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# Annual Meeting of the European Federation of Animal Science



## Abstract n° 34261 - Theatre presentation

Session 61. SMARTER: small ruminants breeding for efficiency and resilience



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Chair: Conington J. / Moreno C.

### Identification of homozygous haplotype compromising fertility traits in dairy sheep

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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 non-carrier 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.