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Evolution of ROH's distribution along the genome over a decade of genomic selection in dairy cattle

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Previous works showed that genomic selection led to an increase in annual genetic gain in major French dairy cattle breeds but, in some cases, the increase in genetic gain was linked with an accelerated loss of genetic diversity. This could have deleterious consequences on the health and performance of the breed with detrimental economic effects. This accelerated loss of diversity was assessed using Runs of Homozygosity (ROH), which represent contiguous homozygous regions of the genome assumed to result from inbreeding. On the other hand, genomic selection selects targeted regions of the genome much more precisely than genetic selection based on progeny testing only. Therefore the structure of genetic diversity should have evolved differently along the genome.

Our objectives were to understand where ROH are located and how they are structured along the genome, to understand what it can tell us about genome structure evolution and genes locations in a selection perspective.

To answer these questions, we studied the evolution over time of the positions, lengths and distributions of ROH with respect to already known selected traits determinism. Our dataset consisted in 8019 sires of three French dairy cattle breeds, Montbéliarde, Normande and Holstein, born between 2005 and 2015 for which we characterized genetic diversity all along the genome.

We observed that ROH were increasingly shared among individuals over the years within a breed. In addition, the most shared ROH tended to be older than the least shared ROH. The position of a ROH within the genome could influence their evolution over time, because of differences in recombination/selection rates along the genome.

This study was the opportunity to better understand the mechanisms of the loss of genetic diversity in selection programs and thus to develop efficient and sustainable breeding schemes limiting the loss of genetic diversity and inbreeding depression. Eventually, this new information about genes potentially linked to traits of economic interest may also be used in future genomic selection programs.