

Gene expression analysis of duck liver steatosis from hybrid and parental species

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Liver steatosis can occur spontaneously in wild waterfowls as a result of energy storage before migration. This ability is exploited since thousand years in domesticated birds to produce "foie gras" by overfeeding. However, different abilities for fatty liver production are known according to species. Common ducks "Pekin" (*Anas platyrhynchos*) have a lower ability when compared to Muscovy ducks (*Cairina moschata*) and to mule ducks (interspecific hybrids produced from a male Muscovy duck and a female common duck), mule ducks representing more than 95% of the foie gras production. To better describe the mechanisms involved in hepatic steatosis development and differences between species and hybrids, next-generation sequencing (NGS) and analyses can be performed on RNAs extracted from the livers of Pekin and Muscovy duck species and of their reciprocal interspecific hybrids, mule and hinny ducks fed ad libitum or overfed. Usually, such RNA-seq analyzes involve the mapping of reads on a reference genome. However, when two different species are involved some mapping biases could be expected. Thus, alternative methods must be developed to be more appropriate for transcriptome analyses and comparisons between the two species and their hybrids.

The whole transcriptomic project includes 80 Illumina paired-end libraries with a read length of 100bp. The raw dataset for each of the 4 species was assembled independently using Trinity, including a reads cleaning process with Trimmomatic then following by an in silico reads normalization step. A global assembly of the 4 de novo transcriptomes was conducted using DRAP for constructing our reference transcriptome. Quality of the reference transcriptome was then validated with an average rate of 85% using pseudoaligner Kallisto and a Busco completeness of 97%. A functional annotation was performed using Trinotate pipelines. Differential expression analysis was conducted using TMM normalization counts in gene level by DEseq2 and edgeR.

Analyses using both reference genome and de novo methods point out a good performance of the de novo method for the different species treatment revealing a new set of genes differentially expressed.

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