## Investigating the RYR1 gene in pigs: A bioinformatic approach

This example aims to show how to find and analyze *the RYR1* gene in pigs using a genomic database. The *RYR1 gene* plays a significant role in regulating calcium release during muscle contraction and relaxation. Students will learn to navigate the genomic database and use various bioinformatics tools to obtain relevant genomic information, including gene sequence, functional annotations, and conserved domains. This exercise will contribute to a better understanding of gene exploration in the context of bioinformatics and its potential use in animal genetics.

Materials:

- 1. Computer or laptop with internet access
- 2. Genomic online databases (e.g. Ensembl <u>http://www.ensembl.org/index.html</u>, NCBI <u>https://www.ncbi.nlm.nih.gov/genbank/</u>)
- 3. Relevant bioinformatics tool for paired alignment: ~ BLAST <u>https://blast.ncbi.nlm.nih.gov/Blast.cgi</u>,
- 4. Text editor (e.g. Word or Notepad)

Tasks:

- 1. Check the GenBank (NCBI) database for information on the *RYR1* gene in pigs.
- 2. On which pig chromosome is the RYR1 gene located and what is its position? What is his ID? What is the length of a gene?
- 3. In which tissues is the gene expressed and what are its functions?
- 4. Find the reference sequence of the *RYR1* transcript (mRNA) and analyze it the length of the transcript, how many exons and introns are there? How long is a protein coded?
- 5. From the publication Fuji et al. (1991), select the sequence with the mutation locus and find in which part of the genome sequence of the gene it is located using the BLAST tool. Identify the position of the mutation causing susceptibility to stress and the occurrence of PSE meat.