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► To cite this version:

Céline Bourdon, Mekki Boussaha, Marie-Pierre Sanchez, Thierry Tribout, Rachel Lefebvre, et al.. Identification and characterization of microRNA genetic variants in dairy cattle, from their detection to the analysis of their biological impacts. Plant and Animal Genome Conference (PAG), Jan 2019, San Diego, United States. hal-03812528

HAL Id: hal-03812528

<https://hal.inrae.fr/hal-03812528>

Submitted on 12 Oct 2022

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***Identification and characterization of microRNA genetic variants in dairy cattle,
from their detection to the analysis of their biological impacts***

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Genomic selection is now widespread in bovine species, leading to the selection of animals through their Estimated Breeding Value (EBV), taking into account relevant traits. The addition of causal mutations to anonymous genetic markers could improve EBV accuracy. To participate in this improvement in a dairy context, genetic variants of microRNAs expressed in mammary gland and localized in dairy QTL were studied in bovine.

Starting from millions of genetic variants from whole genome sequencing data, we selected those i) in a genomic region significant for dairy traits and ii) in a microRNA expressed in mammary gland. Three of them were validated thanks to GWAS data, with a validated link between genotype and phenotype. Biological impacts of the validated variants were analyzed according to their expected effect. The expression level of the microRNA was studied if its biogenesis was thought to be impacted, and the expression levels of targeted mRNAs was studied if the impact was expected on the microRNA/mRNA recognition. Notably, modifications of targeted mRNAs expression levels were observed, emphasizing the impact of a single nucleotide change in the mRNAs recognition.

These steps lead to an integrated pipeline for the analysis of microRNA genetic variants. Thanks to its validation through the achieved results, the developed approach will be applied to ovine and caprine datasets.