

Assessing the adoption of genomic tools in sheep and goat breeding: patterns, challenges, and perspectives

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Brainstorming within the ICAR SGC-WG

Could ICAR contribute to the establishment of a European Reference Centre for the genetic management of small ruminant breeds? (EU Regulation 2016/1012)

Discussion points:

- International genetic evaluation (across-country genetic evaluations are still not implemented in SR);
- harmonization of methodologies;
- services supporting breeding schemes management and the implementation of genomic tools;
- cost-benefit analysis of innovative genomic tools
- Involvement of non-European countries (particularly the southern shore of Med area)
- involving representatives of breeding organizations and experts in breeding and genetic evaluation.
- Other potential partners
- relationships with EURC-EAB

Background



75th EAAP Annual Meeting 1/5 September 2024 - Florence, Italy

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

Antonello Carta, Georgia Hadjipavlou, Christina Ligda

Consultation through a questionnaire of 18 experts from 11 countries,
61 sheep breeds, 20 goat breeds

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The main questions addressed were:

1. Has the **traditional approach of selective breeding** been feasible or successful everywhere ?
2. Which was 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. Could a **technical reference center** be useful?

Main outcomes

1. Feasibility of traditional breeding schemes

Conventional breeding schemes have been fully successful only in a limited number of dairy breeds,

2. Expected evolution of breeding programs

The classical breeding model based on large-scale recording and widespread AI will remain difficult to expand in many production systems.

3. Future role of genomics

Genomics progressively emerged as a “must” for future breeding programs, both for improving production and innovative traits and for preserving genetic variability,

4. Agreement on the utility of a technical Reference Centre

Given these new opportunities, **the establishment of a EURC could provide important support for the harmonized development of genomic strategies** in small ruminants.

WHY A NEW SURVEY ON GENOTYPING ACTIVITIES?

Supporting the SGC-WG initiative

The survey was specifically designed to **investigate the scale of genotyping activities and the level of operational integration** within small ruminant breeding programs,

Main questions:

- Which genotyping tools are currently used?
- For which purposes are genotyping tools applied?
- Are genotyping activities applied routinely?
- Which categories of animals are genotyped?
- How are genotypic data operationally integrated into breeding activities?

QUESTIONNAIRE STRUCTURE

The questionnaire was organized into different sections

General information on: (not shown in the image)

- breeding organization
- population size
- recorded traits
- pedigree recording

Genotyping activities:

- **Applied tools:** size and type
- **Objectives:** pedigree verification and discovery; major genes; genomic selection;
- **genotyping targets;**
- **Use of genotypings in genetic evaluation;**
- **genomic diversity indexes**

| GENOTYPING ACTIVITIES | |
|---|---|
| Molecular markers for pedigree verification and/or discovery | |
| • | Type (microsatellites, low density SNP arrays, ...): |
| | Yearly number per sex |
| • | Number of Females (including young and potential parents): |
| • | Number of Males (including young and potential parents): |
| | |
| Single Loci (major genes) for selection purposes | |
| • | Locus -Trait |
| | Yearly number per sex |
| • | Females: |
| • | Males: |
| | |
| Medium density arrays for genomic selection | |
| • | Type of array: |
| | Yearly number per sex and age |
| • | Young females: |
| | ○ Indicate the proportion of genotyped young females expected to have performance records in the breeding scheme (reference population): |
| • | Total number of breeding females with records |
| • | Number of females with records newly genotyped each year (i.e. that were not genotyped as lambs/kids) |
| • | Young males |
| | ○ Indicate the proportion of genotyped young males expected to have records and/or progeny in the breeding scheme (reference population): |
| • | Males with records and /or progeny |
| | |
| 1) | Genetic evaluation (answer Y or N / specify traits if different methods are used) |
| • | BLUP - Pedigree relationships only |
| • | GBLUP- Genomic relationships only |
| • | Single-Step GBLUP – pedigree and genomic relationships |
| 1) | Genomic diversity index (specify the used indicators or methodology based on genotypes) |
| | |
| Notes or final considerations (optional) | |

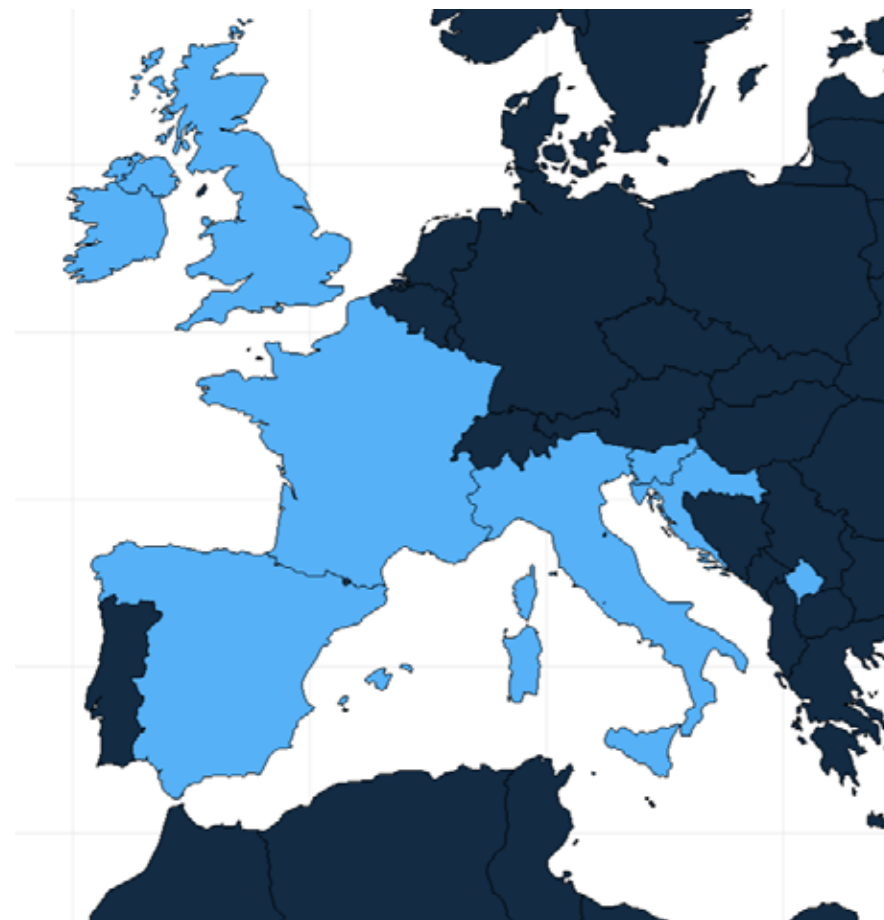
Results

A total of 13 experts from 8 countries participated in the survey, providing information on genotyping activities for 29 breeds, classified as:

- 6 goat breeds,
- 14 dairy sheep breeds,
- 9 meat sheep breeds.

| Surname: | Name: | Country: | Breeding organisation: |
|--------------------|------------------|----------------|--|
| Astruc | Jean-Michel | France | IDELE |
| Clément | Virginie | France | IDELE the breed society Capgènes |
| Gallego | Roberto | Spain | AGRAMA |
| Godfrey | Sean | Ireland | Sheep Ireland |
| González Rodríguez | María Concepción | Spain | ANCA |
| Granado Tajada | Itsasne | Spain | CONFELAC |
| Lambe | Nicola | United Kingdom | SRUC |
| Memaj | Arsim | Kosovo | Ministry of Agriculture Forestry and Rural Development |
| Negro | Alessio | Italy | ASSO.NA.PA |
| Roden | Janet | United Kingdom | Innovis Ltd |
| Simčič | Mojca | Slovenija | University of Ljubljana, Biotechnical Faculty |
| Smith | Ed | United Kingdom | British Texel Sheep Society |
| Špehar | Marija | Croatia | Croatian Sheep and Goats Breeding Association |

Although Australia and New Zealand are known to perform extensive genotyping activities in small ruminants, only limited information from these countries was available through the present survey.



Main findings

Genotyping activities are now widespread across almost all countries

Different genotyping tools are used according with specific breeding objectives:

- **microsatellites** (Italy, Spain)
 - pedigree verification/discovery
- **dedicated low-density SNP arrays** (e.g. Ireland: 800 SNP, France: 226 SNP in sheep, 220 in goat)
 - pedigree verification/discovery
- **medium-density SNP arrays (50–60K)**
 - pedigree verification/discovery
 - genomic selection
 - experimental trials
- **SNP on single loci** (included or not in SNP arrays):
 - PrP (scrapie resistance) in sheep
 - Prolificacy genes in meat sheep
 - PrP ; SOCS2; horn in France sheep
 - PrP, DGAT1, PIS, Pink neck, Cas α 1 in France goats.

| Species: | Country: | Type of medium-density array |
|----------|----------------|--|
| Goat | Croatia | GoatSNP60 BeadChip |
| | France | Illumina 50K SNP chip |
| | Italy | Illumina goatSNP50 bead chip |
| | Slovenija | SNP illumina Caprine 60K |
| Sheep | Croatia | OvineSNP50 v1. and v3. |
| | France | AgResearch "AgR_Ovine Genomics 60K plus" |
| | Ireland | SNP array - 50k |
| | Italy | Illumina ovineSNP50 bead chip |
| | Slovenija | SNP illumina Ovine 54K |
| | Spain | Illumina 50K SNP ship |
| | United Kingdom | Axiom Ovine Genotyping Array (50K, Thermofisher) 50K SNP array (80K) |

Three levels of operational integration of genotyping activities in the breeding schemes

1) Emerging genotyping activities

Genotyping activities are present but remain only partially integrated into structured breeding programs and breeding decisions:

- activities mainly limited to pedigree verification and major genes
- tools mainly based on microsatellites and, in some cases, medium-density SNP chips
- medium-density SNP chips often underexploited within breeding programs
- activities frequently associated with specific research projects or sporadic activities rather than routine breeding operations.

| Country | Breed | Pedigree verification | Pedigree discovery | Type | N | Locus -Trait: | Type of array | N. | Genomic selection | Genomic diversity index |
|----------------|-----------------------------|-----------------------|--------------------|-----------------|----------|------------------|-------------------------------|-----|-------------------|-------------------------|
| Slovenija | G Drežnica | No | Yes | SNP illumina | 50/year | - | - | - | no | - |
| Kosovo | S Balusha | No | No | - | - | - | - | - | - | - |
| Italy | S Delle Langhe | Yes | No | microsatellites | 482 | PNRP scrapie | Illumina ovineSNP50 bead chip | 100 | - | Inbreeding |
| Italy | S Appenninica | Yes | No | microsatellites | 117 | PNRP scrapie | Illumina ovineSNP50 bead chip | 72 | - | Inbreeding |
| Italy | S Merinizzata Italiana | Yes | No | microsatellites | 206 | PNRP scrapie | Illumina ovineSNP50 bead chip | 135 | - | inbreeding |
| Slovenija | S Improved Jezersko-Solčava | Yes | No | SNP illumina | 150/year | - | - | - | No | - |
| Slovenija | S Jezersko-Solčava | Yes | No | SNP illumina | 100/year | - | - | - | No | - |
| Spain | S Castellana | Yes | Yes | - | - | - | - | - | - | - |
| United Kingdom | S Compsites | No | Yes | SNP array | 2225 | BMP3 (Inverdale) | SNP array (80K) | - | not yet | not used |
| United Kingdom | S Scottish Blackface | Yes | No | 50K SNP chip | 25 | - | - | - | No | - |

2) Transition toward genomic schemes

- Routine genotyping activities are already established, although their integration into selection decisions remains only partial.
- Breeding programs are clearly moving toward the implementation of genomic selection strategies.
- In some cases (e.g. Sarda and Croatian populations), genotyping activities include phenotyped females, potentially supporting the development of female reference populations.

| Country | Breed | Pedigree Verification | Pedigree discovery | Type | N. | Locus -Trait: | Type of array | Genotyped animals | Genomic selection | genomic diversity index |
|---------|-----------------|-----------------------|--------------------|-----------------|---------------|---------------|---|-------------------|---|-------------------------|
| Croatia | GIstrian goat | No | Yes | 60K SNP arrays | | | GoatSNP60 BeadChip | 15 M + 158 F | | Inbreeding, ROH |
| Italy | GAlpine | Yes | No | microsatellites | 274 + 535 | | Illumina goatSNP50 bead chip | 530 + 2593 | Start in 2026 for productive related traits | Inbreeding |
| Italy | GSaanen | Yes | No | microsatellites | 109 + 317 | | Illumina goatSNP50 bead chip | 279 + 1150 | Start in 2026 for productive related traits | Inbreeding |
| Croatia | S Istrian sheep | No | Yes | 50K SNP arrays | | | OvineSNP50 v1. and v3. | 37 M + 877 F | in testing phase | Inbreeding, ROH |
| Croatia | S Pag sheep | No | Yes | 50K SNP arrays | | | OvineSNP50 v1. and v3. | 173 M + 3384 F | in testing phase | Inbreeding, ROH |
| Italy | S Comisana | Yes | No | microsatellites | 409 | PNRP | Illumina ovineSNP50 bead chip 96 | | Start in 2026 for productive related traits | Inbreeding |
| Italy | S Massese | Yes | No | microsatellites | 229 | PNRP | Illumina ovineSNP50 bead chip 102 | | Start in 2026 for productive related traits | Inbreeding |
| Italy | S Sarda | Yes | Yes | microsatellites | 7536 (+990 F) | PNRP, TMEM154 | Illumina ovineSNP50 bead chip 150 M + 400 F | | experimental population | Inbreeding |

3) Fully operational genomic schemes

Genotyping activities are fully integrated within routine breeding operations and directly support genomic evaluations and breeding decisions.

- routine use of SNP chips even with different densities according to operational objectives (e.g. Ireland and France)
- progressive extension of genotyping from males to phenotyped females
- systematic SNP genotyping of major genes for selection purposes
- Multi-breed approaches
- preliminary experiences with international evaluations

| Breed: | Pedigree verification | Pedigree discovery | Type | Locus -Trait: | Type of array | Genot. F | Genot. M | Genomic selection | genomic diversity index |
|-------------------------|-----------------------|--------------------|-----------------|---|--|----------|----------|-------------------|-------------------------|
| FR G Alpines/Saanen | Yes | No | Ded. SNP set | PrP, DGAT1, PIS, Pink neck, Cas α S1 | Illumina 50K SNP ship | 1400/yr | 500/yr | ongoing | |
| FR S Basco-Béarnaise | Yes | Yes | Ded. SNP set | PrP ; SOCS2 ; horn | AgResearch "AgR_Ovine Genomics 60K plus" | 840 | 370 | ongoing | |
| FR S Manech tête rousse | Yes | Yes | Ded. SNP set | PrP ; SOCS2 ; horn | AgResearch "AgR_Ovine Genomics 60K plus" | 1200 | 730 | ongoing | |
| FR S Manech tête noire | Yes | Yes | Ded. SNP set | PrP ; SOCS2 ; horn | AgResearch "AgR_Ovine Genomics 60K plus" | 100 | 80 | ongoing | |
| FR S Corse | Yes | Yes | Ded. SNP set | PrP ; SOCS2 ; horn | AgResearch "AgR_Ovine Genomics 60K plus" | 500 | 475 | ongoing | |
| FR S Lacaune | Yes | Yes | Ded. SNP set | PrP ; SOCS2 ; horn | AgResearch "AgR_Ovine Genomics 60K plus" | 1900 | 3600 | ongoing | |
| SP S Latxa | Yes | | Microsatellites | | Axiom Ovine Genotyping Array 50K, Thermofisher 230 | | 190 | ongoing | |
| SP S MANCHEGA | Yes | Yes | Microsatellites | | 50K | | | ongoing | |
| EI S Multiple Breeds | Yes | Yes | 800 SNPs | Scrapie, Prolificacy gene | SNP array - 50k | | | ongoing | inbreeding |
| UK S Texel | Yes | Yes | SNP arrays | Microphthalmia / PrP | 50K | | | ongoing | |

EVOLUTION OF GENOMIC IMPLEMENTATION STRATEGIES

Classical male reference population approach

- Genotyping mainly focused on males
- Progeny-tested sires used as reference populations
- Young males as selection candidates
- typically developed in breeds with efficient conventional breeding schemes (AI, accurate pedigree and extensive performance recording)

Issues: maintenance of the male reference population

Female reference population approach

- Genotyped and Phenotyped females used as reference population
- Young males as selection candidates

In breeds without a performing conventional schemes (limited AI and single sire mating, inaccurate pedigree and performance recording)

Issues: cost/benefit analysis of increased genotyping costs, and the role, size, and number of involved flocks.



Increasing female genotyping



**Progressive convergence
of both approaches**

Take home messages

- The adoption of genotyping activities is progressing faster than the development of fully operational genomic breeding schemes.
- The transition from “having genotypes” to “using genomic information operationally” remains the major challenge for many small ruminant breeding programs.
- Where international collaboration through a possible EURC could contribute:
 - Choice and harmonisation of genotyping SNP arrays (e.g. international 300-800 SNP set for parentage verification/discovery)
 - Optimisation of breeding schemes;
 - development, maintenance, and updating of reference populations (males, females, or combined)
 - Integration of costly or difficult-to-measure phenotypes
 - International genomic evaluations (see the following presentation)
 - Development of Multi-breed approaches
 - Evaluation of the real impact of genomics on genetic progress and cost–benefit analyses of genotyping strategies
 - preservation of genetic variability (adaptive potential to climate and environmental challenges)

Thanks to:

Members of the ICAR Sheep, Goats and Camelids Working Group

Experts who participated in this survey

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