Genetic and demographic signatures of population fragmentation in a cooperatively breeding bird from south-east Kenya

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Habitat loss and fragmentation typically result in smaller and more isolated populations of plants and animals, which are further suppressed by stochastic, demographic and environmental processes, synergistically leading to population extinctions and worldwide biodiversity loss. Currently, few in depth studies exist on genetic and demographic effects of habitat loss and fragmentation in tropical ecosystems, despite the fact that conservation implications may differ largely in tropical and temperate-zone species. Therefore, we conducted research in the isolated Taita Hills in south-east Kenya with the implicit aim of advancing our understanding on how tropical rainforest fragmentation may lead to population fragmentation in cooperatively breeding, forest-restricted bird species. To achieve this aim, we studied genetic and demographic signatures of rainforest fragmentation on populations of the cabanis's greenbul (*Phyllastrephus cabanisi*), the results of which are described in five consecutive chapters.

In Chapter 1, historical shifts in mobility in three *P. cabanisi* populations were evaluated against those of six sympatric forest bird species, by comparing species-specific levels of past population differentiation, estimated from sets of microsatellite genotypes, with contemporary dispersal rates, estimated from multi-strata capture-recapture models. In *P. cabanisi*, severe fragmentation of the original indigenous forest cover resulted in moderate historical loss of mobility over time, combined with genetic subdivision into three distinct clusters.

In Chapter 2, shifts in demographic and genetic properties were quantified within and between five *P. cabanisi* populations over a recent time interval. Contrary to our expectations, genetic and demographic spatiotemporal analyses could not substantiate a decrease in between-fragment connectivity over a more recent, fifteen years time span. Rather, contemporary populations showed higher levels of genetic variation and admixture, and effective population sizes remained largely equal or even showed a weak tendency to increase with time.

In Chapter 3, spatial and temporal variation in predation rates on natural nests of *P. cabanisi* were described in two contrasting forest fragments during three consecutive breeding seasons. Within fragments, predation levels matched the typical high predation rates on tropical bird species. However, daily predation rates on *P. cabanisi* nests in the

Taita Hills were much lower than in similarly-structured forests in a more pristine part of the Eastern Arc Mountains (East Usambara). Predation rates strongly varied in space and time, and a model that combined habitat-, edge- and timing effects was best supported by our data. Nest predation rates increased from the forest edge towards the interior, supporting the notion of an inverse edge effect.

In Chapter 4, the social breeding system of *P. cabanisi* was examined by means of a detailed camera survey. Results revealed complex breeding behavior in *P. cabanisi* with a considerable amount of breeding pairs assisted by helpers, characterizing the species as a cooperative breeder. Through detailed quantification of variation in food provisioning rates at nests with and without helpers, we found that breeding females most likely adopt a load-lightening strategy. They reduce provisioning rates to nestlings when assisted by helpers, which might positively affect their fitness in terms of increased breeding attempts, condition and/or survival.

In Chapter 5, the genetic signature of forest fragmentation was revisited by adopting an individual-based approach. At local scale, we revealed fine-grained spatial patterns of positive local genetic structure, consistent with behavioral observations of natal philopatry. At a landscape scale, individual-based auto-correlation values also showed restricted dispersal, with the decreasing values over time supporting our other findings of increased gene flow over the past decade. Results of this study confirm that individual-based genetic analyses at multiple spatial scales can provide a powerful alternative to population-level analyses.

Based on genetic and demographic results of this doctoral study, we concluded that even though human-induced habitat changes in the Taita archipelago seem to have impacted *P. cabanisi* populations via moderate historical mobility loss and genetic population subdivision, shifts in the genetic population structure over the last decade at least hint towards population reconnection. Our findings are promising in the fact that the detrimental effects of forest fragmentation might be reversible, given that increased dispersal and gene flow at metapopulation level seem to dampen demographic and genetic effects of forest loss and degradation at the local population level. This doctoral study hence supports the recommendation that conservation of fragmented populations of K-selected Afrotropical passerines requires action both within habitat fragments and at the landscape level. Within fragments, habitat loss and deterioration should be kept at a minimum in order to maintain adequate population growth and emigration to other populations. Across fragments, efforts should be made to maximize landscape connectivity in order to allow birds to move between fragments. Finally, although the demographic and genetic implications of cooperative breeding could not be evaluated thoroughly in this study, the initial detection of helpers at the nest provides a potential source for various future explorations on the evolution, consequences and conservation implications of such complex behavior.