

**Abstract:**

Domestic chickens are domestic animals with tremendous economic value. Due to this value, high-production lines have more important role for humans than fancy breeds and rural populations. Production traits of these high-production lines are not comparable with traditional breeds. The preference for larger profit gradually diminishes the importance of the traditional breeds, which leads to their replacement increasing the risk of loss of their genetic variability. Despite this trend, general awareness of this problem increases providing hope in saving these rich sources of genetic variation. We selected sample of 272 individuals representing 33 traditional (fancy) breeds. I evaluated the degree of variability through the analysis of twenty selected neutral markers (mtDNA control region and 19 microsatellite loci) and four immune genes (TLR3, TLR4, TLR5, TLR7). The main aims were: to map the origin of modern breeds between ancient breeds, identify the possible geographic origin of the breeds, to compare the rate of neutral and functional variation between breeds with the level of variation within breeds and to compare the degree of shared polymorphism (gene flow / ancestral polymorphism) of neutral markers and immune genes. The results show that we can genetically differentiate breeds and identify from the range of which ancient breeds modern chicken originate and how they are related to each other. All studied breeds belonged to four mitochondrial families, the most common family was E1, with a likely ancestor *G. g. murghi* from north-eastern India. Some breeds carry more mitochondrial haplotypes. Genetic variability of immune genes and microsatellites was high. Asian breeds showed a higher degree of variability than European breeds. We gained similar results by the analysis of immune genes and neutral markers. Differences in genetic variability of ancient and modern breeds were non-conclusive. Genetic variability among breeds was only slightly higher in neutral markers (32%) than in immune genes (27%). This result is most probably related either with a similar degree of ancestral polymorphism or gene flow between breeds. Rate of shared polymorphism was significantly higher in neutral markers. From a total of 163 alleles only 41 were private alleles. This result shows that 74.8% of alleles were shared between breeds. On the contrary, the TLR had 154 alleles in total and 101 alleles were private. Thus, the breeds shared only 34.4% of alleles, which likely results from higher genetic diversity of the TLR loci.

**Keywords:** chicken, microsatellites, mitochondrial DNA, D-loop, relatedness, gene flow, genetic variability, ancestral polymorphism