A global assessment of population structure and genetic diversity in chicken populations from Africa, Asia, and Europe

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P-20. Genetic diversity and population structure of 114 chicken populations from Africa, Asia, and Europe were studied using 29 microsatellite markers. These populations included three wild chicken populations (RJF), nine commercial purebred lines, and one inbred line with four sublines to be used for comparison. Allele frequencies, mean number of alleles, heterozygosity, and Wright's fixation indices were estimated to investigate the extent of genetic variability between and within chicken populations from different geographical regions. Geographic population structure was determined by using Bayesian model-based clustering. High heterozygosity and lower genetic differentiation were observed in African and Asian chickens relative to European and Commercial breeds. European chicken breeds showed higher range of variability in heterozygosity, while the majority of Asian and African chicken populations had heterozygosity levels above the mean of all populations. The cluster analysis revealed high admixture in African and Asian chicken populations whereas European breeds partitioned into distinct groups with minimum sharing of genetic material.