

Abstract Submission Form

Title (Mr./Mrs/Dr./Prof.)

Dr

Presenting author

Marija Špehar

Institute

Institute/company: Croatian Agency for Agriculture and Food

Adress: Svetošimunska cesta 25

ZIP/Postal code: 10000

City: Zagreb

Country: Hrvatska

Insert all authors and institutions

Špehar M. (1), Astruc J.M. (2), Ramljak J. (3), Kasap A. (3)

(1) Croatian Agency for Agriculture and Food, Svetošimunska cesta 25, 10000 Zagreb, Croatia;

(2) IDELE, Castanet-Tolosan, France;

(3) University of Zagreb, Faculty of Agriculture, Department of Animal Science and Technology, Svetošimunska 25, 10000 Zagreb, Croatia

Preferred presentation

Oral

Preferred session

Session 9: WG DNA – Genomic's impact on Livestock Sustainability

Email of corresponding author

marija.spehar@hapih.hr

Title of your paper

Opportunities and obstacles of the use of genomic data in sheep breeding – large versus small populations

Insert ABSTRACT text

The objective of this paper is to draw the benefit and obstacles of using genomic data in sheep through two contrasting situations: Croatia and France. Istrian (IS) and Pag (PS) sheep are Croatian native breeds undergoing selection on dairy traits (milk, fat, and protein) based on traditional pedigree BLUP. Genetic improvement of dairy performance via selection is important for their long term productive and economic viability, while maintenance of the existing genetic variability is vital for their resilience in unpredictable future environment. Different SNP arrays have been used in many novel breeding programmes for purpose of selection and conservation, and including genomic information in existing genetic evaluation of IS and PS seems promising and beneficial, from both perspectives, selection and conservation. The intention of the stakeholders involved in genetic evaluation of these breeds is to implement the basic principles of genomic optimum contribution selection (OCS) in existing breeding program in order to provide selection progress on targeted trait/s with minimal loss of genetic variability (ultimate goal of project OPTI SHEEP, CSF, IP: 2019-04-3559). Up to now, almost the whole breeding population of IS and PS (altogether ~4,000 animals) was genotyped using the Illumina OvineSNP50K BeadChip®. Transition from pedigree based

BLUP to single-step GBLUP, and development of pipelines for routine genomic OCS are still in progress. However, prior to bigger financial investments in genotyping and picking up the best strategy for long-term OCS, many practical and scientific questions needed to be answered. Since the benefits of genomic selection heavily depend on population specific genetic parameters such as linkage disequilibrium, genetic connectedness between flocks, heritability of the traits, effective population size etc., their estimation brought to light potential benefits of genomic selection, and some weakness that need to be worked on to maximally benefit from this promising strategy. All these efforts will definitely impact long-term sustainability of IS and PS which will benefit the breeders, consumers and corresponding (dairy) industries. By showing how to optimize selection with maintenance of genetic diversity, the results could also be beneficial to other sheep and livestock breeding programs. In France, all the dairy sheep breeds have switched towards genomic selection for five to ten years, with large reference population of artificial insemination (AI) rams, from 362 in Corsica breed to 3,546 in Lacaune breed. Each year, more than 8,000 new genotypings, including all the candidate rams and also some females in flocks with no AI nor control mating, are performed with more and more affordable medium density SNP arrays. In addition to single-step genomic evaluation, genotypings are used for predicting major genes (such as scrapie) and for parentage verification and discovery. The extra genetic gain obtained with the genomic program has already permitted to include more easily novel traits, such as resistance to parasites, and will permit hopefully in the next future to include novel efficiency and resilience traits. As French populations are large, it is not feasible to genotype the whole female population, unlike the Croatian situation. In this respect, and through the comparison between those populations (large vs small populations, ancient vs recent breeding programs), we highlight similarities and differences regarding the opportunities and obstacles of the use of genomic data. We also assess how an initiative to build an EU Reference Centre (EURC) on performance testing and genetic evaluation in small ruminants could offer opportunities to better valorise genomic data, including across country evaluation, in more sheep breeds.

Enter keywords

genomic selection, genotypings, sheep, genetic variability