Mapping genome homozygous regions in the Avileña-Negra Ibérica breed

A. Rubio[1], M. Ramón[1], C. Meneses[2], A. Hernández-Pumar[2], M. J. Carabaño[2], C. Gonzalez[2], C. Díaz[2]

[1] *Instituto Regional de Investigación y Desarrollo Agroalimentario y Forestal de Castilla-La Mancha (IRIAF), Av. del Vino s/n, 13300 Valdepeñas.*
arjuan@jccm.es (Corresponding Author)
[2] *Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria CSIC-INIA, Ctra. de la Coruña km 7.5, 28040 Madrid, Spain.*

Summary

Several studies have reported the high reliability of runs of homozygosity (ROH) to estimate inbreeding in a population. Proportion of ROH relative to the total length of the genome is an indicator of the level of inbreeding of an individual or a population. ROHs are the result of the selection pressure as well as the low recombination events. Furthermore, ROH could be an alternative strategy to detect genomic regions related with important economic traits. This work aimed at mapping homozygous regions in the genome of the Avileña-Negra Iberica beef cattle as a tool to identify regions of low variability that could impact traits of interest such as behaviour, diseases susceptibility, fertility, meat quality or production. It is also viewed as a tool to identify positional candidate genes.

Data consisted of HD genotypes (Illumina® HD-chip) belonging to 284 animals born between 1975 and 2018. ROH were identified as regions that could contain up to 5 missing calls and 1 heterozygous, with at least 50 SNPs per 50 KB. If two consecutive SNPs were more than 1000 KB apart they were no declared part of the same ROH. These regions were classified afterwards into 3 groups according to ROH length: short (<2.5 MB), medium (between 2.5 and 5 MB) and long (>5 MB) ROHs. This classification aimed to differentiate recent and old events, since the smallest regions of homozygosity are associated with older selection events. On the contrary, larger regions of homozygosity are generally related to recent selection pressure. Finally, for each ROH identified we explored which QTLs felt into it in each animal. Only QTLS related to production (body weight at yearling, weaning and slaughter), meat quality (tenderness and meat colour), fertility (age at first calving, calving interval, sperm DNA fragmentation, early embryonic survival and age at puberty), behaviour (temperament, aggressive behaviour and adrenocorticotropic hormone level), and diseases susceptibility (IBR, BSE, TB, BVD and GD) were considered.

Results showed that abundance (number of animals with the QTL) of QTLs associated with body weight at slaughter, meat colour, age puberty, GD, temperament and aggressive behaviour increased from short to long ROH. There were no QTLs decreasing their abundance if we looked at long ranges compared to short or medium ranges. Finally, a number of QTLs associated with body weight at weaning, early embryonic survival, calving interval, age at first calving, BVD and ACTH decreased their abundance from short to medium but increased in long ranges compared to the other two. This phenomenon may be due to the fact that long ROHs occupy a large part of the genome thus, more QTLs are expected to be found within them. Many of the QTLs for a given trait were distributed in all chromosomes. However, ROHs were not observed in all of them. Nevertheless, others appeared in at least 30-80 individuals for each chromosome. The fact that the same QTL appears in ROHs of different lengths provide an insight of continuous selection process. The challenge is now to understand the impact of those ROHs on the traits.