Summary

The American mink (*Neogale vison*, previously known as *Neovison vison*) is a carnivorous mammal species from the *Mustelidae* family. In Europe, it occurs in both wild and farmed forms. Due to the aesthetic qualities of its fur, minks are bred as fur animals. Increasing costs and emerging diseases have been the main zootechnical challenges in mink farming in recent years.

Viral diseases reduce farming profitability and compromise animal welfare. A common disease of American mink is Aleutian Disease (AD), a chronic and incurable condition caused by the Aleutian Mink Disease Virus (AMDV). AD poses a significant threat as it leads to severe immunosuppression, acute progression, and high mortality among mink kits. The ease of viral transmission and its environmental persistence considerably hinder efforts to eliminate the pathogen from farms, necessitating the search for specific prophylactic measures. However, all attempts to develop an effective AMDV vaccine have failed (Markarian & Abrahamyan, 2021). The lack of specific prophylaxis highlights the need for strategies to mitigate breeding losses due to AD. One possible strategy is genetic selection for increased resistance to infection.

Karimi et al. (2021a) investigated signatures of selection in response to AMDV infection and identified genes that could serve as prognostic markers of minks' immune response to AMDV. These genes are strong candidates for selective breeding of minks tolerant to AD. The identified genes, *SRSF5*, *RNF165*, and *SKOR2*, are located in two genomic regions comprising contigs from whole-genome sequencing: scaffold 1: 23,046,774–23,187,210 bp and scaffold 2: 23,424,424–23,969,935 bp.

Based on the literature, *SRSF5*, *RNF165*, and *SKOR2* were selected from Karimi et al.'s (2021a) study for further analysis. The *SRSF5* (*Serine and Arginine Rich Splicing Factor 5*) gene is involved in RNA splicing processes, which are potentially critical in regulating the expression of genes involved in antiviral responses. The *RNF165* (*RING Finger Protein 165*) gene, acting as a ubiquitin ligase, may influence the degradation of viral proteins, while *SKOR2* (*SKIFamily Transcriptional Corepressor* 2) functions as a transcriptional corepressor regulating immune signaling pathways. Sequencing these genes revealed single-nucleotide polymorphisms (SNPs) in all the studied genes.

In the conducted study, several polymorphisms were identified. In the *SRSF5* gene, these included a 173A>C transversion, a 758ins.T insertion, and a nonsynonymous 916G>T mutation (p.S229I) in farmed minks. The *RNF165* gene exhibited two polymorphisms: one

synonymous at position 141A>G and one missense mutation at 596A>G (p.R199K). The *SKOR2* gene contained two nonsynonymous mutations at positions 3000A>T (p.K1000N) and 3017A>G (p.H1006R).

A divergence was observed between the high-throughput sequencing (NGS) results from the Ensembl database and those obtained using the Sanger sequencing method in the analyzed genes. Genetic polymorphisms were found to impact the functional effects of the encoded proteins, leading to potential changes in their structure or function. Moderate functional effects were observed for the SRSF5 916G>T (p.S229I) and RNF165 596A>G (p.R199K) polymorphisms. For the *SKOR2* gene, a negative functional effect was associated with the 3000A>T (p.K1000N) polymorphism, while a neutral effect was linked to the 3017A>G (p.H1006R) polymorphism.

Keywords: American mink, Aleutian Disease, genetic markers of immunity, *SRSF5*, *RNF165*, *SKOR2*