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12. Effectiveness of breeding programs for local breeds in the Mediterranean region and other harsh environments. (S+G, WG)

Prospects of breeding programs for small ruminant breeds in the Mediterranean region

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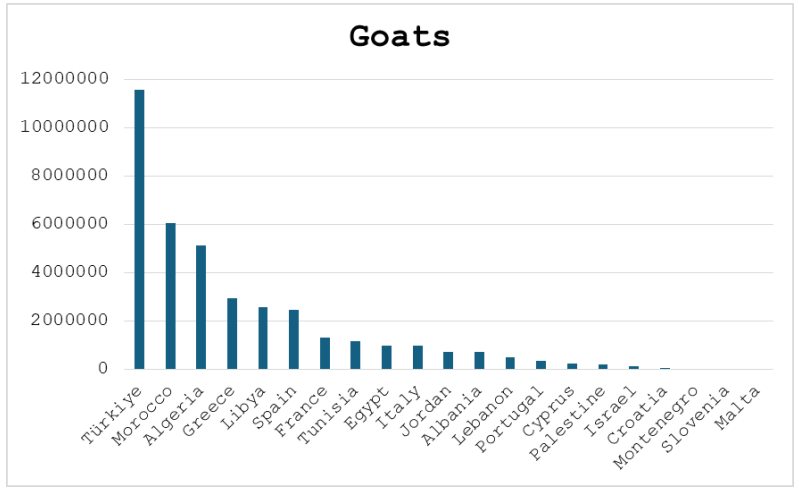
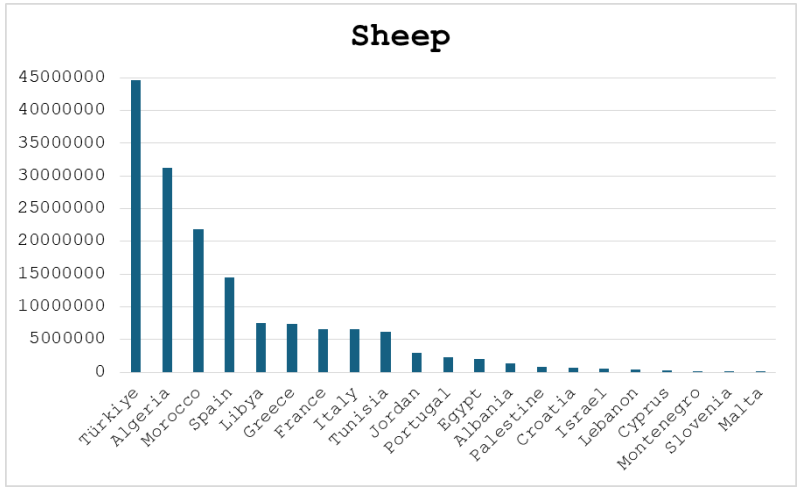
Descriptive statistics of the sheep and goat sectors in the MED area

	heads (% world)	t of Meat (% world)	t of Milk (%world)
Goat	38'348'467 (3.3%)	287'221 (4.5%)	2'837'072 (14.8%)
Sheep	158'156'174 (12.0%)	1'546'945 (15.0%)	4'527'614 (44.9%)

FAOSTAT access 10.07.2024





Important reservoir of genetic variation

Hundreds of local breeds and their crossbreds (many with small number of heads and at risk of extinction)

Few improved breeds with large number of heads spreading in other countries

Need to organize common research to effectively appreciate the contribution of the whole Med population and of single breeds to global biodiversity

Need to identify common strategies to make local breeds attractive for farmers and preserve their genetic potential to adapt to climate change





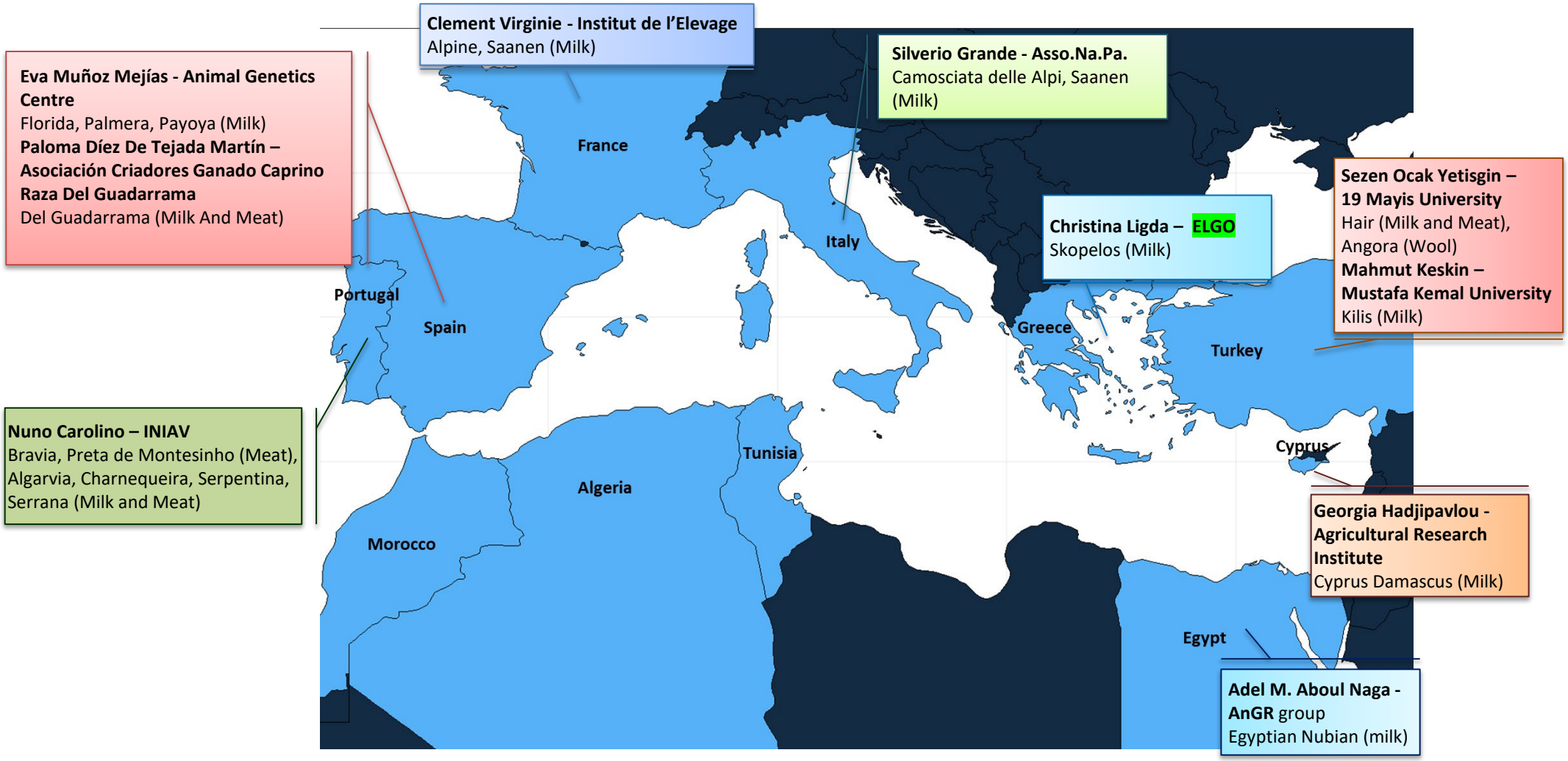
The main questions we will try to answer

1. Has the **traditional approach of selective breeding** been feasible or successful everywhere ?
2. Which is the most likely **evolution** of the breeding schemes?
3. Which approach to follow to implement **genomic tools**, innovative traits and strategies to preserve genetic variability?
4. Is the creation of a technical **reference center** useful?





Consultation through a questionnaire of 10 experts from 8 countries, 20 goat breeds



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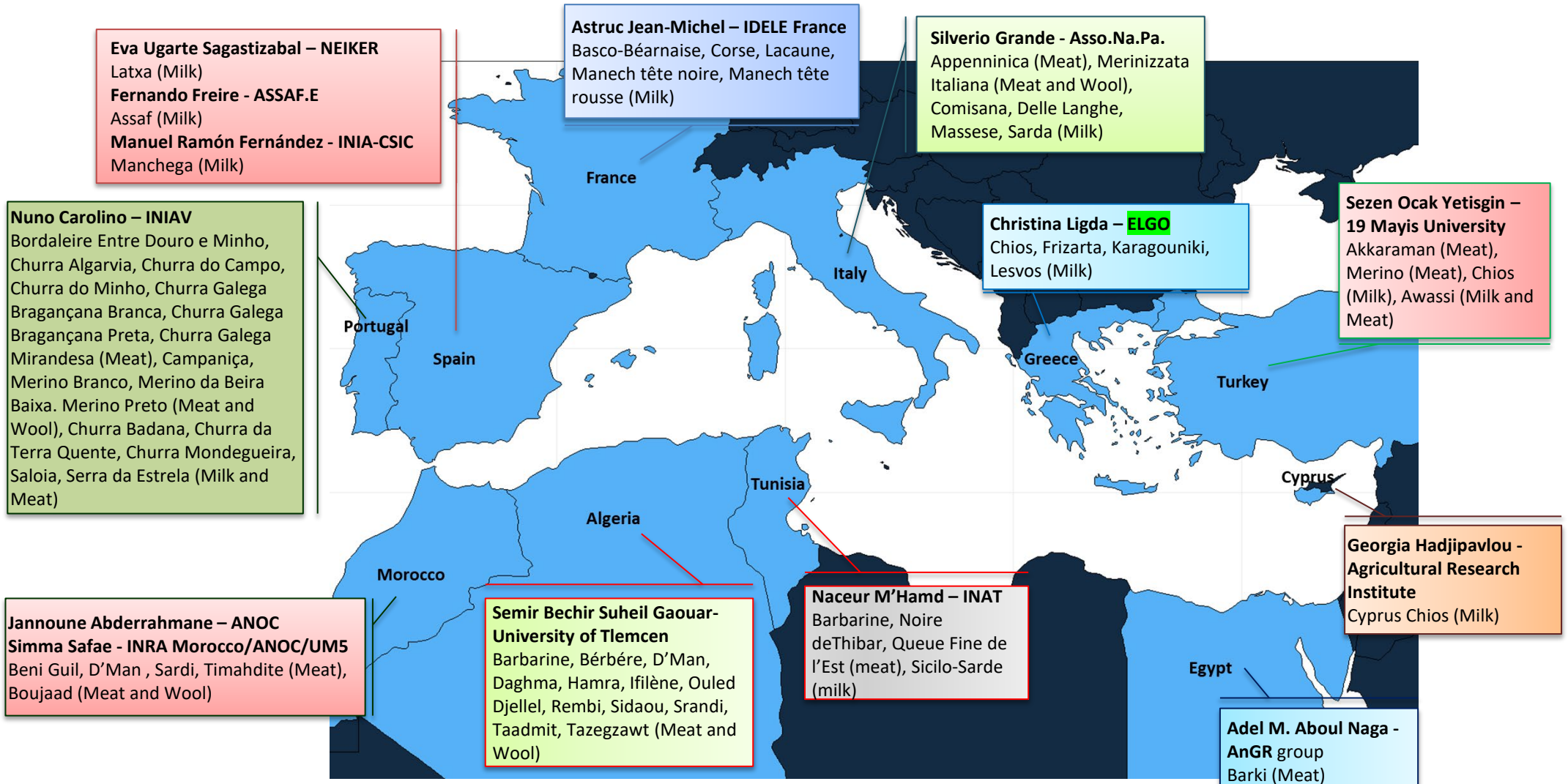
Egyptian Nubian (milk)





Consultation through a questionnaire of 14 experts

from 11 countries, 61 sheep breeds



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Christina Ligda – ELGO
Chios, Frizarta, Karagouniki, Lesvos (Milk)

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Semir Bechir Suheil Gaouar- University of Tlemcen
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Barbarine, Noire deThibar, Queue Fine de l'Est (meat), Sicilo-Sarde (milk)

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Has the traditional approach of selective breeding been feasible or successful everywhere?

Main tools:

Performance recording (ICAR guidelines)
Artificial Insemination and ram centers
Single Sire Mating
Pedigree verification

Main variations to the traditional approach:

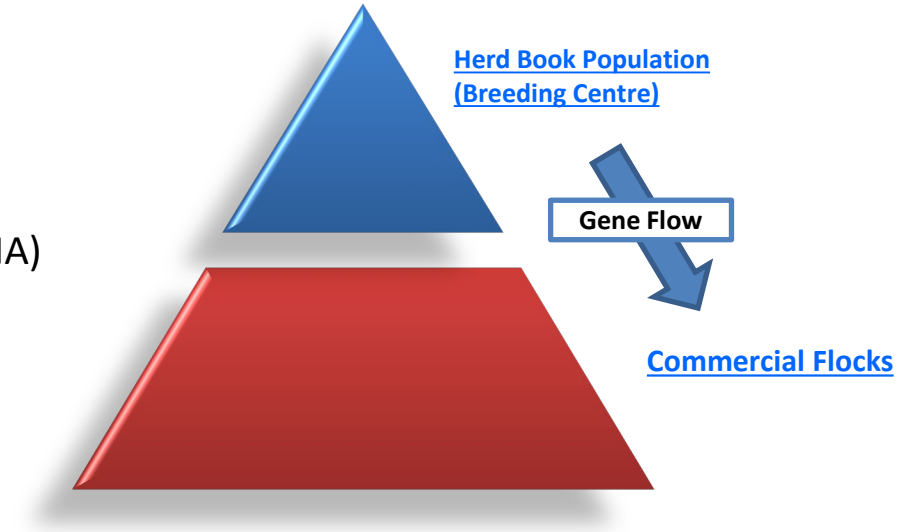
Multiple sire mating with or without pedigree discovery (DNA)

Breeding Centers

Selection per specific genes (PrP – Scrapie in sheep)

More recently:

Genomic selection with a similar approach to dairy cattle



Has the traditional approach of selective breeding been feasible or successful everywhere?

Self evaluation

Evaluation	Goat	Sheep
Highly Efficient	15%	11%
Moderately Efficient	55%	34%
Marginally Efficient	5%	25%
Inefficient	25%	30%

Highly efficient breeding schemes just in few dairy breeds, mainly in France, Spain and for some breeds in Italy and Greece

Lacaune, Assaf, Saanen, Alpine and somo other breeds have been spreading in regions different from the original ones, as purebred or crossbreds, not always with appreciable outcomes

Most experts underline the great difficulties of correctly and efficiently applying the selection tools envisaged by the traditional approach





Has the traditional approach of selective breeding been feasible or successful everywhere?

Main issues:

- Insufficient rates of artificial insemination and single sire mating
- Small effective size of the selected population
- Few recorded traits and low accuracy of phenotypes
- Low accuracy of pedigree
- No effective management of the genetic variability





Has the traditional approach of selective breeding been feasible or successful everywhere?

Issues are the same all over the countries, but it seems that:

- In the northern Med shore, difficulties are due mainly to organizational problems and the lack of breeder awareness;
- In the southern Med shore, issues are due mainly to funding problems, technological delays and difficulties of data recording on a large scale mainly in very extensive systems

Successful implementation of selective breeding even less for meat breeds due to greater difficulties of performance recording in more extensive systems (greater use of performance test in Breeding Centers)

Has the traditional approach of selective breeding been feasible or successful everywhere?

The new challenge in selective breeding for SR is including innovative traits for more sustainable farming possibly without any deterioration of production traits and taking into account the evolution of production and breeding costs

- Behavioural traits (temperament, milkability)
- Fertility and longevity
- Health (mastitis, viral disease, metabolic disorders, immuno-response)
- Ethical value of products (animal welfare, feed efficiency , greenhouse gas emissions)
- Nutritional components of products
- Climate change adaptation and resilience to climate stress
- Sustainability in terms of preservation of genetic variability mainly genome regions involved in adaptation to climate change

Which is the most likely evolution of the breeding schemes?

Most experts believe that it will be difficult to resolve the issues that have prevented the complete implementation of tools envisaged by the traditional approach :

- No way to extend phenotype recording even for traditional production traits
- No way to extend single sire mating and AI
- No way to select for innovative traits (due to the lack of extensive historical recording and deep pedigree, low heritability)
- No way to precisely monitor and preserve genetic variability

Will the advent of new genomic technologies and the constant reduction in application costs make a change in the traditional “large scale recording-artificial insemination” paradigm possible?





Which is the most likely evolution of the breeding schemes?

The overall thought is that genomics will be crucial both for the genetic improvement of production and innovative traits and for preserving the genetic variability to face climate change but ….:

- Experts of breeds with successful traditional breeding schemes and where genomic tools have already been implemented believe that breeding schemes will evolve toward innovative GS approaches for traits difficult or costly to measure on large scale

- Most experts of breeds with unsuccessful results of the traditional approach, envisage innovative genomic selection approaches and phenotypes

- Part of experts still consider genomic tools too expensive and challenging from a technological point of view mainly in the southern Med shore

Which approach for implementing genomic tools and innovative traits?

Genomic applications until now:

- **selection assisted by causative or linkage disequilibrium (LD) mutations** needs long trials based on large population measured for a lot of traits (examples: Scrapie and Maedi Visna)

- genomic selection (dairy cattle approach) implies large scale recording of traits for sire reference populations and the wide use of elite sires

Which approach for implementing genomic tools and innovative traits? Is the dairy cattle approach feasible/effective?

SR: technical issues

- **less accurate progeny testing** due to the low average number of daughters, the lack of genetic connectedness and the low accuracy of the performance and pedigree recording
- difficult to find **well-structured reference populations** to estimate SNP effects
- **Increasing accuracy is more relevant than shortening generation interval**

Which approach for implementing genomic tools and innovative traits? Is the dairy cattle approach feasible/effective?

SR: economic issues

- **Relative high cost** of SNP arrays if related to the value of a single animal and the number of recorded traits:
  - Cattle : 50.000 SNP x 10-27 traits
  - Sheep : 50.000 SNP x 1-5 traits

Most experts consider the cost of genomic applications as still being too high

CAN WE DEVELOP A MODEL OF GENOMIC SELECTION SPECIFIC TO SR TAKING INTO ACCOUNT TECHNICAL AND ECONOMIC CONSTRAINTS?





Which approach for implementing genomic tools and innovative traits?

The trends of breeding costs and funding :

- Strong reduction of genomic technology costs
- Diffusion of automatic systems for measuring some (productive) traits (mainly in intensive systems)
- Still high costs for measuring and sampling animals in extensive systems
- Innovative organizational models that envisage links and sharing of costs between breeding organizations, breeding companies, R&D public bodies and farmers (likely not to the same extent everywhere)

Which approach for implementing genomic tools and innovative traits?

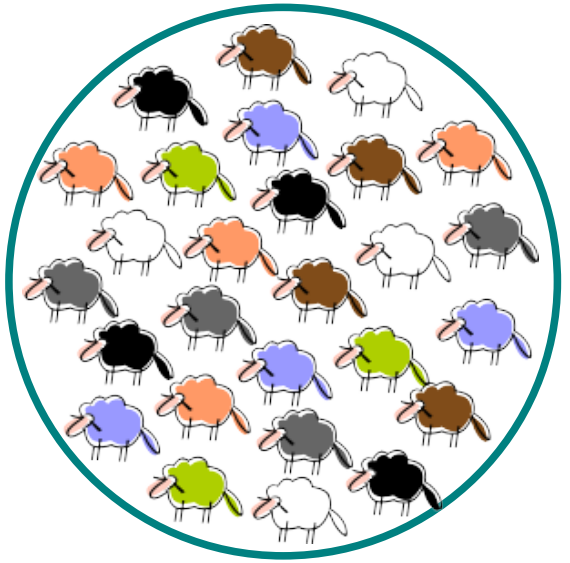
Female Nuclei (GENOTYPING AND PHENOTYPING)

- measured for several traits
- genotyping with medium density arrays
- NGS of more influential animals for imputation
- LD markers and causal mutations
- Rare variants and variants associated with adaptation to CC

Commercial Population (GENOTYPING)

- genotyping with medium density arrays

Sires
AI or NM



Genotypes
Phenotypes

Estimation of Genomic Segments Effects

Effects (b)

Estimation of Genomic Breeding Values (GEBV) of selection candidates

Which approach for implementing genomic tools and innovative traits?

- organize female nuclei in **"genomic herds"**
- accurately plan **the flow of animals from and toward the nuclei** to sample the genetic variability of the whole population including rare haplotypes
- implement optimal combination of **whole genome sequencing for the more influential animals** with medium density array genotyping to impute selection candidate genotypes
- dissect traditional and innovative traits using **more precise trait definitions and phenotypes closer to genotypes** (new proteomic and metabolomic technologies)
- monitor the **frequency of rare variants** to preserve genetic variability and produce a diversity index
- identify **variants involved in adaptation to climate change** and produce a resilience index
- **share costs** between breeding organisations, R&D public bodies and farmers: whole genome sequencing (breeding organization, R&D public bodies); genotyping of females with low density arrays (farmers)

Is the creation of a technical reference center useful?

Almost all experts agree (even if with different nuances) that a Reference Center will be useful to move from traditional to innovative approaches.

Goals :

- Share methods
- Provide guidelines
- Provide technical and analytical services
- Data Repository (models, genetic parameters or even more with specific agreements)
- Provide training
- Organize common research





How to proceed to create a reference center?

The REGULATION (EU) Breeding Law 2019/1012. Article 29 mentioned the EU **Reference Centre** for the scientific and technical contribution to the harmonisation and improvement of the methods of performance testing and genetic evaluation of purebred breeding animals of small ruminant species

EURC – Interbull: The European Union Reference Centre for the "scientific and technical contribution to the harmonisation and improvement of the methods of performance testing and genetic evaluation of purebred breeding animals of the bovine species" (01.11.2018)

EURC - EAB: The European Union Reference Centre for Endangered Animal Breeds is responsible for the scientific and technical contribution to the establishment and harmonisation of methods **for the preservation of endangered breeds, and the preservation of the genetic diversity existing within those breeds**. (01.01.2023)

How to proceed to create a reference center?

Discussion started in the H2020 Smarter Project :

WP6 (task 6.3)
"… The outline of a reference centre in the EU Regulations on animal breeding will be developed and aimed to be operational by the end of the project"

Deliverable 6.4 : Business and operation model for international evaluation of rams and bucks
"It describes the business and operation model for international evaluation of rams and bucks. This deliverable consists in a specification of a ready-to-implement routine international evaluation infrastructure. **This deliverable also describes the outline, expectations and organisations of a reference centre for small ruminants."**

Brainstorming in ICAR SGC-WG on the possibility of an ICAR – Interbull Consortium to become EURC for SR?

EURC must not be Eurocentric, but it must provide benefits/services to other countries mainly MED countries

The main goals should be to harmonise methods and to provide services for the genetic management of SR breeds (across country genetic evaluations do not really exist in SR so far).

The governance must include people from the breeding organizations and experts of selective breeding and genetic evaluations.

Relationships with EURC – EAB

Other partners?





Main remarks

- SR farming in the Med area must solve the eternal antagonism between selecting for productivity or resilience and maintain genetic variation to face climate change
- The exploitation of the large biodiversity reservoir in the MED area is a MUST and the preservation of genetic variation should be included as a selection objective in all breeds
- The management of the local genetic resources must be cooperative and integrated
- Genomic tools must be exploited and implemented through appropriate breeding schemes soon and everywhere
- Sharing methods and results of breeding schemes is necessary to achieve the goal of avoiding the deterioration of the global genetic variability
- Innovative solutions for funding should be envisaged
- A Reference Center might be a good starting point





Thanks to

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