR has 5/77 as S-8's chick,  
3/84 as raised by K-8,  
and y/b-o as 5/86's color band.

S-3

Winter Territory:  
Egg Point/ Lamar

Pair Observations:

Unbanded pair (67-78) Non-fertile eggs. - Kuyt '81b  
Possibly taken over by S-7 ? as to where S-3 went to  
(80 nest) - Kuyt '81b  
1977 considered to have poor reproduction rate - Kuyt '81b  
1978 Possible pair switch of at least one of the pair  
1984 unbanded pair - Kuyt '87  
1990 SP - Kuyt data

Banded Chicks:

7/79	3/82	9/83	20/83	21/84
(M)	(U)	(U)	(U)	(M)
09827	01813	09832	09833	01818
BWB-r/g	White-R/R	Yellow-y/r	BWSP-Red	BWSP-White
2/85	1/86	12/87	7/88	7/88
(F)	(M)	(U)	(U)	(U)
01832	01859	01867	01899	01898
Yellow-Red	Yellow-Red	YBY-RWR	GwG-Yellow	GWG-WBW
				Fostered S-12

Unbanded Chicks:  
1989, 1990

Egg Switch: in out  
'77 (S-4)  
'78 (S-4)  
'88 (S-12)

Gray's Lake:  
GL-7/79

**Captive Offspring:**

1964, Canus 201/R21	Live
1967, Big Ed WB267	Dead
1968, WB264	Dead
1987, Whoopi 87-034	Dead
1990, Josh 13-035	Live
1991, 91-071	Live

**S-4**

**Winter Territory:**

Middle Sundown Island

**Pair Observations:**

Unbanded 67-84 ? CNA taken over by S-11 in '86.  
1977 poor reproductive rate - Kuyt data  
1983 unbanded  
1984 unbanded pair - Kuyt '87  
1985 definitely one unbanded  
1986 definitely one unbanded  
1987 Pair disappeared after nesting (ANWR)  
1988 No birds present - ANWR data

**Banded Chicks:**

11/77	4/78	6/79	1/82	20/83	12/85
(U)	(U)	(M)	(U)	(U)	(M)
09805	09816	09828	01811	09833	01831
Red-Red	RWR-Orange	BWB-g/r	w/r-Green	BWSP-R	Green-Green

**\*10/87**

(U)  
01868  
Y-Y Black Y

**Egg Switch:** in out  
'86 (Lob) '85 (K-7)  
'77 (S-3)  
'78 (S-3)

**Captive Offspring:**

1968, ID Unk	Dead
1969, WB220	Dead
1971, WB426	Dead
1974, B1/250	Dead
1983, R89	Dead

\*ANWR data shows 10/87 wintering with S-11 pair.

S-5

Winter Territory:  
Sundown Island

Pair Observations:  
Unbanded 68-80 - Extinct  
1976 unbanded

Banded Chicks:

1/77  
(U)  
09806  
Red Blue

Captive Offspring:

1968, R11/263                      Dead  
1974, WB244                         Dead

S-6

Pair Observations:  
Unbanded 66-76 then abandoned nest site - Extinct - Kuyt  
'81b

Captive Offspring:

1968, ID UNK                         Dead  
1969, WB217                         Dead  
1971, WB427                         Dead

S-7

Pair Observations:  
Question on the CNA 72-? - Extinct

Captive Offspring:

1974, WB240                         Dead

S-8

Winter Territory:  
South Sundown Bay

Pair Observations:

Unbanded pair 71-90  
1981 unbanded  
1982 unbanded  
1983 SP  
1984 unbanded pair - Kuyt '87  
1987 early nesters (Apr. 23-24) -Kuyt data  
1988 early nesters - Kuyt data  
1990 SP - Kuyt data

**Banded Chicks:**

1/78	2/80	2/82	2/84	1/85	* 6/86
(U)	(M)	(F)	(F)	(F)	(U)
09817	01801	01812	01829	01836	01860
Orange-RwR	Red-r/b	Green-w/r	Blue-White	White-Red	BWSP-o/w

<del>2/87</del>	2/87	1/88
(U)	(U)	(U)
01870	01866	01900
R-YbY	YBY-GWG	Red-Red
	Foster S-9	

**Unbanded Chicks:**

1989, 1990

**Egg Switch:** in out  
'87 (S-9)

**Captive Offspring:**

1971, WB428	Dead
1974, WB242	Dead

\*ANWR has o/w-BWsp as 6/86's color band.

**S-9 (Hippo Lake pair)**

**Winter Territory:**

Middle Matagorda

**Pair Observations:**

Single banded Red-Nil (6/77)(M) Parents K-5 80-88(?)  
at least.  
ANWR RWR-nil starting in summer 1983  
1980 infertile, nest abandoned Red-Nil - Kuyt data  
1981 nest failed Red-Nil - Kuyt data  
1982 Red-Nil - Kuyt '87  
1983 Red-Nil becomes Nil-Silver, infertile eggs - Kuyt data  
1984 one banded - Kuyt '87  
1985 Nil-Silver and (?)RWR-Nil - Kuyt data  
1986 Nil-Silver and unbanded bird  
1987 RWR-Nil (now Nil-Silver) - Kuyt data  
1989 Nil-High Silver and unbanded bird - Kuyt data  
1990 abandoned nest before laying - Kuyt data  
This pair wintered in 1990-91 raising a sandhill chick -  
ANWR

**Banded Chicks:**

16/84	20/85
(M)	(F)
01817	01833
Yellow-BWSP	Yellow-Green

**Egg Switch:** in out  
'87 (S-8)

Gray's Lake:  
GL-8-83

S-10

Winter Territory:  
None defended - N. Sundown Island

Pair Observations:

Both banded 1983 & 84  
1983 BWB-Green\Red and Red-Green, abandoned nest - Kuyt '87  
1984 BWB-Green\Red and Red-Green - Kuyt '87

S-11

Winter Territory:  
Spalding Cove

Pair Observations:

ANWR has R-r/b (8/80) paired with r/b-R (9/80)  
1984 Red-Red and Red-Blue - Kuyt '87  
1985 Red-Red and Red-? - Kuyt data  
1988 male unbanded, female ?-Red  
1989 No nest - Kuyt data

Unbanded Chicks:  
1988, 1990

Egg Switch: in out  
'88 (Lob) '90 (S-1)

S-12

Winter Territory:  
Pipeline Flats

Pair Observations:

One banded 84-90. RWR-Orange (4/78)(M?) parents S-4.  
?Mated with BWB-r/w (17/79) Parents K-8. - Kuyt '87  
1984 RWR-Orange and ?-RWR - Kuyt '87 & Kuyt data  
1985 RWR-faded orange and BWB-R/W, now metal H. left - Kuyt  
data  
1986 RWR-faded orange (now Nil-0) and Silver(H)-Nil - Kuyt  
data  
1987 SP - Kuyt data  
1990 SP - Kuyt data

Unbanded Chicks:  
1989, 1990

Egg Switch: in out  
'88 (S-3)

**S-13**

**Winter Territory:**

S. Matagorda

**Pair Observations:**

1986-88 Two banded birds  
1986 White-Red and red-Yellow, first year - ANWR data  
1987 r-Yellow(19/83) and White-Red(10/82) - Kuyt data  
1988 White-Red now White-Nil, nest destroyed - Kuyt data  
1989 nest not located, presumed present due to  
behavior. - ANWR data  
1990 too dry - Kuyt data

**Banded Chicks:**

26/87

(U)

O1871

BWB/YBY

**Egg Switch:** in out  
'86 (K-10)

**Captive Offspring:**

1987, 87-038 Dead

**S-14**

**Winter Territory:**

Three Island

**Pair Observations:**

One banded Blue-White (2/84)(F) Parents S-8  
1989 Blue-White and unbanded bird - Kuyt data  
1990 SP - Kuyt data

**Unbanded Chicks:**

1989

**Egg Switch:** in out  
'88 (S-2)

**Captive Offspring:**

1988, 88-059 Dead  
1988, 88-063 Dead

S-15

Winter Territory:  
Boat Ramp

Pair Observations:

1987 Yellow-BWSP(16/84)(M) Parents S-9, raised unbanded chick. Unbanded Female lost 12-87. - ANWR data  
1988 Yellow-BWSP (now Yellow-Nil) and WbW-WbW (13/85(F) parents K-3 - ANWR data  
1989 SP - Kuyt data  
1990 SP, too dry - Kuyt data

Banded Chicks:

32/87

(U)

01869

RwR-YbY

Unbanded Chicks:

1989

Egg Switch: in out  
'88 (S-1)

Captive Offspring:

1988, 88-060	Live
1988, 88-062	Live
1989, 89-089	Dead

S-16

Winter Territory:  
S.Fulgrum

Pair Observations:

1988 White-Blue (28/84)(F) Parents by K-7 and B/W-R/B (now White-Red) (7/83)(M) Parents K-8, nest destroyed. ANWR makes no reference to this pair.  
1989 White-Blue and Yellow-Green 20/85 (now Yellow-Nil) - Kuyt data  
1990 Yellow-Nil and Green-Yellow (ANWR doesn't verify) Feels RwR-YbY (32/87(U) parents S-15 - Kuyt data

Egg Switch: in out  
'89 (S-1)

S-New

Winter Territory:  
S.Shoalwater Bay

Pair Observations:

1989 29/89  
1990 23/90  
1989 ByB-WbW (23/85(M) and Yellow-Yellow (24/84(F) - Kuyt data



**Unbanded Chicks:**  
1990

**Egg Switch:** in out  
'90 (S-2)

**Captive Offspring:**  
1990, O'Malley 13-037 Live  
1990, Kane 13-039 Live

**S-New**

**Winter Territory:**  
Salt Creek

**Pair Observations:**  
1990 o/w-BWSP and Nil-Nil - Kuyt data

**Unbanded Chick:**  
1990

**SASS-KLEWI**

**SK-1(Stubby Lake)**

**Winter Territory:**  
South Sundown Island

**Pair Observations:**  
Unbanded 80-87(?)  
1984 unbanded - Kuyt '87  
1985 at least one bird unbanded - Kuyt data  
1987 unbanded one adult lost 12/87 - ANWR data  
1988 No nest present

**Banded Chicks:**

16/82	21/83	8/85	4/86	20/87
(U)	(U)	(F)	(M)	(U)
01816	09829	01834	01856	01872
r/r-Blue	y/g-Green	BYB-BYB	Blue W-Black W	YBY-Red

**Captive Offspring:**  
1982, Matagorda 82-004 Dead

**SK-2**

**Winter Territory:**

North Dunham Bay

**Pair Observations:**

84-90 At least three pair switches  
1984 unbanded and banded - Kuyt '87  
1985 Blue-Red (1/77(M) parents S-5 and unbanded - Kuyt data  
1986 Blue-Red (now Blue-Nil) Dead -ANWR data  
1987 widow and new male - Kuyt data  
1988 widow and unbanded - Kuyt data  
1989 unbanded, female disappears Jan. 1990 - ANWR data  
1990 unbanded male and Red(faded)-Yellow(3/86(F) parents K-8  
- Kuyt data

**Egg Switch:** in out  
'87 (Lob)

**Unbanded Chicks:**

1983, 1984, 1989, 1991

**Captive Offspring:**

1989, Aransas 13-027 Live  
1991, 91064 Dead

**SK-3 (Twin Lake)**

**Winter Territory:**

Twin Lakes

**Pair Observations:**

1984 Red-BWB(8/79(M), possibly BWB-R is mate - Kuyt '87  
1985 Red-BWB (now Nil-BWB) and unbanded - Kuyt data  
1988 SP  
1989 Nil-BWB (now metal) and unbanded female  
1990 Lost unbanded female, Red-BWB (lost all bands) and  
BWB-GWG(85)(?) - Kuyt data

**Banded Chicks:**

24/84	22/85	22/86	21/87	20/88
(F)	(M)	(F)	(U)	(U)
01822	01839	01861	01873	01888
Yellow-Yellow	White-White	R/B-O	White-Y Black-Y	Y-GWG

**Unbanded Chicks:**

1989

**Captive Offspring:**

1987, 934 87-043 Live  
1988, 1423 88-046 Live

**SK-4 (Whale Lake)**

**Winter Territory:**

Dunham Peninsula

**Pair Observations:**

1987-90 Aransas records female as BWB-R. Formed Brady Bunch on Dunham Peninsula in 84-85. Changed winter territory from N. Dunham Bay to M. Sundown Isl. in 87-88 & S. Sundown Isl. in 88-89. Female I.D. uncertain  
1984 BWB-R (2/79(F) parents K-6 lost unbanded male during fall migration - ANWR data  
1985 Female didn't nest - ANWR data  
1987 one banded possibly Red/Orange on right leg (BWB-R?) - Kuyt data  
1988 low silver-nil in fall  
1990 BWB-R not observed at Aransas, maybe band fell off - ANWR

**Banded Chicks:**

26/84	13/87	2/88
(U)	(U)	(U)
01823	01881	01886
W-B	Y/B-YBY	RWR-GWG

**Unbanded Chicks:**

1986, 1989, 1990

**Captive Offspring:**

1988, Tarzan 1424	Live
1990, Chip 13-034	Live

**SK-5**

**Winter Territory:**

Shoalwater Bay

**Pair Observations:**

1989 one banded possibly B/W-R/B (7/83(M) now nil-r parents K-8 and Nil(?). - Kuyt & ANWR data  
1990 No chicks, same pair - Kuyt data

Egg Switch: in out  
'89 (K-10)

**Unbanded Chicks:**

1989

**Alberta**

**Winter Territory:**

Vinson Slough

**Pair Observations:**

77-90 Unbanded  
1983 abandoned nest - Kuyt data  
1984 Unbanded - Kuyt '87

**Banded Chicks:**

3/81	17/87	17/88
(M)	(U)	(U)
01809	01865	09834
Green-R/W (Radio)	GWG-YBY	G-GwG

**Unbanded Chicks:**

1984, 1989, 1990

**Egg Switch:** in out  
'85 (K-15)

**Captive Offspring:**

1982, 8251	Live
1986, Alta 86-027	Live

**Alberta-New 2**

**Winter Territory:**

Pat's Bay

**Pair Observations:**

1988 b/b-Y and BWSP-BWSP nest in unknown location  
1989 BWSP-BWSP shot in 1/89  
1989 b/b-Y repairs with Y-R - Kuyt data  
1990 32-90 nest # - Kuyt data

**Unbanded Chicks:**

1988, 1990?

**Alberta-New 1**

**Winter Territory:**

None mentioned by ANWR

**Pair Observations:**

1990 31-90 W-ybY and Y-YbY present - Kuyt data

**Lobstick**

**Winter Territory:**

West Dunham Bay

**Pair Observations:**

1982 RWR-B (10178) and unbanded bird - Kuyt '87 & Kuyt data  
1984 one banded - Kuyt '87 & Kuyt data  
1985 RWR-B  
1986 RWR-B  
1990 SP - Kuyt data  
Only metal band remains above foot of RWR-B (Low Silver-  
nil) - ANWR

**Banded Chicks:**

10/82	18/85	8/86	1/87	5/88
(U)	(M)	(M)	(U)	(U)
01810	01830	01846	01864	09835
W-R(Radio)	Green-Yellow	o-WBW	YBY-Y	GwG-Green

**Egg Switch:** in out

'86 (S-4)  
'87 (SK-2)  
'88 (S-11)

**NYARLING**

**N-1**

**Winter Territory:**  
Mustang Lake

**Pair Observations:**

Unbanded pair nesting 1971 - present  
1979 abandoned nest - ANWR data  
1980 didn't visit nest - Kuyt data  
1981 bird on nest - Kuyt data  
1982 built and abandoned two nests - Kuyt data  
1983 won't rise off nest  
1984 unbanded pair -Kuyt '87 & Kuyt data  
1985 same as above  
1988 same as above - Kuyt data  
1989 same as above - Kuyt data  
1990 SP - Kuyt data

**Banded Chicks:**

10/77	12/78	7/81	17/86
(F)	(U)	(F)	(F)
09801	09810	01807	01851
Green-Red	RWR-Nil	White-r/w	o(nil)-White

**Unbanded Chicks:**

1984, 1987, 1988, 1989, 1990

**Egg Switch:** in out

'89 (N-3)

**Captive Offspring:**

1971, WB433	Dead
1974, Hal 74-001	Live

**N-2**

**Winter Territory:**  
None mentioned by ANWR

**Pair Observations:**

77-79 - Kuyt '87

N-3

Winter Territory:  
Dunham Point

Pair Observations:

1989 unbanded, most likely 1986 birds - Kuyt data

1990 At Aransas female O-R/B presumably present in 1989 and  
1990 - ANWR data

Egg Switch: in out  
'89 (N-1)

Unbanded Chicks:  
1989

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**SUMMARY TABLE OF CNA GENETIC REPRESENTATION**  
 (Offspring which are alive or possibly reproduced before they died.)

Pair CNA#	WILD		CAPTIVE		G. LAKE WBNP EGG#
	BANDED Band#	UNBANDED Year Hatch	Studbook and Name/ID#		
K-1 Pair Gone 1989	09802 09811 09826 01805 01844 01854 01882	1984?	1031 1040 1053	RATTLER KLEWI MRS.C	
K-2	09819 09825 01877 09812dead	1989 1990	1027 1190	URSULA BARATUX	
K-3		1980? 1982?	1062 1192	74-012?dead MILT	
K-4	01804 01821 01843		1127	84-002	
K-5	09809 09824dead 01802 09818		1042	PAX	
	01849 01878 01894		1189	KOHLER	
K-6	09814 09808?dead 09823?dead 01803		1032	KILLERdead	76/7 78/10
	01883		1153 1165	87-042 88-058	
K-7	01862 01889	1980?			



<b>K-8</b>	09825      1987? 09820dead 1989 01824      1990 01841 01855	1119      KATE	
<b>K-9</b>	Pair Gone 1984		
<b>K-10</b>	09822      1987? 01840      1989 1990	1145      JACK	
<b>K-11</b>	01842      1983? 01863 <hr/> 1990	1148      SADDLEBACK <hr/> 	
<b>K-12</b> Pair Gone	01820?dead 01838 01847?dead 01876		
<b>K-13</b>	01837 01884	1138      WOODY	15/86
<b>K-14</b>	<hr/> 1988 1989	1147      ANDRE' <hr/> 	
<b>K-15</b>	<hr/> 01887	1036      "259"dead 1041      ULYSSES <hr/> 1179      MOUSSE	
<b>K-16</b>	1989 1990	1164      88-055 1182      BOSQUE 1193      HERFY	
<b>S-1</b>	09803dead <hr/> 01857      1989 01897      1990	1022      EKTU 1050      MS.SCREWBILL dead <hr/> 	<hr/> 3/83

S-2	09804?dead ----- 01835      1987? 01858      1989 01896	1020    SCREWBILLdead 1046    PATUXENTdead -----	
S-3	----- 09833?dead1989 01832      1990 01859 01867	1019    CANUS ----- 1195    JOSH 1212    91-071	79-7
S-4 Pair Gone 1988	09805?dead 09816 09833?dead 01831?dead 01868		
S-5 Pair Gone	09806?dead		
S-6	EXTINCT	EXTINCT	
S-7	EXTINCT	EXTINCT	
S-8	01801      1989 01829      1990 01836?dead 01870 01866 01900		
S-9	01817 01833		8-83
S-10	Pair Gone 1984		
S-11	1988 1990		
S-12	1989 1990		
S-13	01871		
S-14	1989		

<b>S-15</b>	01869		
	1989	1167 1168	88-060 88-062
<b>S-16</b>			
<b>S-NEW</b>	1990	1197 1199	O'MALLEY KANE
<b>S-NEW</b>	1990		

<b>SK-1</b>	01816 01834		
<b>SK-2</b>	1983? 1984?		
		1180	ARANSAS
<b>SK-3</b>	01822 1989 01839?dead 01861 01873	1154 1162	87-043 88-046
<b>SK-4</b>	01823?dead		
	01881 1986? 01886 1989 1990	1163 1194	TARZAN CHIP
<b>SK-5</b>	1989		

<b>ALTA</b>	01809 1984? 01865 1989 09834 1990	1077 1144	8251 ALTA
<b>ALTA-N</b>	1988		
<b>ALTA-N</b>			

<b>LOB</b>	01810 01830?dead 01864 09835		
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<b>N-1</b>	09801      1984? 09810      1987? 01851      1988 1989 1990	1063      HAL	
<b>N-2</b>	EXTINCT	EXTINCT	
<b>N-3</b>	1989		

**KEY**

- ? - Question as to whether bird reproduced before dying.  
 == - Definite pair change.  
 --- - Possible pair change.

**SUMMARY OF ANNUAL PRODUCTIVITY OF THE WOOD BUFFALO NATIONAL PARK WHOOPING CRANES**  
 Data Collected by Ernie Kuyt, Canadian Wildlife Service  
 Compiled by Kristi Sprow, Aviculture Intern, International Crane Foundation  
 31 July 1991

Yr	# Nest	# Hatch	% Hatch	# Fledge	% Fledge	# Chicks Arrived at Aransas	% Hatch to Arrive at Aransas	% Nests with a Chick at Aransas
67	9	9	100	9	100	9	100	100
68	10	-	-	-	-	6	-	60
69	11	-	-	-	-	8	-	72.7
70	13	-	-	-	-	6	-	46.2
71	13	-	-	-	-	5	-	38.5
72	15	-	-	-	-	5	-	33.3
73	14	-	-	-	-	2	-	14.3
74	15	-	-	-	-	2	-	13.3
75	16	-	-	-	-	8	-	50.0
76	16	13	81.3	12	75	12	92.3	75
77	17	13	75.6	10	58.8	10	76.9	58.8
78	15	11-15	73.3- 100	8-11	53.3- 73.3	7	46.7 63.6	46.6
79	18	14	77.7	6-14	33.3- 77.8	6	42.9	33.3
80	19	14-15	73.7- 78.9	6	40.0- 42.9	6	40.0- 42.9	31.6
81	17	9	52.9	3-9	17.4- 52.9	3	33.3	17.6
82	17	12	70.6	8	47	6	50	35.3
83	24	13	54.2	10	41.7	7	53.8	29.2
84	16-22	16-22	57.1- 78.6	16-18	57.1- 75.0	15	68.2	53.6
85	28	20	71.4	16-20	80.0- 100	16	80	57.1
86	28	22-24	78.6- 92.9	20-24	71.4- 85.7	20	83.3- 90.9	71.4
87	32	25-26	78.2- 81.2	25-26	78.2- 81.2	25	96.2- 100	78.1
88	30	22	73.3	22	68.8	19	86.4	63.3
89	30	20-27	66.7- 90.0	-	-	20	74.1- 100	66.6
90	32	8	25.0	-	-	-	-	-
<b>Average % (1967-89)</b>			<b>72.3- 78.6</b>		<b>58.7- 70.0</b>		<b>68.3- 72.1</b>	<b>49.8</b>

## Glossary of Terms Used in This Studbook

Stud #	Preliminary Wood Buffalo Studbook number assigned to the crane.
Sex	M = male; F = female; U = sex unknown.
Hatch Date	The year during which the crane hatched.
Sire and Dam	The crane's father and mother. Wild = parent unknown.
Location	WBNP = Wood Buffalo National Park, Canada; ARANSAS = Aransas National Wildlife Refuge, TX;
Date	The date, or estimate thereof, on which the crane hatched or died.
Local ID	The nest number/year the egg was originally found in by the Canadian Wildlife Service.
Death Date	The date, or an estimate thereof, on which the crane died.
Tag/Band	Leg band number assigned to that bird by the Canadian Wildlife Service.
Origin	The WBNP Composite Nesting Area (CNA) from which the bird originated.
Pair	The WBNP Composite Nesting Area (CNA) where the bird established itself as part of a nesting pair.
Band	Color bands assigned to the bird by the Canadian Wildlife Service.

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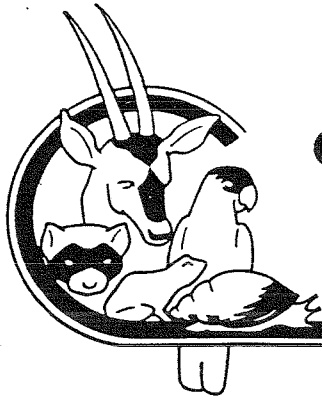
***GRUS AMERICANA***

**WHOOPING CRANE**

**CONSERVATION VIABILITY ASSESSMENT  
WORKSHOP REPORT**

**SECTION 11  
CBSG \ IUCN SSC**





# Captive Breeding Specialist Group

Species Survival Commission  
International Union for the Conservation of Nature and Natural Resources

U. S. Seal, CBSG Chairman

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## CAPTIVE BREEDING SPECIALIST GROUP (Revised 1 January 1992)

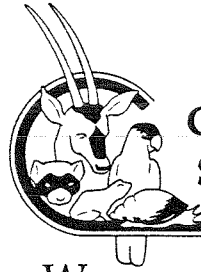
### **Mission**

To conserve and establish viable populations of threatened species through captive propagation programmes and through intensive protection and management of small and fragmented populations in the wild.

### **Terms of Reference**

1. To advise the IUCN, SSC, and the SSC Specialist Groups on the uses of captive propagation for conservation and to organize, facilitate, and monitor international captive propagation programmes.
2. To establish a global network of zoo professionals and zoos to provide facilities and personnel for international collaborative captive propagation programmes for species in danger of extinction.
3. To establish a global network of professionals in captive management, wildlife management, population biology, reproductive biology and technology, and other disciplines to advise on the establishment, development, and conduct of recommended captive propagation programmes of endangered species.
4. To conduct Conservation Assessment and Management Plan (CAMP) workshops and to prepare Captive Breeding Action Plans in collaboration with the appropriate Specialist Groups of SSC and ICBP for all of the vertebrates and selected non-vertebrates. These Plans are to provide analyses of the status of the species in captivity, information on the status of the species in wild, and recommendations for captive propagation programmes.
5. To assist in the organization of captive programmes for species as recommended by the Plans. This would include coordination of studbooks and captive breeding programmes at the global level, recommendations to the regional zoo organizations for selection of species, assisting in arrangements for field studies, and working with relevant Specialist Groups and responsible management agencies to obtain animals from the wild if needed.

6. To assist the adoption and use of effective systems for assembling local and global captive data (such as ISIS, ARKS), and regional systems where appropriate, by all of the world's zoos as essential information resources for support of collaborative captive breeding programmes.
7. To use a global system for continuing collection of information on the status of species in the wild to assist in establishing priorities on a timely basis. This information system would provide a database for the SSC Action Plans, Heritage Species Plans, and assignment of IUCN categories of threat.
8. To assist the SSC and the International Union of Directors of Zoological Gardens with the Heritage Species Programme, specifically the aspects relating to conservation biology.
9. To prepare and distribute a Newsletter to provide a means of communication between all members of the CBSG and the world's zoos. To arrange and hold meetings to facilitate the selection, development, maintenance, and monitoring of collaborative programmes.
10. To conduct Population and Habitat Viability Assessment Workshops, in conjunction with other SSC and ICBP Specialist Groups, as needed to establish the extinction risks for a taxon end to develop the scenarios and recommendations for management actions needed to prevent extinction and to achieve recovery (removal from the threatened species list).
11. To develop, in conjunction with other SSC and ICBP Specialist Groups, Global Master Plans for species as needed and as a basis for providing a focus on the conservation of species in the wild. This would include specific identification of reserves that are in need of support, development of pre-release programmes for species that are to be returned to the wild, and the coordination of the captive programmes.
12. To develop and assist the use Genome Resource Banking for the conservation of threatened species.



## Captive Breeding Specialist Group

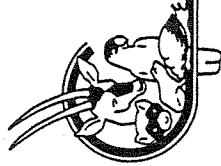
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With increasing encroachment by humans, the biodiversity of our planet is decreasing dramatically. Without active intervention, it is estimated that more than 1,000 vertebrate and uncounted numbers of invertebrate and plant species will go extinct within our lifetime.

As populations of animals and plants rapidly decline in their natural habitats, worldwide coordination of conservation efforts is critical. For many long-term species recovery programs, intensive management efforts in the wild must be reinforced by captive breeding programs, especially when species are threatened by habitat destruction, inadequate protection, or rapidly declining populations.

The Captive Breeding Specialist Group is a global network of individuals with expertise in captive animal management, small population biology, reproductive and behavioral biology, species recovery planning, and other disciplines. Part of the Species Survival Commission (SSC) of the IUCN-The World Conservation Union, the Captive Breeding Specialist Group advises the IUCN, SSC, and other SSC Specialist Groups on the intensive management of small populations in the wild and the uses of captive propagation for conservation, in accordance with the IUCN Policy Statement on Captive Breeding.

As we approach the 21st century, the mission of the Captive Breeding Specialist Group becomes increasingly urgent: *"to conserve and establish viable populations of threatened species through captive propagation programs and through intensive protection and management of small and fragmented populations in the wild."*



# Captive Breeding Specialist Group:

catalyst and coordinator for intensive management of threatened small populations

With over 400 members from over 60 countries, the Captive Breeding Specialist Group (CBSG) catalyzes coordination of conservation programs worldwide. CBSG works closely with institutions committed to species conservation via captive breeding as well as governmental and non-governmental organizations concerned with species and habitat conservation in the wild. Because it does not represent any particular constituency, the CBSG serves as a neutral stimulator and mediator in intensive species conservation management efforts, providing information, technical assistance, and administrative support for a wide variety of programs.

## How do CBSG's programs work?

### Conservation Assessment and Management Plans (CAMPs)

CAMPs allow evaluation of all species and subspecies in a broad group (such as primates) to determine global priorities for intensive conservation, based primarily on status and distribution in the wild. Intensive conservation action includes: intensive care in the wild, collaborative research between captive and field communities, captive breeding, and Population and Habitat Viability Analyses. An important product of the CAMP process is a Global Captive Action Plan (CAP), which recommends strategic priorities for captive program development and resource allocation.

Since 1990, Conservation Assessment and Management Plans have been prepared for:

- Antelope
- Asian Hornbills
- Carnivores
- Deer
- Ducks, Geese, & Swans
- Felids
- Parrots
- Primates

Recommendations from Conservation Assessment and Management Plans, Global Captive Action Plans, and Population and Habitat Viability Analyses provide guidance to regional zoo associations and wildlife management authorities for implementation within their programs.

### Population and Habitat Viability Analysis (PHVA)

PHVA is a method of assessing the extinction risk for a species and of developing management recommendations to enhance long-term survival. PHVA workshops are conducted in the range area of the species in collaboration with the wildlife agencies responsible. Also included in the PHVA process is an evaluation of the status of the species in captivity, possible plans for reintroduction, and problems requiring collaborative research.

Among the species for which Population and Habitat Viability Analyses have been conducted:

- |                          |                       |
|--------------------------|-----------------------|
| Arizland Antelope        | Karnar Blue Butterfly |
| Aruba Island Rattlesnake | Kirtland's Warbler    |
| Asian Wild Horse         | Lion Tamarin          |
| Belt Mynah               | Mexican Wolf          |
| Black-footed Ferret      | Pink Pigeon           |
| Black Rhino              | Puerto Rican Parrot   |
| Florida Key Deer         | Red Wolf              |
| Florida Panther          | St. Lucia's Amazon    |
| Imperial Amazon          | St. Vincent's Amazon  |
| Java Rhino               | Tana Red Colobus      |
| Kaha & Kea               | Whooping Crane        |



### Fauna Interest Groups (FIGs)

FIGs are developing at both global and regional levels for various faunal regions of interest, especially areas of high bio-diversity such as Madagascar, Indonesia/Malaysia, Brazil, Vietnam/Philippines, and Zaire. FIGs coordinate and promote conservation activities by zoos and interact as a collective unit of the worldwide captive community with the countries of interest.

### Communication Network

Annual and regional CBSG meetings provide a forum for CBSG members to discuss and make recommendations for action on current conservation issues of concern.

CBSG News, the quarterly newsletter of the CBSG, is distributed to over 5,000 individuals in 170 countries. CBSG News facilitates international communication by highlighting the activities of the CBSG as well as regional conservation and legislative news of interest.



**Global Captive Breeding Programs**  
CBCG coordinates and facilitates captive breeding efforts for threatened species at the global level via integration of the growing number of organized regional programs around the world:

- African Propagation Program - APP
- Australasian Species Management Program - ASMP
- Association of Meso-American Zoos - AMAZOO
- Chinese Association of Zoological Gardens - CAZG
- Society of Brazilian Zoos - ZSB
- Chinese Association of Zoological Gardens - CAZG
- European Endangered Species Programme - EEP
- Indian Zoo Studbook Programme - IZSP
- Joint Management of Species Committee - JMSC (U.K.)
- Southeast Asian Zoo Association - SEAZ
- Species Survival Committee of Japan - SSCJ
- AAZPA Species Survival Plan - SSP (U.S. & Canada)

The CBSG works closely with the International Species Inventory System (ISIS), a global, central database that provides computerized animal management for over 300 cooperating institutions.



ISIS was founded by CBSG's Chairman, Dr. Ulysses Seal.

## How is the CBSG funded?

Much of the work of the CBSG is accomplished through voluntary contributions of time and labor by its members. A small office with paid staff has been established. Core funding for this office and for some additional CBSG activities is provided by voluntary contributions from over 75 zoos, aquariums, and zoo associations worldwide. However, in the face of the growing environmental crisis facing our planet, the demand for CBSG's services far exceeds our ability to provide needed services with present resources. In order to meet this demand, it is urgent that funding for the CBSG's activities be increased.

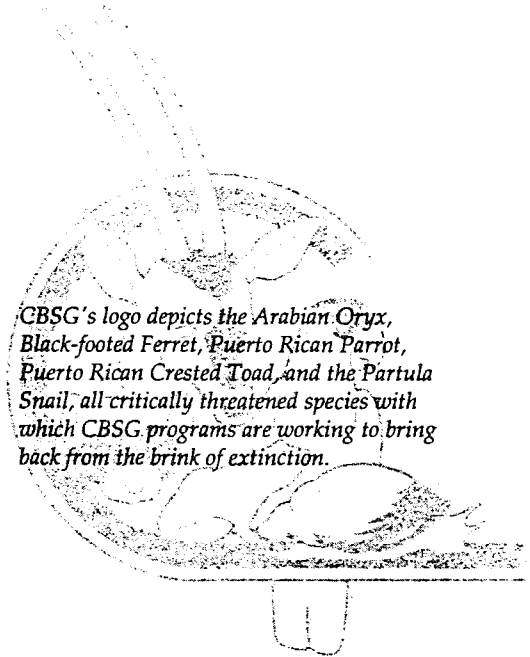
## How you can help

The CBSG is supported entirely by contributions from individuals, institutions, and foundations. You can be a partner in CBSG's important conservation efforts. Your contribution is essential to the success of our programs and will benefit the CBSG, threatened species, and you. A donation of \$25 or more will entitle you to receive our quarterly publication, *CBSG News*, which highlights the activities of the CBSG as well as regional conservation activities and legislative news of interest. Remember, when you give to the CBSG, you are giving to the future of the world's biodiversity. You can help the CBSG in its important work today! Simply complete and return the enclosed reply form.



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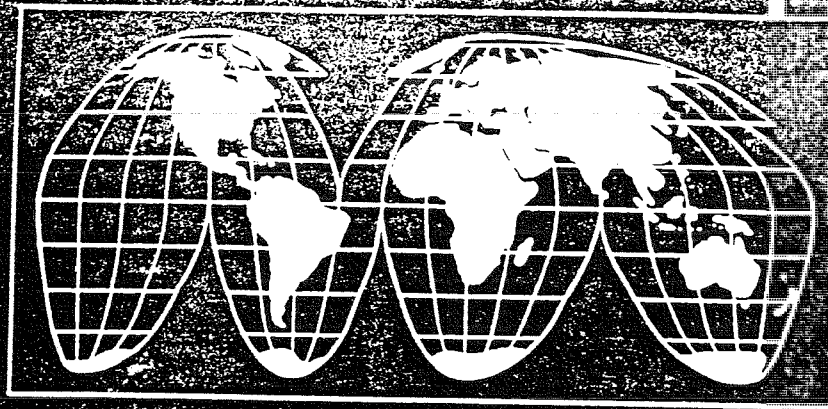


*CBSG's logo depicts the Arabian Oryx, Black-footed Ferret, Puerto Rican Parrot, Puerto Rican Crested Toad, and the Partula Snail, all critically threatened species with which CBSG programs are working to bring back from the brink of extinction.*

### **CBSG Staff**

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# Captive breeding



IUCN POLICY STATEMENT

4 September 1987

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THE IUCN POLICY STATEMENT ON  
CAPTIVE BREEDING

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*Prepared by the  
SSC Captive Breeding Specialist Group*

*As approved by the  
22nd Meeting of the IUCN Council  
Gland, Switzerland*

*4 September 1987*

**SUMMARY:** *Habitat protection alone is not sufficient if the expressed goal of the World Conservation Strategy, the maintenance of biotic diversity, is to be achieved. Establishment of self-sustaining captive populations and other supportive intervention will be needed to avoid the loss of many species, especially those at high risk in greatly reduced, highly fragmented, and disturbed habitats. Captive breeding programmes need to be established before species are reduced to critically low numbers, and thereafter need to be co-ordinated internationally according to sound biological principles, with a view to the maintaining or re-establishment of viable populations in the wild.*

### **PROBLEM STATEMENT**

IUCN data indicate that about 3 per cent of terrestrial Earth is gazetted for protection. Some of this and much of the other 97 per cent is becoming untenable for many species, and remaining populations are being greatly reduced and fragmented. From modern population biology one can predict that many species will be lost under these conditions. On average more than one mammal, bird, or reptile species has been lost in each year this century. Since extinctions of most taxa outside these groups are not recorded, the loss rate for all species is much higher.

Certain groups of species are at particularly high risk, especially forms with restricted distribution, those of large body size, those of high economic value, those at the top of food chains, and those which occur only in climax habitats. Species in these categories are likely to be lost first, but a wide range of other forms are also at risk. Conservation over the long term will require management to reduce risk, including *ex situ* populations which could support and interact demographically and genetically with wild populations.



# 2

## **FEASIBILITY**

Over 3,000 vertebrate species are being bred in zoos and other captive animal facilities. When a serious attempt is made, most species breed in captivity, and viable populations can be maintained over the long term. A wealth of experience is available in these institutions, including husbandry, veterinary medicine, reproductive biology, behaviour, and genetics. They offer space for supporting populations of many threatened taxa, using resources not competitive with those for *in situ* conservation. Such captive stocks have in the past provided critical support for some wild populations (e.g. American bison, *Bison bison*), and have been the sole escape from extinction for others which have since been re-introduced to the wild (e.g. Arabian oryx, *Oryx leucoryx*).

## **RECOMMENDATION**

IUCN urges that those national and international organizations and those individual institutions concerned with maintaining wild animals in captivity commit themselves to a general policy of developing demographically self-sustaining captive populations of endangered species wherever necessary.

## **SUGGESTED PROTOCOL**

**WHAT:** The specific problems of the species concerned need to be considered, and appropriate aims for a captive breeding programme made explicit.

# 3

**WHEN:** The vulnerability of small populations has been consistently underestimated. This has erroneously shifted the timing of establishment of captive populations to the last moment, when the crisis is enormous and when extinction is probable. Therefore, timely recognition of such situations is critical, and is dependent on information on wild population status, particularly that provided by the IUCN/Conservation Monitoring Centre. Management to best reduce the risk of extinction requires the establishment of supporting captive populations much earlier, preferably when the wild population is still in the thousands. Vertebrate taxa with a current census below one thousand individuals in the wild require close and swift cooperation between field conservationists and captive breeding specialists, to make their efforts complementary and minimize the likelihood of the extinction of these taxa.

**HOW:** Captive populations need to be founded and managed according to sound scientific principles for the primary purpose of securing the survival of species through stable, self-sustaining captive populations. Stable captive populations preserve the options of reintroduction and/or supplementation of wild populations.

A framework of international cooperation and coordination between captive breeding institutions holding species at risk must be based upon agreement to cooperatively manage such species for demographic security and genetic diversity. The IUCN/SSC Captive Breeding Specialist Group is an appropriate advisory body concerning captive breeding science and resources.

Captive programmes involving species at risk should be conducted primarily for the benefit of the species and without commercial transactions. Acquisition of animals for such programmes should not encourage commercial ventures or trade. Whenever possible, captive programmes should be carried out in parallel with field studies and conservation efforts aimed at the species in its natural environment.

International Union for Conservation  
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CH-1196 Gland, Switzerland

**PROPOSED  
IUCN RESOLUTION STATEMENT ON  
ANIMAL GENETIC RESOURCE BANKING  
FOR SPECIES CONSERVATION**

**Captive Breeding Specialist Group Annual Meeting  
Singapore, September 29, 1991**

**PROBLEM STATEMENT**

The IUCN holds that the successful conservation of species requires integrated management efforts to sustain available genetic diversity. These efforts include programs to protect and manage animal populations within their natural, native habitat (*in situ* conservation) and supporting programs that manage individuals, gametes and/or embryos outside of natural environments (*ex situ* conservation).

The IUCN recognizes that, although habitat protection is the most desirable approach for conserving biological diversity, supportive *ex situ* programs are essential in many cases. For example, such programs can deal effectively with short-term crises and with maintaining long-term potential for continuing evolution.

The IUCN further recognizes that the efficiency and efficacy of *ex situ* conservation can be increased many fold by applying recent advances in reproductive technology. These include assisted or 'artificial' breeding and the low temperature storage (banking) of viable animal germ plasm, namely spermatozoa, embryos and oocytes. Germ plasm banks: 1) offer a high degree of security against the loss of diversity and, therefore, entire species from unforeseen catastrophes; 2) minimize depression effects of genetic drift and inbreeding; and 3) provide a powerful method for managing the exchange of genetic diversity among populations. Other conservation benefits include banks of serum, DNA and cultured cell lines from germ plasm donors which permit studies on disease status, detection of microbial antibodies, pedigree determination, taxonomic status, geographical substructure and cellular physiology.

The IUCN also recognizes that the establishment of a genetic resource bank must, through basic research, be matched by the development of technologies for its use as a genuine and practical conservation asset.

The development of genetic resource banking programs is hampered by the lack of guidelines for establishing such banks and for integrating them with overall conservation programs. As yet, no single organization with a role in the international coordination of conservation efforts has provided guidance.

## **RECOMMENDATION**

The IUCN regards development of genetic resource banks as an essential component of integrated conservation programs. Therefore, the Captive Breeding Specialist Group recommends that a formal process be developed to formulate global guidelines to establish, operate, use and review animal genetic resource banking programs for species at risk. The framework for international coordination of this type of program must be based upon agreements to cooperatively manage such species for demographic security and genetic diversity.

To achieve this recommendation, a Coordination Committee under the auspices of the Captive Breeding Specialist Group and others to be identified will:

- a) Coordinate animal genetic resource banking activities within the Species Survival Commission and among regional captive propagation groups. This will be accomplished by integrating the genetic resource banks directly into the framework of population viability assessments and conservation Action Plans. These activities require an expert resource network to provide advice on all technical matters.
- b) Establish guidelines for identifying taxa, species or populations that would benefit from genetic resource banks. These guidelines should be detailed and assist in the development of strategic Action Plans for conserving targeted animal populations. The single most important consideration is to ensure that there is a defined conservation goal that requires the collection and storage of biological materials. This requires that an integrated plan for a goal-orientated conservation program be established prior to initiating banking activities.
- c) Establish a globally-standardized, record-keeping database for cataloging, managing and pooling data on banked materials. It will be essential that these biological materials are linked to individually identifiable source animals.
- d) Provide expert technical advice to the appropriate taxon groups to assist in developing animal genetic resource Action Plans. The primary responsibility for developing Action Plans resides with those groups with specific responsibilities for *in situ* and *ex situ* conservation of specific taxa, species and populations. These groups should be encouraged by the Coordination Committee to include genetic resource banks as an integral component in their strategic conservation planning. The Coordination Committee will support the appropriate taxon groups to integrate information on: reproductive and genetic histories of *ex situ* and *in situ* populations; efficiency of reproductive technologies; areas requiring further research; types of biological materials requiring storage; appropriate protocols for banking biological materials; primary and secondary repository sites; strategies for using banked materials; and sources of funding.
- e) Provide a mechanism for approval and periodic review of animal genetic resource banking Action Plans.



***GRUS AMERICANA***

**WHOOPING CRANE**

**CONSERVATION VIABILITY ASSESSMENT  
WORKSHOP REPORT**

**SECTION 12  
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***GRUS AMERICANA***

**WHOOPING CRANE**

**CONSERVATION VIABILITY ASSESSMENT  
WORKSHOP REPORT**

**SECTION 13  
MINUTES**

# WHOOPING CRANE PVA MEETING MINUTES

## FOSSIL RIM WILDLIFE CENTER

### USFWS/CWS/CBSG

#### INTRODUCTION

Jim Jackson: Introduction and welcome.

#### OVERVIEW OF WHOOPING CRANE PROGRAM (Jim Lewis):

Lewis: The timing for this meeting is ideal partly because 1) the DNA work at Patuxent, 2) the ICF/Ernie Kuyt studbook work, and 3) both recovery teams are due to update their recovery plans in the next year. The U.S and Canadian Wildlife Services have been working together closely. I want to thank Jim Jackson and his wife for allowing the workshop to occur here.

Seal: Fundamentally, we want to turn out a product by the end of the three days, one of the ways to do that is to keep the presentations informal. The idea is to bring together a group of experts and to use the tools that are available under the rubric, population viability analysis. The workshop approach is useful in that CBSG, as an international organization, provides a forum that allows people from different backgrounds to bring together the biology and science and to use this information in a variety of simulation models to investigate the probability of extinction and to characterize the other features of an endangered species. All endangered species have problems. This kind of analysis offers an opportunity to reflect on the problems and to arrive at additional suggestions and comments, with the shared goal of attempting to achieve the recovery of the species. The emphasis is biology, not politics, economics, or social constraints. We all come from organizations that are attuned to the politics and needs of our public. The perspective is that we can best influence these institutions if we come up with a consensus using the technical tools available here. Over 90% of our knowledge is in our heads, so one of the parts of this process is to bring this knowledge to bear on the questions. This means your willingness over the course of the next few days to share your knowledge as a manager or researcher of whooping cranes. One of the reasons for discomfort with this process is that there is a large degree of uncertainty in the information, yet you use this information in many decision. The idea is not to expose anyone of us to the scrutiny common to a peer reviewed science article. "Ah, this expert has said this so it must be true." This process is inherently less clearly defined, it deals with probability, tendency, risk. We will try to include an enormous number of outcomes in looking at the persistence of the species. Please express your discomfort and we will deal with it. What we are trying to do is reach a consensus on the biology and science and see what comes out at the other end. So will try to bring the information to bear and summarize it.

There have been areas already identified that are of substantial concern. There will be working groups with the idea that there will be an effort to make an estimate of risk in disease, captive propagation, and genetics. The people who have been involved with propagation will review

productivity in captivity. The genetics group, will review the genetics of the species using the molecular genetic material and the information on the wild.

The fundamental ground rules are: 1) if you want your information included..write it out and give it to Jan and it will be included; 2) we have to respect each individual and accept what each of us is saying...it may seem trivial but disagreements can become profound; and 3) keep the process moving. Occasionally people have so much to say it is difficult to limit them in time and space.

The working groups will develop drafts and by the end of the third day we will come back together and form a consensus. By the end of the first day, the summary, recommendations, there will be agreement on the content and wording. Doing this by mail is approximately 100% unsuccessful. Some of the simulation modeling will need to be done later, 2 to 3 computers over several weeks. We want to have the fundamental product done here. Some of you who are leaving, it is important that you get your drafts completed. Much of today will be spent in summarizing information so by tomorrow morning we will have the first simulations done.

By way of process. Bob Lacy will present on the population overview. I will retain as objective a point of view for the overview. Fundamentals of small population biology is where we will begin.

#### Bob Lacy: Small Population Biology

When populations get small, process, evolutionary and ecology processes become different so all of the things we learn about population management don't work. Small populations are unstable and erratic. There is a lot of fluctuation going on. The population is fluctuating and the population could hit 0. Large populations are made up of small populations many of the small groups will fluctuate, but will be recolonized, a constant dynamic, when . Any single population is vulnerable to extinction. The process, PVA, taking all the information we have doing what we can with to understand the probability of extinction under a variety of scenarios. The classic approach is a life table analysis ...the problem of small populations is that even if the population is on average increasing ( in good shape with the life history calculations) but fluctuating wildly the population could go extinct. The flux is categorized into stochasticity demographic, environmental, catastrophe, genetic drift.

1.Demographic- luck of the draw even if all animals have the same chance. Flux in populations occur even if environment is constant, prob . of male and female, alive or dead, is a coin toss. In a large populations it doesn't matter, small population it could really matter. Could by bad luck, have every animal happen to die one year. Classic example is dusky seaside sparrow have all six of the last birds were male.



## Whooping Crane PVA Minutes

2. Environmental. The flux in demographic probabilities...the prob of birth and death, male or female, and externally imposed additional variation. Some years dying may be 10% the next year because of drought, 90%.

- reproductive rates
- mortality rates
- carrying capacity

3. Catastrophe. This is the extreme of environmental variation. We consider it separately for a couple of reasons. If you look at the typical distribution of environmental flux, catastrophes are outliers. You wouldn't predict hurricanes by studying the wind patterns. It is usually so far out, it doesn't fit the normal day to day, year to year variation. The impact on the population may be very sever. The population could be adapted to year to year but not to catastrophe. Often catastrophes will wipe out the species. A species may hang on and then get hit by a catastrophe. We think of them as aberrant events but over a long time period, they are predictable, hurricanes hit at out every 30 years, forest fires hit with some probability.

- storms
- fire
- disease

The Unexpected

4. Genetic Drift. Small populations flux genetically just as they do in number. It is a sampling problem. In a large pop each generation is a good sample of the one that existed before. In a small population each generation is a poor example of the others. Genes that are flux could hit 0 and alleles get lost, over time there is a loss of genetic diversity. Loss os genetic diversity has been demonstrated vulnerability and susceptibility of environmental problems, reproductive problems, disease, it affects each species differently. Decrease and worsen the demographic situation.

In mammals 1% loss of genetic diversity means 1% loss in reproductive fitness.

All these characteristics feed back on each other in a nasty way in an extinction vortex. External force (hunting, habitat loss), when species become small, you set into effect a series of problems that can spiral down into an extinction vortex. The fluctuation of population size makes inbreeding worse than if it were constant, the demographic fluctuations can negatively impact the population cause further stochasticity, etc. The spiral is fast unless management is very aggressive. Part of management problem is to get populations out of the vortex.

Example: Eastern Barred Bandicoots: Going extinct fast. What-if scenarios in a PVA allow you to look at the data, management schemes,

## Whooping Crane PVA Minutes

George Gee: How do you take into account factors you haven't recognized

Bob lacy: All of the models makes the drastic assumption that we haven't overlooked something. the best we can do is include as many factors as there might be that other people haven't thought about, the models are only as good as the factors that go into them and we clearly recognized that there are things we have left out. We are probably way underestimating the probability of extinction, my intuitions says they are probability negative not positive.

Seal: another way of looking at it is that as you use your expertise and then that does not match the way the pop is reacting, then it points out that there are factors you don't know. This kind of things focuses questions where there is a need for more information. We will try to express these things in terms of risk.

Bob lacy: There are several things that we can do, explore uncertainties in the modeling, you can also do some testing, there is some hint of science, that you can do the model and see of the population is really doing prospectively or retrospectively. We usually do not have the kind of data that you need to do the fluctuation analysis.

There are several approaches to looking at variability on population extinction. One approach is to develop formula, based on various population parameters, Goodman (1987), Scott using mathematically formulations. There are advantages, it looks precise because you get a number at the end. The disadvantage is that the number may not mean much. Usually has limited factors (exponential growth rate, variance, maximum population size) too simple, no genetics, no catastrophes, no carrying capacity, Scott (et.all) assumes no capacity exponential growth, no genetic events, no catastrophes. All the models make assumptions, it is important to think about those assumptions.

The approach I have used to try to understand the Vortex, is quick and dirty, I don't try to develop complicated formula. I try to make the computer think it is the population. Computers are very good at flipping coins, prob is x of something happening.

How small is critical, how big is enough?

Vortex, originated with James Greer, the nice thing about simulation models is that it keeps getting bigger and bigger by adding things on. The model asks the user to input a lot of population parameters. The model is dependent on knowledge, you need to know sex ratios, birth and death, without this information, you can't do anything. You must recognize where data are weak so you can test sensitivity of the model. This allows you to pinpoint where you need more data.

## Whooping Crane PVA Minutes

1. Input population biology parameters
2. Starting population  
size  
sex
3. Determine birth and death rates for year
4. select mates  
for each male of breeding age: determine stochastically if in the breeding pool.  
for each female of breeding age: determine is a successful breeder that year  
select a mate from the breeding males and assign probability of success
5. impose mortality  
age sex genes influence on fitness
6. carrying capacity truncation  
truncation if pop exceeds capacity
7. migration among subpopulations
8. harvest
9. supplementation  
assumes genetically unique additions.
10. report population status at the end of the year  
size, sex distribution, heterozygosity, inbreeding coefficient, number of unique alleles left.
- 11 summary of simulation
- 12 summary across simulations.

All of these are stochastic events so outcomes will differ..So it is critical to run the model at least a 100 times to get an initial feel, to get a more precise definitions, you need 1000 runs, for publication it takes 10,000. To do this it takes weeks to do thousands and thousands of simulations. every model has built in assumption and some exist in Vortex, One, it assumes density independence until it reaches carrying capacity. One gene, two alleles simplification. Modeling unlinked loci.

## Whooping Crane PVA Minutes

George Gee: How many alleles are you starting with?

Bob Lacy: when you talk about mean heterozygosity, however many alleles you start you will lose in the same proportion no matter how many you start with. This is not a good way to do rare alleles. This does not model that very well.

Even if you model with no inbreeding effects, even if it doesn't impact survival, it is still interesting to know how much variability is lost over time. It lets you know what flex they have as environmental change accelerates.

Claire Mirande: Crane Systematics

How the whooping crane fits into the crane taxonomy. Crown cranes are the oldest group. DNA hybridization tests, siberian cranes are in its own group, Remaining are in 4 sister groups. Australasian cranes, wattle cranes, gang-of-five sister group, The gang of five are closely related, there have been hybrids produced between all groups. Only once in the wild. The birds are closely related, the sandhill cranes are probably the oldest, next to the crown cranes and in a separate group.

George Gee: Determining relatedness in cranes  
electrophoresis  
immuno-protein tests  
nuclear RFLP work  
blood typing reagent for histocompatibility in animals.

the problem is that we have huge volume of data and it is not in a publishable form. I prefer to use the founder population (assuming the population is unrelated). I will start with electrophoresis. All show remarkably similar heterozygosity. Low variation in birds in general and low variation in cranes. Looked at 35 loci. Of those we were not able to do all so we cut it down to 27 loci. 14 of these were polymorphic within the cranes.

Seal: How many loci in whoopers?

George Gee: Five of the 27 are polymorphic in whooping cranes. 4-5 polymorphic in all the species.

Evolutionary distance compares more closely to George's behavioral data than to Carry's molecular data.

## Whooping Crane PVA Minutes

John Longmire: Two major questions 1) DNA for parentage 2) DNA to index relatedness mostly for breeding in captivity. Used M13-complementary VNTR closeness from a Charon-40 chromosome-16 (human) library used to develop single locus probes. Single locus probes will highlight particular vertebrate sequences. Using the data to finger print was relatively straight forward, determining relatedness was much more difficult. Used allele (band) sharing, the more closely related, the more bands shared. Assume that alleles are inherited along mendelian lines. the way you tell is that any fragment or band in offspring has to be traced back to parents. Index of relatedness is determined by comparing frequency of shared polymorphic alleles. Whooping cranes relatedness: population (42 ind.) mean was 0.42, siblings (12 pairs) 0.59, parent/parent .46; parent offspring 0.61. Future direction will be to get more detailed using single loci probes. Construct a whooping crane genomic library, screen library for satellite sequences, develop 10-20 VNTR clones.

Claire Mirande: We can also identify the use of band sharing to guide pairing decisions.

Seal: we need to review the limits as well as the advantages

Jon L. : Problem is that if band is not there, you will not know what the alternate loci is. The single loci probe will only pick up the two alleles associated with that loci, it becomes a much more defined system, the offspring also must have 50% of the material from mom and dad.

12:00

Julie: can you get DNA from formalin preserved specimens?

Jon: It becomes more difficult to separate the DNA because they get fixed, in time the techniques will be developed.

Seal: The recommended technique now is alcohol fixing.

Jim Lewis: Historical numbers and distribution

Historically, whooping cranes were most abundant in the Pleistocene probably distributed all over. Allen did his work in 1952, primary areas identified. In the 1800 based on calculations that Allen did population may have been 1500 birds. Banks recalculated 500-700 individuals. Birds in Salt Lake City area, Yellowstone (1915), in the last century. The primary migration route is through the southern prairie provinces and the texas coast and down into the mexican highlands. Birds were present in Utah, east to cape May wintering area and Florida. The birds that wintered along the coast of eastern NA did it in large estuaries and bays. 1857 probably last use of nesting to Atlantic coast. Decline caused by hunting, habitat destruction, museum

## Whooping Crane PVA Minutes

specimens, By 1930+ population very low. 1926 Wood buffalo was protected. Platte River historically was a traditional site for whooping cranes as the habitat degradation occurred the sandbar and river habitat began to fill and they became less attractive, currently it receives very light use. Grays lake is the other population. Two captive populations at ICF and at Patuxent. Two birds at San Antonio Zoo.

All of the birds captive and wild are from the 16 or so individuals that remained in the early 40's from the Wood Buffalo and Aransas population.

Drewien: There is a tremendous amount of speculation there,

Tom Stein: Do you see the figure 5000 before European settlement. I see the 1500 figure and it seems to me thee should have been thousands.

Ernie Kuyt: He used the figure as before settlement.

Tom Stein: The implication is that the birds are not very well adaptive, if you spread the birds over the range, wouldn't there have to thousands.?

Drewien: Somebody published the figure (Allen) and therefor it stuck.

Claire: Does anyone believe it was less than 1000's of birds?

Seal: it is difficult to infer with this kind of information, about the history of the species.

Bob Lacy: Certainly, the model suggests that 500 is still very big as far as most effects, so until you get down to less than 100, you see the effects I was talking about. If you see low heterozygosity, it could have gone through a bottleneck. If there is high variability, it doesn't mean it didn't go through a bottleneck. You can go through a bottleneck with 2 animals and come out with less than a 25% loss in heterozygosity.

Seal: For people to gratuitously state that the numbers have always been small, the data don't support it.

Bob Lacy: The critical questions is not how many were there but what can they expand to now, given the habitat available.

Claire: Brief explanation of PVA exercise.

## Whooping Crane PVA Minutes

Jim Lewis: The question was raised why reintroduce cranes outside their range, I wanted to make the point that cranes were throughout the country. We have tried to establish sites outside the wood buffalo to avoid catastrophes in that population.

Ernie Kuyt: Wood buffalo. Philosophical question or remark, I looked around the table, I decided I was in the minority, so many in captive and so few in the wild. We are interested in perpetuation of wild whooping cranes, not necessarily in populations in captivity. My own involvement has been over many years and will end this year. Brian Johns will take over field work and I will finish data. Work began in 1966. three components, spring pair counts, collection of eggs, banding of young birds in August.

Banding of young cranes 1977- (lead by Rod Drewien). ICF has summarized this data. Banding, capture and selection of a small number of whooping cranes, measured, weighed, banded. The banding work was conceived by getting together and listing priorities objectives. The banding program was stopped in 1988.

Egg collection: End of may. Surplus eggs, Patuxent, Grays Lake, ICF. At the time of the pick up take basic measurements of the nest size, pond conditions, eggs are given viability flotation test and a live egg was left. Since 1984, more selective about this with floating technique we are sure that the egg left in the nest is live. We calculate that between 1984 and 1989, hatching success is improved to 15-19%.

The breeding pair count. The last few days of April, some nest as early as the 24 or 26 of April, The whooping cranes are early nesting birds and they need the whole season to raise their young. Count done by fixed wing aircraft without disturbing effect that helicopters have. All of the work has been done from the air, no landings. Location of nesting pair, counting eggs, Surveys until the middle of may. nests location and egg laying dates.

Gee: What are the experiments on Twining?

Kuyt: The last two years have been very dry, we have a couple that have hatched but because the conditions are so poor we haven't left two in the nest very much. The last time I was in was the June 16, there was one pair of twins, and another pair on the nest with a pair.

Gee: Do you think that leaving two in the nest will improve productivity?

Kuyt: The problem is prediction what kind of year we will have, in wet years yes in dry years could be less.

## Whooping Crane PVA Minutes

**Seal:** Are you dealing with water level variation - environmental variation?

**Kuyt:** Yes, we are dealing with water levels in the Park, the Park people are responsible for collecting the data and we are expecting a progress report. My measurement are elementary, taken at the nest. Last year was the lowest since 1981 and this year was lower. So it does not look good. All of the water bodies are recharged from precipitation. I have a little information on flights in June we saw 51 chicks with nest with 2 unknown.

**Chris Brand:** How many nonviable eggs

**Kuyt:** We send them to Patuxent, we had 5 this year.

**Gee:** We have some information on fertility sometimes they are too rotten.

**Kuyt:**

**Lacy:** Have they found where the non-breeding birds are staying?

**Kuyt:** Yes we have found the areas where the juveniles, Some birds are staying in Saskatchewan. 90% of population without detailed census has been seen returning to the nesting area.

**Jim Lewis:** Boyce identified a 10 years cycle could be related to water conditions.

**Tom Steins:** Aransas Review:

Refuge biologist: 75% of time on whooping cranes, handling my research and that of the refuge. We fly once a week, trying to find every whooping cranes once a week success is 90% + We read the color bands Takes experience to see bands. Sometimes it takes multiple disturbance, we are looking at disturbance now. Winter territories include two birds that are not associating with other cranes, 45 territories, could match Ernie's 45 nesting pairs. The cranes are spread over a 35 mile area. In the last few years we have drought so the birds are flying to fresher water and we have had good acorn crops so birds are going to feed. Aransas area = wintering not just on NWR. Last winter, we had the highest mortality 9 and possibly 11. We haven't done anything different. The spring pop. was 135 birds once died in migration and one died on nesting grounds so 133. Losing 1 to 2 acres of habitat a year just from erosion. 3 feet a year on each bank. Ponds that cranes used to feed in are now gone. We have protected a mile of shoreline with concrete bags with volunteers.

**Jim Lewis:** As there been any check on the food resource to see if the walls affect it?



## Whooping Crane PVA Minutes

Tom: Walls are low so tides go over and food appears unaffected.

There can be no contingency plan...it will be worthless... Within the first hour you could lose 25% of the birds. There is a risk analysis being done right now. The Corp is doing a study of alternatives for the intercoastal water way.

Jim Lewis: There is a contingency plan but it is outdated. The regional office is updating the contingency plan but little progress to date.

Bob: Do you see changes in feeding do to spread of nonendemic species of plants.

Tom: No.

Rod: Could attract birds to other areas with models etc.

Seal: Experience we have had with Corp is waiting will not do it.

Claire: Could Tom do a quick summary on Lewis data>

Tom: I have seen the data, but I don't know what he will conclude. We set of the study because we observed airboat users flushing cranes. There was a federal sting against these guys and they quit running the boats during the course of the study. It is something we will monitor in the future. He found that tour boats, change 3 time a week to 4 to 5 times a week, I have seen 4 to 5 cranes pulled up on one group. The cranes always walk away from the boat. Is that significant or not?

Disturbance is up to 1000 feet impact occurs when boats are really distance.

Brian Johns : Threats to Aransas Wood Buffalo Flock in Canada and Migration in Canada. Habitat conversion has progressed in Saskatchewan since the turn of the century. Grassland to crop, aspen parkland, wetlands, drained and cleared. 70%, in areas 95% of original habitat is gone. 1922 last documented whooping crane. Threats on breeding grounds, drought is major threat. It is protected as Park. 1981 was sever drought, only 3 young produced. 1990, also drought year.

How about forest fires,

Forest Fires have opened up the area.

## Whooping Crane PVA Minutes

**Kuyt:** Fires: no documentation that we have lost any birds as a result, more insidious when you have forest fire years, it tells you something about the habitat condition of the year.

**Johns:** During spring migration, cranes use temporary wetlands, fall migration 80% are permanent or semipermanent, including lakes and river, In the last 30 year may pond average, in the southern prairies, whooping cranes migrate through, there was 2 million average, through the 60's there is no correlation between pond index and survival of cranes during migration. Birds in drought years will shift there location to places where there is more permanent water. Pollutants, agricultural run off is a major problem. Chemical spraying during the spring on 80%, about 15% is insecticides. Run off from the fields affect the roosting sites in the fields.

Grain fields and wetlands are used during migration. Mortality, since records have been kept there have been at least 19 birds killed by power lines. 40% of known death in Grays Lake is power lines. Wood Buffalo 25% due to collisions with power lines. Disease is another problem. We don't know a lot about it in wild flock, parasites in one bird, coccidia, avian TB in the flock, one and possibly two in Aransas and three in Rocky Mt. Flock. Avian cholera, botulism is a possibility in Saskatchewan it does occur in sandhill cranes prevalent in shallow wetlands in Saskatchewan and in the last few years cranes summer in areas botulism occurs. Viral infection is another problem. Predators: black bear on nest and eggs, common raven, grey wolves of flightless young, golden eagles also. Since 1938, at least 5 have been shot, and 2 in Canada, some are willful and some are mistakes. Disturbance, agricultural activities. Birds maybe moved out of traditional stop overs and due to over zealous sight seers.

Whooping cranes occur in prairies for about 2 to 3 months during the year. A single bird will no stay that long, but birds will be coming through over this period of time. Since birds have been migrating through Saskatchewan records have been kept. An attempt to determine where the breeding areas were. The whooping crane records were still be kept. so we have a good database of flock size and migration chronology. Early migrants moving through the southern prairies in Mid april. Breeding adults early. Nonbreeding birds come later and linger longer. 15 April through first few days of May. Fall migration is a more elongated time period. Year to year differences in fall may be explained by water conditions in breeding grounds.

Migration is diagonal across the southern portion of Saskatchewan.

18 areas have been used, 7 are most important, the birds feed primarily in grain fields unknown what invertebrates (or vertebrates) they consume. Appear to stage in traditional sights. One pair uses one wetland and roost site every spring and fall and their young has been thee without the parents. The birds will use a variety of wetlands, sheet water during spring migration and large lakes in the fall. During fall migration, the birds will be with sandhill cranes. Wheat and barley are the primary food resource of cranes during spring and fall. Look for wetlands associated with

## Whooping Crane PVA Minutes

fields. Most of the roost sites and virtually 99% of feeding sites is all private land. Migration habitat is on private lands.

Bob Smith: change in wetland, Hayes anti-wetland bill.

Chris Brand: At the Health Lab, we do diagnostic, field and lab research, Will discuss the results of necropsies at National Wildlife Health Center. 1976-1989. we have received 25 whooping cranes to necropsy. this should represent a complete sample of US birds. 17 from nesting and migration and 8 from migration and wintering of  
Carcasses suitable for necropsy:

predation 8% (1 with TB)

hunting 8%

impact trauma 52%

powerline (2 with TB), fence, auto (right under power line), unidentified, gunshot.

### Disease

TB accounted for 28% of birds, post mortem diagnosed.

4% lead poisoning

4% *P. multocida* otitis

4% congenital defect

29% Grays Lake

25% Wood Buffalo

Sex ratio was not different than non tuberculosis cases. Age ratio, 2 young of year, 1 immature, 4 adults.

These are biased data because of the way we get the carcasses, maybe finding impact is easier than finding diseased birds. Sick birds will hide. Don't know proportion, if waterfowl is an indication, TB is under represented in these data.

We feel 28 % proportional mortality due to TB is very high and that is probably under represented. We conducted a survey of potential sources or reservoirs of infection. Collected 220 greater sandhill, snow geese, 17 lesser sandhills, total 1144 tissues. Low prevalence of TB in sandhill cranes and snow geese, suggests that whooping cranes are super sensitive, fecal contamination maybe a major source of infection. TB may be transmitted through egg in poultry and maybe this is going on in egg.

Many other disease risks in the wild.

## Whooping Crane PVA Minutes

**Gee** : what risk are we bringing into our captive flocks by bringing in eggs from the wild, there could be transmission through egg and material on the eggs.

**Other** diseases: use sandhill cranes has example, avian cholera botulism avian tuberculosis aspergillosis aflatoxicosis (B1), eev, micotoxycosis.

**TB**, avian cholera, eev, micotoxycosis are main problems.

**Avian** cholera is increasing, rainwater basin is whooping cranes staging areas and has cholera and the cranes are harassed off these areas to keep them off. Uncertain about cause and virulence

**Microtoxin**, molds on nut crops, species susceptibility. Immunosuppression and carcinogenic effects. Could be contributing to cholera outbreaks because of immunosuppression.

**Jim Carpenter**: Captivity disease and parasites

**Greatest** impact in times of stress, and other problems. Briefly I will overview the major problems, infectious, bacterial, sporadic infection. No real outbreaks of diseases. E. coli, bacillus, staff, (see papers in the briefing document). Avian cholera has occurred in captive cranes, TB in captivity, viral diseases is unknown. Avian pox is a potential problem for cranes in captivity.

**EEE** is the major problem in captivity, transmitted by mosquito. whooping crane is the only indigenous species that has died of EEE, introduced species as susceptible but haven't found any that have died. Aspergillosis is the main micotic disease. parasitic diseases are major problems. Blood proteins. Helminths. Nematodes. Ectoparasites.

**EEE**, **DVC**, microtoxin are the main captive problems.

**DVC** (parasite) could be over 100% in sandhill cranes

**Microtoxins**: 80% morbidity

**EEE** : bird mosquito bird life cycle.

**Seal**: In a sense there has been a neglect of disease in evolutionary biology.

**Rod Drewien**: Grays Lake. In 1975, Canada and Us initiated jointly an experiment for sandhill crane/whooping cross fostering. Idea initiated by Fred Barr, proposed in 50's. Grays holds highest density of sandhill cranes in continent. Cranes use National wildlife refuges transplanted eggs. 288 eggs 73 from Patuxent and the remainder from Canada. 210 hatched, those that were lost were to predation, or infertile. 73% hatched, 85 birds fledged (40+%) coyote predation, inclement weather, usually before birds were 30 days old. Of 85 birds that fledged only 13 are

## Whooping Crane PVA Minutes

alive today. In Colorado, San Lois valley, was a mortality black hold 12 % on summer ground 11% in winter grounds , 77% occurred in san Lois valley in colorado. 38% were recovered. Collision with fences and power lines, TB 19% (under represented), few others.

Sandhill and whooping cranes were frequently associated with geese and ducks, Our impression from watching this cranes are not every susceptible to cholera. They are highly susceptible to avian TB. Population was growing through 1985, then a series of bad years, five years of drought, during early and mid 80 food shortages on wintering ground. About one third would return to Grays Lake, others would disperse . Starting about 4 years males started setting territories without females, very unusual. pattern has persisted. Females disperse in summer range and do not set up territories, occupy an activity areas, not always consistent. Once males set up a territory, they came back. Pairing experiments unsuccessfully. My feeling is that the females are not responding properly, don't respond sexually. Skewed sex ratio, mortality rate, few females returning. Flexibility in foraging in New Mexico.

Pairing can occur on wintering grounds and breeding grounds at Wood Buffalo. Wood buffalo population returned within the 400 sq. mi. and Grays lake males returned to Grays Lake, 95% of females in Grays lake females dispersing over 100+ square miles radius. Wood Buffalo females do not disperse alone. Because of mountainous terrain, Grays Lake dispersers are very isolated.

Bob Lacy: Best Guesses for Vortex.

First Simulation:

simulation runs: 25

Years of simulation run: 100

Time interval for report: 10

populations to model: 1

Will EV(reproduction) be correlated with EV(survival): no

How many types of catastrophes to model: 3

toxic spill

red tide

fire

hurricane

disease

Do you want inbreeding depression? Y

Recessive lethal or general heterosis model: Heterosis model

## Whooping Crane PVA Minutes

how many lethal equivalents (how severe is inbreeding depressions): 3

Monogamous or polygamous: M

AT what age did females begin breeding: 4

At what age did males: 4

What is the maximal longevity: 30

Sex ratio at hatch: .5

Maximum number per clutch: 2

In an average year what percent of females produce 0 yg.:20%

percent of females produce 1 yg: 75

produce 2: 5

What is the SD in percent females of producing litters (80%) due to EV? 15

Mortality of females between 0 and 1: 50%

What is the SD in the above mortality due to EV? 20

What is the percent mortality of females between ages 1 to 2: 5

What is the SD: 2

What is the percent mortality ages 2 to 3 years:5

SD :2

Constant for the rest of life.

Simplifying assumption of the model is that mortality is same after reproductive age.

Males are the same mortality pattern

Catastrophe:

toxic spill: 2%

severity to reproduction: .9 (reproduction is at a level of 90% of a typical year)

severity to survival: .4

Disease: 10% per year

severity reproduction: .8

severity to survival: .8

Hurricane:

.333

severity reproduction: 1

severity survival: .5

Are all adult males capable of setting up territories and breeding: n

What % of the adult males in the breeding pool: 95

Do you want the starting population to reflect the sable age:y

How many animals: 150

## Whooping Crane PVA Minutes

carrying capacity: 500

What is SD in K due to EV:0

Is there a trend projected in the carrying capacity?y

Over how many years is the carrying capacity expected to change? 10

how many years: 100

percent decline: -.5

Do you want to harvest: n

do you want to supplement population: no

August 7, 1991: Summary and Working Groups  
Modeling, Genetics, Disease Groups

Claire Mirande: Captive Studbook

ICF agreed to put the studbook because it was necessary for pairings enormous work, and cooperation. The exercise is more valuable the more you know about the wild population, the data was there but there hadn't been a need to look at the data yet. Ernie Kuyt had most of the information necessary to do a studbook on the data. What I am going to do is show you what we have in terms of studbook information.

Sheri Snowbank: I got most of the data from Ernie I had to invent some parents. In the back are CNA summary. Egg switch information. Captive offspring. are the parts.

Claire: There is a table in the beginning of the studbook. Each of the years that birds were banded. The number of hatch and number of fledge data is preliminary. Reviewed studbook data.





***GRUS AMERICANA***

**WHOOPING CRANE**

**CONSERVATION VIABILITY ASSESSMENT  
WORKSHOP REPORT**

**SECTION 14  
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