

RESEARCH FRONTIERS IN GENETICS: FUTURE NEEDS AND OPPORTUNITIES
IN SUPPORT OF SELF-SUSTAINING POPULATIONS

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Research involving genetic studies of exotic animals in captivity and, especially, of endangered species has, until recently, been the subject of relatively little attention in comparison to the efforts expended on behalf of domestic livestock and pet animals. Nonetheless, the increasing research effort in population genetics, pedigree analysis, cytogenetics and molecular genetics has produced useful and often unanticipated benefits as zoos establish breeding programs for endangered species.

Genetics research programs have been undertaken in support of many SSP programs and have helped them toward their gene pool conservation goals. Table 1 provides an informal list of genetics research projects supporting SSPs. The specific application of techniques in genetics research has been applied to SSP taxa not so much because they are special in their need for research but, rather, because of the manner in which SSP status focuses concern; similar genetic research efforts are desirable for other taxa, e.g., gibbons, giant tortoises, parrots, cracids, gazelles, manatees, and leopards.

In addition to opportunities for expanded efforts in genetics research to continue to help structure existing and new SSPs, new technologies may be anticipated that will enable analyses more informative than available today and involving relatively less effort in sample collection and laboratory effort.

It is fun to speculate what the future might hold and, indeed, in the halls of laboratories and at the watering holes of conferences, exciting ideas abound. However, in this forum it seems altogether more appropriate to focus less on fantasy and more on frontiers - and what they are likely to be.

In the future, there is likely to be:

- 1) Expanded genetics research activities in support of SSPs,
- 2) New challenges facing captively-bred populations in zoos whose origins lie embedded in the genetic structure of populations and species,
- 3) New technological possibilities helpful in dealing with previously identified and newly identified problems, and
- 4) Increasing opportunity for transfer of the technology, initially developed in zoos to in situ conservation efforts for a variety of species.

Expanded Research Involvement. As SSP programs expand both in terms of the number of taxa involved and their taxonomic diversity, and over an increasing number of generations in captivity, questions concerning systematics and taxonomy and uncertain parentage will inevitably continue to arise. Better methods of marking animals and record keeping will help with uncertainties in parentage but, it is predictable that uncertainties

Ryder, O.A. 1988
 Genetics research frontiers

will continue to exist. It seems even less likely that questions of genetic differentiation of regional populations, ecotypes, and subspecies will subside.

New studbooks are being established and this will continue in the future. As the essential tool for population management, the value of studbooks is eroded by uncertainty in the genetic and taxonomic status of founders and by lack of exact parentage information. Early intervention of research investigations in genetics will help new studbooks correctly classify founders and their offspring - as has been done with orang-utans and Asian lions for example - and keep accurate pedigrees - as has been done with pygmy chimpanzees and squirrel monkeys (Saimiri sp.).

Facing New Problems. Many unresolved issues in systematics and taxonomy and pedigree confirmation and correction may be amenable to investigative approaches now applied. However, it is not clear that collection of sufficient specimens for traditional morphometric analyses will be feasible. As populations of large vertebrates become endangered and exist only in fragmented remnant populations they become less available for collection and deposition in museums. Thus, there may be an increasing reliance on non-lethal investigations involving cytogenetics and molecular genetics. Zoological parks and aquaria are expanding their capabilities to deal with these needs through proliferation and expansion of in-house genetics research efforts. Still, unfilled demand for practical genetic information is growing.

A major issue that zoos will be confronting in the management of their small populations is a logical consequence of the phenomenon of founder effect (Ryder, 1988). Two empirical observations sketch the logic of this argument. First, in humans (the species whose medical genetics are best known) inbreeding over generations in populations that are genetically isolated (usually for religious or other cultural reasons) has, through the chance events of the founder effect, provided explanation for the occurrence and restricted distribution of certain genetic diseases (Diamond and Rotter, 1987).

Overtly lethal genes are, of course, either weeded out by selection or, in the extreme case, contribute to the extinction of the population. Thus, genes producing their deleterious effects after the age of sexual maturity or producing sublethal deleterious effects may produce genetic disease.

The second observation is that all zoo populations are small populations in a genetic sense or otherwise. In his review of the 1986 ISIS data, Conway (1987) reported that only for ten species of birds and mammals did the pooled population size for reporting institutions surpass 200 individuals.

Under these circumstances, genetic diseases are inevitable in our zoo stocks, in our SSP programs and in remnant wild populations. They may lie undetected in early generations of captive breeding in zoos only to become apparent after multiple generations of breeding in captivity or upon return to the wild in introduction programs.

Genetic disease or genetically-determined undesirable characteristics are already known in zoo populations of selected taxa. Examples include the pigmentation anomaly in Przewalski's horses (called the fox-coloration in

Europe), the cross-eyed condition associated with white coat color in tigers, hairlessness in ruffed lemurs and, possibly, diaphragmatic hernia in golden lion tamarins. As pathology information is collected by additional institutions involving greater numbers of taxa bred in captivity over increasing numbers of generations, the identification of additional genetic defects in zoo populations appears certain.

New technologies may greatly aid techniques of pedigree analysis in analyzing, diagnosing, and combating genetic defects. Two resources are essential: accurate pedigree information and reference specimens from founders, affected individuals, their ancestors and unaffected relatives. If we in zoos consider the occurrences of genetic defects in our stocks a realistic future possibility, then we greatly aid ourselves by keeping cell lines - or at least DNA samples - from founders and individuals of known pedigree as our populations expand toward their defined carrying capacity. (DNA samples may be purified relatively inexpensively using common laboratory equipment. Once purified, DNA is stable for long periods of time at low humidity at room temperature.)

Technological Innovation in Zoo Genetics Research. There is no question but that the astounding increase in information about the human genome and its organization now being generated with technology of regularly increasing sophistication can be applied to the benefit of endangered species as can the production technology itself. DNA fingerprinting, a technique exploiting the presence of dispersed arrays of repetitious DNA sequences in vertebrate genomes offers the potential for confirming or refuting parentage assignments in cases that were unresolvable with techniques hitherto available. In selected situations it may be applied to small populations to make useful inferences of kinship generally, thereby providing information about the degree of genetic relatedness of, for example, California condors whose pedigree relationships are uncertain.

Analysis of variable DNA sequences within and among populations and subspecies may also provide data useful for systematic studies, taxonomic identification and estimation of migration rates and other population genetic parameters. Successful demonstration of the utility of analysis of patterns of variable DNA in systematics, population and evolutionary biology has occurred involving relatively few species to date. Clearly, a great deal of additional research needs to be undertaken and significant opportunities exist for zoological parks and aquaria to participate in this exciting research area that holds promise for aiding conservation efforts.

Characterization and management of genetic defects and diseases in humans is now based largely on DNA studies in conjunction with analysis of pedigrees. New techniques of DNA mapping have allowed for the identification of DNA markers that are powerful predictors of whether an individual carries a defect transmissible to his/her offspring. Carrier tests for genetic diseases in endangered species may need to be developed as an aid in management of future populations.

Application of New Technologies to In Situ Conservation. The ability of the technology employed in DNA fingerprinting to resolve genetic variation not detectable with other methods recommends its use in a variety of applications of concern to conservation biologists in the field. Management for

conservation in zoological parks and aquaria and population vulnerability or population viability assessment for conservation of populations in the wild require knowledge of both behavioral ecology and population genetics information.

Behavioral observations and knowledge of pedigree structure (i.e., parentage assignments and kinship relationships) may be combined together to infer the breeding structure of populations and the fitness of individuals. Newer DNA analysis based studies may be used to generate sufficient pedigree information to begin the analyses.

The applications to conservation management include inference of effective population size and, hence, the rate of loss of genetic variability in small populations as now occur in remnant populations of such species as lion tamarins, Asian and African elephants, rhinoceroses, island tortoises and sea turtles.

Rhinoceroses serve as a notable example. In East Africa, Zimbabwe, Zaire and Southern Africa, both black and white rhinos are being sequestered into defensible reserves and private ranches. The breeding structure of rhino populations in these conservation propagules is undocumented. Provided samples for DNA analysis (skin biopsy specimens, ear notches, or blood samples) are taken from the adult population (possibly at time of translocation), the number of genetically effective males may, in principle, be determined by analyzing the offspring produced. With this knowledge, the effectiveness of the reserve design and appropriateness of animal density within the ranches and reserves in terms of gene pool conservation goals may be examined.

A similar argument holds for the analysis of reintroduced populations and useful information obtained for long-range planning of reintroduction efforts.

A final example of the application of new technologies to conservation management highlights the potential of the technique of PCR (polymerase chain reaction). Sufficient DNA may be obtained from skin fragments and shed hairs to allow the selective amplification of defined DNA sequences useful for providing genetic information about individuals. Dr. Karen Garner in the genetics lab at CRES (the Center for Reproduction of Endangered Species) at the Zoological Society of San Diego has recently produced DNA typing information from the shed hairs of lowland gorilla individuals. Extension of these studies to relatively easily obtained mountain gorilla hair samples offers the potential of providing genetic data on this highly endangered flagship animal now at critically low population levels.

References

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Ryder, O.A. 1988. Founder effects and endangered species. Nature 331: 396.

Table 1

GENETICS RESEARCH PROJECTS
UNDERTAKEN IN SUPPORT OF
SSP PROGRAMS

Protein electrophoretic
studies

Arabian oryx
Asian elephant
Asian small-clawed otter
Asian wild horse
black rhinoceros
cheetah
gaur
golden lion tamarin
gorilla
Indian rhinoceros
red panda
scimitar-horned oryx
tiger
white rhinoceros

Chromosomal
studies

Asian small-clawed otter
Asian wild horse
black rhinoceros
gorilla
okapi
orang-utan
scimitar-horned oryx
Sumatran rhinoceros
white rhinoceros
bonobo
Indian rhinoceros
California condor

Mitochondrial DNA
studies

Asian elephant
Asian wild horse
black rhinoceros
cheetah
gaur
golden lion tamarin
gorilla
Grevy's zebra
lion-tain macaque
orang-utan
red wolf
Sumatran rhinoceros
white rhinoceros

DNA fingerprinting
studies

Asian elephant
Bali mynah
bonobo
California condor
lion-tail macaque
orang-utan