

Popular science summary of the PhD thesis

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Title of the PhD thesis	Genomics and epigenomics analysis of animal production and welfare in Denmark
PhD school/Department	DTU Compute

Science summary

* Please give a short popular summary in Danish or English (approximately half a page) suited for the publication of the title, main content, results and innovations of the PhD thesis also including prospective utilizations hereof. The summary should be written for the general public interested in science and technology:

Denmark is one of the largest producers and exporters of dairy milk and pig meat in the world. However, dairy and pig farming is undergoing transformation to be even more cost-efficient and welfare-friendly, partly due to international competitions and European Union regulations. In this context, improving animal efficient production and addressing the animal welfare (e.g., avoiding surgical castration for boar taint (BT) problem) is one of the major goals in Danish farms.

For the animal production, the current study demonstrated a method for the correction of genotyping by sequencing (GBS) genotypes. The results showed that the correction increased the accuracy of GBS genotype and increased the accuracy of genomic prediction. This study also compared imputation methods for GBS genotypes and improvements in genomic predictions from the imputation of missing markers. The results showed that imputation accuracy was relatively low for GBS at a low depth (approximately 0.90 for depth = 2) and high for GBS at a high depth (approximately 0.96 for depth = 5). In addition, imputation resulted in larger gains in the reliability of genomic predictions for GBS at a low depth, which had a larger number of missing genotypes. These results suggest application of IMPUTE2 imputation based on corrected GBS to improve genomic predictions at higher depths. In addition, FImpute software could be a good alternative for practical, routine imputation because of low computational demands.

For the BT problem, we found that the methylation rates were lowest in promoters (0.15) and highest in introns (0.55). Cytosines binding to CpG islands showed different methylation patterns between intron and exon regions. Methylation levels of CpG islands were lower than CpG island shores in different genic features. This study also found the characterization of pig epigenomes/methylation changes between animals with high and low BT and genome-wide epigenetic markers related to BT levels. The correlations between the gene expression levels and methylation levels in different parts of a gene suggested that methylation potentially regulates the expression of genes, particularly genes involved in the development of BT in pigs. In turn, these results could contribute to the functional annotation of pig genomes and aid in the genetic selection of pigs for low BT in breeding programs. Finally, we identified candidate genes undergoing epigenetic modifications, namely, *CRYL1*, *DNMT3A*, *EGFR*, *FASN* and *PEMT*, in an integrative analysis of methylation profiles using reduced representation bisulfite sequencing technology and transcriptome profiles of differentially expressed genes.

Please email the summary to the PhD secretary at the department