



## W707: Broadening the miRNA Catalogue in Livestock Species

Sunday, January 14, 2018

02:30 PM - 02:50 PM

📍 Royal Palm Salon 3-4

MicroRNAs play a crucial role in the regulation of gene expression. Their action is crucial in many biological processes and functions, such as cell development and differentiation, and in response to disease. Moreover, it has been shown that polymorphisms in miRNAs can be linked to diseases and complex traits. An improved annotation of miRNAs in domestic animals is therefore required in order to acquire a comprehensive understanding of their impact on livestock traits. For this, we used 328 quality approved small-RNA-seq datasets available from public repositories for five livestock species (*Gallus gallus*, *Sus scrofa*, *Equus caballus*, *Ovis aries* and *Bos taurus*). The data was used to quantify miRNA expression in different tissues as well as to identify putative novel miRNA candidates. For *Bos taurus*, our analysis allowed an increase of 50% of the total miRNA catalogue currently available. Interestingly, for *Ovis aries*, we have identified a large number of putative novel miRNAs that share the seed with pre-existing miRNAs in other species. Currently we are studying the miRNA convergence at the functional and genomic level, which will be reported along with the list of novel miRNAs. Furthermore, we are also investigating the occurrence of other types of ncRNAs, e.g. tRNAs and snoRNAs in the analyzed data, some of which are known to be processed into miRNA. We have created a comprehensive ncRNA annotation for the studied species as well as interspecies pairwise and multiple genome-wide alignments. We believe these findings will further contribute to the understanding of the functional genome of the studied species.

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