Species survival in 21st century with special reference to tigers in India

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As with other species, the genetic diversity of tigers is crucial for avoiding the well-known hazards of inbreeding. It is well recognized that a healthy population can only survive by sharing a sufficiently large gene pool to evolve and filter its way around the environmental factors. Studies have shown that many of the current captive tiger populations in zoos around the world suffer from severe diseases, weakened immune systems, abnormalities, and birth defects.

The Ranthambhore free ranging tiger populations - resident to an approximate area of 400-500 sq km in the district of Sawai Madhopur in Rajasthan - in the past have had good landscape connectivity with other tiger bearing areas of Kota, Karauli, Jaipur, Bharatpur and Sariska. As a result a large gene pool was available to the tigers. However, due to several factors leading to higher demand for agricultural land coupled with expanding urban clusters, the forests around Ranthambhore have been fragmented. Tiger movement both inter-state and intra-state has thus been drastically restricted since the last several years. The source population of tigers is now confined to about 20 to 25 breeding females and about 18 to 20 males. This population has seemingly grown from a small population of five tigers as reported in 1971, when the area was small (150 sq km) and surrounded by several villages. There is a need to develop and interpret a variety of genetic data in order to answer specific questions regarding tiger populations in Ranthambhore. This would be of immense help to develop effective management strategies for the long-term survival of tigers in Rajasthan.

Population fluctuations and the breeding of tigers in Ranthambhore have been recorded over the last forty years. Almost seven generations of tigers have so far not shown any morphological perturbations. Their populations crashed to ten females in 1992 and then again to fifteen in 2005. Remarkably, the total population bounced-back to 45 and 44 in 2003 and 2009, respectively. Such cycles[1] naturally occur among the wild populations of several species. From each generation to the next, weaker genes are filtered out from wild populations either by predation or fights etc.

This holds true for a normal and constraint free population group, where genetic variability is high and a large free ranging habitat is available. However, a range of questions now arise. How large does the habitat need to be? What determines the breeding? Is there a genetic pressure to move on to the next generation? If so, then what are the key determinants of selecting a good mate in the wild? Is it essentially random and opportunistic? Is avoidance of mating between relatives hardwired in the brains of the wild animals? What about inbreeding? What is the scale/ index to identify the effects and measure it before it has expressed itself in recessive genes to show morphological variations? Why population crashes occur? Such questions cannot be answered straightaway; however molecular genetics when applied to wild animal population groups points to possibilities.

The breeding among wild animal populations has always remained an enigma. While some species survive population bottlenecks others do not. A survey of situational studies reveals varying results. Northern elephant seals were hunted to near extinction in the western US by the early 1920s, with less than 20 individuals surviving the slaughter. Despite the low numbers, populations have since bounced back to over 175,000 – thus showing that even a species on the edge of extinction can rebound. A study, published in the Journal of Heredity[2], estimates that the Hawaiian monk seals were reduced to a total population of around two dozen around 1890. Their genetic diversity is even lower than that of the Mediterranean monk seal, whose population is only 1/5 of the Hawaiian monk seal. The survival of Cheetah[3] despite its population passage through a very thin bottleneck has made it lose its entire genetic diversity, yet it has a growing sizable population in the wild of about more than 10,000. Even the *pundits* of genetics have no clear answers for such differential results of survival found among species - some go extinct on loosing the genetic diversity due to compulsive inbreeding, while others, like the Cheetah, ride the wave of survival.

Inbreeding and Outbreeding: Results in-depth

Inbreeding depression is of major concern in the management and conservation of endangered species. Inbreeding universally appears to reduce fitness, but its magnitude and specific effects are highly variable because they depend on the genetic constitution of the species or populations and on how these genotypes interact with the environment. Recent natural experiments are consistent with greater inbreeding depression in more stressful environments. In small populations of randomly mating individuals –which are characteristic of many endangered species - all individuals may suffer from inbreeding depression because of the cumulative effects of genetic drift that decrease the fitness of all individuals in the population.

The dusky seaside sparrow, a melanistic subspecies of sparrow that inhabited central and eastern Florida, was listed as endangered in 1966. By 1980 the population had declined to six birds. The possible solution conceived was to breed the sparrow with a larger population group that was genetically closer. Five were brought into captivity to be crossbred with a lighter-colored Scott's seaside sparrow from the Gulf Coast of Florida in an effort to save the dusky. The Hybrid Policy memoranda of the US government did not allow the cross breeding. The dusky sparrow is now extinct.

Out breeding in species has been considered by classical conservationists as a threat that crosses the path of evolution and is said to cause genetic pollution. It is believed that nature has its own ways of having interspecies genetic barriers to guard against genetic mixing in order to keep species distinct. When rarely hybridization does occur naturally as in hybrid zones where the ranges of closely related wild species overlap, the hybrid crosses produced, even though they may display hybrid vigour (heterosis) in the first generation (F1 hybrid), are in the long run less fit then the two parent species which have evolved over hundreds of thousands of years specializing in exploiting their own particular niche in nature.

This belief however does not give enough reasons to explain the natural occurrence of certain hybrid species in the wild. This is demonstrated by the new school of conservationists that many species have developed by natural intercrossing among closely related wild species. Like the red wolf, a flagship endangered species for U.S. Fish and Wildlife Service, are found to derive completely from hybridization between coyotes and an extinct wolf subspecies. The neo conservationists armed with the tool of molecular genetics have found several such examples of cross bred wild populations; in Washington State the northern spotted owl had been crossbreeding with a neighboring subspecies, hybrids between blue whales and fin whales were discovered based on new molecular genetic data.

The contention of restricting intercrosses among wild population exclusively for the purpose of maintaining genetic purity at the cost of losing the species was whisked away by the winds of change that genetics brought. Moreover, the new protagonists further believe in using genetic mixing for repair of damage done by inbreeding. They claim that the likes of dusky seaside sparrow should not be penalized for what happens naturally every day, and in emergency cases intercrossing must be allowed to be used as a tool for species survival.

The Hybrid policy of United States was subsequently revised and it took the U.S. Fish and Wildlife Service several years of debate to create a new hybrid policy. On February 7, 1996, the new policy finally appeared in the Federal Register, under the title "Endangered and Threatened Wildlife and Plants; Proposed Policy and Proposed Rules on the Treatment of Intercrosses and Intercross Progeny (the Issue of Hybridization). Stephen O'Brien[5] in "Tears of a Cheetah", describes this issue poignantly in "The Bureaucratic Mischief". Here's an excerpt:

"The political turmoil over the legal ratification of subspecies, intercrosses, and endangered species represents the tip of the iceberg for a critical but highly contentious conservation issue; When should a subspecies be maintained as pure or when might it be encouraged to intermix with another subspecies? The answer has two tiers. One involves natural gene flow introgression, which we simply observe and document, such as nineteenth –century hybridization between Texas and Florida puma subspecies. The second involves management intervention to hybridize, as was carried out in the 1996 panther restoration experiment of the same two groups." In this experiment gene flow was augmented to save the Florida panther, after overwhelming genetic, reproductive, medical, and ecological life history data pointed to its imminent extinction.

The New Paradigm

With rapid growth of human populations, large landscapes have been scissored by highways and canals making it more and more difficult for the survival of many species. The gene pools of several species have been continuously shrinking and inbreeding among some species has become imminent. The second option pointed out by O'Brien is critical to our search for management solutions in this rapidly changing scenario of wildlife. Existing inbreeding provides vital clues to understanding how we can allow mixing and when we should intervene to stop.

In India, the rapidly changing landscape and fragmentation of wild habitats in the last decade has put tremendous pressure on defining the conservation strategy for large carnivores. The dangers of inbreeding in isolated meta population of tigers have now put pressures on the conservationists to make a choice and facilitate breeding with other meta population, generally believed to be done to purge the recessive genes and produce a healthy progeny. However, some scientists argue that since different meta populations, separated in time, develop adequate resistance and adaptations that shield them from certain diseases and have distinct immunological strength that relates to their habitat, we therefore need to preserve and protect them against genetic swamping. They oppose all kinds of out breeding and recommend conserving the purity of such population groups rather than rushing for a robust hybrid.

The tigers living in Sunderbans are believed to be distinctly tailor-made in time to survive in their environment as opposed to the tigers of arid regions of Ranthambhore. The divergence of climate between arid and semi-arid regions is deterministic of the sub-species of that region. Outwardly, we may not see any difference between the tigers of Rajasthan and those of east India as they belong to the same sub-species, but certainly a distinct variation has been found to occur in one such study[4]. mtDNA polymorphisms was analyzed in 59 scat and 18 tissue samples from 13 wild populations of the critically endangered Indian tiger (*Panthera tigris tigris*), along with zoo animals as reference. Northern tiger populations were found to exhibit two unique haplotypes suggesting genetic isolation. Populations were assigned to the regions Northern, Northeastern, Western, Central, and Southern India. Data from Chitwan (Indo-Nepal border) and Nagarhole (Southern India) (Luo *et al.* 2004) was collated. Analysis yielded only six different composite haplotypes. The composite mitochondrial haplotypes are informative regarding geographic population structure. The two closely related haplotypes together had a frequency of 100% in Northern populations (*i.e.* all tigers in Rajaji/Corbett showed one of these two haplotypes), while it was absent in all other regions. This suggests that Rajaji/Corbett harbors a genetically distinct tiger population.

Both, the analysis of molecular variance and the pair wise analyses revealed significant differences among most tiger populations of different geographic areas across India. Genetic analysis of the recently exterminated population of Sariska (Western India) suggests potential connectivity to the extant Ranthambhore population, a scenario further corroborated by historical information on a forest connection among these two areas until 100 years ago.

The divergent features of the meta populations found among the Indian tigers certainly point out that there is merit in preserving these gene pools. Preserving these pure lines of tigers with some currently unknown beneficial properties of their DNAs may be of benefit in the future.

Therefore, it becomes imperative for breeding that the candidate animals of the five different meta populations identified in the study must be put on a monitoring roster for observable inbreeding constituents. Till such time they remain genetically healthy no crosses be allowed.

It will also be necessary to determine a critical level of observable occurrence of recessive expressions of inbreeding among the animals, which should be the deciding factor before any introgression is allowed to take place. In such a situation, decisions on permitting intercrosses must be based on a well crafted threshold protocol that may consider knowledge of heterozygosity, coefficient of inbreeding, evaluation of possible genetic restoration and other factors specific to the habitat, before introduction of a new gene.

While the extent of intervention in dwindling populations is debatable, it is certain that we need to adopt a guarded regime to allow limited intercrosses for genetic restoration. It must be restored to when populations of some endangered species have become so small that they have lost genetic variation and appear to have become fixed for deleterious genetic variants. To avoid extinction from this genetic deterioration, some populations may be allowed to benefit from the introduction of individuals from related populations or subspecies for genetic restoration, i.e., elimination of deleterious variants and recovery to normal levels of genetic variation. We would thus have to collect a database marking the genetic distribution maps of several important and threatened species of wild animals.

However, caution must be observed in the selection of the animals likely to be introduced for such genetic repair of inbred populations. An unfortunate accident that took place over 35 years ago in a National Park in India shows how hazardous it can be for the gene pools of wild populations.

Tara, a hand-reared supposedly Bengal tigress acquired from Twycross Zoo in England in July 1976 was trained by Billy Arjan Singh, a well reputed conservationist, and released to the wild in Dudhwa National Park, in an attempt to prove the experts wrong that zoo bred hand reared Tigers can ever be released in the wild with success. In the 1990s, some tigers from Dudhwa were observed which had the typical appearance of Siberian tigers: white complexion, pale fur, large head and wide stripes. It was subsequently found that Siberian tiger genes polluted the otherwise pure tiger gene pool of Dudhwa National Park. It was proved later that Twycross Zoo had been irresponsible and maintained no breeding records and had given India a hybrid Siberian-Bengal tigress instead. The possibility exists of such genetic pollution in other tiger groups and, at its worst, this could jeopardize the Indian tiger as a distinct subspecies.

References:

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