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**Genome-wide association study in Brown Swiss for udder traits based on sequence data**

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Identification of QTL, especially of causative variants within QTL is still challenging. Higher SNP densities aid the identification and fine-mapping of QTL. Based on imputed sequence data we performed GWAS for udder traits in Brown Swiss cattle. The GWAS was performed using a mixed-model approach with deregressed breeding values as phenotypes. The traits investigated included: udder depth (UD), fore udder attachment (FUA), rear udder width (RUW), rear udder height (RUH), fore udder length (FUL), and central ligament (CL). We found significant associations on BTA 3 (UD, FUA), BTA 5 (UD), BTA 17 (FUL, RUW, CL) and BTA 20 (FUA). A single gene was located in the significantly associated regions on BTA 5 (ABCC9) and BTA 20 (HCN1). The region on BTA 17 spans almost 3 Mb and includes 74 genes (maximal region for all the traits combined) and the region on BTA 3 includes 91 genes across 3 Mb. We also looked for associated missense variants in these intervals. Neither for ABCC9 nor for HCN1 we could identify such a variant. On BTA 17 we identified 2 missense variants that were significantly associated with CL. On BTA 3, 11 missense variants were significantly associated with UD and/or FUA. The advantages of using imputed sequence data compared to SNP chip genotypes are mainly through the inclusion of potential causative variants.

## Session 01

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**Correlation between DNA methylation in CHFR gene promoter and economic traits in J. Black cattle**

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Meat quality of Japanese Black cattle (JB) is known to excel in Wagyu, and the breed has become very popular worldwide. However, the main mechanism of developing these characteristic features are not well understood although many researchers have reported SNPs and QTLs which may be related to them. DNA methylation to C in CG rich of the upstream region of start codon controls the expression of many genes on a genome wide level in relation to environmental effects. This study aims to examine a correlation between genome DNA methylation of CG rich in upstream region of CHFR gene and economic traits in JB. Samples were collected from adipose tissues around the kidneys in each 100 JB's produced from same sire. After DNA extraction and purification, EpiXplore Methylated DNA Enrichment Kit, EpiScope Promoter qPCR Array (Human), SYBR Premix Ex Taq GC (Perfect Real Time) of TAKARA and specific software were then used to analyze DNA methylation degree. The DNA methylation degree of CG rich regions in the upstream regions of CHFR gene which encodes E3 ubiquitin-protein ligase correlated significantly with subcutaneous fat thickness and rib thickness ( $r=0.66$ ). The expression of this gene is required for the maintenance of the antephasis checkpoint that regulates cell cycle. So, this gene may play a key role in cell cycle to progress weight gain and lipid accumulation. In this study, although apparent relationships between the known QTL and this gene could not be found, this information might be an effective marker for monitoring meat quality in JB.