

A global view on prioritizing genomic resources

Hoffmann I, P. Boettcher, R. Baumung Animal Production and Health Division - FAO Livestock Genomic Resources in a Changing World Cardiff, UK 17-19 June 2014





Content

- Domestication history why to conserve
- Why prioritization is necessary
 - Tools with and without molecular data
 - FAO-ISAG
- Genomics in AnGR management
 - Current situation and constraints
- Conclusion and recommendation



Framework - Global Plan of Action

The Global Plan of Action for Animal Genetic Resources was adopted by FAO members in 2007

- internationally agreed framework for the management of animal genetic resources
- 4 Strategic Priority Areas
 - 1. Inventory, monitoring and characterization
 - 2. Sustainable use
 - 3. Conservation
 - 4. Policy, institutions and capacity building

		à	*
¢			1.1
FOR ANI	PLAN OF A MAL GENE INTERLAKE	TIC RESO	
.	and the second	27	
R	R.	Fur	RE





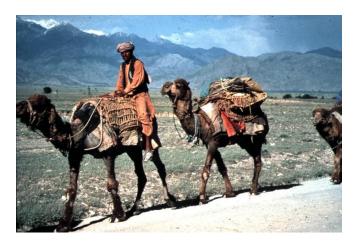


History – why conserve?



m









Domestication and breed history

Present AnGR diversity result of combination of forces

- domestication
- migration and genetic isolation
- environmental adaptation and selective breeding
- introgression and admixture of subpopulations

Molecular tools helped unravel history

Contribute to current decision making



Domestication and breed history

- Different marker types yield different information
- Mitochondrial DNA
 - Assumption is that domestication relied on keeping females
 - maternally-inherited \rightarrow wild ancestral species
 - geographic variation on continental scale
- Y-chromosomal variation
 - highly informative on male introgression
 - breeds
 - species

Autosomal DNA

- within or across continents
- neutral or selective variation





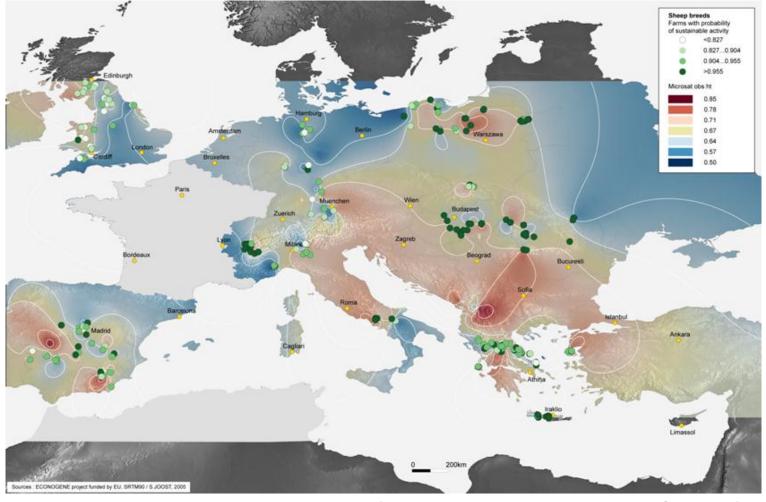
Centres of Domestication

identified through the use of molecular markers and other information





Geographical gradients



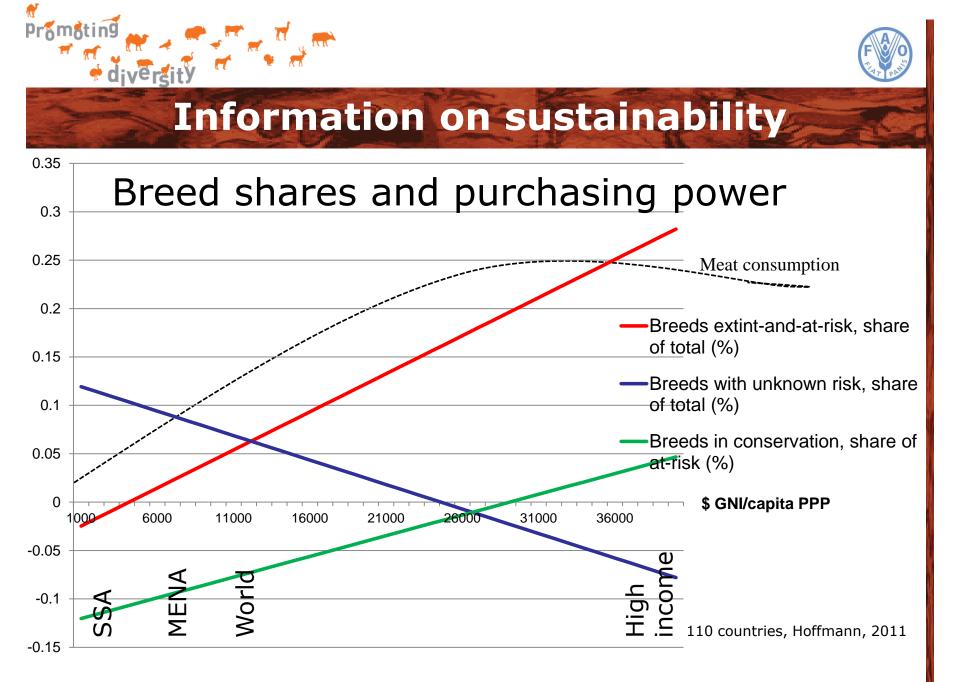
(courtesy Econogene project, S. Joost)





Why is conservation important?

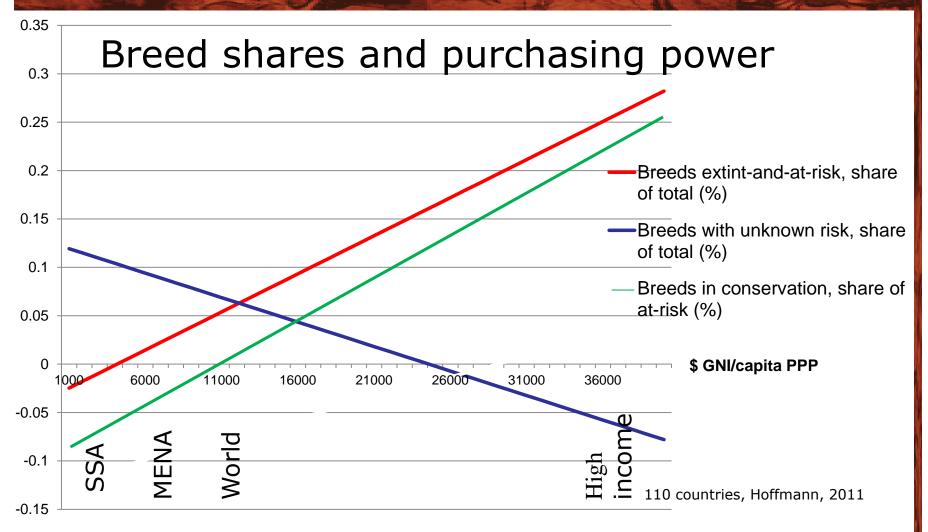
- Genetic diversity is necessary for adaptation
 - changing environments
 - production systems
 - climate
 - changing markets
- Genetic diversity is necessary for continued genetic improvement
- Cultural and historical reasons

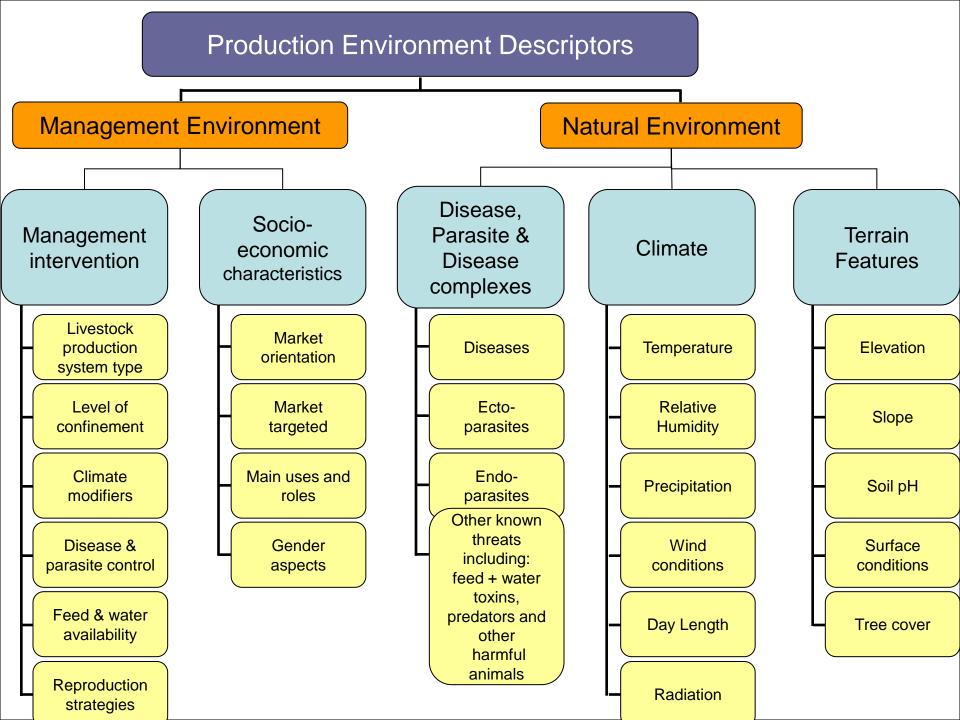


Promoting diversity



Information on sustainability

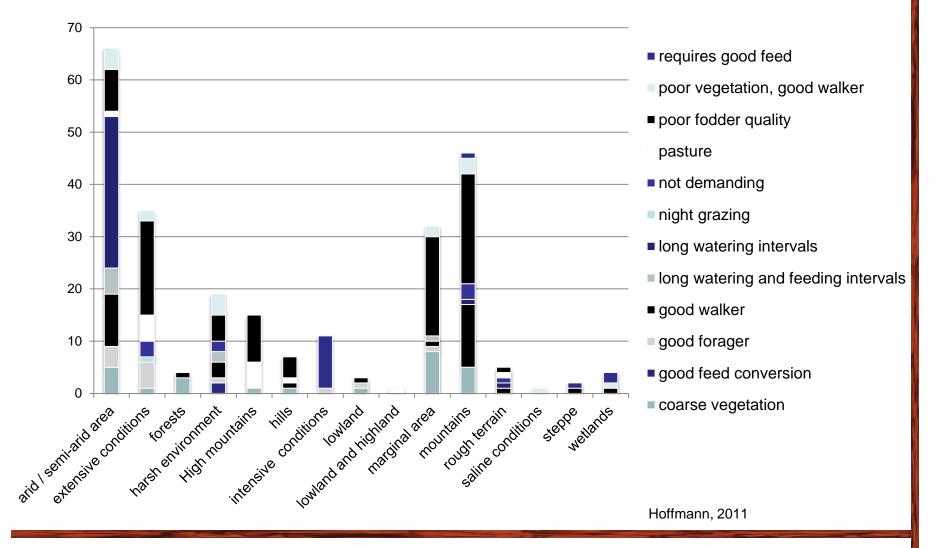








No. of national breed populations of selected species by ascribed habitat and fodder/feeding adaptation



DAD-IS



- Management intervention
- Socio-economic aspects

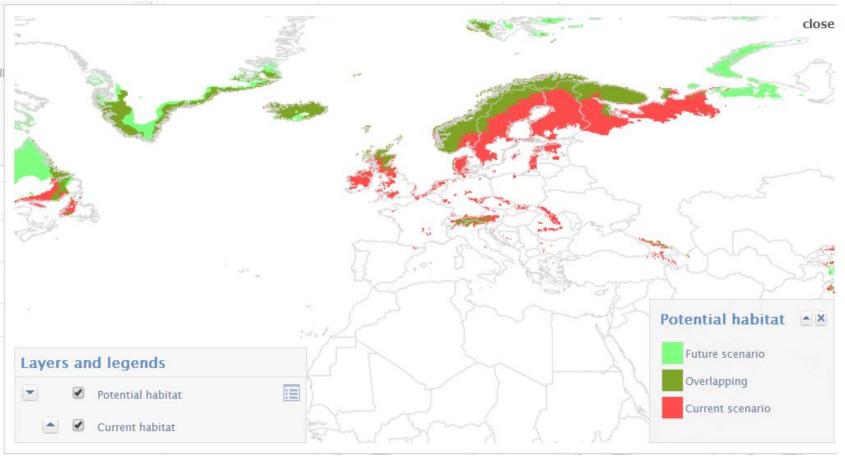
•Natural production environment





Climate change modeling - Norwegian Red cattle

2050 – most optimistic scenario



Model: HadGEM2-ES, rcp26

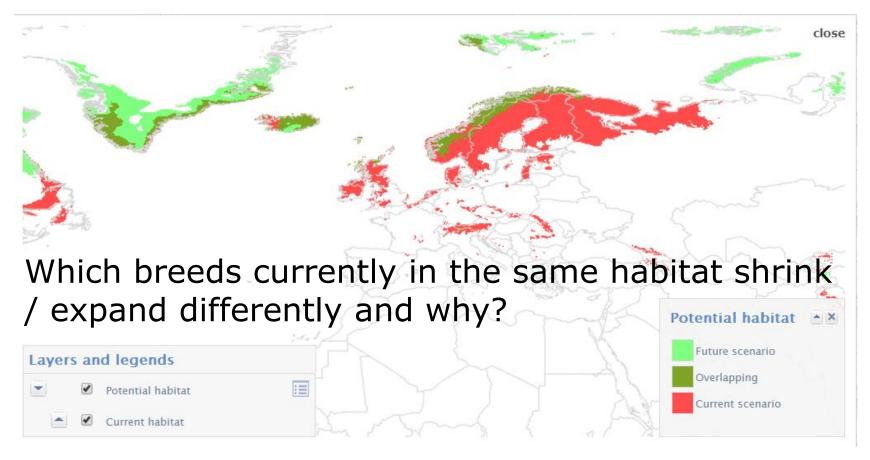
FAO, 2014





Climate change modeling - Norwegian Red cattle

2070 – most pessimistic scenario



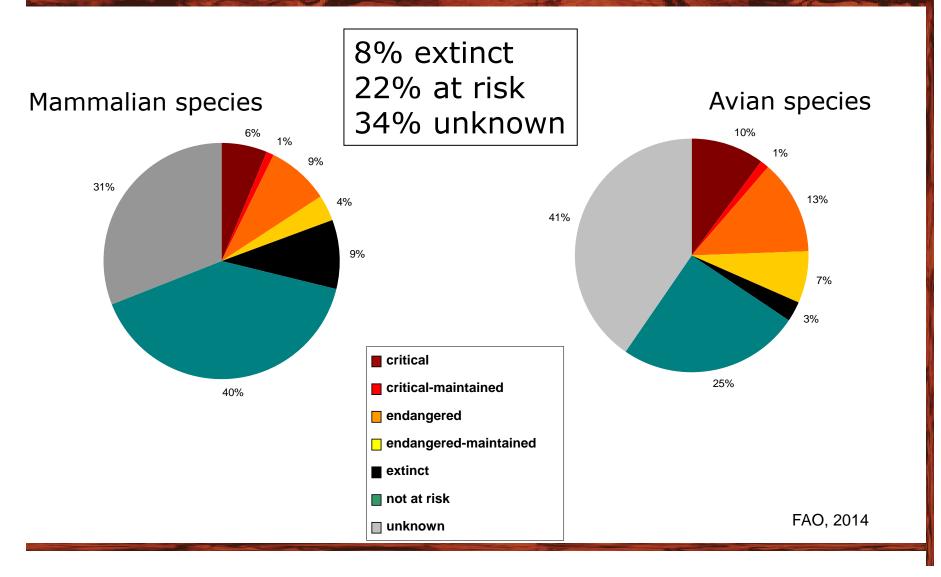
Model: HadGEM2-ES, rcp85

FAO, 2014





Risk status - the global picture (2012)







Conservation programmes: Changes since 2005

	Number of repo	f countries rting		countries with in tion programmes	Proportion of countries with in vitro conservation programmes					
	SoWAnGR 1	SoWAnGR 2	SoWAnGR 1	SoWAnGR 2	SoWAnGR 1	SoWAnGR 2				
Africa	42	40								
East Africa	7	8								
North & West Africa	24	20								
Southern Africa	11	12								
Asia	25	20								
Central Asia	6	4								
East Asia	4	4								
South Asia	7	6								
Southeast Asia	8	6								
Southwest Pacific	11	7								
Europe & the Caucasus	39	35								
Latin America & the Caribbean	22	18								
Caribbean	3	5								
Central America	9	5								
South America	10	8								
North America	2	1								
Near & Middle East	7	7								
World	148	128								

FAO, 2014



Why is prioritization necessary?

Conservation of all breeds impossible

- Many breeds and limited financial resources
 - Food security more important in developing countries
 - Short-term economic return more important in industrialized countries

Wholesale conservation not scientifically justified

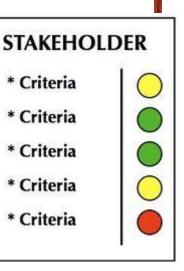
- Breed may have no apparent short- or long-term value
- Breeds may be effectively the same genetically

Decision support may be needed

many factors to consider simultaneously

Objective approaches have been proposed

- use of genetic markers to measure diversity







Factors influencing conservation priority

- Risk of extinction
 - Breed demographics
 - number and distribution
- Genetic variability (seek to maximize)
 - Genetic distance
 - distinctiveness
 - Allelic diversity
 - diversity and distinctiveness
 - Kinship
 - diversity within and across breeds
- Genetic diversity will rarely be only criterion





Factors influencing conservation priority

- Phenotype
 - genetic merit for productivity
- Unique traits
 - adaptive traits
 - environment interaction
- Historical and cultural importance
- Practical considerations
 - species and ease of conservation
 - chance for success







Prioritization without molecular data

Use single criterion

• Risk of extinction or carrier of unique trait or cultural value

Multivariate statistical methods

- Correspondence or principal components analysis
 - reduce many variables to smaller number
- Cluster analysis
 - assign breeds to similar groups
 - choose single breed from each group
- Multivariate Index
 - assign different weights to characteristics of breeds

Farmer Choice models(Zander and Drucker 2008)

Consumer WTP

Geographical approaches valuable when no formal "breeds" exist



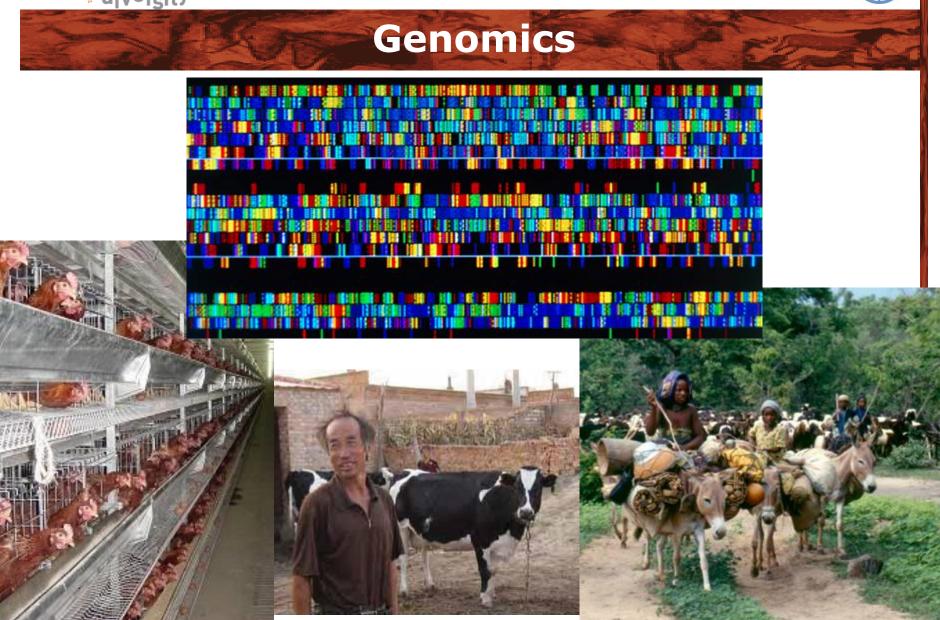


Use of formal approaches to prioritize breeds for conservation

	Number of	Fumber of countries with formal conservation priorization approaches		Criteria for breed conservation priorization. Percentage of countries using each criteria among countries reporting formal approaches for conservation.													
Regions and sub regions	countries			n Risk of extinction		Genetic uniqueness		Genetic variation within breed		Production traits		Non-production traits		Cultural or historical importance		Probability of success	
Africa	40		58		78		87		35		70		30		74		52
East Africa	8		50		75		100		50		50		75		100		75
North & West Africa	20		65		69		77		31		77		15		77		46
Southern Africa	12		50		100		100		33		67		33		50		50
Asia	20		70		71		86		71		93		64		79		71
Central Asia	4		100		25		75		50		100		50		75		100
East Asia	4		50		100		100		100		100		50		50		100
South Asia	6		67		100		75		50		75		50		75		25
Southeast Asia	6		67		75		100		100		100		100		100		75
Southwest Pacific	7		43		67		100		100		100		67		100		33
Europe & the Caucasus	35		89		100		71		74		55		52		87		39
Latin America & the Caribbean	18		56		100		80		60		80		40		110		40
Caribbean	5		60		100		67		33		67		67		100		33
Central America	5		40		100		100		100		100		50		150		100
South America	8		63		100		80		60		80		20		100		20
North America	1		100		100		100		100		100		100		100		100
Near & Middle East	7		29		100		100		100		100		-		50		50
World	128		66		88		81		63		71		46		85		49







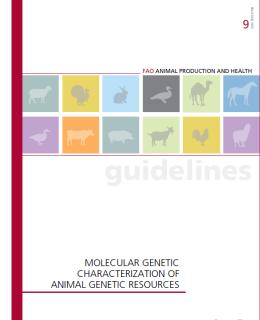


Molecular data is mainly used to measure breed diversity and relationships among breeds

- $-\uparrow$ diversity = \uparrow priority
- $-\uparrow$ distinctiveness = \uparrow priority

History – Use of genetic information

- Measurement of Domestic Animal Diversity (MoDAD)
- ISAG-FAO advisory group on animal genetic diversity
 - 1998 Standardized microsatellite lists proposed
 - cattle, chicken, sheep, swine
 - 2004 new microsatellite lists
 - 4+ Buffalo, goat, horse, donkey, camelids
- Scope of utilization increased
 - several multi-country projects
 - Problems to link studies









Current Situation

- DNA analysis technologies have rapidly advanced
 - more information
 - greatly reduced costs
- Technological advances allow for expansion of objectives beyond those foreseen for MoDAD
 - functional and neutral variation
 - genetic profiling of individuals rather than breeds
- FAO is implementing "Production Environment Descriptors" in DAD-IS
 - Study of links between genomes and environments



- "Genomics Revolution" could increase the utility of molecular genetics in management of AnGR
- Genomics study of genomes of organisms
 - Study of entire sequence
 - Variability in multiple genome regions
 - Fine scale genetic mapping
 - Interactions between genes and their products
- Prompted by large-scale declines in cost of obtaining information





Sustainable Use and Development

- Recent biotechnological advances
 - efficient sequencing
 - increased information about polymorphism in genome
 - denser maps at lower cost = \uparrow increased precision
- Single Nucleotide Polymorphisms (SNP)
 - causative variants of simply-inherited traits
 - genome-wide selection within breeds
 - selection signatures across breeds
 - increased biological knowledge







Conservation

- "Conservation Genomics" = new field
- Improved accuracy of haplotype reconstruction
 - Diploid with linked loci
 - Assign loci to parental origin
- Increased precision of parameter estimates
 - Population structure, Effective population size
 - Direction of migration
- Substitution for pedigree information
 - When not available
 - For refinement for animals with equal pedigree relatedness



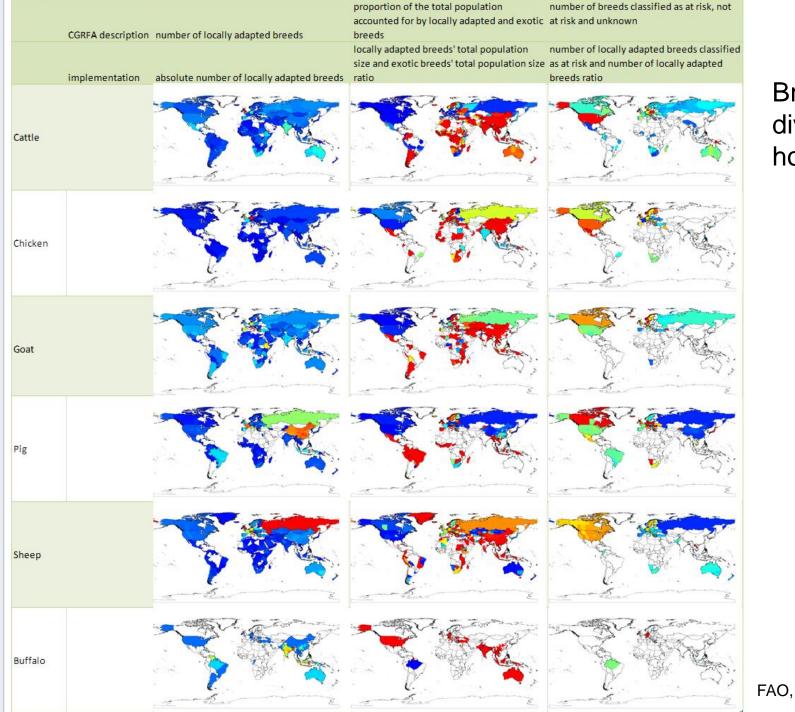
Conservation and Selection

- Improve phenotype of conserved breed to improve productivity
 - Genomic selection to increase accuracy
 - Overcome lack of routine phenotypic data collection
- Overcome effects of inbreeding depression
 - Identify loci responsible for inbreeding depression
 - Increase variability
 - Select for positive alleles
- Introgression
 - Keep desired genes from outside breed
- Recovery from unwanted hybridization
 - Eliminate in general genes from outside breed



Conservation and Distinctiveness

- Take advantage of a breed's uniqueness
- Selection signatures
 - Identify genes responsible for unique phenotypes
- Local breeds tend to be better adapted to harsh environments
- Integrate genomic with other sources of data
 - Phenotypes
 - Climatic variables
 - Geographic data
 - Zones of epidemic disease



Breed diversity hotspots

FAO, 2014





Constraints

- Costs
 - Prices are continually decreasing, but many applications are still "out of reach" for many countries
- Data
 - Genomic selection procedures rely on bank of phenotypic data
 - Cannot easily use data from other populations
 - Linkage phase
 - G x E
 - Data "overload"
- Ascertainment bias
 - Incorrect estimates of genetic variability





Conclusions

- Genomics can be a powerful tool in management of AnGR
 - abundance and precision of data will only increase
 - New standards (SNP, full genome sequencing?)
- Technology can not solve all problems
 - Avoid raising false hopes
 - Raise awareness on importance of non-genomic data
 - Need phenotypes
- Gap in capacity for developing countries





Recommendations

- Reach consensus on diversity measure
 - "Balanced" approaches
- Improve characterization
 - molecular for estimation of diversity
 - phenotypic for consideration of other information
 - Carrier of specific alleles (adaptedness, diseaseresistance, selection signatures....)
- Improve population monitoring
 - identify breeds at risk or of specific value (unique traits)
 - Link of breeds with production systems
- Continued and increased international collaboration and capacity building



