# Abstract

The honeybee, *Apis mellifera*, is a globally distributed species that has spread both naturally and by humans across the globe resulting in many natural and secondary contact zones. The geographic isolation of honeybees is likely to contribute to genetic differentiation. Secondary contact has resulted in hybridization at the nuclear genome, but replacement of mitochondrial. Here, we used a mitochondrial marker and 19 microsatellite markers to test for the variations in the mitochondrial and nuclear genomes of honeybee populations on the Comoros islands. We used samples of 160 workers for mtDNA analysis and 288 workers from 16 colonies spread across the three islands for microsatellite analyses. Our results showed that the wild honeybee populations of the Comoros Islands consist of coexisting mitochondrial haplotypes. One belongs to the typical African A-lineage, and the other, the newly described L-lineage, is closely related to *Apis koschevnikovi*, a honeybee species native to Southeast Asia. The nuclear genomes show complete hybridization, high genetic diversity, and strong differentiation according to the island of origin. Based on our results, we hypothesise that the Asian honeybee could have been transported from Southeast Asia to Madagascar and Comoros via the human migrations that occurred 6000 years ago, and has hybridised with African honeybees at the nuclear genome, but maternal ancestry still can be traced using the mtDNA markers. We conclude that mtDNA plays a pivotal role in adaptation to the local environment, with both haplotypes of the honeybees of Comoros contributing significantly to the mito-nuclear coadaptation resulting in maintenance at almost equal frequency.