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Genomia: across-Pyrenees genomic selection for dairy sheep

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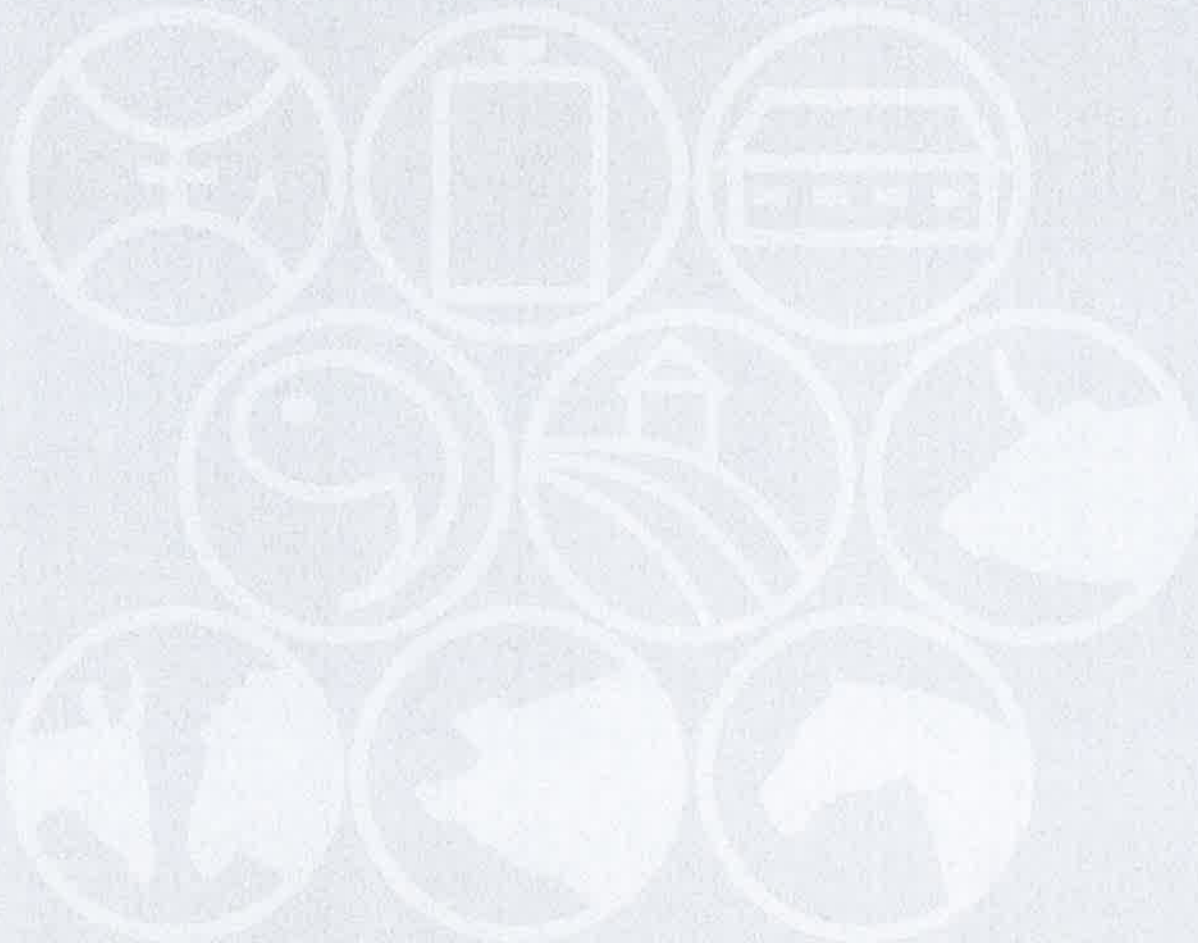
Dairy sheep breeds Latxa (in Spain) and Manech (in France), divided into blond and black strains, are the object of 5 independent selection programs since the 80's/70's. These populations, comprising 164,000 females and a few hundred AI males on the whole, originate in the same ancestral across-borderline breed; frequent Latxa-Manech exchanges occur, in particular in the Blond Face strain, albeit not in a systematic way. The advent of genomic selection has raised the interest of a systematic sharing of resources of these breeds. European Union FEDER funds, through POCTEFA (<http://www.poctefa.eu/>) finances a project called GENOMIA, whose aim is to investigate the possibilities of a joint, international, breeding scheme. Particular focus is given to: description and analysis of the existent schemes; exchange of genetic material; study of sanitary issues for systematic exchange of AI doses; genomic selection. Current similar points involve traits of interest (milk yield) and methodologies (data recording, AI-based selection, BLUP-based evaluation). Current disagreements involve different recording systems for milk composition and type traits, and emphasis on resistance to Scrapie, that has been heavily selected for in Manech whereas in Latxa it is not a major concern. Concerning genomic selection, plans are genotyping ~1400 progeny-tested rams by country, in order to assess, by cross-validation, the accuracy of across-country genomic evaluations and the interest of using both populations together.

Heritability estimates for *Mycobacterium avium* ssp. paratuberculosis in fecal tested German Holstein cows

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Paratuberculosis (ParaTB) or Johne's disease caused by *Mycobacterium avium* ssp. paratuberculosis (MAP) is a chronic enteritis in cows which leads to high economic losses. The world wide classical control programs are based on management arrangements and culling of infected animals. Breeding for disease resistance will be an additional useful tool to inhibit the distribution of ParaTB. Therefore, we estimated the heritability for occurrence of ParaTB based on fecal culture. On the basis of 11,285 German Holstein herd book cows originated from 15 farms we determined heritabilities between 0.157 and 0.228. This led to the conclusion that the MAP detection by fecal culture is from interesting to control the disease as well as an appropriate feature for further genetic analyses to detect MAP associated chromosome regions.

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