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Molecular Population Genetic Studies on Crucian Carp (*Carassius auratus*) in Korea

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Freshwater fish fauna are famous for its large proportion of endemic species as a consequence of regional speciation which came from the nature of freshwater fish species. Freshwater fish, especially obligatory species cannot move across the rivers or river systems to which they are confined. This would meet the sufficient condition for speciation because isolation is requisite for population divergence. Moreover, fluctuation of sea level during the Pleistocene must have facilitated the divergence of this animal group. Crucian carp (*Carassius auratus*) is one of the most common freshwater fish originally distributed over Palearctic region and now all over the world by anthropogenic introduction. *Carassius auratus* composed of six subspecies, however, is located in the center of debates about its species status induced by its various reproductive modes and karyotypes as well as morphological traits. In this study, we described geographical distribution of genetic variation and tried to infer the evolutionary history of *Carassius auratus* based on phylogenetic and population genetic evidences using mitochondrial sequences. Totally 103 sequences of mitochondrial control region were acquired from Korea in our study. 45 haplotypes were identified from 103 sequences based on the analysis of full mitochondrial control region sequences (1066 bp). According to the phylogenetic analysis, Korean populations consisted of two monophyletic clades, one clade, MAC (MAjority Clade) formed 67% of total Korean individuals and the other clade, MIC (MInority Clade) that showed relatively low frequency (33%). Both of them may have experienced population expansion events, which were verified by mismatch distribution analysis and neutrality tests (Tajima's D and Fu's Fs). MAC lineage may be older than MIC one in Korea, which was supported by several molecular evidences. First, higher gene diversity was observed in MAC (0.9506 ± 0.0149) compared to MIC (0.5839 ± 0.0973). Genetic diversity is generally in proportion to evolutionary time because of spontaneous mutations without consideration of other factors. Second, according to mismatch distribution analysis, MAC may have about 2.4 times longer history than the other clade in Korea assuming equal mutation rate and generation time. Third, individuals in MAC was geographically highly structured between the major river systems (Han-Geum/ Nakdong-Seomjin), which was supported by analysis of molecular variance that 44.13% of genetic variation lay among groups ($P=0.005$). But MIC lineage did not exhibit significant genetic structure. It strongly suggested that sufficient time have passed to acquire genetic divergence after the isolation. Haplotypes of Japanese gimbuna (*C. auratus langsdorfi*) were significantly diverged from Korean and Chinese ones, as a result of phylogenetic analyses. Several haplotypes of China and Japan belonged to MAC in the neighbor joining tree, which may be the evidence for dispersal during the Last Glacial Maximum. It is interesting that haplotypes from goldfish, popular ornamental aquarium fish showed close relationship with those of MIC. It was possible that Korean MIC lineage may have recently migrated from the Southern China where goldfish was originated via the Paleo-Yellow River that was formed to connect rivers of Korea, China and Japan as sea level lowered during the ice ages. Following scenarios for evolution of crucian carp in East Asia could be inferred from our molecular data. Ancestors of extant crucian carp originated from southern China had expanded ranges toward northern Eurasia and easterly Japanese Islands through connected river-system. Luo et al. (1999) suggested that *C. auratus gibelio* subspecies may be separated from *C. auratus auratus* according to their maximum parsimony analysis of RFLP data. Therefore, two subspecies groups of *C. auratus* (northerly *C. auratus gibelio* and southerly *C. auratus auratus*) were diverged in the mainland of Asia. Prior to divergence of *C. auratus* in China, *C. auratus cuvieri* had been separated from the species of mainland of Asia about 0.72MYA (Luo et al. 1999). Of these, *C. auratus gibelio* which was suspected identical to MAC clade may have more influence on the populations of Korea than those of Japanese Islands where *C. auratus langsdorfi* departed from *C. a. gibelio* (Murakami & Fujitani 1997) had already dominated with long isolation from mainland of Asia. Ancestors of Korean MIC clade may have migrated into Korea from South China more recent than that of MAC clade and/or have colonized with small number of founder. Additional data will elucidate more exact history and species status of this organism. Alternative explanation for existence of MIC in Korea was the naturalization of goldfish. The goldfish was imported as an ornamental fish, and numerous releases in private ponds had occurred during the last century over the world. Escaping from park and garden pools, the goldfish has become naturalized. Therefore, the possibility of naturalization of goldfish should not be overlooked in case of interpretation of pattern of molecular genetic variation.