

Genetic evaluation systems and breeding programs in sheep and goats: an international perspective

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Genetic selection has been a key tool for improving productive performance in small ruminant populations around the world, especially in Europe. This has been achieved through selective breeding for numerous traits, using diverse genetic evaluation systems and breeding schemes. Knowledge of the alternative approaches taken is paramount to the design of efficient and integrated genomic breeding programs. In this study, we summarised information on 48 sheep and goat breeding programs, genetic and genomic evaluation systems and resources available in 12 countries involved in the SMARTER project. This was done using published reports and surveys distributed to all partners. Responses to the surveys reveals information for more than 9, 16, and 20 dairy goat, dairy sheep, and meat sheep breeds involved in genetic schemes, respectively, with ~3,083,562 animals included in data collection schemes. The main groups of traits recorded across countries are: (1) milk yield and composition, mastitis indicators, udder and body conformation, and reproduction in dairy sheep and dairy goats; and (2) growth, reproduction, health, ultrasound, wool, and carcass in meat sheep. Seven countries have progeny testing schemes, but only 5 use artificial insemination. There are numerous challenges to be addressed (e.g. disparity of trait recording, SNP panels, statistical models used, joining pedigrees across countries as well as grouping breeds based on genetic similarity, and an average of ~30% of animals with unknown sires). However, there are many opportunities to use the current resources and develop collaborative approaches to optimise selection for novel breeding goals such as resilience and efficiency in small ruminants across countries.

Milk transcriptome analysis identifies genes and pathways affecting feed efficiency in dairy ewes

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Improving feed efficiency (FE) reverberates in the profitability and sustainability of dairy sheep production by reducing feed costs and environmental footprint. FE in dairy sheep has been defined as the capability of a ewe to transform the feed nutrient consumed into milk. One of the currently established indexes to evaluate FE is the residual feed intake (RFI). The specific evaluation of the milk transcriptomic profile of ewes with extreme FE phenotypes may be of particular interest to identify genes and metabolic pathways related to this trait. This study aimed to identify differentially expressed genes (DEGs) between sheep with extreme RFI values through the analysis of milk somatic cell (MSC) transcriptome. For that, RNA-sequencing was performed on RNA extracted from 14 milk samples collected from high (n=7) and low (n=7) efficient ewes. An average of 43 million paired-end reads were generated per sample. Samples were aligned against the Ovine genome assembly (Oar_V3.1) using STAR and the quantification was performed with RSEM software. The differential expression analysis, performed with DESeq2, identified 23 DEGs (FDR<0.05) between high and low feed-efficient ewes. Among them, 3 genes were upregulated (logFC≥2) and 20 genes were downregulated (logFC≤-2) in the high feed-efficient group compared with the low feed-efficient one. Interestingly, upregulated genes in high feed-efficiency sheep were associated with metabolic pathways involving lipid biosynthesis and protein secretion. In contrast, genes downregulated in high feed-efficient ewes were related to apoptotic processes, which agrees with previous results in cattle and pigs. In summary, results from this research improve our knowledge of the metabolic pathways underlying milk production-related feed efficiency in dairy ewes, which could be a first step towards improving the favourable phenotype through genetic selection. Projects EU-SMARTER & JCyL CSI276P18, FEDER and ESF.