



**HAL**  
open science

## Using sequence variants to better characterize a QTL region and improve the accuracy of genomic evaluation in Saanen goats

Estelle Talouarn, Isabelle Palhière, Marc Teissier, Philippe Bardou, Hélène Larroque, Virginie Clément, Gwenola Tosser-Klopp, Rachel Rupp

### ► To cite this version:

Estelle Talouarn, Isabelle Palhière, Marc Teissier, Philippe Bardou, Hélène Larroque, et al.. Using sequence variants to better characterize a QTL region and improve the accuracy of genomic evaluation in Saanen goats. ISGC and IGGC Virtual Meeting, Jun 2021, Toulouse-Dunedin, France. hal-03817609

**HAL Id: hal-03817609**

**<https://hal.inrae.fr/hal-03817609>**

Submitted on 17 Oct 2022

**HAL** is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

## 20. Using sequence variants to better characterize a QTL region and improve the accuracy of genomic evaluation in Saanen goats

Estelle Talouarn<sup>\*</sup>, Isabelle Palhière<sup>\*</sup>, Marc Teissier<sup>\*</sup>, Philippe Bardou<sup>†</sup>, H  l  ne Larroque<sup>\*</sup>, Virginie Cl  ment<sup>‡</sup>, Gwenola Tosser-Klopp<sup>\*</sup>, Christ  le Robert-Grani   and **Rachel Rupp**<sup>\*</sup>

<sup>\*</sup> GenPhySE, Universit   de Toulouse, INRAE, ENVT, F-31326 Castanet-Tolosan, France

<sup>†</sup> Sigenae, INRAE, F-31326 Castanet-Tolosan, France

<sup>‡</sup> Institut de l'  levage, F-31326 Castanet-Tolosan, France

The objective of this study was to assess the usefulness of sequence data in Saanen goats (N = 33) to better capture a QTL on chromosome 19 (CHI19) associated with production, udder type and SCS in order to improve the accuracy of predictions and fine map the QTL

A total of 1,207 50k genotypes were imputed to the sequence level. Four scenarios, each using a subset of CHI19 imputed variants, were tested. Sequence derived information included all CHI19 variants (529,576), all variants in the QTL region (22,269), 178 variants selected in the QTL region and added to the updated 50K chip, or 178 randomly selected variants on CHI19. Best overall results were obtained using ssGBLUP on 50k genotypes completed with all variants in the QTL region with +6.2% average increase in accuracy for nine traits (and up to +17.9% for fat yield). Using all CHI19 variants led to an overall decrease of 4.8% in prediction accuracy. The updated chip improved genomic evaluations by 3.1% to 6.4%.

No obvious candidate mutation was identified for the QTL. Phasing imputed sequence variants the region of the QTL highlighted a haplotype however that was present in Saanen (50 %) but almost absent in Alpine. This haplotype was associated with pleiotropic phenotypes : large animals with good production and less favorable udder type. The Alpine like haplotype showed opposite profiles: smaller animals with good udder type and less favorable milk production.

Altogether, using QTL-region variants imputed from sequence data offered a promising perspective for improving genomic evaluation and using QTL information in breeding schemes.