

Genetic variability and structure of common carp (



Domesticated/captive stocks and wild/feral populations of common carp from Europe, Central Asia and East/South-East Asia were examined for allozyme (23 populations), microsatellite (11 populations) and mitochondrial DNA (21 populations) variation. Allozyme variability (1.06–1.81 alleles per locus, expected heterozygosity 0.006–0.136 at 16 loci) was much lower than microsatellite variability (2.5–14.0 alleles per locus, expected heterozygosity 0.426–0.887 at four loci). Differences in variability between domesticated/captive stocks and wild-caught ones were more pronounced at microsatellite loci than at allozyme loci, suggesting that microsatellites are better suited to detect population bottlenecks and loss of variation due to inbreeding. All but one European population were fixed for a single composite mtDNA haplotype, which also dominated in Central Asia but was completely missing in East/South-East Asia, indicating a single origin of European carp in Central Asia. All three classes of genetic markers clustered populations into two highly divergent groups: Europe/Central Asia and East/South-East Asia. Hierarchical partition of

genetic diversity showed that for microsatellite loci most of variation was due to the within-population component while the highest proportion of mtDNA variation and substantial proportion of allozyme variation was accounted for by differences between geographical regions. Genetic data support the subspecies status of *C. c. carpio* assigned to the European carp and *C. c. haematopterus* assigned to the East/South-East Asian carp but do not justify a separate subspecies status (*C. c. aralensis*) for the Central Asian carp. As demonstrated for a wild/feral carp population from R. Danube, Germany, the genetic markers used in our study may be effectively applied to detect mixing and introgression of intra-species units in the presence of sufficient genetic differentiation.

Auteurs du document : Klaus Kohlmann, Riho Gross, Asiya Murakaeva, Petra Kersten

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