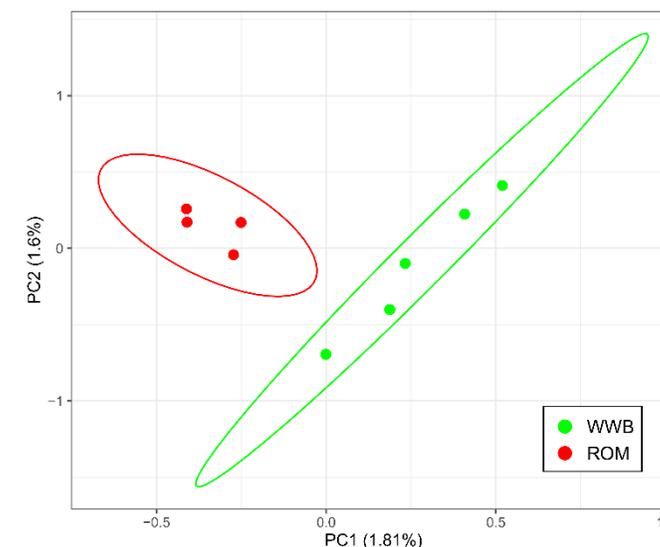


Identification of candidate SNPs associated with high prolificacy in Romanov sheep

Shakhin A.V.¹, Dotsev A.V.¹, Deniskova T.E.¹, Brem G.^{1,2}, Zinovieva N.A.¹

Prolificacy is a very important trait in sheep. Romanov sheep – is the world-wide known Russian sheep breed, which is characterized by very high prolificacy, however the genetic basis of this unique property of Romanov sheep is still unknown. It was reported that Ovine *BMPR1B* gene, located on the OAR6, is associated with prolificacy in several sheep breeds. The aim of our study was to identify candidate SNPs within *BMPR1B* gene, related to prolificacy. To achieve this goal, using NGS technology, we sequenced ovine *BMPR1B* gene in Romanov sheep (n=6), which are characterized by high prolificacy (about 270 lambs per 100 ewes). The sequences of *BMPR1B* gene of Noire du Velay, Tan, Southdown and Australian Horned Merino sheep breeds as well as Asiatic mouflon (n=1), which are characterized by significantly lower prolificacy (from 110 to 180 lambs per 100 ewes) were derived from publicly available sources and used for comparison. F_{ST} analysis performed in PLINK 1.9 program revealed 10 SNPs with values higher than 0.8. The majority of candidate SNPs under putative selection were localized in the region from 29,382,098 to 29,430,387 on OAR6 of Ovine reference genome (Oar_v3.1 (Ensembl release 98)). Thus, we can suggest, that this region of *BMPR1B* gene can be considered as the putative region, associated with high prolificacy of Romanov sheep. Additional studies will be needed to confirm the effect of identified candidate SNPs on prolificacy traits. The research results will be useful for artificial selection of sheep with higher prolific capacity, including introduction of desired alleles in sheep populations using genome editing technologies. This work was supported by the Russian Ministry of Science and Higher Education No. 0445-2019-0024 and RFBR No. 20-516-56002.

Keywords: *Ovis aries*, single nucleotide polymorphism, *BMPR1B* gene



Principal component analysis

¹ L.K. Ernst Federal Science Center for Animal Husbandry, Moscow, 142132 Podolsk, Dubrovitsy 60, Russia

² Institute of Animal Breeding and Genetics, University of Veterinary Medicine, Veterinärplatz 1, A-1210, Vienna, Austria