Genome-wide study of structural variants in French dairy and beef breeds

Didier Boichard, Mekki Boussaha, Cécile Grohs, Rabia Letaief, Sebastien Fritz, Johanna Barbieri, Christophe C. Klopp, Romain Philippe, Dominique Rocha, Aurelien Capitan

▶ **To cite this version:**

Didier Boichard, Mekki Boussaha, Cécile Grohs, Rabia Letaief, Sebastien Fritz, et al.. Genome-wide study of structural variants in French dairy and beef breeds. 69. Annual Meeting of the European Federation of Animal Science (EAAP), Aug 2018, Dubrovnik, Croatia. hal-02736390

HAL Id: hal-02736390
https://hal.inrae.fr/hal-02736390

Submitted on 2 Jun 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.

Genome-wide study of structural variants in French dairy and beef breeds *M. Boussaha[1], C. Grohs[1], R. Letaief[1], S. Fritz[1,2], J. Barbieri[3], C. Klopp[4], R. Philippe[5], D. Rocha[1], A. Capitan[1,2] and D. Boichard[1]. [1]GABI, INRA, AgroParisTech, Université Paris-Saclay, Domaine de Vilvert, 78350 Jouy-en-Josas, France, [2]Allice, Maison Nationale des Eleveurs, 75012 Paris, France, [3]GenPhySE, INRA, Université de Toulouse INPT ENSAT, Université de Toulouse INPT ENVT, 52627 Castanet-Tolosan, France, [4]SIGENAE, INRA, SIGENAE, 52627 Castanet- Tolosan, France, [5]GMA, INRA, Université de Limoges, 87060 Limoges Cedex, France; mekki.boussaha@inra.fr.*

Deep whole genome sequencing coupled with the development of several computational approaches provide opportunities to investigate chromosomal alterations between individual samples across the genome. These structural variants (SVs) affect DNA segments greater than 50 base pairs and correspond to deletions, inversions and tandem duplications and translocations. Several studies revealed involvement of structural variants in phenotypic changes in many species including cattle. In the present study, we performed genome-wide study of SVs using whole-genome sequence data from 360 bulls corresponding to 20 dairy and beef breeds. Bioinformatics detection of potential SVs was performed using Pindel, Delly and BreakDancer. Predicted SVs were filtered using different strategies in order to minimize false positive results. Filtered SVs were subsequently merged in order to define potential SV regions. A panel of SV regions were genotyped using the bovine LD beadchip. Genotyping data were used for validation studies. Furthermore, a genome-wide association study (GWAS) was performed on several thousands of dairy animals in order to assess the impact of validated SVs on routinely measured traits in dairy cattle.