

## Animal genetic biodiversity - methodological considerations

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### 1 Introduction

The livestock sector in the world, especially in developing countries, will face a strong challenge to satisfy a rapid increase in the demand for meat, milk and fibre due to the continuing population growth, rapid urbanisation and rising incomes. In the past the demand for an increased food production has been realised by a combination of genetic improvements, greater farming inputs and cultivation of more land. It has to be recognised that the potential for increasing arable areas is limited, hence the future demand for livestock products will have to be met through intensification, increasing the productivity of land and livestock. Production objectives will become more specialised, reducing the number of distinct breeds of farm livestock and putting many of those in danger of extinction. The Domestic Animal Diversity Information System (DAD-IS) of FAO states that there are 332 cattle, 407 sheep, 123 goat, 156 pig and 213 horse breeds maintained in 37 European countries of which about one third are in danger of extinction. Similarly, in 14 countries of sub-Saharan Africa there are 66 cattle, 64 sheep, 61 goat, 15 donkey and horse breeds considered as indigenous breeds of which about 10% are considered as endangered. Main causes for the breed substitution in those developing countries are seen as urbanisation, modernisation and productivity differentials between indigenous and exotic breeds which are rarely proven since unbiased comparisons are scarce. This is particularly true in some cattle breeds where artificial insemination permits very rapid replacement of existing populations. This paper focuses on ways to identify the value of indigenous breeds, also in comparison to exotic breeds, for reducing the danger of their continuing depletion.

### 2 Reasons for conservation

In general the depletion of livestock breeds is a consequence of economic change. To a certain extent there is a conflict between the desire of preserving the present variety of livestock breeds and increasing production efficiency by concentrating on more productive genotypes. On the other hand there are some important reasons why the variety of livestock breeds should be conserved. First, production environments and market requirements vary so much throughout the world that a variety of breeds is needed. Developments, such as the growing demand for specialised food, diversification in production systems (intensive versus hobby farming), and use of animals for sports, require a large variation in animal species and breeds within species. Second, the high-input high-output systems are characterised by high use of fertilisers, drugs and other factors. Agricultural pollution and resistance against drugs can encourage changes in production systems in which management traits are of higher value as compared to production traits. This is demonstrated by the shifts in European dairy cattle over the last 25 years in the light of market saturation and quotas from milk and butterfat production to protein and management traits. Third, due to our inability to envisage long-term

requirements in production and market conditions and in the light of rapid changes in identifying the genetic background of species, breeds and animals at the gene level it is prudent to ensure that animal breeds having survived to the present are to be conserved.

### **3 Techniques for conservation**

The techniques for maintaining indigenous and endangered breeds depend on the conservation objectives and the degree of breed extinction.

- In general, in situ conservation which means keeping a breed in its normal production environment allows for better characterising the breed, further genetic development of the breed and adaptation to changing production and market environments. Since very little is known on the performance of most indigenous breeds there is a need to better understand their genetic and economic value
- Ex situ techniques are applicable for endangered breeds which are to be conserved and eventually re-established knowing their genetic and economic value. Cryoconserved embryos, somatic cells and semen are possible choices. Using semen for backcrossing females requires four generations to achieve over 90% of genes of the endangered breed. Through this process cytoplasmatic effects are lost or altered. Semen can also be used for creating synthetic breeds and for gene introgression to apply breeding programmes in live populations.

### **4 Identifying the value of breeds**

The methods to conserve breeds in technical terms are clear, but prior to conserving breeds it is necessary to counteract the process of a breed decline through several actions within countries. Such important actions are: getting reliable data on the phenotypic and economic performance of the breed, improving infrastructures and technical assistance, developing and installing selection programmes for raising productivity and profitability, and optimising production systems. Such actions have been spelled out in several breed conservation projects as proposed within the CDAD for CEE countries and others.

Factors important in such breed evaluation studies are:

#### Describe production environment

Describing the environment in which the population is kept is essential for understanding the value of the breed. The location, climate and feed resources are to be recorded. Also management conditions such as housing systems, herding practise, watering, supplementation and health intervention should be described.

#### Estimate population size, breeding structure and degree of endangerment

Due to uncertainty about future production systems and markets the major goal may be to maintain as many breeds as possible. Conserving genetic variation is also best obtained by retaining separate pure breeding populations instead of just one big population (*Hall and Bradley, 1995*). This is because market forces can push the selection within a population to a narrow breeding goal, also modern reproduction techniques can give few families or animals a major influence within a population.

For estimating population size macro studies as proposed by *IEMVT (1989)* are to be carried out which are based on rapid and reliable survey techniques providing estimates on the population size, breeding and age structure. Number of males and females, number of castrates, use of artificial insemination and number of animals moving out or into a herd are valuable bits of information. Phenotypic estimates on reproduction and production parameters become available if a large number of herds (more than 100) are surveyed within ecological zones.

As pointed out by *Ruane(1999)* the degree of endangerment depends also on other factors such as rate of change of population size, rate of immigration in the past, risk of crossing with other breeds , degree of organisation of farmers and distribution pattern of animals across herds.

#### Selecting important variables

Knowing the economic importance of traits is of paramount importance for developing and conserving breeds. If a breed is known to have one or several traits such as high fertility, disease resistance or any other trait which is of high economic importance today or in the future then it will be developed or conserved. The today's importance can easily be derived, but to quantify the situation in the long-term is very difficult if not almost impossible.

In countries with expected population growth and urbanisation, emphasis may be given to quantitative traits such as milk yield and growth rate, in developed countries food quality and other secondary traits may gain importance as production intensity may decrease. Political decisions such as reduction or removal of subsidies may influence rapid and dramatic changes in the economic value of traits. Some breeds may have unique behavioural or physiological and adaptive traits, e.g. Meishan pigs are extremely fertile, N'dama cattle are known for their resistance to trypanosomiasis.

The only conclusion for describing populations which provides some information on their actual and future value with some degree of certainty must be to collect as many traits as possible including those with little or no economic relevance today, i.e. production and productivity traits, physiological and adaptive traits.

#### Collect reliable data

Characterising breeds should be based on performance data within their production environment, i.e. performance data are to be collected in on-farm studies. In many developed countries a system of breeding organisations and herdbooks has been set up over the last 100 years providing large databases on pedigree and performance data, whereas in some central and eastern European countries this is not necessarily so. In most developing countries there is no regular system of data recording. The activities of CDAD are aiming at collecting pedigree and performance data.

Table 1: Precision of estimated phenotypic mean of breeds in on-farm studies

Farms	No. of Sires per farm	<i>Standard error of mean</i> (in % of mean)		80% error of mean <sup>*)</sup> (in % of mean)	
		$\sigma^2_f=10\%$	$\sigma^2_f=40\%$	$\sigma^2_f=10\%$	$\sigma^2_f=40\%$
40	1	2.7	3.6	3.5	4.6
20	2	3.0	4.8	3.8	6.1
8	5	4.2	7.2	5.4	9.2
80	1	1.8	2.4	2.3	3.1
40	2	2.1	3.3	2.7	4.2
16	5	3.0	5.1	3.8	6.5
160	1	1.2	1.8	1.5	2.3
80	2	1.5	2.4	1.9	3.1
32	5	2.1	3.6	2.7	4.6

No. of dams(offspring) per sire=5, variance between farms  $\sigma^2_f$ , heritability  $h^2=16\%$ ,  $CV=30\%$   
<sup>\*)</sup> =1/2 confidence interval (80%)

Certain requirements for estimating sufficiently precise means of breeds are calculated by *Bruns (1992)* which are summarised in table 1. On-farm studies with the objective of describing populations are constrained by small farm sizes and by the small number of sires used in breeding and within farms only. Unknown sire identification is another constraint. In general, the precision of estimated means is given by the standard error or the error of the mean which equals half the confidence interval. The numbers in table 1 indicate that at least 400 animals should be sampled to describe a population if the error of the mean should be between 2.5% and 5%. More precise estimates of the mean require a sample of 800 animals per breed or more. Important factors influencing the sample size are the distribution of sires across farms (here a hierarchical structure assumed), number of sires per farm, number of mates and offspring per sire, the relative size of the variance between farms and the heritability. The requirements for estimating variances or standard deviations within breeds can be derived in a similar way as for estimating means, but the errors of estimated standard deviations are about 50% larger than the errors of estimated means for the same number of observations.

More precise estimates of animals' performances are obtained if the environmental effects can be reduced, i.e. performance testing is carried out under controlled and standardised, but population-typical environmental conditions. Testing performance in such environments can be necessary if data collection is technically difficult and costly, e.g. measuring feed intake, pulling power, physiological traits etc. If the testing environment is very distinct from the production environment then the problem of genotype-environment interaction arises.

#### Estimate genetic parameters

For a genetic characterisation of breeds either genetic parameters of the important traits are to be estimated and/or allele frequencies can be used to estimate genetic diversity between and within populations at the level of genes. For estimating genetic parameters, such as genetic variances and covariances or heritabilities and genetic correlations, data from on-farm and on-station studies are useful if ordinary animal identification is guaranteed. The precision of the estimated parameters depend on the total number of animals, the number of offspring per sire, and on the size of the population parameters (see table 2). In general, 400 animals or 40 sire groups are the minimum requirements for estimating heritabilities, whereas for estimating

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genetic correlations 800 animals or 80 sires are needed. Therefore genetic parameters can only be estimated in sufficiently large populations which are not in great danger of extinction. Specific biases in estimating genetic parameters may occur in populations with incomplete and incorrect animal identification, with farms of small size (single-sire farms) and in case of selection of animals.

Table 2: Precision of estimated genetic parameters in on-station studies

sires	No. of offspring	Standard error of heritability (in % of pop. value)		Standard error of genetic correlation (in % of pop. value)		
		per sire	$h^2=.16$	$h^2=.32$	$r_A=.25$	$r_A=.50$
5	20		156	106	340	136
10	10		169	97	340	136
20	5		200	109	392	156
10	20		100	69	220	88
20	10		112	69	232	94
40	5		144	78	280	112
20	20		69	47	152	60
40	10		75	47	156	62
80	5		100	53	192	78

No. of dams per sire=1, half-sib analysis, *Bruns (1992)*

The field of molecular genetics is rapidly developing. For studying genetic relations within and between breeds polymorphism of marker loci are important. In the past some types of markers used in such studies were biochemical markers, bloodtypes, genetic markers, microsatellites and nowadays random amplified polymorphic DNA (RAPD) or DNA-chips. Genes that code for functional proteins are less favourable than noncoding loci like microsatellites since mutation in functional genes will in general have a deleterious effect and become extinct after some time. Polymorphism found in microsatellites are better estimates of the genetic diversity than polymorphism of functional genes. Estimating genetic diversity is a statistical method similar to estimating genetic parameters shown above. Again the sampling process is of importance. The animals sampled should be randomly drawn and should reflect the actual composition of the population. Generally, samples of 25 unrelated animals are taken to be the minimum requirement (*FAO, 1998*) with 50 drawings of alleles per locus.

#### Organise breed comparisons

The decline of many indigenous breeds has been reinforced through breed comparisons which were based on poor experimental designs producing misleading results (*FAO, 1998*). Often the samples were too small, genetic parameters were not estimated, secondary traits such as feed intake, longevity, mortality, fertility which affect productivity are not recorded. Better assessment of breed performances could be achieved if national recording schemes exist and market prices of products are kept.

More accurate comparisons of breeds can be done in on-farm and on-station studies. The following points are important for good evaluations of indigenous and exotic breeds:

- In the design of such comparisons the sampling process and the sample size are important and discussed above.

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- Due to possible genotype x environment interactions performance testing has to be under environmental conditions which resemble the original production system of the indigenous breed; since environmental conditions are not constant over time, production systems may change from extensive to semi-intensive or intensive, comparisons are ideally carried out in differently intensive management systems.
- Genotype : environment correlations which are often positive, i.e. the better breed is receiving better environmental conditions, have to be avoided.
- For a proper economic comparison secondary traits as indicated above affecting productivity are to be evaluated.
- For identifying the genetic value of indigenous breeds in crossbreeding production systems evaluations of crossbreds having different genetic composition (e.g. F1, R1, F2) are necessary. Synthetics can only correctly be evaluated after several generations of recombination.
- An overall economic evaluation of the breeds has to be based upon different prices for input and output factors.

Devise selection program

Based on the breed evaluation as discussed above a local population can have a commercial value and then it should have an organised breeding program to maintain its competitiveness against other breeds. Such a scheme for improving the important production and adaptive traits and for monitoring genetic variability has to be set up and involves:

- Unique identification system necessary for optimal genetic evaluation of individual animals and for checking matings
- Decision on traits to be recorded under on-farm or on better controlled conditions which includes production traits but also adaptation and other secondary traits making up the economic and conservation value of the local breed,
- Genetic evaluation systems should adjust records for both production environment and information from relatives,
- Depending on the population size selection and mating plans are to be developed for improving the genetic value of the breed, but keeping inbreeding at a predefined rate (*Meuwissen, 1997*),
- Applying cryopreservation of semen and embryos or oocytes helps improving efficiency of selection, but also provides a back-up in case of genetic problems and can help increasing the effective population size with an appropriate mating plan if needed.

## **5 Concluding remarks**

The genetic diversity found in animal breeds allows to select animals and to develop new breeds in response to changes in the environment, threats of disease, market conditions, all of which are almost unpredictable. Breeds which are rare today may carry traits which are of commercial importance in the future. To stop the gradual depletion of indigenous breeds that are able to survive in extreme conditions helps reducing the danger of genetic erosion. Many local breeds best-adapted to their environments have a potential for increase of production. This paper summarises methodological considerations for identifying the genetic and economic value of local breeds. Fortunately, the common approach of importing exotic animal breeds to boost production in livestock in developing countries is being rethought and more weight will be given to develop local indigenous breeds which includes building up

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appropriate infrastructures. New technologies in population and molecular genetics and in reproduction can be valuable tools for conserving and improving indigenous populations, but if not properly used can play a role in depleting animal genetic resources.

## **References**

- Bruns, E. (1992): Synthesis of research methodology. African Animal Genetic Resources: Their Characterisation, Conservation and Utilisation. ILCA, Addis Ababa, Ethiopia, 19-21 Feb 1992
- FAO (1998): Secondary Guidelines for Development of National Farm Animal Genetic Resources Management Plans – Management of Small Populations at Risk. FAO, Rome, Italy
- IEMVT (1989): Les enquetes sur la productivité du bétail. Fiches Techniques D'Elevage Tropical 5, Sept 1989
- Meuwissen, T.H.E. (1997): Maximising the response of selection with a pre-defined rate of inbreeding. *Journal of Dairy Science* 77, 1905-1916
- Hall, S.J.G. and Bradley, D.G. (1995): Conserving livestock breed diversity. *Trends in Ecology and Evolution* 10, 267-270
- Ruane, J. (1999): Selecting breeds for conservation. Genebanks and the conservation of farm animal genetic resources. DLO Institute for Animal Science and Health. ISBN 90-75124-06-6, 59-74