

1. The objective of the project and reasons for choosing the research topic

Recent trends in dairy farming are moving in the direction of selecting individuals with high efficiency, while maintaining good health status and the feed efficiency. As a result, we have more and more data describing the welfare and health of animals. Such features are included in the category of so called “novel traits” since they have been collected only recently, and thus their genetic background has not yet been extensively studied. The aim of this project is to analyze the genetic basis of traits describing the hoof and leg quality in the context of the causes lameness of dairy cattle with particular emphasis on epistatic effects i.e. on the interaction between pairs of genes.

2. Research steps

The data available for the analysis comprise 985 cows for which hoof and leg quality data and genotypes of 76 934 single nucleotide polymorphisms describing the genetic variability of cows are available. In addition, we have information on the exact location of polymorphisms in the genome, cows' pedigree, the cases of cows' elimination from the herd and elimination reasons, some additional information such as date of birth, or the number of completed lactations.

The first stage involves editing the data in order to identify and remove erroneous observation. Then correlations between polymorphisms expressed as linkage disequilibrium coefficient will be calculated. The next step will be to develop a function which describes the dependence of the linkage disequilibrium coefficient from the distance between polymorphisms localized on the same chromosome. These polymorphisms that deviate from the standard dependence will be selected for further investigation following the assumption that between these polymorphisms genetic epistasis exists. The next stage of the project comprises calculating the additive and dominance genetic effects of all 76 934 polymorphisms using two different statistical approaches: (a) many models, each taking into account only the effect of a single polymorphism followed by multiple testing correction taking into account the correlation between polymorphism and (b) a single model including additive and dominance effects of all polymorphisms simultaneously. These models will be used to select polymorphisms with additive and dominance genetic effects with significant impact on the variability of the analyzed traits of hoof and leg quality. The final stage of statistical modeling of the genetic variability of the quality of hoof and leg quality traits is to create a model that includes polymorphisms with significant additive, dominance and epistatic effects. In the final phase of the project for these polymorphisms we will conduct a genomic annotation, which will determine their position relative to the functional elements of the genome, such as exons, UTR regions or intergenic regions. For genes, which are marked by significant polymorphisms located within a gene in the vicinity (up to 1 000 nucleotides) of a gene we are going to determine the metabolic pathways, as defined by the databases: Kyoto Encyclopedia of Genes and Genomes as well as Reactome. By this we will try to determine which metabolic processes have an impact on the probability of occurrence of the locomotory system of cattle.