



P0421: Ovarian mRNA and miRNA Transcriptome Profiling of Domestic Sheep Breeds

The highly prolific breeds of domestic sheep (*Ovis aries*) are valuable genetic resources for global sheep industry. E.g. the native Finnsheep is well-known for its prolific traits and has been imported into 40 countries to develop new breeds and to improve fertility of local sheep breeds. Female prolificacy traits of sheep, such as the high ovulation rate and litter size, are critical factors which effect on biological and financial performance of sheep production. To improve our knowledge of the sheep prolificacy traits, we analysed mRNA and miRNA sequences of ovarian tissues from two pure breeds with large (Finnsheep) vs. small (Texel) litter sizes and their F1 crosses. Half of the ewes in each group were fed a flushing diet in order to investigate the effect of feeding on ovulation rate. We found that among the samples, 16,402 genes (60.6% known ovine genes) were expressed. We detected 79 novel miRNAs and a cluster of miRNAs on chromosome 18. The majority of the differentially expressed genes between breeds were upregulated in the low-prolific Texel, owing to the flushing diet effect, whereas a similar pattern was not detected in the Finnsheep. F1 ewes responded similarly to Finnsheep rather than exhibiting a performance intermediate between the two pure breeds. We observed in detail the variants of four major candidate genes for prolificacy (*GDF9*, *BMP15*, *BMPR1B* and *B4GALNT2*) identified previously in sheep. None of the previously studied mutations at these candidate genes were present in any of the samples. Interestingly, the mutation V371M in *GDF9* (C-T transition at 5:41841285) was present in five Finnsheep and four F1 crosses but was not present in Texel. In addition, the three genes (*CST6*, *MEPE* and *HBB*) that were differentially expressed between the group of Finnsheep and Texel ewes kept in normal diet appeared to be candidate genes of prolificacy traits and will require further validation.

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