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Genome specific expression in the liver of mule and hinny duck hybrids

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Among different duck genetic types, Muscovy and especially mule ducks are the only ones involved in fatty liver production. Mule ducks are hybrids from male Muscovy ducks (*Cairina moschata*, *Cm*) and female common ducks (*Anas platyrhynchos*, *Ap*). They benefit from a heterosis effect on feed ingestion capacity and fatty liver weight and thus they account for 95% of fatty liver production. Conversely, common ducks and hinny hybrids (male common duck X female Muscovy duck) are not used to produce fatty liver.

In order to better characterize these reciprocal hybrids, genome specific expression was analyzed. RNA sequencing was conducted in the liver of common, Muscovy, mule and hinny ducks fed ad libitum or overfed (n=10). SNPs with genome specific alleles were selected in common and Muscovy duck RNA sequences by discospn++, a *de novo* assembly method that does not require a reference genome. Sequence reads corresponding to the two alleles of genome specific SNPs were then counted in RNA sequences from mule and hinny hybrids. These counts were considered as expression levels.

Only three loci were found to be expressed in a strict genome specific manner. They were localized in the mitochondrial genome and, as expected, the maternal allele of the hybrids was found to be expressed.

Interestingly, some genes were also found to be expressed with allelic imbalance, i.e. the ratio of *Ap* allele expression on *Cm* allele expression being < 1 in at libitum fed and > 1 in overfed ducks or conversely > 1 in at libitum fed and < 1 in overfed ducks, pointing out orthologue genes with and without regulation by (over)feeding.

In conclusion, genome specific expression and allelic imbalance could be observed in duck hybrids, strongly suggesting regulatory divergence between parental alleles.