Local and genome-wide admixture levels in cattle indicate selective sweeps

Anamarija Frkonja¹, Urs Schnyder², Ino Curik³, Johann Sölkner¹

¹University of Natural Resources and Life Sciences Vienna, Department of Sustainable Agricultural Systems, Division of Livestock Sciences, Gregor Mendel Str. 33, A-1180 Vienna, Austria (anamarija.frkonja@boku.ac.at)
²Qualitas AG, Chamerstrasse 56, Ch-6300 Zug, Switzerland
³University of Zagreb, Faculty of agriculture, Department of Livestock Sciences, Svetošimunska 25, 10000 Zagreb, Croatia

Summary

Large-scale genotyping of SNPs has shown great promise for identifying markers which could be linked to ancestry. In this work, we focus on the obtaining regions under selection according to F⁰ST as a measure of population differentiation. Furthermore, after obtaining region with large F⁰ST, differences in allele frequency in two pure breeds were compared. The cattle population investigated is Swiss Fleckvieh, a composite of Red Holstein Friesian and Simmental cattle with very wide range of crossing. Nine chromosomes had SNPs with very high Fst (>0.7), based on information of 100 Holstein Friesian and Simmental animals, each. The top signal both according to F⁰ST and average difference in allele frequency for every SNP in region (0.41) was found on chromosome 6, close to insulin-like growth factor binding protein 7. A total of reported 28 QTL regions are overlapping the region on CHR 6 reported here, many of them responsible for milk yield and composition. Even more (36) QTL regions overlap another of our candidate regions on CHR 5 many of these connected to reproduction. This is indicating selective sweeps in one of the breeds.

Key words: Swiss Fleckvieh, selection signatures, local admixture