



Inclusion of candidate mutations in genomic evaluation for French dairy cattle breeds

Pascal Croiseau, Chris Hozé, Sebastien Fritz, Marie-Pierre Sanchez, Thierry Tribout

► To cite this version:

Pascal Croiseau, Chris Hozé, Sebastien Fritz, Marie-Pierre Sanchez, Thierry Tribout. Inclusion of candidate mutations in genomic evaluation for French dairy cattle breeds. 69. Annual Meeting of the European Federation of Animal Science (EAAP), Aug 2018, Dubrovnik, Croatia. hal-02948756

HAL Id: hal-02948756

<https://hal.inrae.fr/hal-02948756>

Submitted on 25 Sep 2020

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.

Inclusion of candidate mutations in genomic evaluation for French dairy cattle breeds.

Pascal Croiseau¹, Chris Hozé^{1,2}, Sebastien Fritz^{1,2}, Marie-Pierre Sanchez¹, Thierry Tribout¹

¹ *GABI, INRA, AgroParisTech, Université Paris Saclay, F-78350 Jouy-en-Josas, France*

² *Alice, F-75012 Paris, France*

The 1000 Bull Genomes project offers an excellent opportunity to move from QTL detection to causal mutation identification. In this aim, all French genotyped animals were imputed to the sequence level and we performed GWAS for all the available traits in the three main dairy cattle breeds (Holstein, Normande and Montbéliarde). Based on the results of these analyses, main candidate mutations were selected and designed on the custom part of the 6th version of the EuroG10K SNP chip (10KV6).

The aim of this study was to assess whether the use of the genotypes for these candidate mutations could improve the accuracy of genomic predictions, compared to the use of the Illumina Bovine SNP50BeadChip® (50K). For that purpose, the pool of genotyped animals was split into training and validation populations. The three following alternative scenarios were compared to the reference situation (use of the 50K chip):

- Virtual 50K chips (V50K) were designed by replacing all or part of the 50K by candidate mutations identified from GWAS on imputed sequences from the run4 population of the 1000 Bull Genome project. Different strategies to define these V50K were proposed (scenario 1).
- The 50K was augmented with the candidate mutations of the custom part of the 10KV6 chip. The genotypes of the bulls for these latter SNP being imputed using as reference population either the run4 population of the 1000 Bull Genomes project (scenario 2) or the animals currently genotyped for the 10KV6 chip (scenario 3).

At best, the various strategies tested in scenario 1 led to very limited gains in accuracy compared to the 50K. On the opposite, scenarios 2 and 3 resulted in substantial improvement in prediction accuracy for some traits. In addition, we applied the scenario 3 on three regional dairy cattle breeds (Abondance, Tarentaise and Vosgienne) and we observed similar results.