Development of High-Density SNP Markers for Evaluating Genetic Diversity and Population Structure in Pingwu Red Chicken

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Abstract

Broilers supply humans with an abundance of high-quality chicken, and the utilization of local poultry genetic variety is crucial for the development of high-performing and efficient broiler breeders. Pingwu red chicken is an outstanding native poultry genetic resource in Sichuan Province, yet research on Pingwu red chicken DNA polymorphism lags behind that of standard broiler breeds. To uncover the genetic variety of Pingwu red chickens, blood genomic DNA from 18 Pingwu red chickens was extracted, and high-throughput locus-specific amplified fragment sequencing (SLAF-seq) was utilized for SNP marker analysis and phylogenetic tree construction. To investigate the genetic evolutionary relationship of Pingwu red chickens, a total of 952,944 high-quality SNPs (integrity > 0.5 and MAF > 0.05) and SLAF fragments were gathered, according to the study. This study successfully uncovered the genetic foundation of Pingwu red chicken, indicating the existence of three tiny clusters across all samples. Specific-length amplified fragment sequencing (SLAF-seq) is a high-resolution technique for identifying and genotyping de novo SNPs. This study concludes that slaf-seq is an effective method for revealing the genetic variety of Pingwu red chickens and provides a scientific basis for its use in Pingwu red chicken evolution.

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