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## Using genomic information provided by selection schemes to assess French dairy breeds diversity

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► **To cite this version:**

Denis Laloë, Sophie Allais, Guillaume G. Baloché, Francis F. Barillet, Jérôme Raoul, et al.. Using genomic information provided by selection schemes to assess French dairy breeds diversity. 63. Annual Meeting of the European Federation of Animal Science (EAAP), Aug 2012, Bratislava, Slovakia. 476 p., 10.3920/978-90-8686-761-5 . hal-02745491

**HAL Id: hal-02745491**

**<https://hal.inrae.fr/hal-02745491v1>**

Submitted on 3 Jun 2020

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**Discovering the unique value of indigenous livestock populations: the opportunities of genomics**

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The advent of next generation sequencing and associated high throughput genome screening technologies are providing new opportunities in livestock breeding improvements. Their potential application in the areas of genetic characterization in connection to the conservation of indigenous livestock genetic resources is yet poorly documented. Human and natural selection have shaped the genetic make-up of these populations. Besides a fine understanding of haplotypes and nucleotides diversities, at individuals and populations levels, these technologies allow us unravelling the unique adaptive genetic make-up of local livestock populations to their environments and production systems. The detection of signatures of selection across the full genome is offering to stamp out the genetic uniqueness of these populations while valuing them as adaptive traits. It is applicable to reproductively isolated livestock populations, often already characterized intensively; but as well for the larger number of the non-descript indigenous livestock populations for which their genetic uniqueness remained largely hidden behind a mosaics of phenotypic diversity. We will illustrate these points through example from our work in African indigenous cattle, fancy and village chicken, ending by an advocacy of the unique value of indigenous livestock genetic diversity as reservoir of adaptations and unique research models for the mapping of the genetic control of adaptive traits.

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In France, selection programs in ruminant species are extremely efficient and a major contributor to the proficiency of the meat and dairy industries. These programs are characterized by the selection of few elite breeding animals. The drawback is a loss of genetic variability in most breeds, which means that selection programs should take into account this parameter. There is, therefore, a need to provide genetic variability indicators, on a regular basis, so that breed associations can adjust their management accordingly. The aim of the project VARUME (Genetic Variability of RUMinants and Equine species) is to set up an observatory of the genetic variability of the French ruminant and equine species, based on pedigree and molecular data. In dairy cattle and sheep, there are now numerous molecular data generated for the needs of selection programs. The project evaluates the feasibility of setting up a genetic variability observatory based on these SNP data. A first step is to define which type of indicators can be generated from SNP data in order to characterize a breed's diversity. An inventory of all the molecular (SNP) data available to build up the observatory is done, in three cattle breeds (Holstein, Montbéliarde and Normande) and two sheep breeds (Lacaune and Manech Tête Rousse). A list of the best indicators to monitor a breed's diversity is defined by testing them with the various molecular data available and evaluating their usability depending on various contexts. The indicators are also used to target males with outstanding indicators so that their semen can be transferred to the French Cryobank. Finally, the indicators are compared with the ones obtained with pedigree data.

# **Book of Abstracts of the 63<sup>rd</sup> Annual Meeting of the European Federation of Animal Science**



**Book of abstracts No. 18 (2012)  
Bratislava, Slovakia  
27 - 31 August 2012**