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Genomic Adaptation of Local Cattle Breeds in the Alpine Massif

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Understanding adaptive ability of livestock is a key factor in the context of global climate change and become a crucial focus in conservation and management for a sustainable farming in a changing environment. One way to better understand adaptation abilities is to identify genes underlying adaptation phenotypes. This goal can be achieved by genetically characterizing livestock species and detecting footprints of selection in the animal genome. The recent availability of genome-wide SNP panels allows providing background information concerning genome structure in domestic animals, opening new perspectives to livestock genetics.

In order to investigate the genetic regions with a potential adaptive role, we investigate 24 cattle breeds, (high productive specialized breeds and several autochthonous populations) reared in six different neighboring nations from East to West Alpine Massif. Several analyses have been performed to detect footprints of selection and genomic regions associated with climate variables. More precisely, using breed GPS coordinates, 4 climatic variables (annual mean temperature, annual precipitation, annual mean radiation, and annual mean moisture index) were extracted from the Climond database. In order to identify footprints of selection, a whole genome scan for adaptive differentiation were performed using Bovine 50K SNP chip genotyping data with the XtX model implemented in the BAYPASS software. In addition, across-population whole genome scans for association with the population-specific climatic variables were performed using the AUX model. Footprints of selection were detected on BTA6 and BTA18 pointing out several candidate genes (i.e. LCORL, PDGFRA, KDR and SPG7); moreover different genomic regions (on BTA 6, 10, 19 and 20) were associated with annual mean radiation. Ongoing analyses will specify candidate regions and genes involved in local adaptation in the Alpine massif.

Acknowledgements

The research was funded by the National Institute of Agronomic Research (INRA AIP “Bio-Ressources”, BOVDIV project)