



HAL
open science

Genome regions and metabolic processes associated with tick resistance in beef cattle

P Martin, T Hüe, J Mante, A Lescane, D Boichard, M Naves

► To cite this version:

P Martin, T Hüe, J Mante, A Lescane, D Boichard, et al.. Genome regions and metabolic processes associated with tick resistance in beef cattle. 74th Annual Meeting of the European Federation of Animal Science, Aug 2023, Lyon, France. Wageningen Academic Publishers, Book of Abstracts of the 74th Annual Meeting of the European Federation of Animal Science, 10.3920/978-90-8686-936-7 . hal-04195830

HAL Id: hal-04195830

<https://hal.inrae.fr/hal-04195830>

Submitted on 4 Sep 2023

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.

Frequency of genetic disorders in genomically tested females in the NetherlandsC. Schrooten¹ and E. Mullaart²¹CRV Cooperative, Animal Evaluation Unit, P.O. Box 454, 6800 AL Arnhem, the Netherlands, ²CRV B.V., Global Genetics, P.O. Box 454, 6800 AL Arnhem, the Netherlands; chris.schrooten@crv4all.com

In 2007, CRV started to use genomic chips to obtain genotypes of a large number of SNPs. The chips that have been used since 2014 contained SNP for the most relevant genetic disorders, with a few disorders added on later versions of the chip. Some of the disorders are lethal when animals carry both recessive alleles (for example BLAD, Bovine Leucocyte Adhesion Deficiency), whereas others are less detrimental. In this research, the development of the frequency of the disorders among genomically tested females in the Netherlands was analysed, for female animals born from 2008 onwards. Frequencies were based on real genotypes, imputed genotypes were not taken into account. Number of genotypes used in the analyses ranged from 79,000 (CVM, patent expired end of 2021) to around 500,000 for the disorders that were present on the chip since 2014. For the lethal haplotypes, HH1 and HH3-HH7, highest frequency of carriers was found for HH3 in 2012 (8.2%), HH4 in 2009 (8.3%), and HH5 in 2016 (4.8%). Frequency of carriers decreased for all HH-haplotypes, highest frequency for animals born in 2023 was observed for HH3 (2.6%). The frequency of BLAD carriers gradually decreased from 1.8% in 2006 down to 0.10% in 2022. For cholesterol deficiency haplotype (CDH), which was discovered more recently, carrier frequency decreased from 6.6% in 2015 to 1.9% in 2022. Highest carrier frequency for CVM was for animals born in 2013 (4.2%), carrier frequency for CVM in recent years was less than 1%. For other disorders, like mulefoot, citrullinemia and dumps, carrier frequencies were always lower than 0.4%. The development in frequency of carriers was favourable for all disorders studied, resulting in better health and viability, due to actively selecting against these disorders by AI organizations worldwide.

Session 28

Poster 13

Genome regions and metabolic processes associated with tick resistance in beef cattleP. Martin¹, T. Hüe², J. Mante³, A. Lescane⁴, D. Boichard¹ and M. Naves⁵¹Université Paris-Saclay, INRAE, AgroParisTech, GABI, Domaine de Vilvert, 78350 Jouy-en-Josas, France, ²Institut Agronomique néo-Calédonien, ARBOREAL, Port Laguerre, 98890 Païta, New Caledonia, ³France Limousin Sélection, Pôle de Lanaud, 87220 Boisseuil, France, ⁴Unité Néo-Calédonienne de sélection et de promotion des races bovines, Port Laguerre, 98890 Païta, New Caledonia, ⁵INRAE, ASSET, Domaine Duclos, 97170 Petit-Bourg, French West Indies, France; pauline.martin@inrae.fr

Ticks cause significant production losses in cattle and consequences of infestation can go up to the animal death. The geographical areas of the parasite keep expanding due to climate change. For these reasons, a better understanding of the genetic control and the metabolic processes involved in host resistance appears of primary importance. To address this question, regular phenotyping have been implemented in 11 commercial farms of French New Caledonia from 2014 to 2021. Six different traits were considered: score of adult female ticks, score of juvenile ticks, total score, and the logarithm of the three previous traits. A total of 556 Limousin animals and 302 Charolais animals were phenotyped, with 1 to 8 visits per animal for the Limousin breed (mean=2.3, s.d.=1.6, total=1,273), and 1 to 12 visits for the Charolais breed (mean=4.2, s.d.=2.8, total=1,281). All the animals were genotyped with the 50K EuroGMD SNPchip. First, a generalized linear model was used to correct performances by the effects of sex, age, herd, technician and period. Then, genome-wide association studies were performed with the GCTA software using an average corrected performance per animal. Five genomic regions in Charolais and 13 regions in Limousin were found to be associated to at least one trait, with two regions in Limousin being highly significant ($P < 10^{-11}$) and shared between traits. Finally, all the significant regions have been included in a Gene Ontology analysis, using the Cytoscape software. Results shows that 37 terms from 9 functional groups are overrepresented, with the three most overrepresented group being the linoleic acid metabolic process, the negative regulation of insulin secretion and the excitatory extracellular ligand-gated ion channel activity. These processes appears as a promising candidate that requires deeper investigation.