A scan for signatures of selection in Russian Romanov sheep breed based on ROH hot spots analysis

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Introduction. The world-famous Romanov breed of sheep fits easily into different production systems including private households, smallholders, and large farms. Such a resilience and extraordinary reproduction traits combining with good meat qualities have made the Romanov breed as a choice to produce mutton in the Central Russia regions. However, little is known on genetic mechanisms underlying the complex of specific traits of this breed.
In this regard, we performed a scan of signatures of selection by identification of runs of homozygosity (ROH) islands in the Romanov sheep population

Materials and Methods

- 48 samples of the Romanov sheep
- Genotyping using Ovine Infinium® HD SNP BeadChip (Illumina, CA, USA).
- ROHs were estimated in the R package "detectRUNS" using window-free method for consecutive.
- The ROH shared in more than 50% of sheep were considered as ROH islands.
- Annotation using Ensembl genome browser 103.
- Enrichment for functional categories using DAVID tool.

Results. More than 88 SNPs were found in ROH islands located on OAR1, 10, 11, 13, 14, 15, 16, 17 and 18.
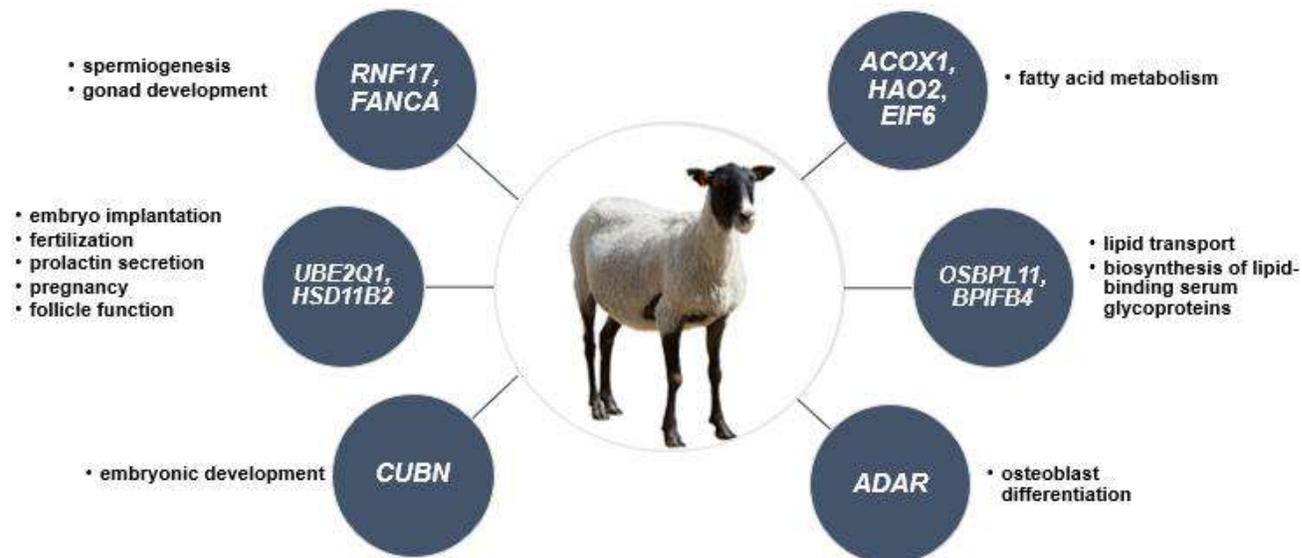
We detected a major group of genes related to reproduction traits (*UBE2Q1*, *RNF17*, *HSD11B2*, *FANCA*, and *CUBN*).

In addition, several identified genes were involved in lipid metabolism (*ACOX1, HAO2, EIF6, OSBPL11, and ADAR)*.

The studies will be continued on a larger sample with further validation of the most promising candidate genes.

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