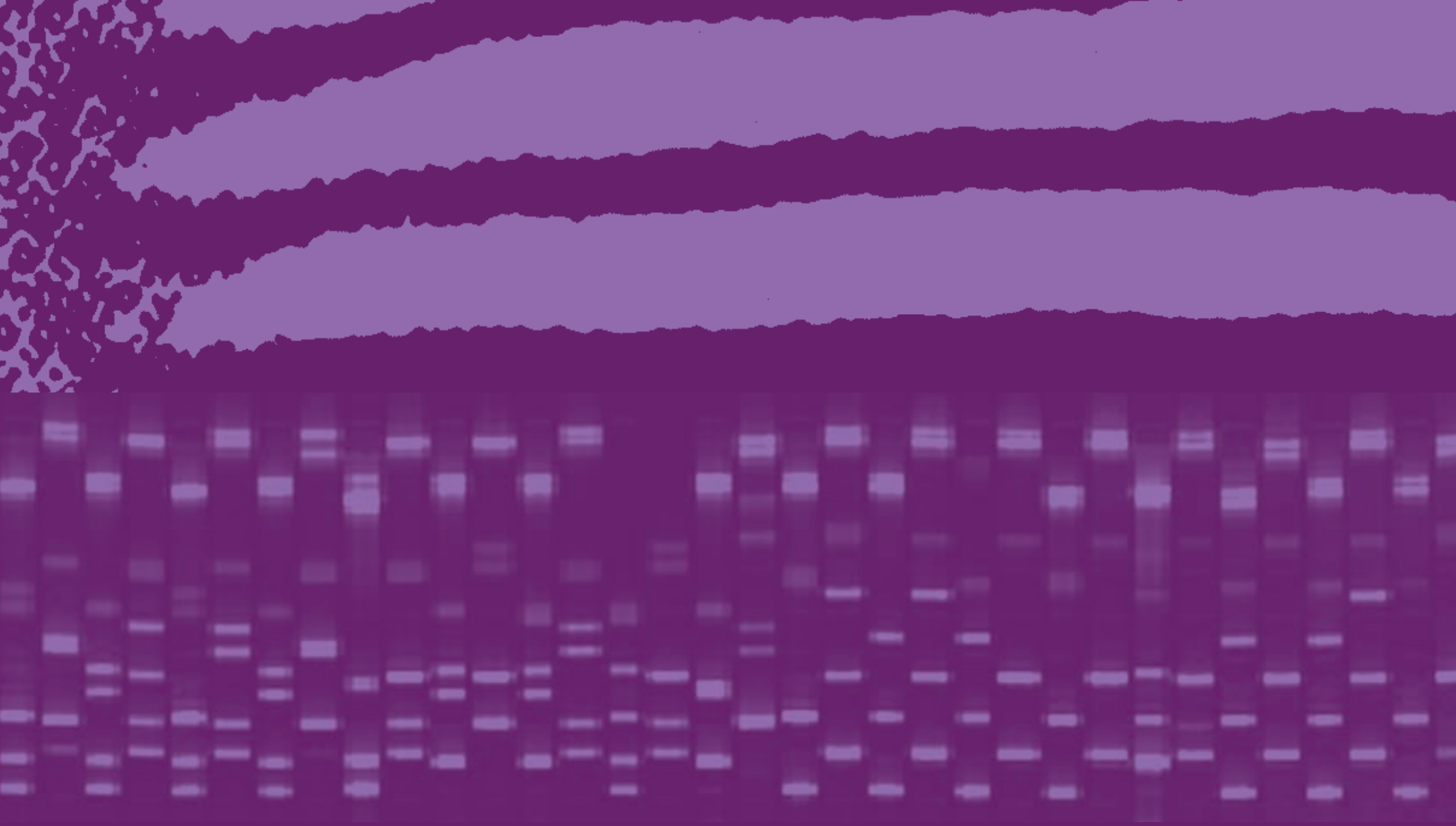


Annual Report of the Institute of Zoology

Science for Conservation 2000

The research of The Zoological Society of London

the institute of zoology aims to maintain and strengthen its position as a leading centre for research which benefits the conservation of animal species

Contents

To this end the Institute:

Carries out research of the highest priority for species conservation in the fields of animal behaviour, population and evolutionary ecology, conservation genetics, reproductive biology and veterinary science.

Puts this work into practice through the application of sound scientific principles to the conservation of animal species in the wild, in captive breeding programmes and in reintroductions to natural or restored habitats.

Disseminates information about the science underpinning conservation and the application of this knowledge through a programme of teaching and training and by the transfer of advanced biological techniques to other organizations and countries.

Through its Veterinary Science Group, maintains the highest standards of health and welfare in the animal collections at London Zoo and Whipsnade Wild Animal Park in support of their programmes in conservation education and the husbandry and breeding of threatened species.

foreword

For the Institute of Zoology, the year 2000 saw fundamental changes with far reaching consequences. The Institute has long aspired to become a National Centre for Conservation Biology and now, with our new and synergistic association with the University of Cambridge, we are working together in this role.

The appointment of Dr Georgina Mace OBE as the Institute's new Director strengthens further our academic leadership of this field. Georgina has worked closely and successfully with eminent theoretical, laboratory and field biologists from across the world to make conservation biology an applied science. The result is that ever more accurate predictions about population changes in the light of environmental pressures can be made to inform international and national decision-making processes. Academic distinction has been interwoven with other activities in the career of the Institute's new Director. Georgina has led ZSL Discussion Meetings and Symposia, and edited several books as well as the Society's successful new journal 'Animal Conservation'. She was also instrumental in forging and formalizing the new association with the University of Cambridge.

It is my pleasure as Secretary of The Zoological Society of London to present this report of a selection of the Institute of Zoology's scientific activities over the past year. The report spans not only scientific research of the highest quality, but also the Society's scientific publications from journals to books, postgraduate training, veterinary work, and practical conservation. Each of those facets of the Institute's scientific activities is set to flourish with the new administrative structures and academic input available to its staff.

Paul Harvey FRS
Secretary, The Zoological Society of London

director's introduction

It was a great privilege for me to be appointed as Director of Science. My thanks go to Dr Bill Holt who was a most capable Acting Director during the difficult period following Professor Morris Gosling's departure in 1999.

Our scientific mission to undertake research in conservation biology has been greatly strengthened this year through a new funding partnership with the University of Cambridge. The Institute's core research work is supported by an annual grant of about £1.7 million from the Higher Education Funding Council for England (HEFCE). Since 1988 we have received this grant through the University of London. However, following an audit by HEFCE in 1998, it became clear that to strengthen our standing as a conservation biology research institute we needed to identify a new funding partner. Much time over the year was spent investigating and evaluating alternative new arrangements. Our preferred choice was for a strategic partnership with the University of Cambridge, which would provide a first class research environment as well as linkages to the network of conservation NGOs in the Cambridge area. A new strategic plan for the Institute was drawn up with colleagues in the Zoology Department in Cambridge, and was accepted by HEFCE as a basis for future funding. The new arrangements came into effect at the end of the year. As I write this we are pursuing various routes to strengthen the linkages with Cambridge: we expect this to be a closer academic partnership than was the case previously with the University of London.

All staff participated in various stages of strategic planning to define our five-year plan for HEFCE. This exercise was particularly helpful for highlighting our comparative strengths and weaknesses, and the way in which our work relates to that of our parent organizations – The Zoological Society of London (ZSL) and the University of Cambridge. We reviewed all current projects according to three criteria: scientific excellence, mission-relevance and potential for external funding. Ideally our work should score highly on all of these but we aim to support some important, but difficult to fund, projects where they are of great strategic value. Our research should develop at the interface between significant practical conservation programmes (by ZSL among others) and the excellent academic work of our partners in Cambridge, to support the conservation of animal species. We value our position as a conservation biology research institute with a wide network of collaborators incorporating academic, governmental and non-governmental organizations, and hope to develop further our role in forging linkages and providing solutions to pressing conservation problems.

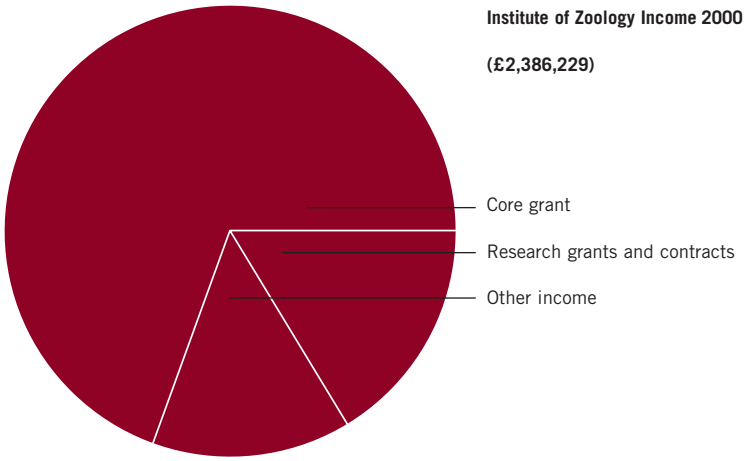
The year included some important scientific publications, international prizes, new grants and other successes. Despite this having been a somewhat uncertain year with changes in academic partner and director, the IoZ staff have continued to deliver excellent scientific results in an increasingly competitive field. This report bears testament to that work which will, I am sure, continue to flourish under our new arrangements.

Georgina Mace
Director of Science

funding and collaborations

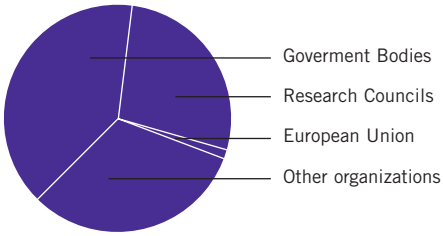
FUNDING ORGANIZATIONS

A H Schultz-Stiftung (Switzerland)
Alistair Voller Overseas Travel Fund
Association for the Study of Animal Behaviour
Association of British Wild Animal Keepers
Bat Conservation International
BBC Natural History Unit
BBSRC
Cook (UK) Ltd
Dalgety/PIC
Department of the Environment, Transport and the Regions
English Nature
European Union
FFI
G & A Claraz-Schenkung (Switzerland)
GlaxoWellcome
Goethe-Stiftung (Switzerland)
HEFCE
Intervet
IUCN
Joint Nature Conservation Committee
Lincoln Park Zoo
MAFF
Merial Animal Health
National Geographic Society
NATO
NERC
North American Freshwater Fishes TAG
Novartis Stiftung (Switzerland)
People's Trust for Endangered Species
Primate Conservation Inc. (USA)
Royal Geographical Society
Royal Society for the Protection of Birds
Schweizerische Akademie der Naturwissenschaften (Switzerland)
Schweizerischer Nationalfonds zur Förderung der Wissenschaftlichen Forschung (Switzerland)
Smithsonian National Zoological Park Fund
The British Andrology Society
The British Council
The Leverhulme Trust
The Natural History Museum
The Royal Society
The Wellcome Trust
Times Cheetah Appeal
Universities Federation of Animal Welfare
UPB Porcofram
Wildlife Conservation Society
WWF-UK
XY Inc., Fort Collins (USA)



Institute of Zoology Income 2000

(£2,386,229)



Research Grants and Contracts (£383,093)

COLLABORATORS

Universities

Anglia Polytechnic
Berne (Switzerland)
Brigham Young (USA)
Bristol
California (USA)
Cambridge
Cardiff
Columbia (USA)
Duke (USA)
Dundee
East Anglia
Edinburgh
Georgia (USA)
Hong Kong (China)
Imperial College, London
Ishinomaki (Japan)
King's College, London
Lausanne (Switzerland)
Leeds
Lisbon (Portugal)
Liverpool
Louisiana (USA)
Luton
Mahajanga (Madagascar)
Michigan State (USA)
Montpellier (France)
Murcia (Spain)
National University of Ireland (Cork)
New England (Australia)
Oxford
Pierre et Marie Curie (Paris)
Princeton (USA)
Queen Mary & Westfield College, London
Queensland (Australia)
Regensburg (Germany)
Royal Veterinary College, London
San Juan (Puerto Rico)
Sheffield
Surrey Roehampton
Sussex
University College, London
Vermont (USA)
Wageningen (The Netherlands)
Washington (USA)
West of England
York
Zurich (Switzerland)

Other

Animal Gene Storage and Resource Centre of Australia
BBSRC Silsoe Research Institute
Bombay Natural History Society (India)
Centre for Ecology & Hydrology (NERC)
Centre for Environment, Fisheries and Aquaculture Science
Chinese Academy of Science, Beijing
CSIRO Australian Animal Health Laboratory
Department of Agriculture and Rural Development for Northern Ireland
Desert Research Foundation of Namibia
Direction Générale de Forêts (Tunisia)
Dulwich Hospital
Durrell Wildlife Conservation Trust
English Nature
Estación Experimental de Zonas Aridas, Consejo Superior de Investigaciones Científicas (Spain)
Fisheries Research Services (Aberdeen and Pitlochry)
Foundation for Nature Research (Norway)
GlaxoWellcome
Hungarian Academy of Sciences
Institut für Zoo- und Wildtierforschung, Berlin
Institute of Animal Health
Instituto Nazionale per la Fauna Selvatica, Bologna
IUCN Species Survival Commission
King Khalid Wildlife Research Centre (Saudi Arabia)
KORA (Switzerland)
MAFF Veterinary Laboratories Agency
Marwell Zoological Park
Moredun Research Institute
National Museums of Scotland
National Wildlife Health Center, Wisconsin
Pig Improvement Company
Poultry Diagnostic and Research Centre of the Venkateshwara Hatcheries Ltd (India)
Queensland Department of the Environment and Heritage (Australia)
Royal Society for the Protection of Birds
Tanzania National Parks
Tanzanian Wildlife Research Institute
The Natural History Museum
The Wildfowl & Wetlands Trust
Universities Federation for Animal Welfare
Wildlife Conservation Society
ZooDent International

evolutionary ecology

Causes and consequences of genetic structure in the greater horseshoe bat *Rhinolophus ferrumequinum*

Bats represent nearly one quarter of all mammal species world-wide and contribute most to Britain's mammalian biodiversity. The majority of species are highly social, forming colonies in caves, mines, trees or buildings. Over the past few decades many of the suitable roosts and foraging sites on which bats so critically depend have been lost, contributing to a decline of European populations. Yet ecologists have afforded surprisingly little attention to these highly elusive animals. Breeding behaviour in particular, which can have important consequences for the maintenance of genetic variation and is therefore of interest to conservation biologists, is poorly understood in most species.

In collaboration with Drs Gareth Jones and Roger Ransome at Bristol University, we used microsatellites to study breeding in the endangered greater horseshoe bat *Rhinolophus ferrumequinum* which underwent a dramatic tenfold decrease in Britain during the last century. Female greater horseshoe bats form summer breeding colonies, returning annually to the same roost. Single offspring are born in early summer. During autumn females visit and mate with territorial males in caves, some of which guard their territories for many years. Shortly after copulation a plug forms in the reproductive tract of the female, probably preventing further matings. Sperm are then stored throughout

Studies on the breeding system and social structure of the endangered greater horseshoe bat *Rhinolophus ferrumequinum* led to a PhD award.

hibernation until fertilization occurs in spring.

To determine paternity, we compared the paternally derived genotypes of five cohorts of offspring born at a colony in Gloucestershire, south-east England, with those of adult males sampled throughout the surrounding area. We found that breeding in this species is polygynous; while some males sire few offspring born at the roost, others are repeatedly successful over successive years. Females breed with males from both within and outside their natal colony, thereby promoting gene flow among populations. Interestingly, a few successful males are revisited by the same females in separate years, leading to full-siblings within the roost.

By combining data on highly successful males with observations of territory tenure we have been able to identify several important male territories which can now be safeguarded from future disturbance. Our ongoing work will hopefully shed more light on this interesting breeding system, as additional individuals are sampled.

ROSSITER S J, JONES G, RANSOME R D & BARRATT E M (2000). Parentage, reproductive success and breeding behaviour in the greater horseshoe bat (*Rhinolophus ferrumequinum*). *Proceedings of the Royal Society of London Series B* 267: 545-551.

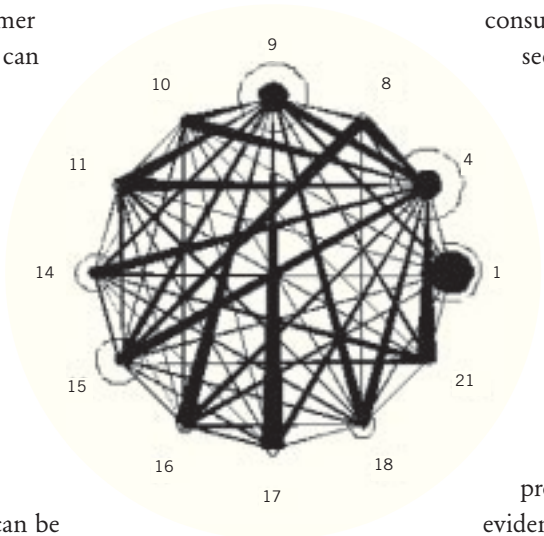
ROSSITER S J, JONES G, RANSOME R D & BARRATT E M (2000). Genetic variation and population structure in the endangered greater horseshoe bat *Rhinolophus ferrumequinum*. *Molecular Ecology* 9: 1131-1135.

Quantified interaction webs

It would be useful if we could predict what happens to communities when a species extinction occurs or when a new species invades because this would allow us to establish better management plans for the conservation of whole communities. These predictions are difficult because not only do direct effects on resident species occur but also a whole sweep of indirect effects may result. One such indirect effect is 'apparent competition' which occurs when two prey species share a predator. If a new prey species invades the community, the predator population is able to persist at a higher population density. The higher density of predators will cause greater consumer pressures and can lead to the extinction of all prey species except the one that resists highest predator pressure. Therefore apparent competition can be responsible for additional species exclusions and ultimately the organization of a community.

One way to evaluate the potential of apparent competition is the sampling of fully quantified food webs. Food webs depict trophic relationships and energy flows between interacting species. They are abstractions and, as such, often pool data into classes or groups, blurring species boundaries and therefore important species interactions. We have used a model system of aphids and their parasitoids (page 8) that, because of the one-to-one relationship of host to adult parasitoid, offers a unique opportunity to fully quantify all species interactions within the web.

The potential for apparent competition to occur is analysed by overlap diagrams (below) which show the extent to which parasitoids are shared and how symmetrical the interactions are. We found the strongest potential for apparent competition via the highest consumer level of secondary parasitoids. Although quantified webs are valuable for predicting the most important species interactions, they do not provide direct evidence for such interactions or how they affect species distribution and these need to be tested in controlled field experiments. This can conveniently be carried out on model assemblages of insects but would be impossible for most vertebrate systems of major conservation concern. The accumulation of similarly resolved webs from various communities can tell us whether some properties of food webs are general. If generalities across



Parasitoids are insects that feed and develop mainly on other insects. Aphids maintain large communities of parasitoids that occupy different trophic levels within a web: 'primary parasitoids' attack the aphid host and 'secondary parasitoids' attack the primary or secondary parasitoid.

insect model food webs exist, this could lead to significant insights on important species interactions for the composition and complexity of any natural community.

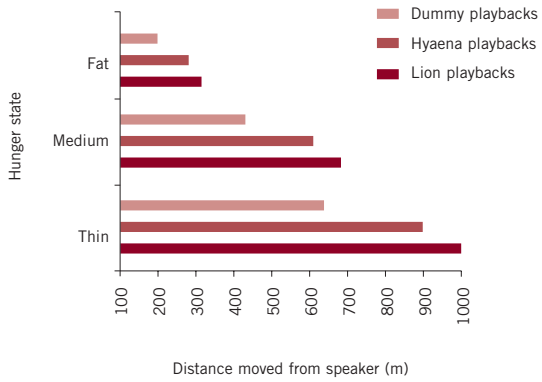
MÜLLER C B, ADRIAANSE I C T, BELSHAW R & GODFRAY H C J (1999). The structure of an aphid-parasitoid community. *Journal of Animal Ecology* 68: 346-370.

Innately vulnerable to extinction?

New compilations of information on the severity of threat faced by the world's mammals have made it possible for us to undertake a systematic study on the relationship between basic biological traits of species and their vulnerability to extinction. From general observations it has been suggested that relatively large-bodied, slow-reproducing species and those at the top of food chains would be more vulnerable to extinction. However, this had not previously been tested, nor had it been possible to evaluate the relative contributions to threat status from the biological traits of species compared to the impacts from human activities. Our study included over 300 species of mammals belonging to the orders Carnivora and Primates where we had independent information on the severity and nature of threats they face, as well as on their life history, distribution and ecology. Using methods that control for phylogenetic relationships, we showed that species at a high trophic level, with low population density, slow life history and, in particular, a small geographical range size are all more likely to have a high extinction risk, even when the associations between these variables are controlled for. Altogether these traits explain *c.* 50% of the variation in extinction risk between species. We show how much of the remaining variation is directly attributable to the intensity of human-induced processes that can threaten species, whatever their basic biology. For example, several of the Madagascan lemurs are, according to our model, biologically robust against extinction but they have a high threat rate because their habitat is disappearing. In contrast, other species, such as baboons, that appear biologically vulnerable are apparently quite secure because they have significant populations in relatively undisturbed habitats.

PURVIS A, GITTLEMAN J L, COWLISHAW G & MACE G M (2000). Predicting extinction risk in declining species. *Proceedings of the Royal Society of London Series B* 267: 1947-1952.

Distance moved from playback experiments and hunger state



Living with the enemy: cheetahs, lions and hyaenas in the Serengeti

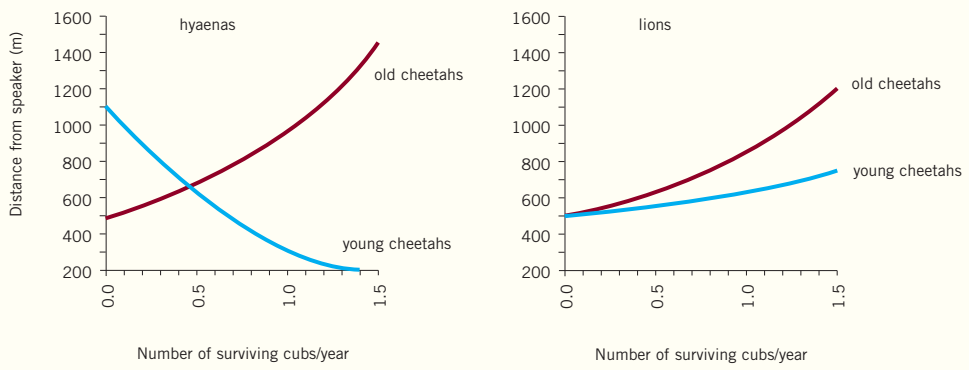
Predator avoidance has been documented for a number of species and could potentially play a key role in structuring species communities. This is the case even when the actual mortality owing to predation is low, as mortality may be low because predator avoidance is effective. Where competition is intense, then competitor avoidance may also be important. This year we documented avoidance behaviour within a large carnivore community for the first time. Cheetahs in the Serengeti, Tanzania, lose kills and their cubs to two species of large carnivores: lions and spotted hyaenas. Cheetahs can do little to defend themselves because they have small jaws and are of a much lighter build than these other carnivores. Cheetahs might therefore be expected to employ avoidance behaviours, particularly when they are likely to be hunting and hence more likely to attract attention. Lion and hyaena calls were played to cheetahs through a loudspeaker to examine the risk perceived by cheetahs from these carnivores. The results show that cheetahs actively moved away from both lion and hyaena calls. Cheetahs were also much less likely to hunt after lion and hyaena calls than when no sound was played through the loudspeaker. This reduction in hunting activity resulted in a lower kill rate suggesting that the perceived presence of other carnivores by cheetahs caused them to suffer reduced food intake rates. Also, while cheetahs moved just as far after lion calls as after hyaena calls, they spent significantly more time looking at the loudspeaker and were less likely to make a kill after lion calls, suggesting that cheetahs perceived lions to be a greater threat than hyaenas.

Does avoidance have implications for the distribution of cheetahs within the Serengeti ecosystem? A previous study has shown that whenever cheetahs are found near high densities of lions or hyaenas they are less likely to be hunting and more likely to be moving than at low densities. Furthermore, both lions and hyaenas are found near high densities of gazelle, the main prey of cheetahs on the Serengeti plains, whereas cheetahs are more frequently found near low densities of gazelle, while avoiding areas with no gazelles. By avoiding competitors, cheetahs might move away from areas with high prey densities to areas of lower prey densities, where they can survive because of their higher hunting success on small groups or isolated individuals. The mobility of cheetahs and their ability to avoid direct competition in an ever changing landscape of competitors and prey may be the key to their coexistence with lions and hyaenas.

DURANT S M (2000). Predator avoidance, breeding experience and reproductive success in endangered cheetahs (*Acinonyx jubatus*). *Animal Behaviour* 60: 121-130.

DURANT S M (2000). Living with the enemy: pedator avoidance of hyaenas and lions by cheetahs in the Serengeti. *Behavioral Ecology* 11: 624-632.

Distance moved from lion and hyaena playbacks



Investigating a recent mass mortality of Caspian seals *Phoca caspica*

The Caspian seal *Phoca caspica* is unique to the Caspian Sea and is listed as Vulnerable by the IUCN (World Conservation Union). Between April and August 2000 a mass die-off occurred affecting many thousands of individuals. The die-off, first reported in Kazakhstan in the northernmost part of the Caspian Sea, spread southwards to Azerbaijan and Turkmenistan. Our scientists formed part of an international team of researchers (predominantly from the UK and The Netherlands) investigating the cause of the mortality. The investigation was funded in Azerbaijan by the World Bank Ecotoxicology Project via the Japanese Consultant Trust Fund, and in Kazakhstan by the Offshore Kazakhstan International Operating Company.

Initial postmortem examinations of dead seals from Kazakhstan and Azerbaijan did not produce any consistent findings, although many seals were emaciated. However, microscopic examination of tissue samples from these seals revealed a consistent pattern of lesions that was highly suggestive of distemper, a disease of terrestrial and aquatic mammals caused by specific viruses of the genus *Morbillivirus*. Tissue sections were subsequently examined using an immunohistochemical technique with a primary monoclonal antibody that is known to cross-react with canine and phocine distemper viruses, and cetacean morbilliviruses. Morbillivirus

Bladder epithelial cells from Caspian seals stained with H&E (right) or a monoclonal antibody against distemper virus (left) gave results which are characteristic of distemper virus infection.

antigen was detected in a range of lesions and tissues in seals exhibiting distemper-like lesions. These multisystemic tissue lesions associated with positive morbillivirus-specific immunohistochemical tests confirmed the presence of distemper in Caspian seals during the mortality event.

Morbillivirus nucleic acid was also positively identified in tissues from seal carcasses found on the coasts of Kazakhstan, Azerbaijan and Turkmenistan by carrying out reverse-transcriptase polymerase chain reaction (RT-PCR) with two pairs of 'universal' morbillivirus primers. This technique detects morbillivirus RNA and transcribes it to DNA, which is amplified to allow subsequent purification and sequencing. The resulting sequences matched those of canine distemper virus (CDV) and were clearly distinct from those of other members of the genus *Morbillivirus*. The high degree of similarity of the RT-PCR sequences from these regions of the Caspian Sea indicated that these seals were infected with the same strain of CDV, thus establishing clear spatial and temporal links between the seal mortalities in these widely separated regions.

The origin of CDV infection in Caspian seals and its overall effect on the seal population remain to be determined although it is possible that the CDV virus may have originated from contact with terrestrial carnivores. Although tests for algal toxins in seal tissues were negative, very high levels of organochlorine contaminants (particularly DDTs and PCBs) have been identified in Caspian seals, including some individuals that died in this mortality event. The possibility that high-level exposure to such potentially immunosuppressive pollutants may have played a secondary role in the mortality event must be considered.

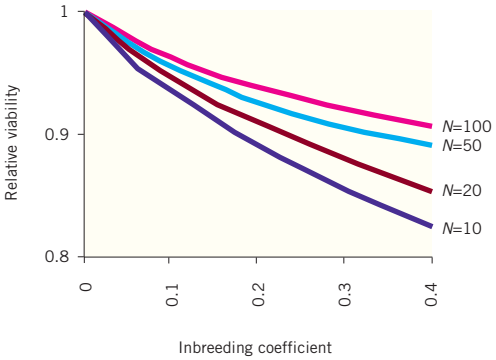
KENNEDY S, KUIKEN T, JEPSON P D, DEAVILLE R, FORSYTH M, BARRETT T, VAN DE BILDT M W G, OSTERHAUS A D M E, EYBATOV T, DUCK C, KYDYRMANOV A, MITROFANOV I & WILSON S (2000). Mass die-off of Caspian seals caused by canine distemper virus. *Emerging Infectious Diseases* 6 (6): 637-639.

Purging inbreeding depression resulting from deleterious mutations

The phenomenon of inbreeding reducing fitness, known as inbreeding depression, has been widely observed in most species of plants and animals. Although still in dispute, substantial evidence from studies involving various fitness traits in diverse organisms has accumulated, supporting the hypothesis that most inbreeding depression is a result of many partially recessive and deleterious alleles that are maintained by mutation and selection balance, and not to a few overdominant loci.

Inbreeding increases homozygosity and thus exposes the harmful effects of the partially recessive and deleterious mutations on fitness. This results in inbreeding depression which may endanger the immediate survival of small populations. At the same time, however, there is a potential for purging these mutations and the resultant depression in fitness. In recent years the effectiveness of purging inbreeding depression by deliberate inbreeding has been explored both theoretically and empirically. The various empirical studies yield conflicting results, and the broad discrepancy about the effectiveness of purging inbreeding depression is understandable considering the many factors involved. For example, among the factors which may influence purging are: the genetic basis of inbreeding depression, such as distributions of selection coefficients and dominance coefficients of mutations; rates of inbreeding and genetic drift; the pattern and strength of selection; reproductive capacity; organization of the genome.

An important issue in purging inbreeding depression that has not been investigated in previous theoretical studies is the effect of selection between inbred lines. Because genetic variation is progressively reduced within lines and increased between lines, particularly for recessive genes, between-line selection should become increasingly effective with inbreeding, compared to within-line selection. Successful highly inbred lines, with a performance at least as good as the ancestral outbred population, in organisms such as mice and maize are usually developed by inbreeding a large number of lines in parallel and applying between-line selection so that the poorest lines are eliminated and the best are retained. Therefore one possible strategy for more effectively purging inbreeding depression is to apply artificial between-line selection, in addition to



Effects of rate of inbreeding (population size, *N*) on the mean viability relative to the initial population. One deleterious mutation was assumed to occur per diploid genome per generation, with mean homozygous and heterozygous effects of 0.05 and 0.02 (both in exponential distributions), respectively. The lethal mutation rate is 0.03 and the dominance coefficient of lethal alleles is 0.02.

within-line selection and natural extinction of lines.

Another issue that has received little attention is the interaction between inbreeding, genetic drift and selection. Inbreeding facilitates the selective elimination of partially recessive deleterious mutations, while genetic drift hinders the purging process and may drive the deleterious mutations to fixation. Usually inbreeding and genetic drift cannot be separated and operate simultaneously at the same strength (measured by inbreeding and variance effective sizes) in a small population. However, under certain circumstances, such as partial inbreeding in a single population or subdividing the population into lines and limiting migration, inbreeding can occur at a higher rate than drift, at least temporarily. In a highly subdivided population a deleterious mutation is quickly eliminated from, or fixed in, a line owing to the high rate of inbreeding and genetic drift within lines. However, even if the mutation is fixed in a line, it segregates and is subject to selection again after migration or crossing among lines.

The effect of population subdivision, combined with within-line and between-line selection and line crossing, on purging deleterious mutations of variable effects was investigated. Extensive simulations indicated that the breeding scheme with equal within- and between-line selection and crossing alternatively with full-sib mating is generally the most efficient for purging deleterious mutations. However, unless most deleterious mutations have relatively large effects on fitness in species with reproductive ability high enough to cope with the depressed fitness owing to inbreeding, it is not justified to apply a breeding programme aimed at purging inbreeding depression by inbreeding and selection to a population of conservation concern.

WANG J (2000). Effects of population structures and selection strategies on the purging of inbreeding depression due to deleterious mutations. *Genetical Research* 76: 75-86.

WANG J, HILL W G, CHARLESWORTH D & CHARLESWORTH B (1999). Dynamics of inbreeding depression due to deleterious mutations in small populations: mutation parameters and inbreeding rate. *Genetical Research* 74: 165-178.

Sarcoptic mange and spatial organization of red foxes

Theoretical studies have viewed territory size as a function of the trade-off between different costs and benefits to territory holders. Among group-living carnivores, two territorial strategies have been described. Based on co-operative behaviour, 'expansionists' may occupy territories greater than the minimum necessary to support the basic social unit (a breeding pair) in order that additional animals can share the territory. In contrast, 'contractionists' show little or no co-operative behaviour and breeding individuals defend territories of the minimum size necessary to provide their requirements. Despite the absence of co-operation, groups may arise as a result of the rules by which territories are configured. The resource dispersion hypothesis (RDH) assumes that the basic social unit occupies territories that are just large enough to provide the minimum requirements of the breeding pair during limited resource availability. Outside critical periods of limited resource availability, these minimum territories may contain more resources than needed by the breeding pair alone, and can sustain philopatric subordinate animals.

In collaboration with Professor S Harris, Bristol University, we have examined qualitative predictions arising from the RDH in relation to resource availability using red fox as a model. Red foxes have previously been described as exemplifying a 'contractionist' strategy. The outbreak of sarcoptic mange in an urban red fox population provided an opportunity to test the RDH and the 'contractionist' strategy because fox density changed

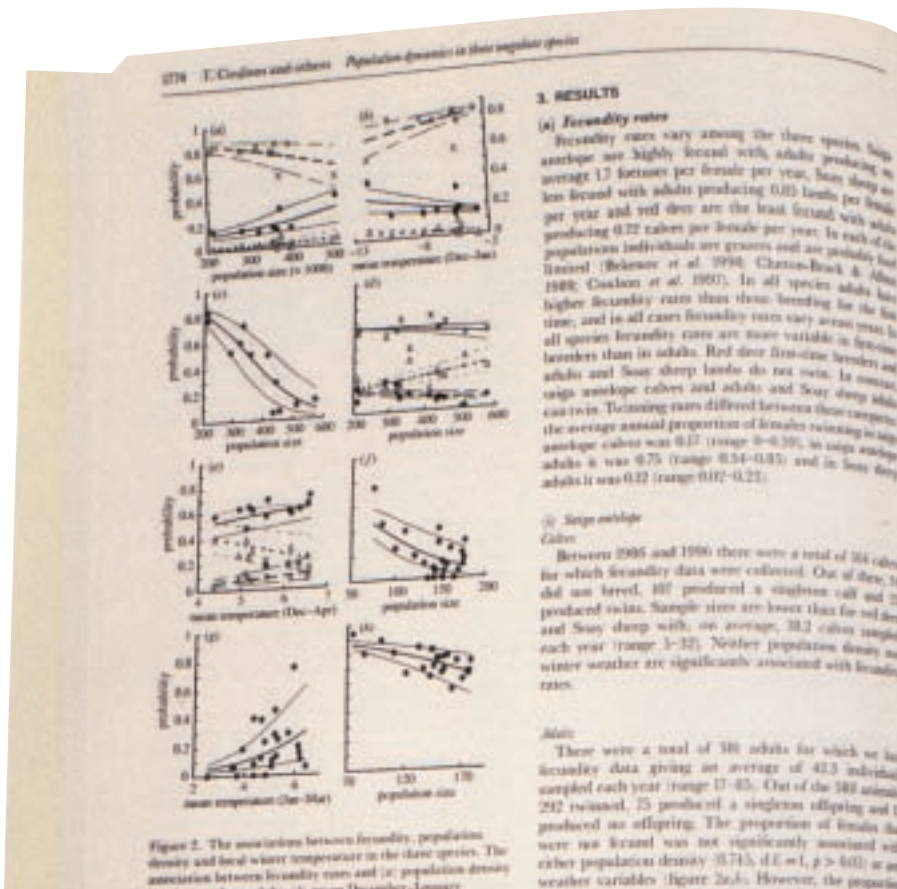
dramatically as a result of mange, and data from previous intensive ecological studies were available. In contrast to the predictions of the RDH and the 'contractionist' strategy, foxes surviving the mange epidemics increased their territories after neighbouring groups had died out but the increases were neither accompanied by the relinquishment of other parts of the existing territories, nor were they a response to a decline in food availability strategy.

BAKER P J, FUNK S M, HARRIS S & WHITE P C L (2000). Flexible spatial organization of urban foxes, *Vulpes vulpes*, before and during an outbreak of sarcoptic mange. *Animal Behaviour* 59: 127-146.

Population dynamics in ungulates

The relative influence of density-dependent and density-independent processes on population dynamics has been debated in ecology for over half a century. Although both processes are now known to be potentially important, it is currently not possible to make many generalizations. Previous research has typically used pattern-orientated approaches to decompose time-series into contributions from density-dependent and density-independent processes. An alternative process-orientated approach is to estimate the relative roles of each process on inter-annual variation in vital rates. We compared pattern-orientated analyses of time-series with process-orientated analyses of a vital rate in three contrasting ungulate species. Analyses of time-series and vital rates gave different results. Analyses of fecundity rates in Soay sheep (right), saiga antelope and red deer identified that both density and winter temperature were important in one or more age class. In each species, high density and cold winters depressed fecundity. In contrast, analyses of the time-series for each species did not identify significant effects of density on population fluctuation. The approach of analysing relationships between vital rates, density and climatic variables may detect important processes influencing population dynamics that time-series methodologies may overlook. However, an approach to analysing population dynamics data that uses both process-orientated and pattern-orientated methodologies would be best.

COULSON T, MILNER-GULLAND E J & CLUTTON-BROCK T (2000). The relative roles of density and climatic variation on population dynamics and fecundity rates in three contrasting ungulate species. *Proceedings of the Royal Society of London Series B* 267: 1771-1779.



origins and maintenance of biodiversity

Ecological basis of extinction risk

A high proportion of mammal and bird species is threatened with extinction. In the last decade or so, huge efforts have been made by international conservation agencies to describe the geographic distribution of biodiversity and extinction risk in these taxa. Now we can be reasonably sure of which species are threatened with extinction and which regions have unusually high concentrations of threatened species. However, while the description of biological diversity and extinction patterns among mammal and bird species is becoming more complete and precise, we have little knowledge of the evolutionary processes and ecological mechanisms that underlie these patterns. Until very recently we could not answer such deceptively simple questions as why some species are threatened while others appear secure, and why some families contain large numbers of species while others have only a few.

Understanding the evolutionary processes and ecological mechanisms that underlie extinction is fundamental to conservation biology. Previously, using statistical and phylogenetic approaches, we established that not all bird families are equally vulnerable to extinction. For example, parrots and albatrosses are unusually vulnerable whereas woodpeckers and cuckoos are unusually secure. However, the reasons for these differences are poorly understood. This may be, in part, because different bird taxa are threatened by different mechanisms. Among 1012 threatened bird species,

habitat loss, human persecution and introduced predators were by far the most common threats. Habitat loss was cited as a source of risk for over 70% of threatened species, while human persecution and/or introduced predators were cited in 35% of cases. Furthermore, twice as many species (54%) were classified as being

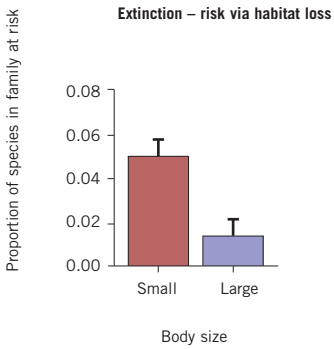
threatened by either habitat loss alone or by human persecution/introduced predators alone, than being threatened by both sources together (27%).

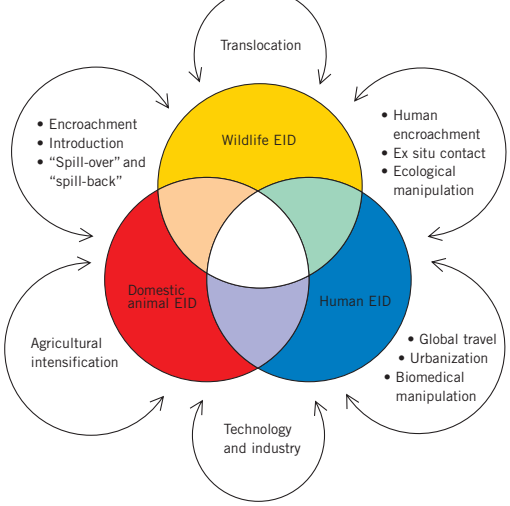
Theoretically, sources of extinction risk that perturb the balance between fecundity and longevity, such as human persecution and introduced predators, should be particularly hazardous for taxa that have slow rates of population growth. In contrast, sources of extinction risk that reduce niche availability, such as habitat loss, should represent a particular threat to taxa that are ecologically specialized. We tested these predictions using a phylogenetic comparative method and a database on 95 families of birds. Our analyses support the predictions that different lineages are threatened by different mechanisms of extinction, and that different ecological factors predispose taxa to different sources of extinction risk. As predicted, extinction risk from persecution and introduced predators is associated with large body size and long generation time but is not associated with degree of specialization, whereas extinction risk incurred through habitat loss is associated with habitat specialization and small body size but not with generation time.

Thus, our results corroborate the prediction that there are multiple routes to extinction among birds. One route is for large-bodied, slow-breeding species to become threatened when an external factor, such as human persecution or introduced predators, disrupts the delicate balance between fecundity and mortality in bird populations. In our analysis, this applies to families such as the kiwis, cassowaries, megapodes, penguins and albatrosses. A second route is for ecologically specialized species to become threatened by habitat loss. Such families include the trogons, scrub-birds and logrunners. A small number of families are prone to both sources of extinction risk. These include the parrots, rails, pheasants, pigeons, cranes and white-eyes. It is this last set of families that we previously identified as being significantly over-prone to extinction.

Our results demonstrate the importance of considering separately the multiple mechanisms that underlie contemporary patterns of extinction.

OWENS I P F & BENNETT P M (2000). Ecological basis of extinction risk in birds: habitat loss versus human persecution and introduced predators. *Proceedings of the National Academy of Sciences USA* 97: 12144-12148.





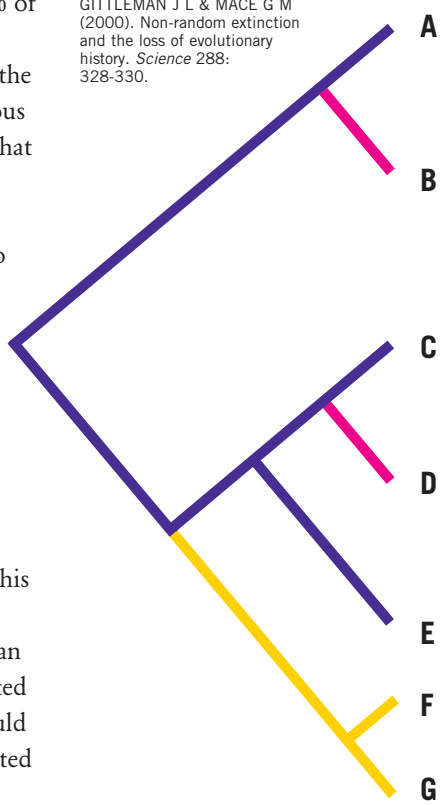
The relationships of emerging infectious diseases in humans, domestic animals and wildlife. Arrows indicate key factors which drive disease emergence.

Reprinted with permission from Daszak, P., Cunningham, A.A. & Hyatt, A.D. (2000) Emerging Infectious Diseases of Wildlife-Threats to Biodiversity and Human Health. Science. ***287****: 443-449. Copyright 2000 American Association for the Advancement of Science.*

Phylogenetic misfortune

Evolutionary trees are hierarchical in structure. An inevitable consequence of this is that even if species extinction rates are quite high, if they are more-or-less randomly distributed across species, then whole higher taxa are nearly always likely to persist simply because some constituent taxa do. This means that surprising amounts of evolutionary history (measured as the complete branch length of a phylogeny) can persist even if a large proportion of species dies out. In an influential paper, Nee and May (1997) illustrated the potential significance of this effect by simulating the consequences of species extinctions in hypothetical phylogenies. For example, in one very large hypothetical phylogeny they showed that just 5% of species could capture 81% of the evolutionary history represented in the phylogeny. However, there are various reasons to doubt their assumption that species extinctions will in fact be randomly distributed. Extinct and threatened species are more likely to be clumped in their distribution on a phylogeny because they share traits that increase vulnerability to extinction and because related taxa are often located within the same broad geographical or habitat types where human-induced threats are concentrated. We were able to test this directly using recently developed complete phylogenies for mammalian carnivores and primates. We estimated how much evolutionary history would be lost if all the species currently listed as being threatened with extinction were to actually go extinct, and we compared this estimate to the amount predicted by the random model. Our results show that threatened species are far from randomly distributed among taxa and among phylogenetic clades. As a consequence of this, the amount of evolutionary history that stands to be lost as a result of the current species extinction spasm is much higher than expected – for primates we expect about an extra 10 million years of evolution to be lost per genus compared to random expectation. Past estimates of the effects of species extinctions on overall biodiversity loss have therefore given results that were too optimistic.

PURVIS A, AGAPOW P-M, GITTLEMAN J L & MACE G M (2000). Non-random extinction and the loss of evolutionary history. *Science* 288: 328-330.



Emerging infectious diseases of wildlife: threats to biodiversity conservation and human health

Emerging infectious diseases (EIDs) of humans have been a focus of public health interest for the past two decades. Recently, we have shown how EIDs can be a significant threat to the conservation of animal biodiversity. Increases in the number of reports of epizootic wildlife EIDs (*e.g.* marine mammal morbillivirus disease, kangaroo blindness, amphibian ranavirus disease, herpesvirus-associated mass mortalities of pilchards) suggest that these are a current and serious global concern. Some of these diseases, such as cutaneous chytridiomycosis of amphibians, have been implicated in the declines, and even extinctions, of whole populations. This can happen either through the direct (*e.g.* infection causing death) or the indirect, or 'knock-on', (*e.g.* infection causing loss of prey species) effects of disease.

Although many of these disease outbreaks are seemingly 'natural' occurrences, we have shown that anthropogenic (human-mediated) ecological changes have driven the emergence of the majority of recent wildlife EIDs, including those in otherwise pristine areas. These changes include the 'spill-over' of pathogens from domestic animals to wildlife, human encroachment into wildlife habitat, deliberate or accidental translocation of pathogens (with or without their hosts) into 'naïve' areas or populations (a process we have termed 'pathogen pollution'), and the management of wildlife for agriculture,

Sika stag (foreground) and red deer stag and red/sika hybrid hind (background) on a deer park in Ireland. Sika deer of both sexes are about half the size of Scottish red deer.

hunting and even for conservation reasons. Further analyses demonstrate that these anthropogenic changes to wildlife ecology directly affect the emergence of disease in human beings, which can lead to significant morbidity and mortality (*e.g.* the emergence of Nipah virus disease in SE Asia, West Nile virus disease in the USA). Furthermore, it appears that pathogen pollution could be as important and far-reaching a threat to biodiversity conservation as other major forms of anthropogenic impacts, such as habitat loss or chemical pollution. Our work demonstrates a need for increased vigilance and research into the impact of anthropogenic change on the ecology of disease in wildlife, domestic animals and human beings.

DASZAK P, CUNNINGHAM A A & HYATT A D (2000). Emerging infectious diseases of wildlife: global threats to biodiversity and human health. *Science* 287: 443-449.

DASZAK P, CUNNINGHAM A A & HYATT A D (2000). Conservation conundrum - Response. *Science* 288: 2320.

Hybridization between red deer *Cervus elaphus* and introduced Japanese sika deer *Cervus nippon* in Argyll, Scotland

Human introductions of exotic species frequently have detrimental effects on native ecosystems. Typically this occurs via competition for resources, predation on naïve species or through hybridization with related native taxa. A current example of hybridization in the UK is that of red deer *Cervus elaphus* and introduced Japanese sika deer *Cervus nippon*. This hybridization is progressing rapidly and has the potential to have a serious impact both in biological and economic terms on Britain's largest remaining land mammal.

Sika deer were first brought to the British Isles in the 1860s and were bred and distributed to parks throughout Ireland, England and Scotland. Later, sika deer were either deliberately released or escaped from deer parks, establishing feral populations in several places around the British Isles. In Scotland, around ten introductions were made between the 1860s and 1930s and the descendants of escapees from these introductions now occur across 50% of the available deer habitat in Scotland. Phenotypic hybrids have been reported in Scotland from the 1950s onwards where the two species have come into contact.

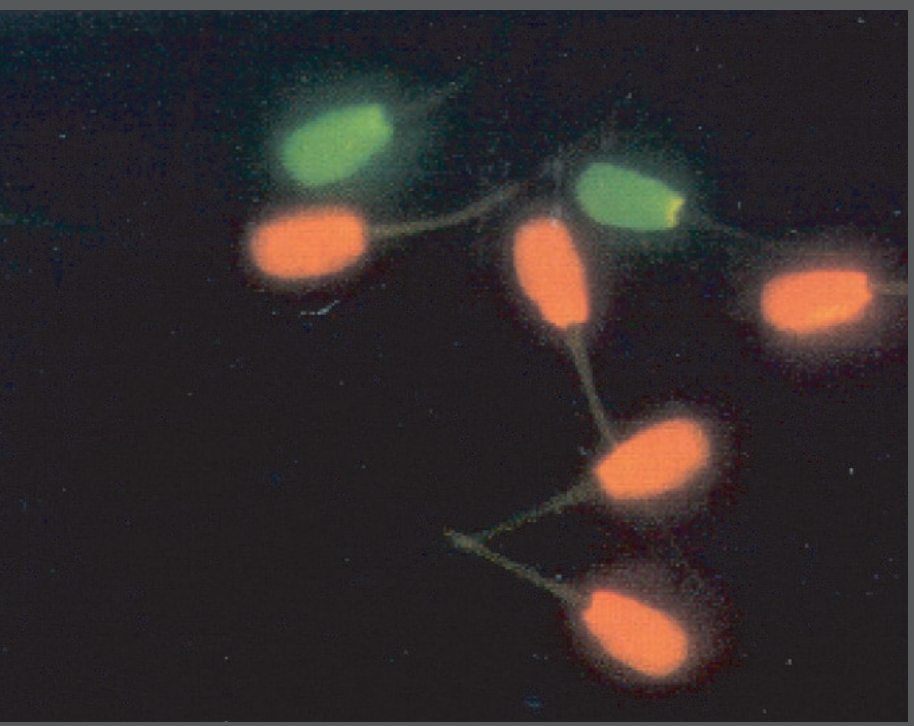
Following genetic studies of hybridization between red and sika deer in Scotland carried out at the Institute of Cell, Animal and Population Biology, The University of Edinburgh, a further analysis of these data is under way at the Institute of Zoology. The data are from an intensive survey in Argyll, including *c.* 700 deer sampled during the 1996–1997 annual cull which were screened for 25 species diagnostic microsatellite markers and one mitochondrial marker. This new analysis confirms the strong assortative mating and rarity of F1 hybrids between red and sika deer which was observed previously. The F1 hybrids are generated at a frequency of only 1/500–1/1000 matings, however, these hybrids go on to backcross successfully into both parental taxa. This leads to substantial introgression between the taxa and 62% of sika deer and 33% of red deer had some hybrid ancestry. This new analysis suggests that in sika deer selection is acting to remove introgressed alleles. This may be because sika hinds with introgressed alleles tend not to breed in their first year whereas pure sika almost all become pregnant in their first year. If this selection is strong enough to prevent introgressed alleles from accumulating in the long term, it might mean that red and sika deer phenotypes will be maintained, despite ongoing hybridization, instead of collapsing into a continuous distribution of hybrid forms, as observed in County Wicklow, Ireland.

A new project at the Institute also supports the view that distinct phenotypes of red and sika deer can be maintained despite ongoing hybridization. Red and sika deer from an ancient natural hybrid zone in eastern Siberia were analysed using the same genetic techniques. Preliminary results show that most deer have some hybrid ancestry in the recent past but that they can all be classified as red or sika on the basis of phenotype.

Finally, recent analysis of new data from microsatellite screening shows that the introduced sika deer originated from the area around Nagasaki, Kyushu, Japan: until now, the origins of these deer had been obscure because of poor records of the introductions.

GOODMAN S J, BARTON NH, SWANSON G M, ABERNETHY K & PEMBERTON J M (1999). Introgression through rare hybridisation: a genetic study of a hybrid zone between red and sika deer (genus *Cervus*) in Argyll, Scotland. *Genetics* 152: 355-371.

conservation biology and management



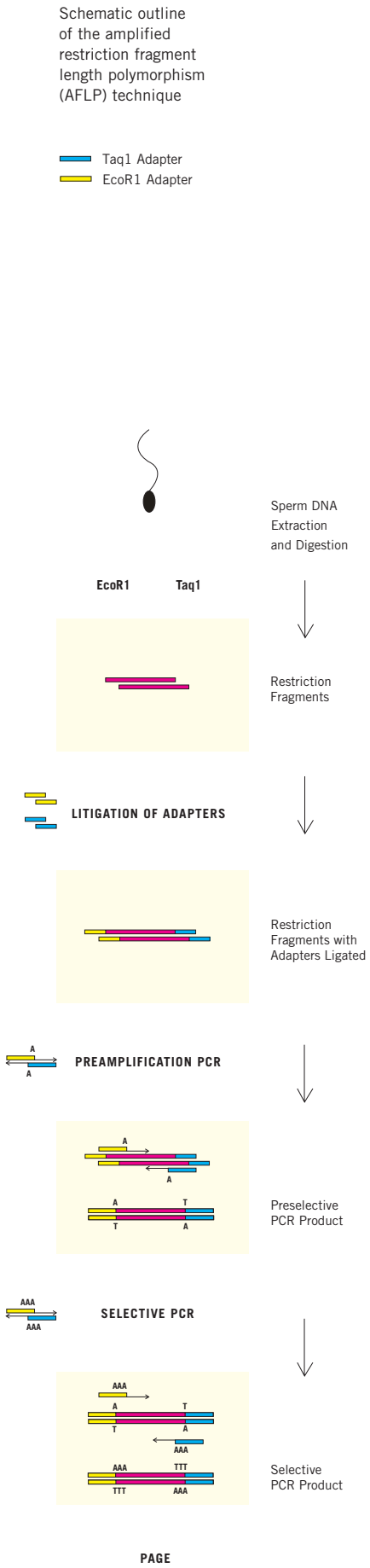
Variation in boar spermatozoa fertility after freezing was investigated and genetic markers associated with this variation were identified.

Our future in the freezer: a genetic basis for boar sperm survival following cryopreservation

Many threatened wild populations are small in number and fragmented in distribution, and captive-bred populations are also inevitably limited in size. Genetic variation is lost rapidly in small populations, leading to less viable inbred individuals. A classic example of inbreeding causing reduced reproductive fitness is the Florida panther *Felis concolor coryi* in which a loss of genetic diversity has led to abnormal testis development and resulting infertility.

One possible solution to this problem is genetic resource banking, whereby sperm and other tissues from threatened species are frozen and stored for use in controlled breeding programmes. By cryopreserving the spermatozoa of 'genetically valuable' males we could maintain maximum genetic diversity in an endangered population. Of course it would be naïve to suggest that gamete preservation alone would end species extinction, however, gene banking has a valuable role to play when used in conjunction with other conservation strategies.

The concept of preserving genes from threatened species is an attractive option but although semen cryopreservation has been applied successfully in a few species, extensive variation in post-thaw semen quality exists between individuals. Our recent studies, using pig as a model species, have confirmed that consistent inter-individual variation in sperm



'freezability' exists and is inherited. Three groups of boars were identified on the basis of a consistent response to semen cryopreservation (poor, average and good freezers). Semen viability was determined using % motility, computer assisted semen analysis (CASA) of motility parameters, plasma membrane integrity (SYBR-14 +ve by flow cytometry) and acrosome integrity (fluorescein-labelled peanut agglutinin +ve stained smears).

DNA from boars classified as good and poor freezers was analysed using the amplified restriction fragment length polymorphism (AFLP) technique to identify molecular markers linked to genes controlling the ability of sperm to freeze successfully. The AFLP technique is based on the selective PCR amplification of fragments of genomic DNA and allows us to screen the genome without prior knowledge of nucleotide sequence. The DNA fragments are visualized on a sequencing gel and assessed rather like a DNA 'fingerprint'. Clear differences in the DNA profiles of individual boars were observed and these were related to the variation in semen freezability, confirming that freezability is inherited. Sixteen candidate molecular markers linked to genes influencing semen cryopreservation were identified.

Important practical applications of this research extend to both domesticated and endangered species. By identifying markers for genes which may influence semen freezability, we have the potential to influence animal production systems. Current methods of sperm preservation impose significant costs on UK agriculture through wastage of semen held at ambient temperatures and the loss of genetic information from important boars. The identification of genetic markers linked to semen freezability will have a direct impact on methods of semen preservation in the artificial insemination (AI) industry and promote cryopreservation as a viable option for porcine AI. Rigorous validation of these molecular markers as a predictive measure of semen freezability will provide an opportunity to improve the quality of cryopreserved semen through selective breeding programmes, leading to improved efficiency for UK agriculture.

The identification of genetic markers linked to 'freezability' genes will allow us to promote genome banking as a viable conservation tool. Future work must aim to identify what aspects of sperm function are controlled by the freezability genes and develop protocols to minimize the effects of freezing on these cellular components. The development of successful cryopreservation protocols would ensure the maintenance of viable stored spermatozoa, protecting both genetic and species diversity for future generations.

THURSTON L M (2000). *An investigation into sources of variation and the genetic basis of boar sperm survival following cryopreservation.* PhD Thesis, University of London.

THURSTON LM, SIGGINS K, MILEHAM A, WATSON P F & HOLT W V (2000). Identification of amplified restriction fragment length polymorphism (AFLP) markers linked to genes controlling boar sperm viability following cryopreservation. *Journal of Reproduction and Fertility Abstract Series* 25.

Veterinary monitoring of scimitar-horned oryx *Oryx dammah* reintroduced to Tunisia

The reintroduction of a mammal into part of its former range is not straightforward. In order to succeed, the reason for the disappearance of the species from the area must have been identified and removed or dealt with, and sufficient habitat for the animals' requirements must be available. Disease is another important factor. Animals raised in captivity may carry pathogens that were natural in their former range but may also carry exotic pathogens, contracted from domestic animals or other exotics, especially closely related species. The stress of transportation may exacerbate infections or lower resistance and the mixing of animals from different collections may expose some to pathogens to which they are unaccustomed. Finally, on arrival at the reintroduction site, the animals may encounter novel pathogens to which they have no immunity.

The scimitar-horned oryx *Oryx dammah* was formerly widespread in the arid grasslands of the Sahel but is now extinct in the wild in most, if not all, North African countries. The captive population has increased dramatically over the last 30 years and there are many animals available for reintroduction. In 1985 ten oryx were returned to the Bou Hedma National Park in central Tunisia. This population has grown to *c.* 100 animals but is inbred owing to the relatedness of the founders. In March 1999 two male and 11 female scimitar-horned oryx were sent from European institutions to southern Tunisia for reintroduction to two National parks, and a further male was sent to Bou Hedma to introduce a fresh genetic line.

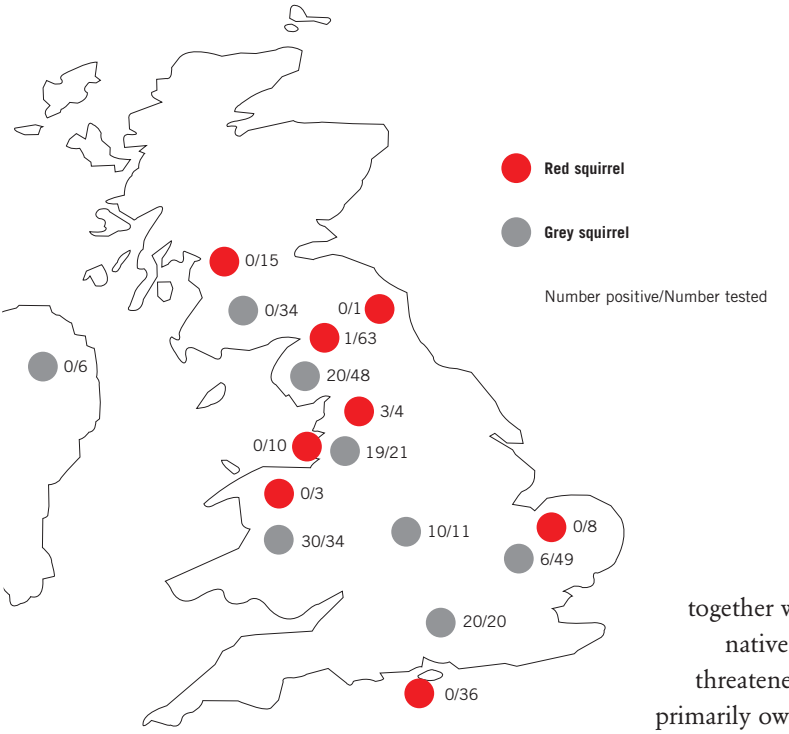
Our veterinary involvement with the oryx reintroduction included: (1) co-ordination of pre-export health checks performed by the veterinarians at the zoos providing animals, (2) monitoring the oryx during transportation and the 30 day post-import quarantine period, and carrying out treatment and preventative health measures, and (3) monitoring health after release and assisting with movement of oryx between release sites. All 14 oryx were transported to Tunisia without incident and were quarantined at the Sidi Toui National Park. After 1 month, several animals were immobilized; one male for transport to the Bou Hedma Park, one male and two females for transport to start a third group at Oued Dekouk reserve, and two females for fitting radio-collars. At each opportunity the animals were re-examined and all were in good health. Further monitoring has been continued by a zoologist and Park staff.

A follow-up visit was made in November 2000. The majority of the released animals, plus six offspring born since the reintroduction, were sighted during visits to the Bou Hedma and Sidi Toui National Parks. Training workshops on immobilization and health checks were held for Tunisian National Park staff. At a meeting with the Tunisian Direction Générale de Forêts, Park officials and vets from the Ministry of Agriculture and Veterinary Faculty considered the management and monitoring of disease in wildlife.

FLACH E J, D'ALTERIO G-L, ZAHZAH K, MOLCANOVA R, WAKEFIELD S, BAROSSI D, EULENBERGER K, KOPCOK M, OLLIVET F, PETIT T, VAHALA J & FRÖLICH K (2000). Veterinary monitoring of captive-bred scimitar-horned oryx (*Oryx dammah*) prior to reintroduction in Tunisia. *Proceedings of the 3rd Scientific Meeting of the European Association of Zoo and Wildlife Veterinarians (Paris).* 31 May - 4 June 2000: 91-97.

Parapoxvirus disease and mortality in red squirrels *Sciurus vulgaris*

In our studies to explain the effects of infectious disease on the population size of endangered species we have used red squirrel parapoxvirus (RSPPV) and squirrels as a model. The epidemiology of this infection was of interest because there is good evidence that parapoxvirus disease causes significant mortality in red squirrels *Sciurus vulgaris*, a species which is undergoing a marked decline on the UK mainland. A serological survey was carried out on red squirrel and grey squirrel *Sciurus carolinensis* populations using an enzyme-linked immunoabsorbant assay (ELISA). The results showed that 61% of grey squirrels, an introduced species, had antibody levels consistent with exposure to RSPPV, compared with 2.9% of red squirrels. This finding represents evidence of endemic infection of low pathogenicity in grey squirrels and suggests that they are a reservoir host of the virus. This could explain why outbreaks of parapoxvirus disease continue to occur in small, isolated populations of red squirrel.



The survey results suggested a relationship between the geographic distribution of grey squirrels with antibody to RSPPV and locations where parapoxvirus disease is either known to, or believed to, have occurred. At sites where parapoxvirus disease, or disease of similar description, has never been known to occur, grey squirrels were seronegative. The transmission of infectious agents from an abundant reservoir host to a smaller population of another species is now a well recognized threat to endangered species, a good example being the occurrence of rabies in African wild dogs *Lycaon pictus*, which was transmitted from a reservoir in domestic dogs. Where such threats are shown to be attributable to human activities, the case for intervention to protect the endangered species deserves consideration. Vaccination of red squirrels against parapoxvirus is now under investigation.

SAINSBURY A W, NETTLETON P, GILRAY J & GURNELL J (2000). Grey squirrels have high seroprevalence to a parapoxvirus associated with deaths in red squirrels. *Animal Conservation* 3: 229-233.

Monitoring reproduction in the wild mongoose lemur *Eulemur mongoz* of Madagascar

The lemurs of Madagascar make up a substantial proportion of the mammalian diversity on the island and, together with most of the native fauna, are threatened with extinction primarily owing to habitat alteration and destruction. Zoo, field and laboratory scientists have been collaborating for a number of years in order to gain more insight into the biology of one particular species, the mongoose lemur *Eulemur mongoz*, classified as Endangered by IUCN. A study of mongoose lemur socio-ecology carried out in 1994/95 provided basic knowledge of *E. mongoz* in the wild and, in order to improve the immediate success of captive-breeding, a detailed chemical analysis of the diet was carried out. Genetic variablity in wild and captive populations is currently being assessed and a species management group, which includes researchers from zoos and universities, was formed last year.

As part of this collaborative effort our reproductive biologists have studied female reproductive traits in one of the first attempts to monitor reproduction in a group of wild primates using non-invasive methods. In 1995 sexual behaviour was monitored in two wild family groups and faecal samples were collected from adult females and their sub-adult daughters over a 20 week period. Samples were stored in ethanol and subsequently analysed for progestagen and oestrogen content. These data were compared with results from samples collected from two captive animals in the UK.

Ethanol storage was a successful method of preservation for samples collected in the field. The hormones were extracted into the ethanol during the storage period thereby reducing the laboratory processing required. Furthermore, although faecal samples contained variable amounts of indigestible fibrous matter and seeds, as well as stones, these did not interfere with the hormone assays. Our results showed that most females conceived during the first oestrus of the breeding season and conception was preceded by a pseudooestrus, which probably did not result in ovulation. Pseudooestrus and oestrus were identified by investigating the oestrogen:progestagen ratio on each day. Pregnancy was reliably diagnosed *c.* 47 days after conception when progestagen and oestrogen excretion increased above breeding season levels. Gestation was further characterized by high progestagen concentrations and a decline in oestrogen excretion 70–80 days after conception. A sub-adult daughter in the wild conceived while still a member of her natal group and aborted at 70–80 days of pregnancy, when progestagens declined but oestrogens remained high.

Our results will make a significant contribution to the captive-breeding and conservation of *E. mongoz* and its relatives, and have furthered our understanding of their reproductive physiology.

CURTIS D J, ZARAMODY A, GREEN D I & PICKARD A R (2000). Non-invasive monitoring of reproductive status in wild Mongoose lemurs *(Eulemur mongoz)*. *Reproduction Fertility and Development* 12: 21-29.

scientific publications and meetings

An essential part of ZSL's work is facilitating the communication of information between professional zoologists, researchers and the general public. We achieve this through a varied programme of meetings, which is open to the public and members of staff, and the publication of scientific journals and books.

The *Journal of Zoology,* ZSL's pre-eminent international journal dedicated to academic zoology, continues to attract contributions from top researchers. During the year 160 original peer-reviewed articles were published in 12 monthly parts of Volumes 250–252, providing comprehensive coverage of the latest research and developments in zoology.

ZSL's quarterly journal, *Animal Conservation*, provides an important forum for the rapid publication of rigorous empirical or theoretical studies relating to species and population biology. The journal continues to bring together exciting new research and ideas from evolutionary biology and ecology that contribute to the scientific basis of conservation biology.

The Conservation Biology book series, published in association with Cambridge University Press, includes internationally significant advances in the science that underpins conservation biology. Titles are based either on symposia held at ZSL or on other topics which meet these aims. Three titles were published during the year: *Behaviour and conservation*, edited by L Morris Gosling and William J Sutherland, *Priorities for the conservation of mammalian diversity,* edited by Abigail Entwistle and Nigel Dunstone, and *Genetics, demography and viability of fragmented populations*, edited by Andrew G Young and Geoffrey M Clarke.

Volume 37 of the *International Zoo Yearbook* was published and contains 43 articles, 32 of which are on the conservation of Psittacines. Nigel Collar, BirdLife International, gives an authoritative overview of the 90 species of parrots which are threatened with extinction, while others provide information on breeding, husbandry, conservation, health and captive management of these fascinating and beautiful birds. Articles in Section 2, The Developing Zoo World, range from the husbandry and breeding of the Kerry spotted slug to hand-rearing and reintroduction of a Sumatran orang-utan. The Guest Essay by Sally Walker addresses the continuing establishment of regional or national networks of the Conservation Breeding Specialist Group.

After five years in preparation, this year also saw the publication by Chicago University Press of *Primate Conservation Biology* by Guy Cowlishaw (Institute of Zoology) and Robin Dunbar (University of Liverpool). This work is both a review and synthesis of current theory and practice in primate conservation. Beginning with an overview of the diversity and biology of primates, the book goes on to address extinction processes in primates and the key forces that currently drive them, namely habitat disturbance and hunting. The last part of the book focuses on possible conservation solutions to these problems, including

protected areas, sustainable tourism, and captive-breeding and reintroductions.

The first ZSL Symposium of the new millennium *Reproduction and Integrated Conservation Science*, was held on 9th and 10th November. The objectives were to critically evaluate the role of reproductive sciences in conservation and to suggest priorities for the future application of reproductive research in this field. The meeting was organized by Bill Holt and Amanda Pickard (Institute of Zoology), David Wildt (Smithsonian Institution, USA) and John Rodger (Marsupial Conservation Research Center, Australia). There was a large international attendance with over 160 delegates from the Americas, Antipodes, Africa, Asia and Europe. The papers will be collated in an edited book to be published in the ZSL/Cambridge University Press series on conservation biology.

At our regular Scientific Meetings, three speakers provide an overview of important research within a particular field. The eight Meetings held during the year covered diverse subjects, such as *Can parks protect Africa's predators?*, *The conservation of animal diversity in river basins* and *Cycles in animal populations*.

Tuesday Talks are aimed at a general audience. Nine talks were held during the year covering a wide range of topics, including *Gorilla tactics, Mudflats, misconceptions and the millennium,* and *From concrete to warblers - the story of the Wetland Centre. The Living Wild,* a collection of stunning images presented by internationally recognized wildlife photographer Art Wolfe, was particularly popular.

The Science and Conservation seminars held by the Institute of Zoology included talks by invited speakers on subjects relevant to our research, for example, *Biology after the human genome, Snake venom proteins: a new male contraceptive* and *Life history and extinction risk in bats*.

The 2000 Sir Stamford Raffles Lecture, *How the brain generates consciousness*, was presented by Professor Susan Greenfield, Director of the Royal Institution of Great Britain. The event was sponsored by the Singapore Tourism Board and Singapore Airlines; we are most grateful for their continuing support of this event.

The *Zoological Record*, published jointly with BIOSIS, is the oldest continuous information service for the life sciences. As a record of all aspects of zoological research, it is considered the foremost publication in its field. The continued generous support of various institutions, principally the British Library Document Supply Centre at Boston Spa and the Natural History Museum, London, in providing access to material for indexing is greatly acknowledged.

education and training

Our PhD students continue to be one of the Institute's greatest assets. Their individual and scientific backgrounds, sources of funding support and thesis subjects reflect the range of research and collaboration typical across the rest of the Institute. Students regularly present their work through informal discussions, at the Institute's annual Student Conference and outside the Institute at research meetings.

Eighteen PhD students were registered at the Institute at the end of 2000. Gina Caplan, a BBSRC CASE student, joined us in October to investigate the potential use of the field vole *Microtus agretis* as a novel environmental biomarker. In a project combining the bioengineering skills of staff at the Silsoe Research Institute with the Institute's expertise in non-invasive hormone monitoring, she will develop techniques for the automated monitoring of reproductive status in field voles under both laboratory and field conditions.

Three NERC-funded students started in 2000. Julie Anderson will study individual dispersal decisions and emergent metapopulation dynamics of the Angolan black and white colobus monkey in East Africa. Sonya Gowtage-Sequeira will investigate the importance of jackals and domestic dogs in the transmission of infectious canine disease to endangered carnivores in southern Africa, and Fredi Devas will study mechanisms which mediate the impacts of both predators and competitors on foraging success in a social forager, the desert baboon.

Four students, Stephen Casey, Jim Groombridge, Stephen Rossiter and Lisa Thurston, were successful in obtaining their doctorates during the year. The key results from Stephen Rossiter and Lisa's research are featured elsewhere in the report.

Stephen Casey received his PhD for research on the evolutionary and population genetics of seahorses *Hippocampus* spp., funded by NERC. Seahorses are threatened by loss of habitat, trade and by trawls, and the impact of this exploitation has been difficult to determine; with few variable external characters which can be scored, species identification has been difficult. A taxonomic revision of Vietnamese species was completed and phylogenetic analyses of species world-wide were carried out. Population studies of the heavily fished *H. comes* in the Philippines showed low levels of genetic differentiation over tens of kilometres, indicating high levels of gene flow and suggesting that marine protected areas may be effective at promoting the recovery of adjacent sites.

Jim Groombridge, funded by the Mauritius Wildlife Foundation and Durrell Wildlife Conservation Trust, carried out molecular genetic studies on three critically endangered bird species endemic to Mauritius (Mauritius kestrel *Falco punctatus*, pink pigeon *Nesoenas mayeri*, echo parakeet *Psittacula echo*). His research on the Mauritius kestrel showed that recovery of the population from an extreme bottleneck (a single wild breeding pair in 1974 to over 250 wild pairs) occurred despite the erosion of

Frank Clarke (below right) received the Thomas Henry Huxley Award for his PhD research on naked mole-rats from Sir Martin Holdgate (left) and Mr Brian Marsh (centre).

previously high genetic diversity. Therefore although half of all endangered bird species are island endemics, some can make remarkable recoveries. This collaborative study will help to promote the conservation priority of other critically endangered island species. Jim is now Project Co-ordinator on the Maui Forest Bird Recovery Project in Hawaii.

Stephen Rossiter, funded by a NERC CASE award, investigated the breeding system and social structure of the greater horseshoe bat *Rhinolophus ferrumequinum* in the UK. Patterns of genetic exchange and differentiation were investigated together with the consequences of population structure on individual fitness and the evolution of kin-biased behaviour at colony level. Stephen is now at Queen Mary and Westfield College, London.

Lisa Thurston, a CASE student funded by BBSRC, studied sources of variation in boar spermatozoa fertility following cryopreservation. Her results provided evidence of a genetic basis for the individual variation in post-thaw semen quality, and AFLP technology was used to identify molecular markers linked to genes influencing this variation. Ultimately this work could lead to the identification of specific genes which are crucial to aspects of sperm function. Lisa is now at the Royal Veterinary College.

Frank Clarke was presented with the Thomas Henry Huxley Award for original work submitted as a doctoral thesis, a highly competetive and prestigious award with contenders from

all over the UK. Frank is a graduate of Glasgow University where he was President of the Zoological Society, Vice-Chair of the Exploration Society and team leader of expeditions to North Cyprus and Trinidad. His PhD research was on the hormonal, behavioural and genetic correlates of dominance and breeding status in captive colonies of naked mole-rats. After completing his PhD Frank worked at the University of Pretoria, South Africa, and is now at The University of Aberdeen.

Our second Student Conference, open to Institute staff, external supervisors and collaborators, was held on 28 September in the ZSL Education Department. Research Councils stress the importance of transferable skills and training in the career development of students. Our aim is to provide students with excellent experience in research and help them gain skills to make informed choices about their future careers. One crucial skill is the ability to prepare and present information in a way that inspires and informs those receiving it, and by asking students to give yearly talks within the conference setting we provide an opportunity for them to develop these skills, and to learn from and support each other. The informal nature of the conference is ideal for those who are presenting work for the first time.

The presentations this year were all excellent and the standard was even higher than last year, reinforcing the fact that this is an opportunity for students to progressively develop their presentation skills. SaffronTownsend, Lisa Thurston and Octavio Paulo gave particularly well structured and polished presentations on sheep domestication, boar sperm cryopreservation and phylogeography of the Iberian lizard, respectively. Projects currently range from studies of bumble bee foraging ecology in London, to human-bear interactions in South America, MHC polymorphism and fitness in the great tit, leking in topi and analysis of giraffe subspecies designations.

In October the Institute held its Annual Research Conference which is also open to all staff and students and provides another forum for exchange of ideas and discussion.

In addition to supporting PhD students, the Institute provides valuable resources and skills for training and collaboration with many researchers in the laboratory and the field. In any one year we host a large number of visitors, including undergraduate and MSc students, visiting postdoctoral researchers and others. This year was no exception, with undergraduate students from Queen Mary and Westfield College and the University of

education and training

Becki Lawson was awarded the prize for best student on the MSc Wild Animal Health course. The prize is sponsored by Mazuri Zoo Foods.

East London, MSc students from University College London, Berne and Montpelier, and postdoctoral researchers from the Royal Veterinary College, Paris and the USA. For example, Janice Long (MRes Studies, Environmental Science, UCL) worked with Georgina Mace for 3 months on 'Global conservation priorities for mammals and birds – comparing diversity and threat among regions', and Conrad Scofield (MRes Studies,York University) carried out his research project with Chris Carbone examining predator–prey size relationships in snakes. In the field, John Shemkunde, a Tanzanian student with a wildlife management diploma from Mweka College, was seconded to the cheetah project from Tanzanian National Parks. As part of his Masters degree (University of Wales) he will conduct a leafleting campaign to solicit photographs from visitors to the Parks to help estimate numbers of cheetahs and cub survival across the northern circuit in Tanzania. If successful, this scheme may be incorporated within National Parks as part of a carnivore-monitoring plan, enabling us to anticipate and prevent problems to cheetah populations across Tanzania.

The Master of Science Course in Wild Animal Health (MSc WAH), run jointly with the Royal Veterinary College (RVC), continues to be oversubscribed and a maximum compliment of 15 students started the 2000/2001 course in October. This highly successful course is now in its seventh year and the current group of students maintains the international mix, with five students from Spain and others from Egypt and Japan. There are now 70 course graduates, from 31 countries on six continents. We regularly hear news from the graduates as they develop their careers and we continue to advise them as and when necessary. All veterinarians on the 1999/2000 course passed and Becki Lawson (left) won the prize for the best student. Some graduates have gone on to key posts in zoo and wildlife medicine, for example, Dr Maud Lafortune who is now a veterinarian at Calgary Zoo.

The Quality Assurance Agency (QAA) carried out an assessment of the standard of teaching in January 2000, and, like the other courses run by the RVC, the MSc WAH was awarded a score of 24/24 (100%). The QAA report noted the high level of enthusiasm and satisfaction expressed by the veterinarians on the course and that the pass rates were excellent.

Institute staff also teach on the 'Sex, genes and evolution' course at University College London, and on reproductive biology at King's College London, St George's Medical School and the RVC.

The Centre for Ecology and Evolution (CEE) was set up in 1994 to create a centre of excellence for research and teaching in the fields of ecology and evolution and is now a partnership between many UCL Departments, the Institute of Zoology and the Natural History Museum. As well as weekly

Andrew Cunningham (below second from right), our Veterinary Pathologist, was one of the international Amphibian Disease Team awarded the prestigious CSIRO medal (pictured above).

seminars, the CEE sponsors a series of workshops. This year the ZSL Meeting Rooms were the venue for a workshop on 'Adaptive Molecular Evolution' and a one-day conference entitled 'Sex and asex from microbes to multicells', with speakers including John Maynard Smith (Sussex), Matthew Meselson (Harvard), and Bill Rice (Santa Barbara).
www.gene.ucl.ac.uk/cee/

For students and more experienced scientists alike, explaining the details of your research to fellow scientists is often a difficult task. However, explaining it to an audience comprising Nobel laureates, Members of Parliament, Fellows of the Royal Society, school teachers, sixth form pupils and the general public is more of a challenge. The research on the social behaviour of ants being conducted by Andrew Bourke, Rob Hammond and Mike Bruford (Cardiff) formed one of the invited exhibits in this year's New Frontiers in Science exhibition organized by the Royal Society. Assisted by Roselle Chapman, the exhibit was shown for 3 days in London and a further 2 days in Edinburgh. The aim is to promote a wider understanding of science and this is an excellent opportunity to inform a wider audience about the work of the Institute.
www.royalsoc.ac.uk

Andrew Cunningham, our Veterinary Pathologist, was one of the Amphibian Disease Team, comprising researchers in Australia and the USA, which solved one of the world's most puzzling environmental problems; the reason for the sudden disappearance of rainforest frogs in protected habitats in Australia and Central America. The study demonstrated how a multidisciplinary approach could solve a complex environmental problem. The Team determined that the frog declines were the result of mass die-offs and identified the cause of the deaths as a new genus of chytrid fungus which infects the skin. The research strategy has been identified internationally as the way forward in investigating global problems associated with wildlife

diseases and related fields of conservation. The research has highlighted the potential of introduced/new pathogens as a major threat to natural ecosystems, including those previously considered pristine and outside the sphere of human influence. The research also indicated that disease threats to global biodiversity may be as significant as other forms of anthropogenic environmental threats, such as global warming or chemical pollution.

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