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Investigation of metabolic pathways of genes related to the QTL of reproduction traits in sheep genome using gene network and gene ontology

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Abstract

Naturally, Fertility characteristics such as ovulation rate, litter size, total number of lambs born, stillbirth and age at first puberty are regulated by different genes with different effects in sheep and all have a significant impact on the economy of the sheep industry. The development of DNA-based marker technology and genomic tools opened an opportunity to identify and annotate functional genes associated with economic traits. In this study, QTLs related to fertility in sheep were prepared through AnimalQTL database. The genes for each QTL were then obtained from the sheep reference genome in the NCBI database. Then, in order to understand the relationship between the obtained genes, gene networks for each trait were drawn using Cytoscape_v3.8.0 software, and finally, Cytoscape software was used to interpret gene networks and study gene ontology. The results of this study showed that there are a total of 124 QTLs for the parasite resistance trait that are controlled by 388 genes. Most of these markers were mapped using methods such as the Genome-Wide Association Study (GWAS), Regional Heritability Mapping (RHM), or Single Nucleotide Polymorphisms (SNPs). Ontological analysis showed 32 biological pathways related to this trait in sheep and some pathways contributed more than others were including: positive regulation of organelle assembly, positive regulation of canonical Wnt signaling pathway, smoothed signaling pathway, neuron fate commitment, NF-KappaB binding, ovulation cycle process, regulation of viral life cycle. In this study, the ontology of genes was investigated and the metabolic pathways associated with the reproduction trait in sheep were obtained through experimentally validated QTL reports. To our knowledge, this was the first study pointing out the related pathways from known and valid QTLs. This method could be applied for other traits as well.

Key Words: *Ontology, QTL, Marker, Fertility*