Lacy

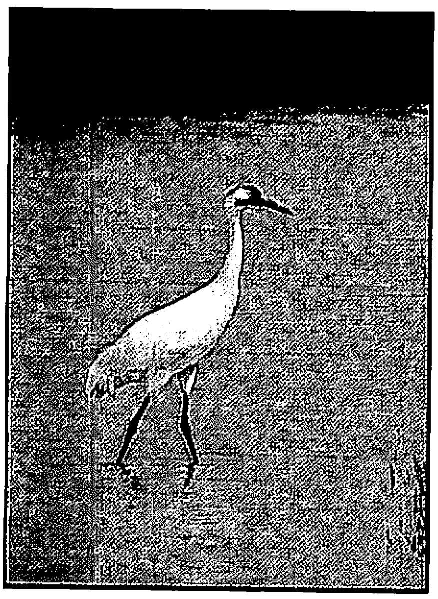
Fighting extinction with PVA

Any population of animals or plants faces threats to its survival. These threats can be human-induced or intrinsic to biological processes. If they cause a population to become small and isolated, then additional threats intrinsic to small biological populations can arise. Population biologists have come up with a number of ways to tell when a population is in danger of extinction.

By Robert Lacy

Threats caused by human actions include habitat destruction, over-harvesting, pollution, and the introduction of exotic predators, competitors and diseases. The combined effect of human-caused and intrinsic threats can be disastrous, leading to the extirpation of the population – or, if the local population was all that remained of the taxon, its ultimate extinction.

Population Viability Analysis (PVA) is a collective term for the various quantitative methods used to determine the probability of extinction of a population, and has become a useful a tool in conservation assessment and planning.



When only a single population of the whooping crane *Grus americana* persisted in the wild, a PVA determined that additional populations needed to be established to avoid its decimation by a local catastrophe such as an epidemic or severe storm. PVAs showed that the black-footed ferret and the Puerto Rican parrot faced similar threats. *WWF/Sture Karlsson*

PVA can be used to measure "minimum viable population", or MVP. When a population falls below its MVP, its days may be numbered: subsequent chance events can cause it to fluctuate and decline even further. The smaller and more erratic its size, the greater the probability that its number will, by chance, hit zero.

In the 1980s researchers Michael Gilpin and Michael Soulé found that the destabilizing processes are synergistic: a combination of demographic, environmental, and genetic processes can exacerbate the instability produced by other factors, causing what has been depressingly referred to as "extinction vortices". Although Mark Shaffer first defined MVP as the size at which a population has a 99% probability of persistence for 1000 years, it might be more meaningful biologically to consider it to be the size below which a population's fate becomes determined largely by the intrinsic random factors that characterize extinction vortices.

We are finally beginning to understand how extinction works.

How can we estimate MVPs?

Perhaps the best way to determine an MVP would be through empirical observation of the long-term fates of a number of populations of various sizes. In 1990 Joel Berger presented a good example of this approach, in which he observed that populations of bighorn sheep in the mountains of the western USA persisted only when the populations had more than 100 animals.

We need more such empirical studies, but the time and numbers of populations required for them are precluded in the cases of most species threatened with extinction – exactly those for which estimates of MVP are most urgently needed.

A more elegant approach would be to calculate the probability of extinction from a small number of measurable parameters. Although there have been some valiant attempts in this direction, our understanding of population biology is not yet sufficient to provide fully adequate analytical models of the extinction process.

A third method is the use of computer simulation modelling to project the probability distribution of the possible fates of a population. Such models can incorporate a very large number of threatening processes and their interactions.

Evolution of the MVP/PVA/PHVA approach

Shaffer's original term "minimum viable population" has fallen into disfavour among many conservation biologists, even as the PVA approach has risen in popularity. To some, the term MVP implied that there was a precise number below which extinction was certain and above which persistence was assured. In keeping with the probabilistic nature of the extinction process, a number of conservation biologists have focused on PVA methods for estimating the probability of extinction over defined time periods for a designated population exposed to a specific scenario of environmental conditions, threats to persistence, proposed management actions and other foreseeable events.

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desert. Wild dog populations have declined precipitously during the last 20 years and perhaps no more than several thousand now exist. The east and west African populations are the most endangered, having recently suffered severe population declines.

Molecular genetic analyses showed that eastern and southern populations form two genetically distinct clades that warrant separate preservation. Thus plans to reintroduce south African wild dogs to areas of east Africa where populations have recently gone extinct would mix populations with separate evolutionary histories. In addition to causing the potential loss of genes that are unique and adaptive in the east African population, introduced south African dogs could put the native eastern population at risk with south African diseases to which they have not developed immunity. Moreover, wild dogs in zoos are all of south African origin indicating the captive breeding of the wild dog is not directed towards those populations most at risk.

Breeding success

In small captive and wild populations, some animals may have less reproductive success than others, with important implications for conservation management. Molecular genetic techniques can be used to deduce parentage in wild and captive populations if all potential parents and their offspring are sampled. Even in populations for which little information is available, inferences can be made about the breeding structure from molecular genetic data.

An important aim of the genetic management of captive populations is to reduce inbreeding by selecting breeding pairs of low relatedness. Newly developed techniques of DNA analysis can be used to assess genetic variation directly, and DNA fingerprinting can be used to group individuals into relatedness classes.

For example, in the captive breeding programme for the critically endangered Mauritius pink pigeon *Nesoenas mayeri* good parentage records stretch back over several generations, but all captive birds are descended from just six founder birds, and the relationships among these are not known. When researchers saw evidence for inbreeding depression in captive pigeons, DNA fingerprinting proved useful for determining levels of relatedness among them and deciding how to manage their breeding.

Molecular techniques have recently called into question some of the assumptions around which rainforest conservation plans have been designed so far.

Forensics

The forensic applications of molecular techniques are wide ranging. The species and regions that samples have originated from may be deduced and samples from the same individual obtained from different places and at different times can be matched. Genetic typing can often be done on trace materials such as hair, horn, tusks, faecal material, ruminant boli and mummified or museum preserved remains. One of the most intriguing recent cases concerns monitoring the legal market for whale meat in Japan. Whales taken under strict scientific collecting permits can be sold in the Japan's domestic market, but concern has been raised that such legal sales allowed a route for illegal marketing. Palumbi and colleagues have shown that the whale meat for legal sale in Japan does involve several banned species, suggesting that the legal market is a vehicle for illegal trade and may be difficult to police.

Gene conservation

Molecular genetic techniques can be used on small, isolated populations to measure the loss of genetic variability and identify those populations that have been most severely affected.

One example concerns the Northern hairynosed wombat *Lasiorhinus kreffti* in Epping Forest National Park, Queensland. Once abundant, this species now exists as only a single colony of less than 80 individuals as the result of drought and cattle grazing. Because this remaining population is small, random genetic drift will cause loss of genetic variability, particularly of rare alleles, over time. Through the use of the polymerase chain reaction applied to DNA isolated from museum samples, researchers compared historical levels of genetic variability in a population from New South Wales to the levels found in the current Epping Forest population and to a related but abundant wombat species. The molecular analysis showed that the Northern hairy nosed wombat had only about 40% of the genetic variability expected in a widely distributed abundant species, and that the loss of genetic variation was well advanced even in the historical population. Such information can be used to estimate effective population size over the period of decline in Epping Forest wombats and expected future losses in genetic variability, and provide the basis for a captive breeding programme.

Limitations and problems

The preservation of evolutionary diversity is an essential part of conservation. Molecular genetic techniques are useful tools for this purpose, whether in choosing appropriate taxa or sites for conservation or for making plans that will increase the prospects for long-term viability. Our increased ability to measure genetic variation could result in both improved preservation of genetic variability and avoidance of inbreeding depression in captive and wild populations of rare and endangered species.

However, there are limitations to the use of genetic techniques and problems in their application: demand for laboratory services is growing, and resources are increasingly scarce. We must find cheaper, less demanding techniques, and greatly increase training. We now possess a powerful set of molecular tools with which to approach many important conservation questions; we have only to apply them more widely.

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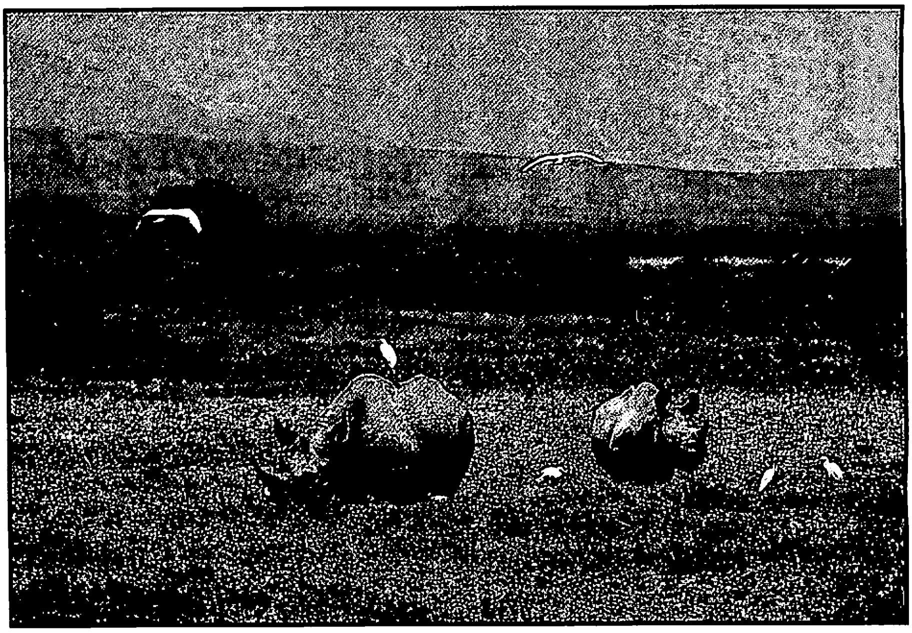
Beginning about 1989, we began to see that PVA can be most usefully incorporated into a conservation strategy if it were the focus of a conservation workshop. Such an event would encourage collaboration between conservation professionals, NGOs and local communities.

The Conservation Breeding Specialist Group (CBSG) of the IUCN Species Survival Commission has used workshops centered on PVAs to provide guidance to conservation assessment and planning. Over the past few years, the PVA workshops have expanded beyond the quantitative analysis of extinction probabilities. They now often incorporate consideration of such factors as resource use by local human populations (for example, in the PVA on the Tana River primates in Kenya; education programmes for local human populations (Aruba Island rattlesnake PVA); trade issues (Kenya black rhino PVA); and trends in human demographics and land-use patterns (greater one-horned rhinoceros PVA). Such workshops have thus come to incorporate more than population biology modelling, and are now called Population and Habitat Viability Analyses, or PHVAs.



Inbreeding and demographic fluctuations are threats to Kenya's black rhinos, according to a PVA. *WWF/Mauri Rautkari*

How is a PVA used?

Which factors are important to consider in a PVA? This depends on the biology of the species, the present population size and distribution, and the threats it faces. For example, orang utans may be threatened by forest destruction, but inbreeding and randomly skewed sex ratios are unlikely to be problems, at least not on a species-wide basis.

On the other hand, even if the remnant Atlantic coastal rainforest of Brazil is secured for the future, the populations of golden lion tamarins *Leontopithecus rosalia* which can persist in that remnant forest may not be sufficiently large to be stable in the face of chance events.

The identification of the primary threats facing a taxon via a comprehensive PVA is important for conservation planning. For example, tamarin populations might be stabilized by the translocations and reintroductions that are under way and planned, but an orang utan PHVA recognized that releases of confiscated "pet" orang utans are unlikely to have a conservation benefit for those populations which are facing habitat destruction rather than stochastic fluctuations and inbreeding.

For many species, such as the whooping crane *Grus americana*, the temporarily extinct-in-the-wild black-footed ferret *Mustela nigripes*, and the Puerto Rican parrot *Amazona vitatta*, only a single population persisted in the wild. Although those populations may have been maintained or even increased for a number of years, PVAs helped to identify that the principal threat was that a local catastrophe (e.g., disease epidemic, severe storm) could decimate the population. The primary recovery actions therefore needed to include the establishment of additional populations.

PVA modeling also allows one to test the expected results of any given management action on the computer before implementation in the field. This process can help us select the best management option and define target recovery goals. For example, a PVA carried out on the black rhinoceros in Kenya's 11 rhino sanctuaries has suggested that periodic movement of rhinos between fenced sanctuaries to reduce inbreeding and demographic fluctuations would be necessary to stabilize the populations in the smaller parks.

What is the future of PVAs?

We are finally beginning to understand how extinction works. This was reflected in the recent decision to base IUCN categories of threat on quantified criteria indicating probability of extinction, or changes in such indicators as species range, numbers, and trends. Much more needs to be done, however, to develop more comprehensive and predictive models, gather relevant data on status and threats, and apply the PVA techniques.

To date, most PVA models are too simplistic, treating organisms as independent actors in homogeneous environments. We also need to include other factors, such as dispersal patterns; complex social processes; effects of loss of genetic variation; interactions with other species; and the effects of changes in the global environment.

Unfortunately, the urgency of the current biodiversity crisis does not permit us the luxury of waiting until we have a better understanding of all the factors that drive population, community, and ecosystem dynamics. We are ethically required to take aggressive conservation action now, and PVA provides a way to make immediate use of the information we do have, in a well-documented process that is open to challenge and improvement.

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This text was adapted from an article in press in *Primate Conservation* by Robert C. Lacy, Daniel F. and Ada L. Rice Center, Brookfield Zoo, Brookfield, IL 60513 USA.

Saving endangered plants

The Royal Botanic Gardens at Kew has pioneered the science of plant conservation.

By Charles Stirton and Michael Maunder

Botanists have a number of new techniques which show their usefulness in identifying areas of high biodiversity, thus building the scientific basis for the conservation of biological diversity. Some, such as Geographical Information Systems (GIS), help to convey complex scientific arguments to non-specialists particularly politicians and decision makers clearly and succinctly (see page 21).

The Royal Botanic Gardens at Kew, (RBG, Kew) represents a huge resource for international plant conservation at its two sites, at Kew just outside London and at Wakehurst in West Sussex. The two sites contain the world's largest collection of living and preserved plants, extensive glasshouses, laboratories and the Wakehurst seedbank. In line with the Convention on Biological Diversity and Agenda 21, these collections and research facilities are increasingly managed to support plant conservation programmes throughout the world. This utilization is based on collaborative projects with a wide variety of organizations. Key conservation priorities are botanical inventory, production of floras and monographs of key plant groups, professional training, promoting a resurgence in economic botany, the continued development of applied plant conservation techniques and increased local capacity.

Henk Beentje beside the endangered Madagascan palm *Chrysalidocarpus decipiens*. *John Dransfield*

The new Millennium Seed Bank at the Wakehurst Place site, to be opened in 2000 and designed to house seed of 25% of the world's plant species, is a major *ex situ* conservation project involving many countries with dryland floras.

Species recovery

The Living Collections Department of RBG, Kew is managing several integrated species recovery programmes. For a number of species, now extinct in the wild – such as the sacred toromiro tree *Sophora toromiro* of Easter Island – the only hope of long-term survival lies in careful genetic analysis and management. RBG, Kew and the University of Reading are screening all known toromiro trees to verify their identity and assess surviving genetic diversity. Using the developing techniques of molecular fingerprinting, genuine toromiros have been identified in European, Australian and Chilean botanic gardens, whilst wrongly identified trees have been removed from the breeding programme.

This work is coordinated by the Toromiro Management Group, which is co-chaired by representatives from CONAF an IUCN member in Chile, and Bonn Botanical Garden, Germany. This is an international group, supporting the conservation and reintroduction of this species – the first international pedigree management scheme for a threatened plant.

Similar programmes are being undertaken with other island plant species as part of Kew's Island Plant Programme. This includes botanical inventory, habitat restoration and reintroduction projects in the Mascarenes in collaboration with the Mauritius Wildlife Fund, the government of Mauritius and the Indian Ocean

Local people watch as a toromiro tree is planted on Easter Island by a warden of the Rapa Nui National Park and Dr Wolfram Lobin, Curator of the Bonn Botanical Garden. *Alberto Bordeu*

Commission. This is funded by the Global Environment Facility (GEF) of the World Bank and the Indian Ocean Commission.

Botanical inventory

Much of Kew's work is based on the belief that without an accurate and comprehensive inventory of plant species, and a mechanism for identifying that diversity, a national or regional strategy for plant conservation is dead-on-the-ground.

For example, Madagascar has a diverse palm flora with representatives of several evolutionary lines, yet until recently information on these spectacular plants was incomplete. Since 1991, Dr Henk Beentje has worked with Dr John Dransfield to prepare a comprehensive book on the palms of Madagascar. So far, he has discovered some 35 new species and a rare aquatic palm. This book appeared in 1995, providing a definitive treatment of this difficult group.

Scientific exchange

The GEF is funding scientific exchange between Kew and the National museums of Kenya as part of its programme for institutional support for the protection of East African biodiversity. Kenyan and UK botanists are exchanging visits and collaborating on the production of the