LATXA AND PREDICTION OF BREEDING VALUES

<https://www.journalofdairyscience.org/article/S0022-0302(20)30340-4/fulltext>

Latxa is a breed from Western Pyrenees with two strains based on colour, Cara Negra-black and Cara rubia-red. Black splits in two geographical areas with slight morphological differences, Euskadi (LCNEUS) and navarra (LCNNAF), cara rubia is (LCR).

They claim that breeding programs are well and show increased genetic gain (what is it exactly and how is it measured)

READ MORE Intro mentions some studies where Genetic Gain (AGG) increased slightly using SNPs compared to pedigree. Also mention genomic selection in French sheep showing improvement of rams using genomic selection (GS).

They say that 2014 legarra had some results difficult to understand and argue that is due to poor genotyping, poor modelling,

They keep talking about AI rams, what are those?

Main objective: check the effect of including genetic info the evaluation of LCR and LCNEUS (they dont do LCNNAF)

Main result: selection of latxa using pedigri info or genetic info is the same, there is not added value yet of using genomic selection.

<https://www.sciencedirect.com/science/article/pii/S1751731117003688?via%3Dihub>

REVIEW of genomic selection of rumiants using SNP chips

<https://www.journalofdairyscience.org/article/S0022-0302(14)00204-5/fulltext>

first study of implementation of GS in pyrynee breeds (2014 legarra) including laxa and French breeds, showed gain in accuracy (estiation of breeding values more reliable) when using GS in some breeds, but not in latxa. READ MORE, do they do machine learning somewhere? They mention PCA on introduction

<https://gsejournal.biomedcentral.com/articles/10.1186/s12711-018-0426-6>

statistical methods used to predic breeding values and phenotypes.

<https://academic.oup.com/genetics/article/200/2/455/5936198?login=false>

metafounders theory to better model and predict genetic relatioonships and genetic values when pedigri info is missing.

WGS AND AGRONOMICAL TRAITS LOCI

<https://www.nature.com/articles/s41467-020-16485-1>

WGS of Ovis orientalis (wild sheep) and Ovis aries (domestic sheep) identify NSmut and genes with CNV possibly related to domestication

They use **Muflon** (wild ancestor), **landraces**(domestic without selection, only adaptation to local habitat, like latxa or Manech breeds), and **improved breeds** (exhaustive breading like Merino for wool or Dorset for meat)

From genes selected on previous studies with known functions (check supplementary data for gene list) they find NS-SNPs in 59 genes , and significan differences in *PDE6B*, *BCO2*, *ADAMTSL3*, *NKX2-1*, and an olfactory receptor 51A4-like gene *LOC101108252* and distinct genotype pattern in *LOC101108252 between* muflon and landraces

They also find CNV in genes associated with domestication, and deletions

Identify PDGFD for tail configuration differences

Also, identification of putative genes involved in reproduction, milk yield, wool fineness, meat production, and growth rate as well as for morphological traits

<https://academic.oup.com/mbe/article/39/2/msab353/6459180>

Very similar to work above, with some updates 🡪 Genes involved in wool production and focus on origin of wild and domestic Asian sheep breeds. Better introduction than previous paper.

<https://www.sciencedirect.com/science/article/pii/S0022030216302703>

RNA seq of milk somatic cells from Asaf breed and churra breed.

Check 77 transcripts related to cheese yield

Identify 9 genes (*CTSL*, *CTSK*, *KLK10*, *KLK6*, *SUCNR1*, *SERPINE2*, *FABP4*, *HSP70*, and *HSPB8*) that are significantly differentially expressed between the 2 breed, possible implication into differences in milk yield and quality traits.