**Tiger Endangerment**

A lot of tiger population has diminished due to human development. Only 7% of the historic range has survived. However, corridors that have attempted to link regional tiger populations have lost their importance. Corridors still may be functional by contemporary migration. Small and isolated populations are "prone to local extinction."

**Historic Decline**

After the British rule there was a severe decline in the number of tiger recovery began in 1970s with the idea of tiger reserves.

**Tiger Reserves**

Every reserve has its own, prohibiting human inhabitation and development. Size varies from 344 km² - 3,150 km² [in Asia: India & Nepal].

**Gene Flow & Migration**

Gene flow and "spatial dispersal" allows us to study migration patterns and understand how the habitat linkages are being used by tigers in both historical and contemporary times. Habitat connectivity models are made using GIS layers, allowing gene-flow among populations which prioritizes habitat corridors.

**Urbanization**

Urbanization prevents long-range dispersal for tigers due to high density human (pop)
Prioritizing Tiger Conservation through Landscape Genetics and Habitat Linkages

Bibek Yumnam, Yadendradev V. Jhala, Qamar Qureshi, Jesus E. Maldonado, Rajesh Gopal, Swati Saini, Y. Srinivas, Robert C. Fleischer

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RQ: How do tiger corridors affect tiger populations in Asia?

Abstract

Even with global support for tiger (Panthera tigris) conservation their survival is threatened by poaching, habitat loss and isolation. Currently about 3,000 wild tigers persist in small fragmented populations within seven percent of their historic range. Identifying and securing habitat linkages that connect source populations for maintaining landscape-level gene flow is an important long-term conservation strategy for endangered carnivores. However, habitat corridors that link regional tiger populations are often lost to development projects due to lack of objective evidence on their importance. Here, we use individual based genetic analysis in combination with landscape permeability models to identify and prioritize movement corridors across seven tiger populations within the Central Indian Landscape. By using a panel of 11 microsatellites we identified 169 individual tigers from 587 scat and 17 tissue samples. We detected four genetic clusters within Central India with limited gene flow among three of them. Bayesian and likelihood analyses identified 17 tigers as having recent immigrant ancestry. Spatially explicit tiger occupancy obtained from extensive landscape-scale surveys across 76,913 km² of forest habitat was found to be only 21,290 km². After accounting for detection bias, the covariates that best explained tiger occupancy were large, remote, dense forest patches; large ungulate abundance, and low human footprint. We used tiger occupancy probability to parameterize habitat permeability for modeling habitat linkages using least-cost and circuit theory pathway analyses. Pairwise genetic differences (FST) between populations were better explained by modeled linkage costs (r=0.5, p<0.05) compared to Euclidean distances, which was in consonance with observed habitat fragmentation. The results of our study highlight that many corridors may still be functional as there is evidence of contemporary migration. Conservation efforts should provide legal status to corridors, use smart green infrastructure to mitigate development impacts, and restore habitats where connectivity has been lost.


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Introduction

By virtue of being at the top of the food chain tigers are a group of population that are separated by space but the same species. Background info about tigers.
populations [51]. Though initially restricted to analyses correlating with linear distances [51], [52], the developing field of landscape genetics has now advanced to include more complicated connectivity modeling incorporating ways in which habitats are actually traversed in nature. The use of landscape heterogeneity parameters and habitat permeability obtained from geographical information systems (GIS) layers to model habitat connectivity by least-cost pathways (LCP) analysis [53] and circuit theory based isolation-by-distance (IBD) model [54], [55] that permit gene-flow between populations provide an objective criteria for detecting and prioritizing habitat corridors. There is a small but rapidly growing body of literature investigating the relationship between genetic and corridor connectivity, with both LCP and IBD models finding promise in gene flow studies on taxa with lower dispersal capabilities and that readily form viable metapopulations such as amphibians (tiger salmanders, Ambystoma sp. [56], [57]), to wide-ranging carnivores (cougar, Puma concolor [58]; bobcat, Lynx rufus [59]; wolverine, Gulo gulo [60]; black bear, Ursus americanus [61]). Where available, researchers have incorporated information from animal habitat use and movement behavior in the cost parameterization schemes to approximate realistic paths of least resistance, as in Redig et al. [62]. However, such data are not readily obtainable, and hence the vast majority of studies rely on expert opinion and a priori assumptions on animal presence to assign cost schemes and parameterize landscape resistance to gene flow. Although informative, the parameterization schemes used in landscape resistance surfaces to model movement paths and the assignment of cost schemes to grids in GIS-rasters could easily introduce biases which may be more reflective of habitats as perceived by humans rather than by animals [63]. Incorporating information obtained from fine-scale species and landscape-specific ground data on suitable habitat, cover, prey availability, disturbance and threats in considering the attribute of surrounding cells, is one way which could help reduce subjectivity involved when assessing resistance or cost of cell and the likelihood of path usage [63].

In this study, we investigate parameters of connectivity and spatial genetic structuring to identify barriers and minimal habitat corridors for gene flow between populations within the fragmented tiger habitats in Central India. The Central Indian landscape is a globally recognized area for tiger conservation, with significant potential for long-term persistence of the species [15], [31]. The area supports one of the largest global concentrations of tiger populations (~20% of an estimated 1,700 adult Indian tigers, [31] in patchily connected habitats. Although the populations were historically connected, rapid infrastructural development and urbanization in recent years threaten to fragment barriers to dispersing tigers by isolating tenuously connected small populations, thereby effectively reducing long-term population persistence. Recent population and spatial genetic studies have observed genetic structure among populations indicative of gene flow [64], [65] and long-range dispersal which are affected by increasing urbanization in the area [66]. Although tigers can move huge distances in undisturbed habitats [67], the complex fragmented habitat mosaic in the area, interspersed with high density human settlements and increasingly urbanized centers, have generally been thought to limit long-range dispersal [41]. Dispersal in tigers (Panthera leo [19]) is male biased, as female offspring tend to reside and breed close to their maternal ranges, while male offspring disperse long distances, establishing home ranges farther from their natal areas [41]. This study explores a strategy that utilizes genetic assignment methods to detect population genetic structuring and determine which populations are in migratory contact, extensive occupancy modeling and GIS analysis to delineate social connectivity between populations, and a correlation process between landscape connectivity versus population pairwise genetic distances to determine which of the movement cost schemes and modeled corridors best explain the observed genetic structuring of the tiger.

We extensively and intensively collected scat and a few tissue samples across seven tiger reserves in the Central Indian Landscape and first identify tiger individuals by genotyping the DNA extracts using eleven autosomal microsatellite loci. We next assessed spatial genetic structuring and gene flow in the identified individuals through individual clustering methods. We use likelihood-based [49] and Bayesian [48, 60] assignment methods to assign first and second generation migrants between the identified genetic population clusters. Since resident tigers do not occur outside of forested habitat, we surveyed all of the forested area (76,813 km²) within 185,100 km² of Central India. Based on our understanding of tiger ecology, we predicted a priori that tigers should occur in vast, undisturbed, productive forest patches, with high density of large wild ungulates, prey which would be negatively impacted by human disturbances [20], [31], [41], [67]. We tested these a priori hypotheses by spatially extensive sampling of occupancy to detect and quantify the extent of tiger occupancy that accounted for imperfect detections, using covariates obtained by remote sensing and ground surveys covering all forest patches within our study area. We then used this spatially explicit information of tiger occupancy as a resource selection probability function [69], [70] to model habitat corridors joining tiger populations using LCP [71] and circuit theory [72] analyses in a GIS setting. With genetic data we tested if the observed population structure and dispersal between populations is in accordance with genetic quality of tiger connectivity. Our comprehensive study highlights the importance of particular tiger source populations and intervening forest corridors in Central India. It provides a basis to formulate conservation policy and assist informed decision making for land-use planning at the landscape scale.

Materials and Methods

The majority of field sampled was conducted non-invasively from tiger scat without animal capture and handling. Permits for collection of tiger scat samples were obtained from the National Tiger Conservation Authority and the State Forest Departments. Capture and radio collaring of tigers required the approval of the Ministry of Environment and Forests, Government of India and the Chief Wildlife Warden, Madhya Pradesh State, under the Wildlife (Protection) Act 1972. The permissions define the conditions required for capture of tigers, which include an approved protocol and participation by a Park Official and supervision by a qualified veterinarian in the capture and collaring exercise. Both these permissions were obtained and strictly adhered to. Capture operations were conducted by trained veterinarians and wildlife biologists as per the protocols of the Wildlife Institute of India and the National Tiger Conservation Authority. A tiger tissue sample was obtained from Sabhara Tiger Reserve where the tiger died due to natural causes (was killed by another tiger in a territorial strife). This research project was conceived and radio-collared reported in this paper was done prior to the formation of an animal ethics committee at the Wildlife Institute of India.

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