

Abstract

Approximately 850 bp of the mitochondrial control region was used to assess the genetic diversity, population structure and demographic expansion of the endangered cyprinid *Barbus altianalis*, a species known to be potamodromous in the Lake Victoria drainage system. The 196 samples taken from the four main rivers draining the Lake Victoria catchment (Nzoia, Yala, Nyando and Sondu–Miri) yielded 49 mitochondrial DNA haplotypes; 83.7% thereof were private haplotypes restricted to particular rivers. The overall mean haplotype diversity was high (0.93663 ± 0.008) and ranged between 0.566 (Sondu – Miri) and 0.944 (Nzoia). The overall mean nucleotide diversity was low (0.01322 ± 0.00141), ranging from 0.0342 (Sondu – Miri) to 0.0267 (Nzoia). Population differentiation tests revealed strong and highly significant ($P \leq 0.001$) segregation of populations in the four river basins. F_{ST} values among the four river-based populations ranged from 0.05202 to 0.44352. The samples formed two main haplotype networks based on a 95% parsimony criterion, each exhibiting a strong signature of past population expansion. The smaller network was restricted to the River Nzoia, whereas the larger network contained representatives from all four rivers; within this the central haplotypes were found in more than one river, whereas the peripheral haplotypes tended to be river-specific. The degree of population differentiation and the number of river-specific haplotypes are too high to be explained by recent anthropogenic impacts alone and suggest that the species has probably existed in the Lake Victoria catchment as two populations: the now ‘extinct’ migratory population and the extant river restricted non-migratory populations.