

Fragmentation genetics in the tropics

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Received: 18 June 2012 / Accepted: 29 August 2012 / Published online: 11 September 2012
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Abstract On the 23rd of February, some 50 Conservation Geneticists from around the globe gathered for a half day symposium entitled ‘Fragmentation Genetics in the Tropics’ held at the Friedrich-Alexander University, Erlangen, Germany as part of the German Tropical Ecology Society annual meeting 2012. The overall aim of this symposium was to showcase the latest novel research applying molecular methods (landscape genetics, conservation genetics and phylogeography) to advance our understanding of genetic consequences of fragmentation in the tropics, particularly in the context of how population size and isolation influences population and species extinction. I provide a brief overview of the symposium and finish with a call for papers for a special issue of the sister journal *Conservation Genetics*, for which submission is now open.

Keywords Fragmentation · Gene flow · Conservation genetics · Extinction · Tropical biodiversity

Introduction

Habitat fragmentation remains the most pressing threat to global biodiversity, so it was apt that the 2012 annual meeting of German Society for Tropical Ecology (GTÖ), held in the historic German town of Erlangen, was entitled

‘Islands in Land and Seascape: the challenges of fragmentation’.

Some two-hundred scientists gathered for the meeting to discuss a plethora of ecological topics centred on the emerging challenges for conserving biodiversity in the tropics. It will be of no surprise to the reader that molecular ecology and particularly conservation genetics featured prominently at such a meeting. Indeed, recognition of the power of molecular techniques to address the pertinent questions in tropical conservation biology is increasing in prominence. It was with some satisfaction that the symposium ‘Fragmentation Genetics in the Tropics’ proved to be one of the largest sessions of the whole conference, with nine oral presentations and six poster presentations, and authors from ten countries (including first authors from three tropical countries).

The aim of this session was to present the most up-to-date and novel research applying molecular methods (landscape genetics, conservation genetics and phylogeography) to advance our understanding of fragmentation in the tropics, particularly in the context of how population size and isolation influences population and species extinction. Habitat fragmentation affects different organisms in a myriad of complex ways, at different temporal and spatial scales. Molecular methods provide a very powerful tool for investigating contemporary dispersal, colonization and connectivity, key ecological processes which are notoriously difficult to study using classical field ecological studies.

The session showcased some of the latest world-class research on conservation genetics from botanical to zoological disciplines. Papers from the symposium will form part of a special issue of *Conservation Genetics* to be published later this year edited by Chris J Kettle and Michael Bruford.

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Oral presentations

The session was commendably kick-started by a plenary talk from Professor Ute Radespiel (Institute of Zoology, University of Veterinary Medicine, Hannover, Germany), who provided an enlightened synthesis of current work on the conservation and populations genetics of a range of tropical fauna, including her own work on the Malagasy lemurs. This was tempered by some cautionary words on misinterpretation of patterns of genetic differentiation and the challenges of disentangling the effects of historical natural fragmentation and anthropogenic effects in both space and time.

We remained with mammals but shifted to the winged variety with the excellent presentation by Simon Ripperger (University of Ulm, Germany) on the effects of habitat fragmentation on the genetic structure of the frugivorous bat species *Dermanura watsoni* from the Caribbean lowlands of Costa Rica. Using a novel combination of nuclear SSR (Microsatellite) loci and mitochondrial D-loop markers, this study was able to demonstrate landscape barriers to gene flow in this important seed dispersal agent.

Samuel Boff (University of São Paulo, Brazil) presented a wonderful study system for exploring the effects of fragment size on the genetic diversity and inbreeding in populations of orchid bees, occupying islands of different size and the mainland near São Paulo, Brazil. Boff et al. explored the relationship between ‘diploid male production’ and genetic diversity at 7 nuclear SSR loci. They reported evidence of elevated diploid male production in correspondence with reduced genetic diversity, possibly due to small population size. This has implications for the persistence of these important species in fragmented habitats.

We moved from insects in South America to birds in the cloud forests of East Africa with Jan Habel’s (Natural History Museum, Luxembourg) presentation of a very nice study of the Mountain White-eye *Zosterops poliogaster*. Habel et al. combined morphological and genotype data (19 nSSR loci) across some 650 individuals with a Circuit Scape analysis to explore barriers to gene flow in this mountain archipelago. They demonstrated that the highest variability is found along the interconnected Central Kenya Highlands, while populations on isolated mountains show lower diversity and elevated fluctuating asymmetry. He discussed the implications of this in the context of increased anthropogenic fragmentation of the White-eye’s habitat compared to naturally fragmented habitat.

Moving from animal to plants and transported across continents from Africa to India, Sascha Ismail (ETH Zurich, Switzerland), introduced us to the highly fragmented and extraordinary agro-forest landscapes of the Western Ghats India. Ismail et al. have been applying molecular methods (12 nSSR loci) using a combination of parentage and paternity analysis to gain a detailed

understanding of the gene flow in the tropical tree *Dysoxylum malabaricum* over an extensive landscape scale (nearly 300 km²). By genotyping all adult trees over the entire study area and sampling different age cohorts they demonstrated that despite the capacity for long distance dispersal, fragments with low densities of adult trees have a higher frequency of mating among related individuals.

We then remained with trees but moved to focus on the island of Borneo, when Chris Kettle (ETH Zurich, Switzerland) provided a synthesis of their work applying genetic approaches to understand the reproductive ecology and patterns of genetic diversity in the globally important timber family Dipterocarpaceae. Kettle et al. highlighted the importance of understanding fine-scale spatial genetic structure for both sustainable forest management, and seed sourcing for forest nursery establishment and restoration. He also provided a nice example of how inappropriate seed sourcing can lead to extreme genetic bottlenecks in the Seychelles endemic dipterocarp *Vateriopsis seychellarum*.

In another study of dipterocarp trees in Borneo, Kirsty Nutt (University of Aberdeen, UK) presented a study of heterozygosity-fitness correlations in the critically endangered timber species *Parashorea tomentella*. Nutt et al. genotyped seedlings collected from mother trees with different neighbor distances and degrees of spatial isolation and tracked the survival and growth performance of these seedlings under experimental nursery treatments. This empirical study of the fitness consequences of inbreeding in this important timber family has relevance for forest management policy and understanding the implication of fragmentation in the region’s remaining forest.

Staying with trees but moving from Borneo to Myanmar, Yazar Minn (Georg-August Göttingen University, Germany) presented a comparative study of the genetic variation (at 10 nSSR loci) in populations of Teak (*Tectona grandis*) across life stages (adults and seedlings) and between selectively logged and unlogged populations. Minn et al. results have potentially important implications for the management of genetic resources in this important timber species.

Finally, we moved to Africa where Kathleen Prinz (Georg-August Göttingen University, Germany) presented a study combining AFLPs and chloroplast markers to evaluate the distribution of genetic diversity across four species of tropical trees from East to West Africa. They reported contrasting patterns of genetic diversity related to fragmentation levels, and discussed their potential implications for in situ and ex-situ conservation of tree genetic resources in the region.

Posters

Ivana Kirchmair (Biodiversity and Climate research Center, Frankfurt, Germany) presented work on the biogeography

and intraspecific relationships among four riverine West African tree species. Fernando Rodrigues (University of Brazil) presented a survey of the genetic diversity in populations of the Woolly-mouse Opossum in highly fragmented landscapes. Eliana Fischer (Federal University of São Carlos, Brazil) presented a study of genetic diversity in the White-eared Opossum across the Morro do diabo state park and adjacent fragments of Atlantic rain forest. Janine Wojacki (University of Kassel, Germany) presented microsatellite data from four species of the important genus of tropical tree *Macaranga* from a study site in Sarawak, Malaysian Borneo. Randy Villarín (Georg-August Göttingen University, Germany) presented a comparative study of genetic diversity in natural and planted populations of two important dipterocarp species in the Philippines. Finally, Claire Tito de Moraes (ETH Zurich, Switzerland) presented preliminary results from a study exploring the genetic processes underlying species coexistence in dipterocarp trees of Borneo.

In summary, this half day symposium presented studies applying molecular data to support the conservation of some 28 plant species and more than ten animal species. It

highlighted the challenges faced by a diverse range of tropical taxa associated with fragmentation. The toolbox used by conservation biologists is increasingly sophisticated. Genetic tools are among the sharpest and most powerful for advancing our understanding of how different taxa respond to human induced fragmentation of natural habitat. The tropical glass houses of the Erlangen Botanic gardens provided a retreat to these tropical conservation geneticists from the February chill, but also a sober reminder of the urgent need to ensure that tropical biodiversity survives in situ, not just in botanical or zoological gardens.

We welcome submissions for the special issue of Conservation Genetics so please contact the author or visit: <http://www.springer.com/life+sciences/ecology/journal/10592>.

Acknowledgments We would like to thank the organizing committee of the GTÖ 2012 for their support and the comments of a reviewer. Chris J Kettle's attendance at this meeting was supported by the Ecosystem Management Group ETH Zurich, Switzerland.