Evaluation of genetic diversity in Sri Lankan Indigenous chicken using microsatellite markers

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Sri Lanka is rich in indigenous chicken (IC) genetic resources which are adapted to wide range of production systems with varying climatic and natural environments. Although they play a significant role in rural poultry production systems, and also they harboring a wealth of genetic diversity, an adequate attention is not been paid due the absence of significant production standards. Hence, systematic evaluation and characterization have so far been limited to few studies. Here, we investigate the genetic diversity of IC from 5 distinct regions of the country. A total of 150 birds were genotyped with 20 microsatellite markers on 11 chromosomes. There were 188 alleles observed and number of allele ranged from 5 to 18 with a mean of 9.4. Heterozygosity (H) values of 5 populations were more than 0.5. The average H value and polymorphism information content (PIC=0.663) suggested that Sri Lankan IC population possesses a high genetic diversity compared to many reported to-date. The high average gene diversity (0.676) and the presence of a high number of population specific alleles (privet alleles=36) also prove genetic distinctiveness of IC in Sri Lanka. The fixation coefficients of subpopulations within total population (FST) for 20 loci were 0.05 with moderate genetic differentiation. Estimates of Nei's genetic distance and Neighbor-joining method revealed that, the IC populations have been clustered according to their geographic distribution. High genetic diversity of Sri Lankan IC is in agreement with high phenotypic diversity exhibited by them, and also supported by the existing breeding system at village level. The genetic diversity and relationships among populations estimated may be useful as a guide for designing future investigations and conservation strategies for Sri Lankan Indigenous Chicken genetic resources.

SNPs in candidate genes for intramuscular fat in Parda de Montaña and Pirenaica beef cattle breeds

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Intramuscular fat (IMF) content influences sensory quality traits, such as tenderness, taste and flavor. Due to its interest, there is a search for genetic markers associated to IMF deposition. The aim of this study was to evaluate the association with IMF content of 9 SNPs located at TG (BTA14: g.9509309C>T), SCD1 (BTA26:g.21144730C>T), LEP (BTA4:g.93261931T>C), RORC (BTA3:g.19010079T>G), FASN(BTA19:g.5140203G>A), CAST(BTA7:g.98535683A>G) and CAPN1(BTA29:g.1827088G>C; g.1843665G>A; g.1845653T>C) genes in Parda de Montaña (n=225) and Pirenaica (n=68) beef cattle breeds. IMF was determined following the Ankom procedure in Longissimus thoracis muscle and all SNPs were genotyped by PCR-RFLPs. All SNPs were in Hardy-Weinberg equilibrium in both breeds. In Pirenaica breed, TG gene was the only gene that affected IMF content (P=0.03). The CT genotype had greater IMF content than the CC one (1.50 vs 0.70%, respectively; P=0.03), after the Bonferroni adjustment. These results are in agreement with other authors that found similar results in German Holstein and Charolais breeds. In Parda de Montaña breed, IMF content was affected by 2 SNPs in CAPN1gene: g.1845653 T>C (P=0.03) and g.1843665 G>A (P=0.05). IMF content of TT was greater than that of CT genotype (1.91 vs 1.49%, respectively; P=0.02) for g.1845653 T>C. In g.1843665 G>A, AA genotype tended to have greater IMF content than AG and GG genotypes (2.09, 1.65 and 1.65%, respectively; P>0.10). These results are consistent with those found by others authors suggesting an association between the CAPN1 gene and IMF and marbling in several beef breeds. The lack of consistent candidate gene effects between breeds could indicate that association between markers and IMF content could be influenced by different genomic backgrounds. Thus, different polymorphisms should be used to predict IMF content in each breed.

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