A stakeholder view on fair and equitable exchange of AnGR: a research perspective

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Importance and Access to AnGR

- **Domestication of livestock and further development of AnGR contribute significantly to the civilizations of human societies;**
- **Ways to access to AnGR: commercial trading (e.g. dairy and egg-layer & broiler breeds), formal exchange often involved in indigenous breeds from south to north (e.g. gifted unique animals and birds), smuggling, etc…**
- **Advantages and benefits from the ‘easy’ access to AnGR of commercial breeds and lines – development of improved breeds with good local adaptations, breed replacements wherever the local conditions fit, and terminal-crosses with local breeds – leading to a dramatic increase of livestock production, particularly in southeast Asia over past 30 years;**

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Current knowledge and challenge on genetic characterization of AnGR

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- **Advantages of a global view on biodiversity distribution pattern of AnGR at phenotypic and DNA structural variations, possibly also proteomics, epigenetics;**
- **Exchange of data, phenotypes, DNA samples, knowledge, management practice of production systems etc.;**
- **Centralised collection of research materials, e.g. DNA samples, databases;**
- **However, a significant fragmentation of research on biodiversity of AnGR.**

Fragmentation of research on AnGR

A few of continental scale projects
– regional and global collaboration

Europe (EU projects)

Africa (ILRI projects)

Asia (ILRI and FAO/IAEA projects)

Most of the biodiversity studies included samples within a continent, only a few of them across continents (e.g. ILRI projects, EU Pigbiodiv2, AVIANDIV)

However, never a global view for any major species!

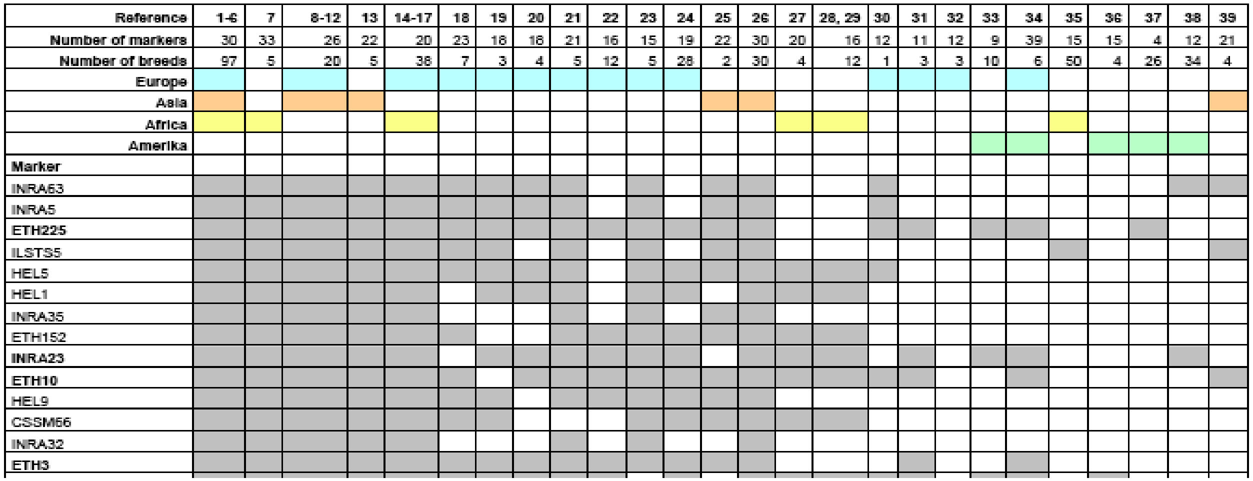
Fragmentation of research on AnGR (Baumung *et al.*, 2004)

- More than eight breeds with an average blood sample size > 50 included in 50% of 87 projects;
- Most of the breeds have a long history of isolation, unique phenotypic qualities or an evolution within a unique environment;
- Small ruminants were investigated in the majority of projects;
- The most preferred markers are microsatellites, but the ISAG/FAO recommended loci were adopted very differently between species and projects with the highest acceptance in pig but the lowest in chicken.

Fragmentation of research on AnGR
- an example from cattle microsatellites

Markers

Experiments



Reference	1-6	7	8-12	13	14-17	18	19	20	21	22	23	24	25	26	27	28, 29	30	31	32	33	34	35	36	37	38	39
Number of markers	30	33	26	22	20	23	18	18	21	16	15	19	22	30	20	16	12	11	12	9	39	15	15	4	12	21
Number of breeds	97	5	20	5	38	7	3	4	5	12	5	28	2	30	4	12	1	3	3	10	6	50	4	26	34	4
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INRA23	▨	▨	▨	▨	▨		▨	▨	▨	▨	▨	▨		▨	▨	▨		▨		▨	▨				▨	
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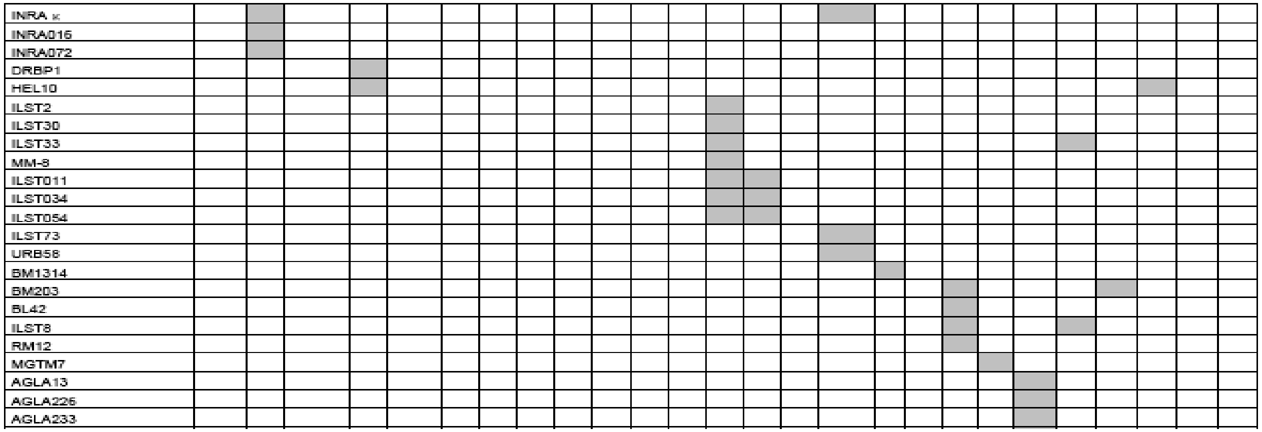
Fragmentation



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MGTM7																				▨						
AGLA13																					▨					
AGLA226																					▨					
AGLA233																					▨					

[Courtesy: J-A. Lenstra – Utrecht University]

Advantages of a global view on biodiversity of AnGR

- **Deep understanding of the origin, route of dispersal and distribution pattern of the biodiversity (geographic centers of domestications and subsequent dispersal routes);**

- **Identification of biodiversity hotspots and distinctiveness on a global scale for an improved and sustainable utilization strategy of AnGR;**

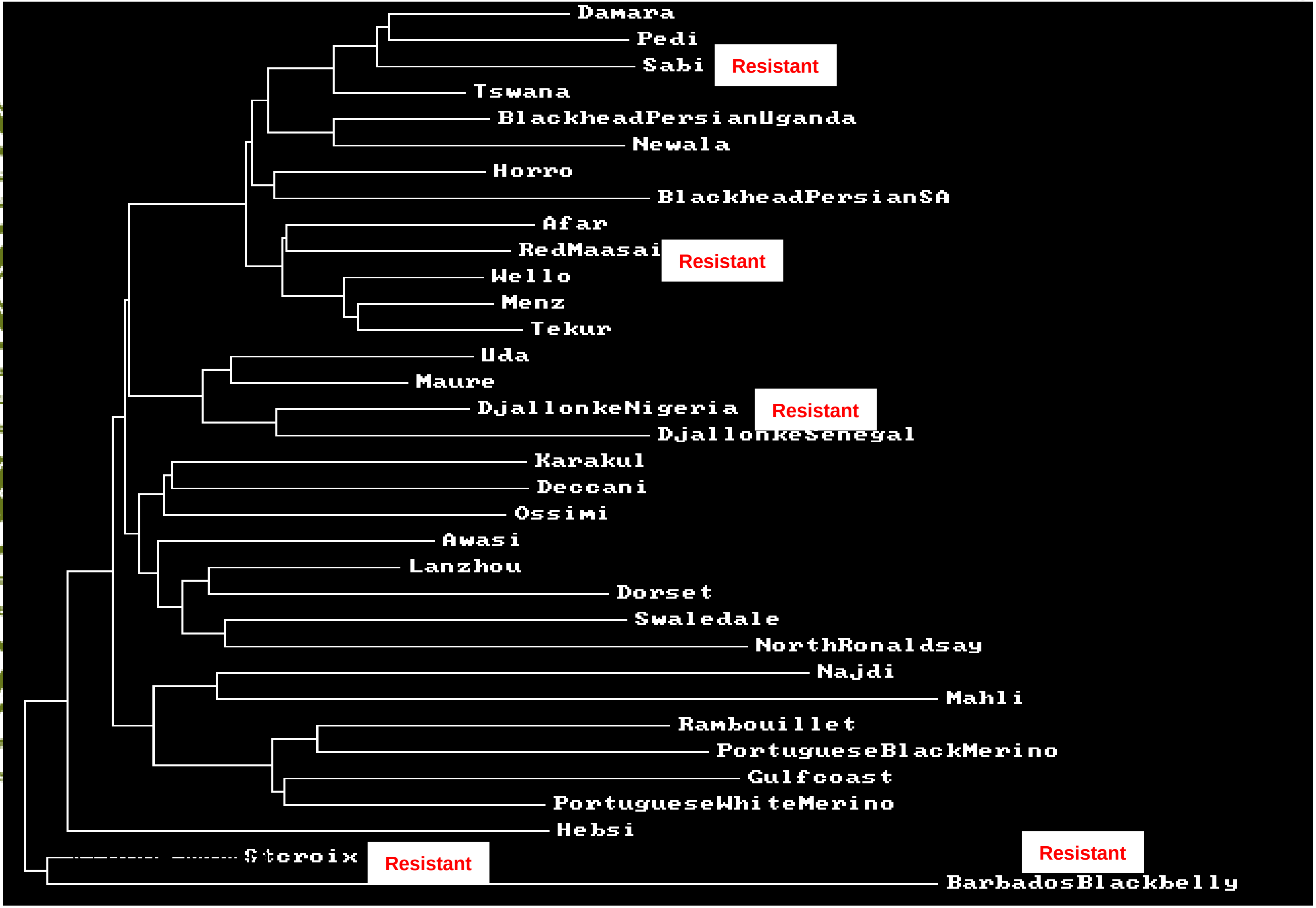
- **Identification of synonymous but non-identical or identical but non-synonymous breeds to rationalize and optimize the efforts and allocation of resources to conserve the maximum global biodiversity of AnGR.**

Advantages of a global view on biodiversity of AnGR

Also complementarity to:

- **Breeds sharing similar traits (e.g. resistance to same disease) in different genetic background might have evolved different and complementary genetic resistant mechanisms;**
- **Parallel investigation of breeds in different agro-climatic regions facilitates the investigation of the genetic basis of adaptation (key traits in a time of rapid climat change);**
- **Selection signatures?**
- **Across breed genetic evaluation and genomic selection?**

Sheep helminth resistance



Origin and migration routes of domestic cattle in Africa

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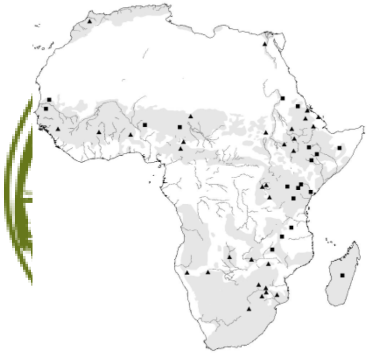

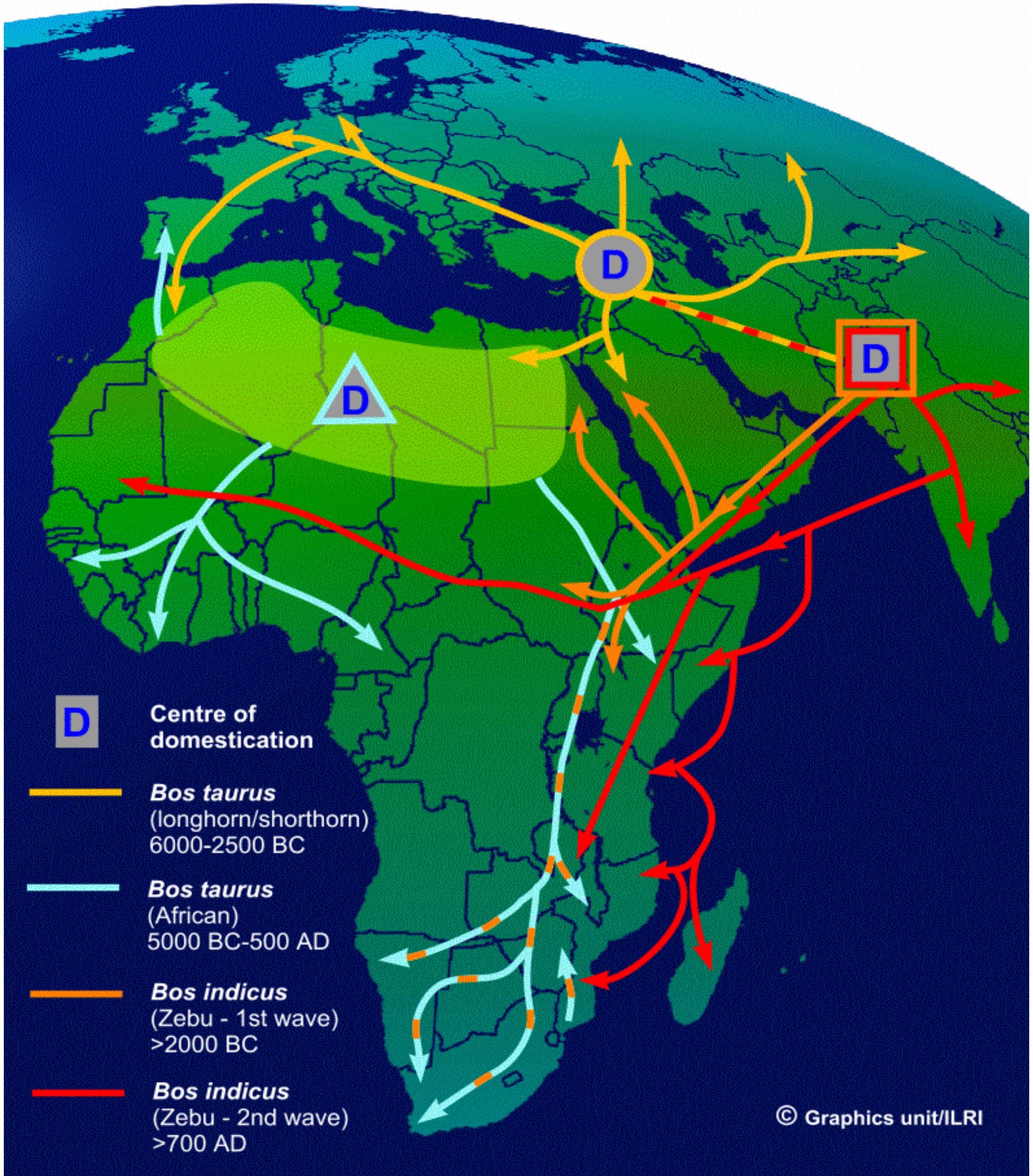

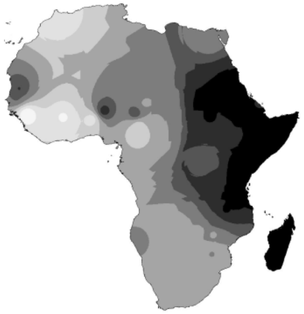

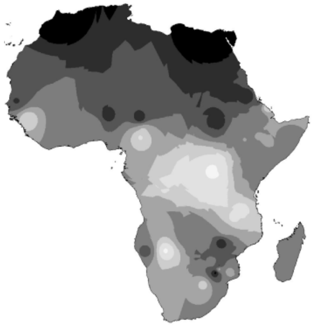

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Livestock genetic diversity hotspots

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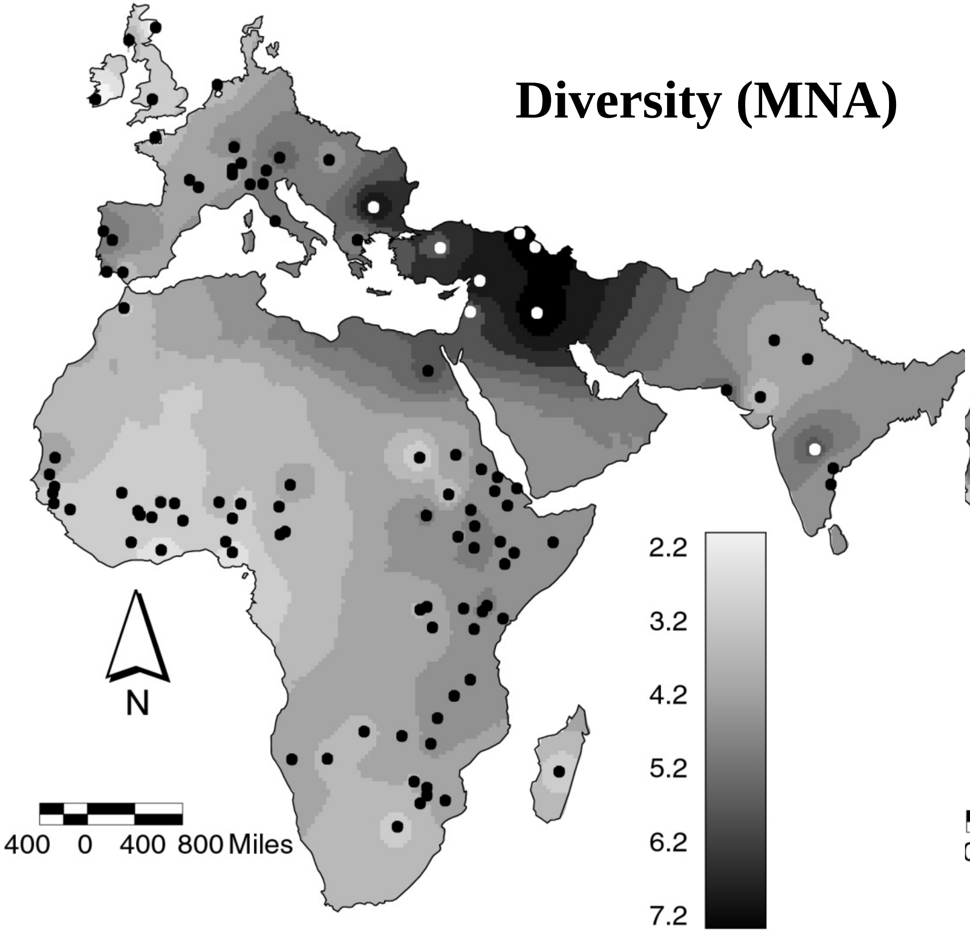
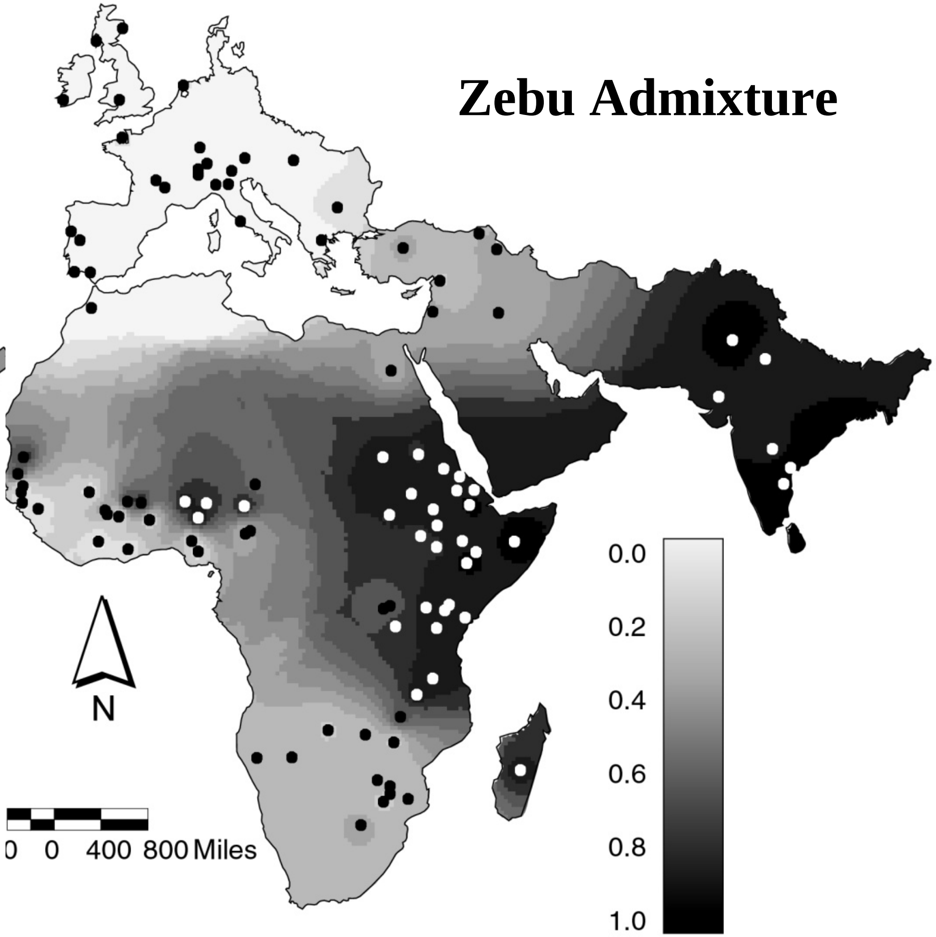


Diversity (MNA)



Zebu Admixture

Freeman et *al*. (2005)

Yak genetic characterization

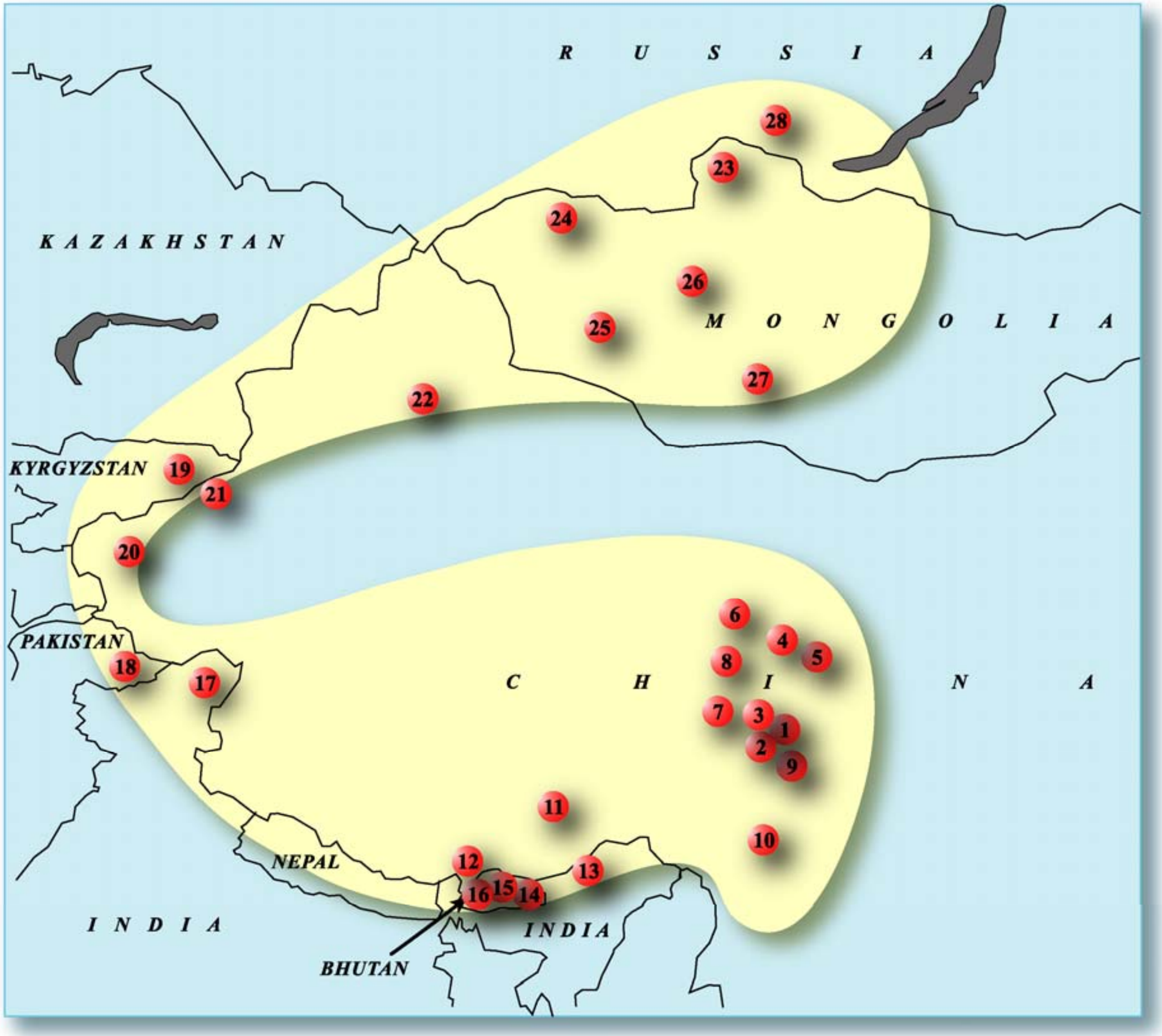
Sampling

- Country = 7
- Populations = 28
- Individuals = 1051

mtDNA sequencing

MS markers

- 17 cattle-derived autosomal MS markers



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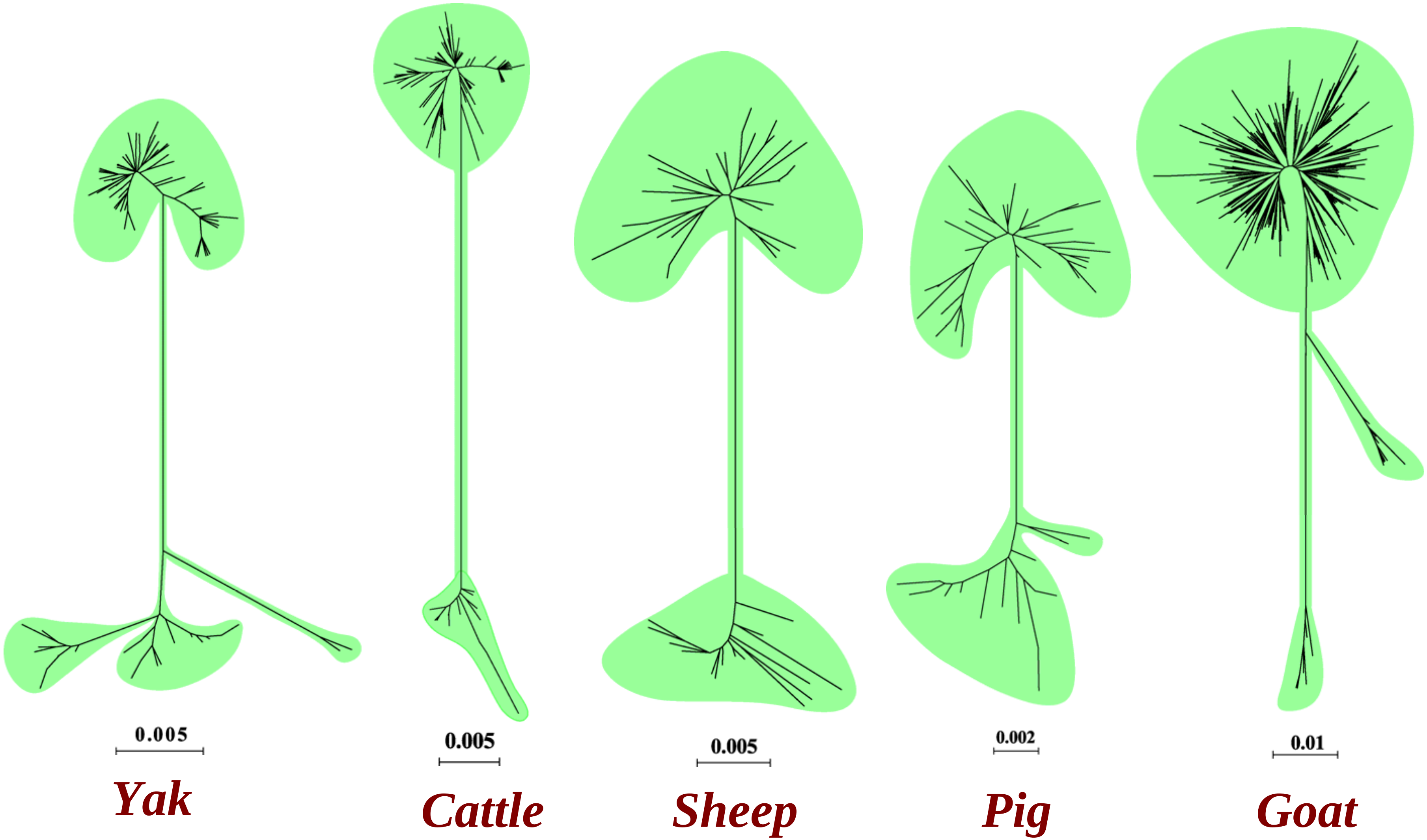
Comparison of phylogenies of yak with other livestock species, uncorrected mtDNA D-loop sequences



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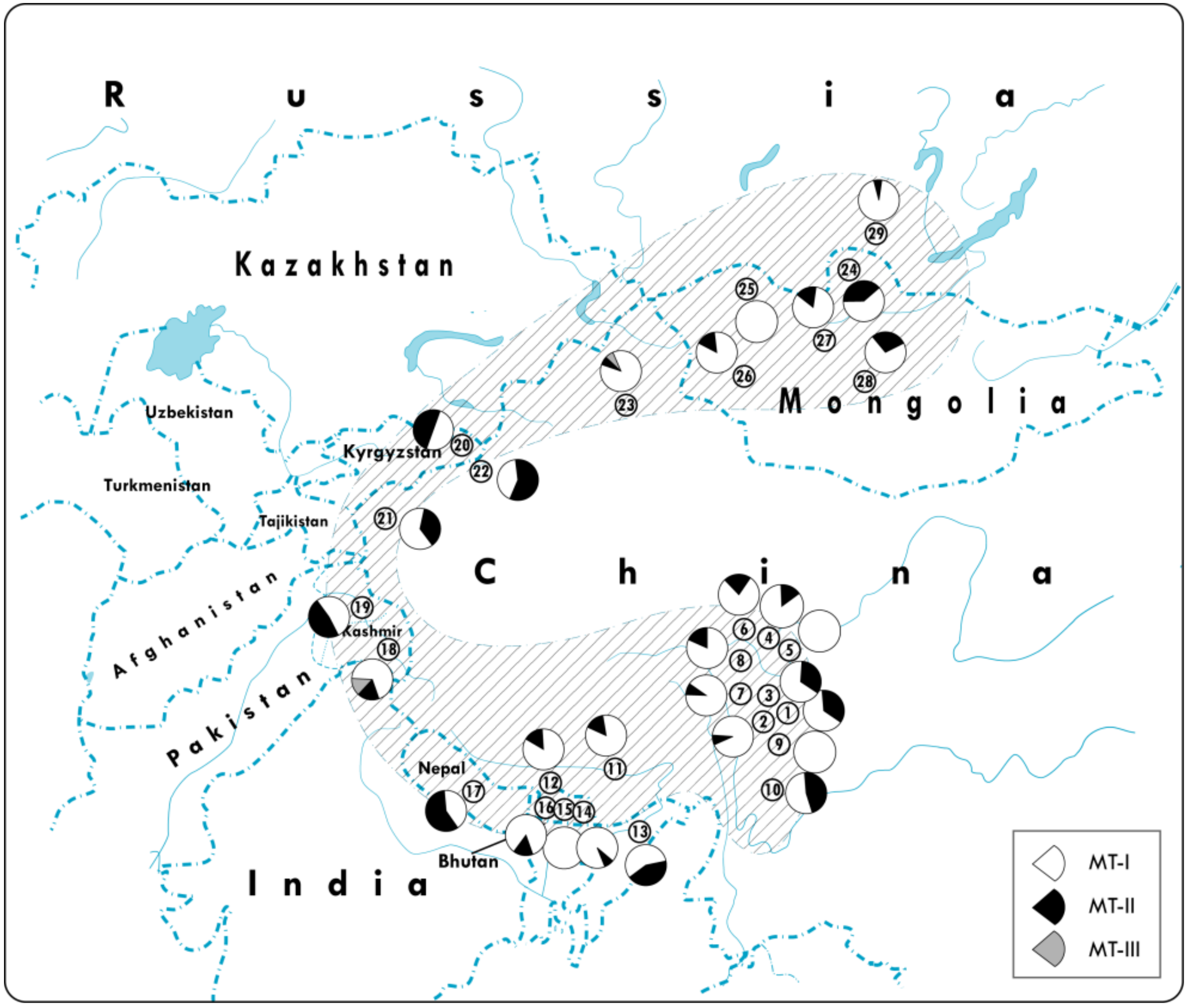
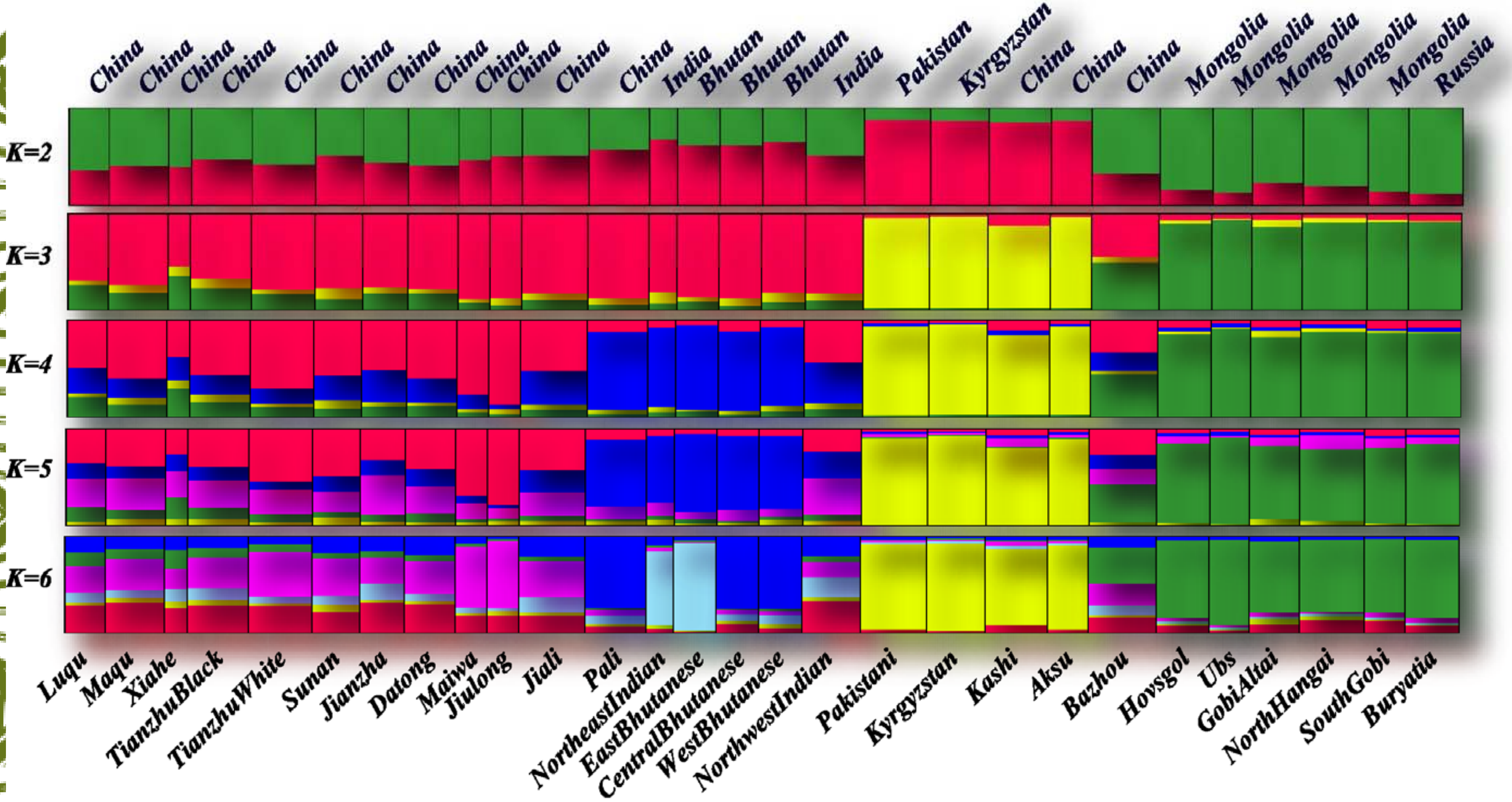
Maternal origin of domestic yak



Phylogeographic analysis of diversity support a single ancestral admixed population of origin for domestic yak.

Population structure of domestic yak microsatellite data



Requirements to facilitate data exchange

- International standard DNA samples to be made available upon request;
- A public reference marker dataset that includes genotyping scores of standard animals and of reference industrial breeds with easy assess;
- A shared, validated, and unbiased marker set;
- An international standard nomenclature of genotyping data;
- An international standard for data storage format;
- A common database to deposit data and make them available after publications (as now happens with sequencing data),

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Centralized collection of research materials

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- Bilateral exchange often difficult for safety reasons and due to the laws and regulations in different countries;
- International repository (genebank) of DNA/gametes/ cells/tissues serving both conservation and research would be ideal;
- Definition of the terms of conditions for equitable access and exchange of data and materials to preserve rights following standard MTAs;
- Appropriate recognition of the origin of DNA samples and information and also personal contriubtion to publications, e.g. authorship.

New “-omics” for collaborative research and benefit sharing

- New technologies is promoting a new modle of collaborative research (outsourcing in advanced countries or commerical companies);
- Highthroughput platforms for genotyping large number of SNPs or targeted re-sequencing of individual genomes (standard definitions for scoring alleles of SNPs with and between different platforms and for selection and coverage of the genome regions);
- Capacity building for young generation scientists in developing countries so that to build deeper trust based on a better understanding of the collabotive research.

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Conclusions

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- **A global approach is a perquisite to understand the general value and uniqueness of biodiversity of AnGR for an equitable access and benefit-sharing;**
- **Though some regional and international efforts have been undertaken, e.g. the ongoing attempts on meta-analysis for ruminants and chickens, an open access to and exchange of data and research materials following standard MTAs and based on the full recognitions of the origin of information & samples and also personal contriubtion to publications is a must for effective collaborative research on AnGR;**

Conclusions

- New “-omics” research tools facilitate and encourage more opportunities for collaborative research but effective training of young scientists and minimum infrastructure support in developing countries needs to be strengthened to build trusts among future generations;
- Prompting collaborative research leading to more efficient production systems with a reduced imprint of livestock;
- Strengthening north-south collaborative research with double objectives of improving local breeds and valuating AnGR.

Thanks for your attention!