

Identification of homozygous haplotype compromising fertility traits in dairy sheep

Maxime Ben Braiek, Stéphane Fabre, Chris Hozé, Jean-Michel Astruc, Carole

C. Moreno

▶ To cite this version:

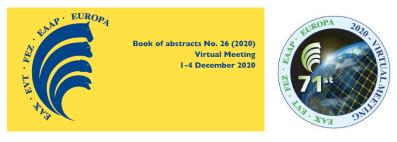
Maxime Ben Braiek, Stéphane Fabre, Chris Hozé, Jean-Michel Astruc, Carole C. Moreno. Identification of homozygous haplotype compromising fertility traits in dairy sheep. Annual Meeting of the European Federation of Animal Science (EAAP), Dec 2020, On line, France. hal-03627607

HAL Id: hal-03627607 https://hal.inrae.fr/hal-03627607

Submitted on 1 Apr 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.

Annual Meeting of the European Federation of Animal Science



Abstract n° 34261 - Theatre presentation Session 61. SMARTER: small ruminants breeding for efficiency and resilience



Date: Friday 4 December 2020; 9.00 – 11.45 Chair: Conington J. / Moreno C.

Identification of homozygous haplotype compromising fertility traits in dairy sheep

*M. Ben Braiek*¹, *S. Fabre*¹, *C. Hozé*², *J.M. Astruc*³ and *C. Moreno-Romieux*¹

¹INRAE, 24 chemin de Borde-Rouge, 31326 Castanet-Tolosan, France, ²Allice, 149 rue de Bercy, 75595 Paris, France, ³Institut de l'Elevage, 24 chemin de Borde-Rouge, 31326 Castanet-Tolosan, France; <u>maxime.ben-braiek@inrae.fr</u>

In the frame of H2020 project SMARTER no. 772787 and HOMLET (APIS-GENE, Région Occitanie) project

In livestock population under selection, the small effective size and inbreeding can cause the emergence of recessive deleterious mutations. When homozygous, these mutations may be responsible for embryo or neonate lethality, or genetic defects, affecting female fertility and animal welfare. To detect such mutations, a reverse genetic screen was applied on phased 50k SNP genotypes and pedigree data to identify Homozygous Haplotype Deficiency (HHD) in Lacaune (LAC, n=19,102) and Manech Tête Rousse (MTR, n=4,900) dairy populations. We detected 10 significant HHD, 5 presenting a complete deficit of homozygous animals (3 in LAC, 2 in MTR), and 5, a partial deficit of 79 to 96% compared to the expected (4 in LAC, 1 in MTR). These haplotypes spanned regions from 1.2 to 3.0 Mb with a frequency of heterozygous carriers between 4.4 to 17.4%. Then, we defined risky mating as mating between heterozygous rams at a HHD and females coming from heterozygous rams at the same HHD. Using logistic binary models, we tested the effect of risky mating for each HHD on two fertility traits: conception at AI and stillbirth rates. HHD in complete deficit were mainly associated with a decrease in conception rate in LAC breed and an increase of stillbirth rate in MTR breed. Only 2 HHD in partial deficit in the LAC breed were associated with an increase of stillbirth rate. Finally, we tested a putative selective advantage of heterozygous rams at the 10 HHD. The daughter yield deviation of 4 main traits (milk, fat and protein yields, somatic cell score) selected in dairy sheep in France were tested by variance analyses comparing carrier and noncarrier rams. Among the 10 HHD, 4 detected in LAC breed had significant positive impact on at least one of the selected traits. Thereafter, using available and newly generated sequence data of HHD carriers and non-carriers, we will try to identify putative causal mutations. The further management of these mutations in the LAC and MTR selection schemes will allow to improve the overall fertility and lamb viability.