

## Annotation of selection signatures in the bovine breed Asturiana de Valles

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Past events of positive selection leave characteristic signatures in the genetic diversity of a population, which can be detected by genome-wide scans based on present time molecular data. However, determining the adaptive trait or the onset and intensity of selection at a given locus is often difficult from such data. By providing direct access to the temporal evolution of allele frequencies, the analysis of genomic data extracted from gene banks might significantly improve our understanding of selection history in livestock species. The aim of this study is to evaluate whether the analysis of genomic samples collected at different times in the recent past allows: (1) detecting recent selection events; and (2) annotating selection signatures found by classical approaches based on present time data only. To answer these questions, we considered the case study of the Spanish bovine breed Asturiana de los Valles (RAV), for which genotyping data was available for 137 animals with birth dates between 1980 and 2010. Fifteen additional RAV animals born in 2008-2013 were sequenced at ~8X coverage. These data were used to detect historical selection signatures in RAV using a classical statistic (nSL) based on a single sampling time. A new statistical approach allowing detection of selection from genomic time series was developed and applied to the combined dataset including nine distinct generations. This approach pointed out several candidate regions with a clear shift in allele frequencies over the few last generations. Besides, the analysis of recent allele frequency trajectories at nSL candidate SNPs outlined that selection at these SNPs was likely completed before 1980. Combining the time series and nSL approaches, 13 candidate regions under selection in RAV were detected, including genes related to carcass and meat traits (such as MSTN, RBPMS2 or OAZ2), immunity (GIMAP7, GIMAP4, GIMAP8), olfactory receptors (OR2D2, OR2D3, OR10A4, OR6A2) and milk traits (ARFIP1). In conclusion, these approaches were found complementary and the time series approach provided relevant new information concerning selection history in Asturiana de los Valles.