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Population genomics reveals adaptive divergence in global populations of common carp (Cyprinus carpio)

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The common carp, Cyprinus carpio, is one of the most important cyprinid species cultured in Europe and Asia and globally accounts for over 70% of freshwater aquaculture production worldwide. Various populations of C. carpio distribute all over the world and mainly in the Eurasian continent, showing distinct biological characteristics including scale, color, body shape, etc. However, the genetic mechanism underlying the traits were not very clear yet. Here we present a population genomic analysis on 14 populations of C. carpio. High throughput SNP genotyping of 2,587 representative individuals from worldwide 14 populations demonstrates different genetic component for C. carpio in two subspecies (C. carpio subsp. haematopterus and C. carpio subsp. carpio). Quality control of SNPs were conducted with following parameters (call rate>95%, genotype rate>95%, MAF>5%). A maximum-likelihood tree was constructed with RAxML and displayed with iTOL software (http://itol.embl.de/upload.cgi), and all SNPs were used to investigate the PCA with SMARTPCA. Population structure were finished using STRUCTURE with 2,000 iterations. The resulting structure matrix was plotted using STRCTURE PLOT v2.0. LD (linkage disequilibrium) block average lengths of 14 populations range from 3.94kb to 36.67kb. We calculated the π distribution for each linkage group using a sliding window method in VCFTOOLS. The window width was set to 10 kb, and the stepwise distance was 10 kb. The π values from the main populations were compared, and the ratios were sorted. Fst and Tajima's D values were also calculated using VCFTOOLS with the parameters "–weir-fst-pop" and "–TajimaD", respectively. We identified the regions with the 5% highest p ratios and the regions with the 5% highest Fst values. Genes within selective sweep regions were identified by genome scanning among different populations, including gdf6a, grb7, mtnr1ba, tgfbr2, etc. Gene ontology and KEGG enrichment analyses by DAVID software unveiled potential trait-related GO terms and pathways which were associated with body shape, scaling patterns and skin color, such as TGF-beta signaling pathway, ECM-receptor interaction and so on. The population genomics analysis paves the way for better evolutional studies and improved genome-assisted breeding of C. carpio.

Biography

Jian Xu has completed his PhD from Peking Union Medical School, China. He is an Associate Professor and Vice Director of Center of Aquatic Genomics of Chinese Academy of Fishery Sciences, Beijing, China. He has published 33 papers in reputed journals and has been serving as an Editorial Board Member of *Frontiers in Genetics*.

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