

Whole-genome Resequencing Identifies Candidate Genes Regulating Tail Fat Deposition in Two Indigenous Sheep Breeds

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Abstract

Excessive tail fat buildup will lower feed utilization efficiency, disrupt insulin sensitivity and weaken reproductive performance of sheep. The hidden genetic drivers that create distinct tail fat phenotypes between long-fat-tailed local sheep breeds and short-fat-tailed counterparts still lack systematic clarification. This research intends to screen vital genes regulating tail fat lipid metabolism via phenotype contrast between Lanzhou fat-tailed sheep with long fat tails and Hu sheep featuring short fat tails. We selected 15 healthy adult sheep individuals from each breed to conduct whole-genome resequencing. Three mainstream selection signal detection metrics including fixation index, cross-population extended haplotype homozygosity and cross-population composite likelihood ratio were jointly adopted to pinpoint differentiated genome segments, followed by GO functional annotation and KEGG pathway enrichment analysis. Seventy-five genome regions with notable selection pressure were screened out, eight candidate genes were repeatedly detected across all three analytical pipelines. Among these candidates, DAB1 and GPC5 had prominent enrichment on lipid metabolism biological processes. Existing functional research confirms DAB1 accelerates adipocyte differentiation relying on the PI3K-AKT signaling pathway, while GPC5 restricts lipid accumulation through suppressing the Wnt/ β -catenin pathway; the two genes collaboratively shape breed-specific tail fat fatness differences. The two screened core genes supply reliable molecular markers for indigenous sheep germplasm preservation and marker-assisted selective breeding practice.

Keywords

Tail Fat Deposition, Whole-genome Resequencing, Selection Signature, Lipid Metabolism, Dab1, Gpc5