



haplotypes. Furthermore, the introduced populations showed a higher sequence and haplotype diversity than their native counterparts. This analysis suggests that elevated gene diversity was largely due to *C. afra* populations being founded by individuals from several genetically distinct and geographically separate populations. In Chapter 4, I discuss the role of introgressive hybridisation with native *P. zebra*, and its impact on mtDNA variation in the introduced *C. afra* gene pool. In Chapter 3, I show that in contrast to the signal obtained from the mtDNA, the genetic variation at the microsatellite loci exhibited a significant reduction in the introduced range. Introduced *C. afra* populations have a lower mean effective number of alleles ( $n_e$ ) than *C. afra* populations in their native range. I use an approximate Bayesian analysis and show compelling evidence that at least two independent introductions have contributed to the introduced *C. afra* gene pool, a conclusion that is supported by high probability values. This conclusion differs from that of previous studies which suggested a stepping stone introduction pattern around Thumbi West Island. Surprisingly, a population of *C. afra* at Domwe Island was founded by a source population from Thumbi West Island, and this stepping stone introduction pattern is supported with a high probability (95%). Microsatellite analysis furthermore suggests that the founder event of *C. afra* in Lake Malawi National Park was associated with strong genetic drift associated with a genetic bottleneck. I was not able to detect this signal from the mtDNA genetic marker alone, which showed an increase in genetic variation at the mtDNA due to different source populations contributing to the founder event (see Chapter 2). These combined studies reported in Chapter 2 and 3 thus demonstrate that microsatellites may be well-suited to investigate questions related to conservation issues such as bottlenecks associated with founder events, while mtDNA is more suited to reveal the evolutionary processes and establish different source populations that have contributed to the introduction. In Chapter 4, I analyse the level of genetic differentiation at microsatellite loci, and show that the introduced *C. afra* and native *P. zebra* populations at Thumbi West Island are genetically more similar ( $G'ST=0.36+/-0.05$ ) than the species-pair at Otter point ( $G'ST=0.94+/-0.18$ ) and Domwe Island ( $G'ST=0.55+/-0.09$ ). In addition, *C. afra* and *P. zebra* at Thumbi West Island showed a lower genetic distance than allopatric *C. afra* or *P. zebra* populations from Otter point and Domwe Island. Further analysis using a Bayesian assignment approach supports previous findings and demonstrates the likelihood of introgressive hybridisation between an introduced *C. afra* and a native *P. zebra* population at Thumbi West Island. No evidence of introgression is found at Otter point and Domwe Island, where the *C. afra* and *P. zebra* populations show distinct genetic structure. The occurrence of introgressive hybridisation at Thumbi West between species from distinct genera shows that translocations can have a dramatic impact even on the gene pools of heterospecific recipient populations. The results from this work have crucial implications in evolution of cichlid fishes and in invasion biology when predicting the evolution of invasiveness. In summary, the thesis shows that hybridisation, as well as the introduction of multiple genetically differentiated source populations has increased the genetic diversity of introduced *C. afra* populations, and this may have facilitated their establishment in Lake Malawi National Park. Translocation of cichlid species in Lake Malawi can have a dramatic impact even on heterospecific gene pools.

This textbook shows readers how models of the genetic processes involved in evolution are made (including natural selection, migration, mutation, and genetic drift in finite populations), and how the models are used to interpret classical and molecular genetic data. The material is intended for advanced level undergraduate courses in genetics and evolutionary biology, graduate students in evolutionary biology and human genetics, and researchers in related fields who wish to learn evolutionary genetics. The topics covered include genetic variation, DNA sequence variability and its measurement, the different types of natural selection and their effects (e.g. the maintenance of variation, directional selection, and adaptation), the interactions between selection and mutation or migration, the description and analysis of variation at multiple sites in the genome, genetic drift, and the effects of spatial structure.