

POPULATION BIOLOGY: THE SCIENCE OF POPULATION MANAGEMENT FOR CAPTIVITY, REINTRODUCTION, AND CONSERVATION.

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Population Biology and Conservation

Captive populations, as well as wild populations requiring conservation action, are typically small. As a result, biological and logistical challenges to their successful management exist. Small populations experience high levels of demographic stochasticity (random variation in individual reproduction, mortality, and sex ratio) and deleterious genetic effects, which combine to greatly enhance extinction risk. As genetic effects influence reproduction and mortality rates, populations decline further and demographic stochasticity increases. These declines lead to smaller populations and increased inbreeding and loss of gene diversity. Genetic and demographic effects are therefore highly synergistic. Populations of sizes less than 200 are generally considered to be especially susceptible to synergistic dynamics of demographic and genetic risk (Frankham et al 2002).

Through the application of standardized methods for population management, these potentially detrimental demographic and genetic effects can be mitigated, and optimal management strategies for captive populations can be devised. Examples of such strategies include those employed by the Species Survival Plan® (SSP) of the Association of Zoos and Aquariums and the EEP of European Association of Zoos and Aquariums.

The goals of these programs include rapid growth of founding populations to achieve demographically stable populations at program carrying capacities, creation of stable age structures, and limiting extinction risk. Management strives to maintain the genetic variation present in the founder stock to the greatest extent possible, avoiding loss of heterozygosity due to genetic drift and inbreeding, and thus maintaining adaptive potential in populations. These populations are managed both for genetic health in captivity and as genetic reservoirs in the event of future reintroductions to wild populations.

To ensure the suitability of these captive populations as genetic reservoirs, management goals also include avoidance of artificial selection, including both the unintentional selection of animals with characteristics “well-suited” to captivity, and the intentional selection for or against specific traits. The role of selection in captive populations is poorly understood and maintaining maximum genetic variation is therefore prioritized over selection for or against specific traits.

Data for Population Management

A prerequisite to the development of a population management plan is the compilation and maintenance of a studbook. This is a computerized database of parentage information and life history events (births, deaths, transfers, etc.) for individuals within the population from the time of population founding to the present. Data entered into the studbook should be as complete as possible, but unknown or missing data is to be expected. “Analytical studbooks” incorporating potential or assumed values for missing information can be created and evaluated.

Population Status

Once compiled, studbooks can be analyzed using a variety of software tools. Studbook analysis is used to examine population history, evaluate current population status, and predict future population status under varying management conditions. Analyses are conducted as part of informed population management planning resulting in specimen-by-specimen recommendations for breeding and non-breeding individuals.

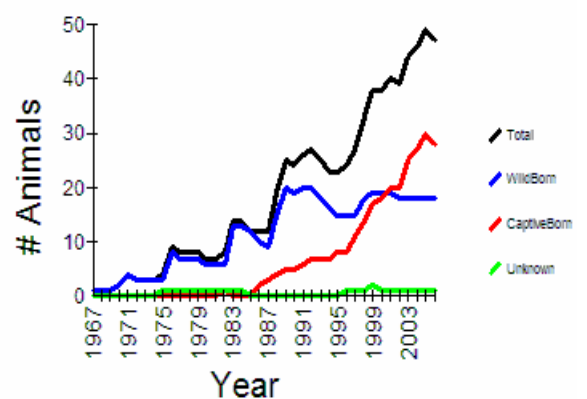


Figure 1. Population census of rhinoceros hornbills in AZA facilities.

Demography

Demographic analyses are used to investigate population size, structure, and distribution. The population census is used to examine historic population growth and decline in captivity (Figure 1.).

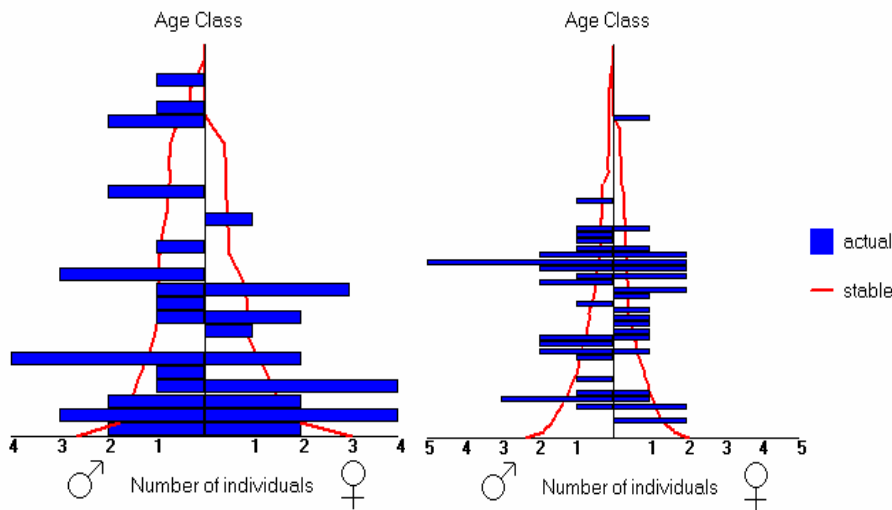


Figure 2. Age distribution of blue-faced honeyeaters and of white-naped cranes in AZA facilities in 2006.

Age distributions, illustrating the number of individuals in each age and sex class, are plotted to examine structure in populations. This structure determines the population’s overall potential for reproduction and growth.

Population vital rates are calculated for males and females using individual life histories; age-specific birth rates (m_x), mortality rates (q_x), and survivorship (l_x) are used to construct life tables (Table 1.). These values, based on historic studbook data, can be

used to inform decisions about the management of living specimens as they indicate expectations for the likelihood of reproduction and mortality for individuals in given age and sex classes.

The accuracy of demographic analyses and their value as predictive tools are dependent on both the quantity and quality of studbook data; rates based upon the observation of few individuals will lack the robust nature of larger data sets. Challenges therefore exist for analyses of highly endangered populations. For species lacking the data necessary to construct life tables, “surrogate” species can be utilized to provide vital rates for the purposes of population modeling. Data “surrogates” should be closely related species with similar life histories.

Genetics

Genetic analysis of populations begins with founders. A founder is an individual entering a population in which it is assumed to be unrelated to all other individuals. Wild-caught specimens are usually considered to be founders, as are specimens entering a managed population from another unrelated managed population. To be considered founders, animals must also contribute descendants to the population; they are considered to be potential founders until offspring have been produced. The number of founders contributing to a breeding program is of great concern, as higher numbers of founders will more accurately represent the genetic composition of the source population.

Age	Males			Females		
	Qx	Lx	Mx	Qx	Lx	Mx
0	0.330	1.000	0.050	0.330	1.000	0.040
1	0.060	0.670	0.470	0.090	0.670	0.760
2	0.040	0.630	0.650	0.070	0.610	0.840
3	0.050	0.605	0.720	0.110	0.567	0.850
4	0.040	0.574	0.630	0.110	0.505	0.920
5	0.080	0.551	0.820	0.150	0.449	1.000
6	0.050	0.507	1.010	0.200	0.382	0.740
7	0.060	0.482	1.120	0.150	0.305	1.090
8	0.110	0.453	1.230	0.240	0.260	0.360
9	0.060	0.403	0.410	0.200	0.197	0.250
10	0.110	0.379	0.550	0.200	0.158	0.000
11	0.170	0.337	0.030	0.170	0.126	0.000
12	0.130	0.280	0.000	0.440	0.105	0.000
13	0.360	0.244	0.000	0.200	0.059	0.000
14	0.400	0.156	0.000	0.500	0.047	0.000
15	0.000	0.094	0.000	0.000	0.023	0.000
16	0.470	0.094	0.000	0.500	0.023	0.000
17	0.000	0.050	0.000	0.000	0.012	0.000
18	1.000	0.050	0.000	1.000	0.012	0.000
19	1.000	0.000	0.000	1.000	0.000	0.000

Table 1. Life table for Guam rails in AZA facilities. This life table indicates first year mortality (q_x) for males and females has been observed to be 33%. Both sexes have a high probability of breeding (m_x) in their first year. While life span has been observed to be as great as 18 years, reproduction has not been observed in individuals of ages greater than 13 years.

From the pedigree, values of pair-wise kinship coefficients (Falconer 1981) are derived, and individual mean kinship is calculated. Individual mean kinship (mk_i) is equal to the average kinship between each individual and all individuals in the population. This value indicates the relative rarity of an individual's genome within the population (Table 2.). Individuals with low mean kinship are "under-represented". Individuals with high mean kinship are "over-represented". Mean kinship is utilized in the creation and prioritization of breeding pairs, with pairs preferentially consisting of individuals with low and similar mk_i values (Ballou and Lacy 1995). This breeding strategy is the most effective way of retaining gene diversity (Lacy 1995).

The inbreeding coefficients (F) of individuals and their potential offspring are also calculated from the pedigree and used in population management. F is equal to the probability that alleles at a locus sampled in two individuals are identical by descent (Ballou 1983). Inbreeding is expected to result in reduced fitness (Ralls and Ballou 1983) and is avoided or minimized in most managed breeding programs (Ballou and Foose 1996).

Population Management Plans

Using demographic and genetic analyses, population biologists create population management plans suited to needs of specific programs. These needs vary from the creation of breeding and transfer recommendations for individual animals to overall strategies for long-term management of healthy populations in captivity and the wild. Plans include designating animals for breeding, holding, or release. They may include the transfer of individuals between holding facilities or between captive and monitored/managed wild populations through meta-population analysis. Plans also are able to address the special needs of conservation programs by creating genetically informed evacuation strategies for breeding facilities, nest or den protection prioritizations for monitored wild populations.

In the selection of individuals for conservation programs such as reintroductions, it is critical that the genetic and demographic integrity of the source population be maintained. Indiscriminately selecting animals for reintroductions can have serious genetic and demographic effects, such as skewed founder representation or loss of founder lines, and destabilization of age structure through overharvest of targeted age classes. Selection of animals for reintroduction must consider the maintenance of the remaining captive population's ability to serve its conservation role into the future, for the perceived extent of the program.

Conclusion

Whatever their role, captive populations must themselves be stable and secure, being managed for demographic and genetic health, to support these functions. Mean kinship management strategies are generally employed, though they may be customized to meet specific program needs. Monogamous, polygamous, and colonial breeders can all be accommodated. Using this strategy, populations can

Males			Females		
SB#	MK	Age	SB#	MK	Age
1292	0.104	6	853	0.08	7
1293	0.104	7	727	0.104	9
1314	0.138	5	508	0.106	5
1591	0.14	1	747	0.113	8
1593	0.14	1	1460	0.133	3
1594	0.14	1	1595	0.14	1
1596	0.14	1	1459	0.154	3
988	0.142	6	1564	0.154	2
985	0.144	6	1412	0.164	4
1313	0.148	5	1584	0.167	1
872	0.152	7	1319	0.168	5
986	0.154	6	1410	0.171	4
981	0.161	7	871	0.174	7
1579	0.167	1	1580	0.174	1
1582	0.167	1	1556	0.175	3
1583	0.167	1	1557	0.175	2
994	0.168	6	1559	0.175	2
1322	0.168	5	993	0.178	6
1569	0.174	2	995	0.178	6
1578	0.174	1	1573	0.183	1
1581	0.174	1	1574	0.183	1
1558	0.175	2			
1318	0.178	5			
1565	0.183	2			
1572	0.183	1			

Table 2. Individual Mean Kinships of Guam rails in AZA. The population Mean Kinship is equal to 0.1576.

be managed to maintain at carrying capacity or to supply surplus individuals for reintroduction or for export to other managed programs.

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