

Description for the general public

Litter size in pigs is a complex multi-factorial trait. It is affected by many physiological aspects of the condition of the animal and its genetics. So far over 50 regions in pig genome have been described as controlling litter size. However, until now only one study reported SNPs controlling the variability of this trait in pigs, but further research is needed to confirm causative mutations.

It has been observed that not only the mean of traits is under genetic control, but also variation around that mean, which is called the “phenotypic variability”. Genes that can buffer hard to predict (e.g., diseases) or avoid (e.g., changes in temperature) environmental factors are highly desirable, as those genes control the variation of a trait and maintain it on expected level. Those genes can also give the indication why some animals perform on the same level despite changes in the environment, when others do not. Thus the hypothesis of this project is that individual’s ability to buffer various environmental factors is controlled by certain genomic regions, and such regions are involved also in regulating the phenotypic variability of litter size in pigs.

This will be done by firstly addressing the background of variation between parities of the sow which will enable to fully understand the genetic basis of litter size variability, as it will allow accounting for variability between the sows and within the production lifetime of one animal. Then the animals will be genotyped and their genomes will be screened for the regions associated with phenotypic variability of litter size. Next, the most promising regions and animals with the best genotypes will be selected for the sequencing. Finally, the sequenced regions of the genome will be studied in order to detect causative mutations.

Increasing our understanding of genetic mechanisms regulating litter size and its phenotypic variability in pigs will facilitate knowledge on genetic architecture of those traits. Furthermore, detecting and confirming presence of genes associated with buffering unfavorable environmental factors will help us understand why some individuals are more susceptible to changes in the environment than others. This project is the first study aiming to detect and confirm presence of those genes in pigs. Such findings could be very important for the livestock production of the future, which needs to fulfill requirements of different conditions and production systems around the world.