AFRICAN ANIMAL GENETIC RESOURCES: THEIR CHARACTERISATION, CONSERVATION AND UTILISATION

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Preface

A combination of high population growth rate and the desire for higher living standards is putting pressure on African livestock owners to increase production. This has necessitated concentration on a narrow range of genotypes supposedly suited to current production and market conditions. At the same time, developments in communication and advances in biotechnology (especially AI) have accelerated the international movement of germplasm, thereby shifting local attention to the more specialised exotic breeds. Consequently, indiscriminate crossbreeding with, and/or replacement by exotic germplasm represent serious threats to indigenous populations. Moreover, interbreeding among indigenous breeds as a result of increased intermingling, through trade and social exchanges of previously isolated populations, and effects of protracted civil wars, worsened by drought and famine in some regions, represent additional pressures on indigenous African animal genetic resources (AGR). Unfortunately, inadequate attention has been given to evaluating these resources or to setting up realistic and optimum breeding goals for their improvement. As a result, many African AGR are endangered and, unless urgent concerted efforts are taken to conserve them, may be lost even before they are described and documented.

Several expert panel meetings involving, among others, the Food and Agriculture Organization of the United Nations (FAO), the Organization of African Unity (OAU) through its Inter-African Bureau for Animal Resources (IBAR), the United Nations Environmental Programme (UNEP), National Agricultural Research Systems (NARS) and other International Agricultural Research Centres (IARCs), including ILCA, have addressed the issue of endangered breeds, both at global and regional levels. However, efforts in support of AGR have remained primarily at the stage of studies to identify priorities. There is now growing consensus that it is time to move beyond studies of options and priorities to their implementation.

At the ILCA Programme Planning Meeting of October 1991, a project on characterisation and conservation of Africa's indigenous AGR was proposed. In taking on this challenging task, ILCA recognised that it could not succeed without substantial collaboration with NARS colleagues. However, we also recognised the need to work out standard characterisation methodology and to outline the implementation process. This workshop was organised by ILCA, as part of the research planning process, to address these issues. The workshop took place 19-21 February 1992 at ILCA headquarters in Addis Ababa, Ethiopia. In addition to NARS scientists, the workshop was attended by AGR experts from FAO, several IARCs and other institutions outside Africa.

Workshop participants reached the consensus that this project was timely and that activities should be initiated to document Africa's AGR, with a view to developing strategies for their conservation and sustainable utilisation. While stressing the importance of breed characterisation, participants reiterated that those breeds identified as currently endangered should be conserved even if their value is not presently apparent. Considerable attention was given to development of experimental designs which would optimise collection of data on population dynamics, physical characteristics and phenotypic and genetic parameters of biological performance traits.

With the exception of breeds in imminent danger of extinction, the workshop did not come up with recommendations on which breeds should be targeted first. However, it was proposed that the breed characterisation process should begin with a few (2–3) pilot projects and that this would be expanded as and when funds became available.

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Acknowledgements

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Logistic support for the workshop was provided by ILCA's Department of Training and Information; our most sincere thanks to Ato Getahun Kifle. Appreciation is also extended to the Publications Section, particularly Ato Tekleab H/Micheal, Ato Mahmoud Saleh and their staff for the final production of this document.

Welcoming address

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The Director General (DG) of ILCA welcomed participants to the workshop and expressed the hope that the ensuing discussions would provide a framework for future ILCA research activities in the area of animal genetic resources. He provided an overview of the Centre's research activities, organisational structure and mode of operation.

The DG added that ILCA is presently at the end of its five-year programme plan and budget. The Centre is now in the stages of preparing a strategic plan of action for the next five years. The output generated from the workshop is expected to form an integral part of the deliberations that will determine ILCA's future involvement in the area of characterisation and utilisation of the diverse pool of animal genetic resources in sub-Saharan Africa.

SESSION I

Animal genetic resource characterisation, conservation and utilisation

Chair: H.A. Fitzhugh

Introduction

H.A. Fitzhugh

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ILCA recognises the value of genetic diversity and variability in Africa. There is an opportunity to better utilise these resources. But, to do so, we need to characterise what exists and find ways of conserving the genetic diversity with the directed aim of utilisation.

Concern with utilisation should not be underestimated. ILCA statistics indicate that the value of livestock products in sub-Saharan Africa is estimated at US $16.7 billion. The real figure might well be higher by several billion dollars.

FAO statistics, developed in support of the Agriculture 2000 Study, indicate that livestock, as a proportion of GDP for all of sub-Saharan Africa, stands at 7%. In terms of the contribution of livestock to agricultural GDP, this figure rises to 25%. These figures indicate that the contribution of livestock is more important than previously thought.

The appropriate role for livestock in developing regions is to improve the quality of life for farmers and consumers of livestock products. Livestock are a critical component of the rising standard of living for developing countries, particularly Africa. They provide incentives for environmentally and economically sustainable agriculture. As the developing world moves towards greater sustainability, the value of livestock will increase.

ILCA is particularly interested in specific adaptive abilities of breeds, for example, trypanotolerance in N'Dama cattle or the prolificacy of the Barbados Blackbelly sheep. They represent genetic resources that have contributed to cattle/small ruminant production outside Africa.

The interest in genetic diversity in part stemmed from our ability to safely move germplasm across the world. Originally, the thought was to upgrade indigenous breeds to improved European types in order to create what was considered a "good animal". However, efforts in this area ignored the fact that indigenous breeds are quite adaptive to African conditions and that crossing/upgrading breeds runs the risk of diluting a valuable genetic resource base.

Experience has also shown that upgraded breeds do not necessarily respond well to problems that exist under African conditions (e.g. tsetse challenge, trypanosomiasis). Thus, we need to be careful that when we attempt to move "improved genotypes" into unimproved environments, we do not run the risk of losing important adapted genetic resources. We also need to be concerned with the trade-offs between productivity and adaptability.

Funds and resources are being mobilised and brought to Africa in recognition of the importance of livestock to Africa and the rest of the world. Yet, the challenge exceeds the resources and capabilities of a single institution such as ILCA. Success will come only through partnerships, particularly with scientists in NARS that have access to the genetic resources and will be in place for the long-term, day-by-day requirements for adequate characterisation. Thus, maintaining the diverse genetic resource base will require collaboration, not only with NARS, but with donors and other institutions (e.g. FAO, European universities, research institutes) as well.

If we work together in an effective, well-planned and adequately funded fashion, we will be able to serve the needs of people in Africa and around the world.

We are hopeful and grateful for your attendance. This workshop provides us with the opportunity to move ahead on an important problem where we can make a useful contribution.

Animal genetic resources: The perspective for developing countries

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Prior to his presentation, Dr. Cunningham noted that the workshop represented an opportunity for FAO to reinforce associations with individual NARS. When we focus on animal biodiversity, all paths seem to lead back to Africa.

ILCA and NARS have concluded that traditional animal breeding efforts and techniques are important, but that more information is needed regarding the genetic populations that exist in the system. This background information should precede any major interventions. The motivation for our work is improved harnessing of these animal populations for the betterment of the human population.

Introduction

The livestock sector is responsible for over half of the agricultural output in the developed world. In developing countries as a whole, it is responsible for a quarter of the output. This proportion is growing. In addition, when account is taken of the non-commercial contributions of livestock, such as work, fuel and manure, livestock are responsible for almost half of the output of agriculture (FAO, 1991). Furthermore, in many countries with large pastoral resources, livestock are the mainstay of the economy. These points emphasise the fundamental importance of livestock resources for future agricultural and economic development in developing countries.

In the short evolution of agricultural systems, covering somewhat less than 10,000 years, surprisingly few animal species have been domesticated. Evidence from the earliest human settlements (Ammerman and Cavalli-Sforza, 1984) indicate that the same species have been used from the start: sheep, goats, cattle, pigs and buffaloes. Though other species (camelidae, rabbits) are locally important, practically all of animal agriculture can be accounted for by less than 20 mammalian and avian species. These are a small subset of the 40,000 known vertebrate species (including 4,000 mammalian and 9,000 avian).

Despite this narrow species range, the animals used in agriculture represent an enormous breadth of biological diversity. Much of this diversity is undoubtedly due to the fact that, with the spread of settled agriculture to all sectors of the globe, specialised and adapted strains from each species have evolved for a wide range of environmental conditions.

This great pool of diversity is now under threat. As development proceeds, livestock agriculture moves from subsistence to commercial farming systems. Production objectives become more specialised and competitive pressures increase. The effect of this process can be seen in Europe, where of the surviving 737 distinct breeds of farm livestock, one third are in danger of extinction (Maijala et al, 1984). In these countries, an awareness of the potential value of endangered breeds has been combined with the necessary resources in

most cases to put in place a variety of conservation programmes. In developing countries, particularly Asia and Africa, the development process is far less advanced and a much higher proportion of the historical pool of variability survives. However, here too economic pressures are having the same effect. This is particularly true in some cattle breeds, where artificial insemination permits very rapid replacement of existing populations.

Conserve or develop?

It is clear that the depletion of genetic resources is a consequence of economic change and development. Therefore, is there an inevitable conflict between the desire to conserve the present variety of genetic resources and the need to concentrate increasingly on a narrow range of genotypes in the interests of more efficient production? To a certain extent there is. Because of the competitive nature of livestock farming, it is clear in certain circumstances that more productive individuals, strains or breeds will tend to replace less productive ones. However, this drive is tempered by three main factors. First, production circumstances and market requirements vary so much throughout the world that a variety of breeds and types is needed within any one species. Second, in any one set of production and market conditions, requirements change over time. This is well illustrated by dramatic shifts in objectives for European dairy cattle in the last 20 years; initially from dual-purpose to specialised dairy types, and, more recently, in the wake of market saturation and quotas, from milk and butter fat production to protein and management traits. The third element can be called the insurance factor. While short-term trends in livestock farming systems are evident, we cannot accurately envisage requirements more than a few decades into the future. Furthermore, the actual genetic patrimony of most breeds and strains in the world has only been observed at the most superficial level. There may well be genes and gene combinations of great value but at this stage are totally unknown. For these reasons, it is prudent to ensure that the breadth of genetic resources which have survived to the present are conserved.

FAO's programmes

Animal genetic resources (AGR) have been part of the FAO programme since the establishment of the organization, but a significant new approach was taken during the last decade following a Technical Consultation in Rome in June 1980. The approach was further developed by an FAO/UNEP Expert Consultation, held in Lomé, Togo. The programme was initiated in 1982, and was supported financially by the FAO Regular Programme and UNEP funds. From 1982–1990, a large programme of work, based on the recommendations of the 1980 Expert Consultation, was implemented. The methodologies for a global programme for AGR have been researched and defined and the necessary infrastructures established. The work has been documented in a series of publications in the FAO *Animal Production and Health Paper* series.

The current programme addresses the needs of both development and conservation in different parts of the world. An example of the former is the nuclear selection scheme for Awassi sheep in Turkey, aimed at increasing productivity of an important Middle Eastern breed *in situ*. An example of conservation activities is the recently published major inventory of livestock resources of the former USSR. More than 30 field projects addressing problems of development or conservation of AGR throughout the developing world are in progress.

In 1989, a major review of the programme in this area was carried out, and the groundwork has now been laid for a new global programme on animal genetic resources. It has the following five main elements.

Global Inventory of AGR and World Watch List

Initially, the global inventory will be prepared in its simplest form, essentially describing each breed, its effective population size and a limited set of key production parameters. A first edition will be published at the end of the first year of the project. Over the life span of the project, data inputs to the inventory will be expanded such that by the end of the project, a comprehensive Global Inventory of AGR will be compiled and published and a permanent data base established.

Based on the data collected for the Global Inventory, a World Watch List will be published at regular intervals focusing attention on breed populations considered to be at risk. The attention focused on particular breeds will enable national governments to take action to preserve endangered breeds and to seek technical assistance where necessary.

Breed preservation

As and when endangered breed populations are identified and if, following detailed evaluation, the breed is considered to have genetic uniqueness, preservation plans will be drawn up. The preservation strategy will be country-specific, and may involve semen or embryo collection and storage or *in situ* preservation. Priority will be given to utilising in-country facilities such as national AI centres and government farms. Regional genebanks will evolve to the extent that they are justified on cost-benefit analysis.

Many countries throughout the developing world have placed their indigenous livestock populations at risk through programmes of exotic breed importation and/or crossbreeding. Rarely has adequate attention been given to evaluating and setting realistic and optimum breeding objectives prior to embarking on breed improvement programmes. Mistaken objectives are sometimes then followed by breed improvement schemes that are totally inappropriate to the existing or available infrastructures. It is proposed to assist selected member states in planning and initiating realistic breeding strategies in order to avoid inappropriate breed replacement/dilution programmes. The intention is to link any such activities in developing countries with parallel technical programmes in the developed world.

Indigenous breed development/conservation programmes

The genetic improvement of selected indigenous breeds is a major objective of this programme. In many cases, a local breed which remains static in the face of competition and changing requirements will not survive. Breed improvement programmes, tailored to fit the conditions in which the breeds are farmed, will therefore be planned and implemented. A total of 12 unique populations have been selected for attention in the first phase of what will be a five-year programme. These have been selected on the basis of their regional importance and genetic uniqueness and are listed below.

Species	Asia	Africa	Latin America
Cattle	Sahiwal	N'Dama	Criollo
		Kenana	Guzera
Sheep	Awassi	Djallonke	Pelibuey
Goats	Zeraby		
Buffalo	Murrah	–	–
Pig	Taihu	–	–
Camelidae	–	–	Alpaca

The breed improvement programmes developed for each of these populations will vary from case-to-case. However, they will share common methodologies, e.g. based on the Genetic Screening/Open Nucleus Breeding Strategy. Participating country inputs will be substantial, including physical infrastructure, feed and operational costs. In the second phase of this project, an additional cohort of indigenous breeds will be identified for development.

Gene technology/genome mapping

The economics of germplasm preservation could be made significantly cheaper if it were demonstrated that many breeds shared a common DNA heritage. DNA level studies may enable geneticists to categorise breeds in terms of genetic distance and in this way to sharpen the scientific rigour with which breeds should be selected for preservation. Furthermore, genome mapping may eventually lead to the isolation of DNA segments that code for particular traits, such as trypanotolerance. This would revolutionise the overall approach to genetic resource preservation. It could also have a dramatic effect on the cost of preservation or use of genetic resources. A venture research fund is being proposed to stimulate, coordinate and guide particular lines of research, which in the longer term, may lead to new and more efficient mechanisms for the conservation of animal biodiversity.

Legal and international framework

As in the plant world, but with significant differences, there is a growing need for a framework of internationally agreed conventions to protect legitimate rights and to guide and regulate access to the world's animal genetic resources. As part of the overall programme, the development of the necessary legal and regulatory instruments is being undertaken.

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Conservation of livestock breeds

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Introduction

The conservation of local breeds should be considered whenever the development of animal production systems is discussed. This essay concerns the importance of breed conservation with particular reference to Africa.

From a European standpoint, breed conservation is seen as the protection of rare breeds (up to 1500 breeding females). Most conservation initiatives are private and generally proceed by breed-society type activities aimed at fostering breed ownership to maintain living populations. These owners usually do not depend on such flocks and herds for their livelihood.

This is clearly not a helpful paradigm for African livestock. The following is suggested as a more appropriate definition of breed conservation:

"The rational use and protection of existing local genotypes from genetic introgression."

Livestock development programmes: General considerations

In many areas of Africa, animal production has been neglected, possibly because a tradition of husbandry is lacking and crops tend to predominate. Agency-funded livestock development programmes in Africa might involve the introduction of a hitherto unknown husbandry system, such as a first-world type dairy, pig or poultry operation ("industrial farming"), the encouragement of newcomers such as farmers who previously grew only crops to livestock production or the improvement of the productivity of a pre-existing livestock system.

Industrial farming and Africa

Industrial farming involves the introduction of genotypes such as Holstein-Friesian cattle, Large White-Landrace pigs and hybrid fowl that thrive in high-input production systems in developed countries. Provided enough resources are allocated, probably any livestock breed can survive, produce and reproduce in any country. However, the substantial recurring expenditure on imported feed, veterinary care and housing may mean that unless subsidies are forthcoming, the enterprise would not be profitable. Such enterprises are not sustainable. They are appropriate only if privately funded and could be seen as an abuse of aid funding because they tend to increase dependence on donor countries and are an inappropriate model for rural development.

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The use of imported breeds

The possible role of imported breeds in more traditional forms of husbandry should be examined. This includes breeds imported from other parts of the same continent. If the resources available are predicted to improve, the genotypes of the livestock that are to use them should be developed in step. However, local breeds may already possess sufficiently responsive genotypes. Accordingly, the response of local breeds to achievable improvements in husbandry should be investigated as should the constraints on productivity of traditional husbandry practices. There are already many examples of local breeds which have been shown to have the genotype enabling them to respond to improved husbandry. In these cases, the importation of genetic material could be unnecessary.

Strategies for genetic improvement of livestock and their consequences for breed conservation

The use of locally existing genotypes

Indigenous genotypes may well be adequate and able to respond sufficiently to reasonable economic improvements in the system. Over many generations they will have evolved to perform various functions under local conditions. For example, indigenous cattle can provide fuel, manure, traction, meat and milk and will probably have resistance to local diseases. Breeding stock would be locally available and their purchase would create cash flow and contribute to the confidence, willingness to innovate and prestige of competent breeders.

The *disadvantage* of using indigenous genotypes is that this approach is not as glamorous as the importation of new genotypes and is perhaps less likely to attract aid funding since heavy expenditure on imports from donor countries is not involved. Also, to discourage the importation of “high performing” (well adapted to first-world husbandry) livestock might fuel the suspicion that the latest advantages in technology are being withheld from the aid recipient.

Local breeds can be improved by selection, without the admixture of imported genetic material. However, it is difficult to predict whether the results would justify the investment. The strategy most likely to work, though the organisational problems may be insuperable, is a nucleus breeding scheme, whereby participating breeders contribute their best females to a central unit and are entitled to purchase stud males from the unit.

Supplementation of local stock with imported genotypes

Is there scope for upgrading local African stock by progressive crossing with imported genotypes? In principle the answer is yes. However, there is not enough time for a new, highly productive yet locally adapted genotype to emerge. There is also a major risk that the best females of local breeds will be the first to be used for upgrading, which would erode the local breeds. Upgrading will foster a climate of contempt for local breeds and devalue traditional husbandry skills. It is unlikely to benefit the smallholder farmer and hence may have limited contribution to the alleviation of rural poverty. However, such developments are very attractive to governments and aid agencies and are likely to continue. Accordingly, they should be accompanied by conservation programmes which would ideally find a role for the local breed as part of a stratified crossbreeding system. If this is not possible, cryogenic conservation should be practised. For example, for each ten doses of semen imported, one dose from a purebred local male should be frozen. Additionally, analogous to the environmental impact statements now demanded of infrastructure development programmes, a *Genetic impact statement* should be included in every livestock development proposal.

Replacement of local stock by other breeds from nearby

Sometimes local breeds may be replaced by supposedly more profitable breeds from the same or neighbouring countries. In Nigeria, for example, the West African Shorthorn or Muturu cattle, a dwarf trypanotolerant breed of the coastal and central zones (adult body weight about 200 kg), is under threat of replacement by other West African breeds. Although the breed population is still large, this is a long-term threat. These cattle are kept under a form of communal ownership in villages where the main interest is crop production. Numbers suffered greatly in the civil war of the late 1960s and ground lost by the breed was not regained, since there is little local interest in their husbandry for profit.

Schemes aimed at promoting cattle-raising in these areas are based on the N'Dama, another trypanotolerant breed mainly from the far west of the continent. In the central zone, tsetse fly eradication and a preference by traders for larger-bodied cattle has resulted in the replacement of trypanotolerant breeds by the White Fulani or Bunaji, a humped and apparently trypanosomiasis-sensitive breed. It is also possible, though data are lacking, that the Kuri, a large-bodied humpless breed with giant bulbous horns, kept in the Lake Chad area by sedentary communities, could be under pressure as a consequence of fighting in Chad, the spread of cultivation around the Lake and pressure from the Red Bororo cattle kept by migratory pastoralists. In these cases, a subsidy might be paid to owners of the threatened breeds.

The extent to which local breeds are threatened

There is pressing need for a central inventory of livestock breeds, supplemented by a data base of genetic data enabling the genetic distance among breeds to be calculated, so that criteria of taxonomic distinctiveness can be applied in conservation assessments.

Due to lack of inventories and status reports on local African breeds, the worst is often assumed, i.e. that breeds or varieties are disappearing or are unknown. Additionally, lack of support for local breeds in development programmes represents a lost opportunity.

An indication of African breeds

The breed dictionary of Mason (1988) was re-cast into tabular form. These tables deal only with breeds native to each country and distinguish breeds that are considered to have become extinct since 1892. The 459 breeds of ass, buffalo, cattle, goats, horse, pig and sheep reported to have become extinct is most certainly an underestimate (Table 1). This total does not tally precisely with the country totals (Table 2) because several breeds have as their native area more than one country, and these were tabulated once for each country. Relatively small numbers of breeds (mostly cattle) are extinct (Table 3). Again, this probably reflects a lack of information.

References

Mason I L. 1988. *A world dictionary of livestock breeds types and varieties.* 3rd ed. CAB (Commonwealth Agricultural Bureaux) International, Wallingford, UK.

Table 1. *Summary of world distribution of extinct, rare and commercial breeds.*

		Ass	Buffalo	Cattle	Goat	Horse	Pig	Sheep	Totals	% rare
Africa	Rare			10		1		4	15	
	Extinct			22		3		1	26	
	Commercial	15	4	168	61	33	6	131	418	
	Total	15	4	200	61	37	6	136	459	3
Asia	Rare		2	8	4	14	2	1	31	
	Extinct			5	1	3	8	2	19	
	Commercial	17	53	180	144	71	140	219	824	
	Total	17	55	193	149	88	150	222	874	4
Europe	Rare	10		101	29	49	37	109	335	
	Extinct	5		154	19	58	79	97	412	
	Commercial	8	8	209	91	137	76	356	885	
	Total	23	8	464	139	244	192	562	1632	27
N & C America	Rare			8	4	9	5	7	33	
	Extinct			1	1	4	17	10	33	
	Commercial	6	1	58	8	34	33	38	178	
	Total	6	1	67	13	47	55	55	244	16
S America	Rare	1		4				1	6	
	Extinct			19					19	
	Commercial	4	2	45	11	21	18	16	117	
	Total	5	2	68	11	21	18	17	142	5
Oceania	Rare			1		1	2	5		
	Extinct			2		1	1	5	9	
	Commercial			23	7		5	35	70	
	Total			26	7	2	7	42	84	7
Former USSR	Rare			9	4	23	2	11	49	
	Extinct			21	6	20	21	31	99	
	Commercial	15	1	49	15	37	32	122	271	
	Total	15	1	79	25	80	55	164	419	15
Totals		81	71	1097	405	519	483	1198	3854	

Table 2. *Numbers of extant breeds of each species in each country in Africa with native breeds.*[1]

	Ass	Cattle	Goats	Horse	Sheep
Algeria	1	2	2	1	10
Angola		5			4
Benin		4		1	1
Botswana		7(2)[2]	1	1	
Burkina Faso		2	1	4	1
Cameroon		11(4)	1		2
Chad		7	4	3	3
Egypt	3	6	6	1	9(1)
Ethiopia	2	17(1)		2	11
Gambia		3	1		1
Ghana		3	1		2
Guinea		1	1		1
Guinea-Bissau		3(1)	1		1
Ivory Coast		1	1		
Kenya	1	14	3		5
Liberia		3	1		1
Libya	1	1	1		4
Madagascar		4(1)			1
Malawi		1	1		1
Mali		6	2	5	8
Mauritania		1	2	1	5
Morocco	1	3	3	1	29(1)
Mozambique		2	2		1
Namibia		6	1		1
Niger		5	3	3	5
Nigeria		11	9	5	6
Senegal		6	1	4	3
Sierra Leone		1	1		1
Somalia	1	8	8	1	2
South Africa		11	4	4	25(2)
Sudan	4	20	11	2	16
Tanzania	2	9(1)	1		2
Togo		4	1	1	1
Tunisia	1	4	1	2	5
Uganda		12	3		1
Zaire		8	2		3
Zambia			1		
Zimbabwe			4		

[1] In addition to breeds noted in table, there are four breeds of buffalo native to Egypt, two breeds of pig native to South Africa and one breed of pig native to Cameroon, Ghana, Nigeria and Seychelles, respectively.

[2] ( ) refers to rare breeds, which are included in cell totals.

Table 3. *Number of breeds extinct since 1892.*[1]

	Cattle	Goats	Horse	Pig	Sheep
Algeria	4				
Benin	1				
Cameroon	1				
Gambia	1				
Lesotho			1		
Malawi	1				
Nigeria	2				
Rwanda	1				
South Africa	4		2		1
Tanzania	4				
Zimbabwe	3				
China					2
Hong Kong				3	
India	2		2		
Japan			1		
Pakistan		1			
Philippines	1				
Taiwan				5	
Turkey	2				
Canada			2		1
United States	1	1	2	17	9
Brazil	15				
Chile	1				
Uruguay	1				
Venezuela	2				
Austria	16		1		9
Belgium	2				2
Bulgaria	2		2		4
Czechoslovakia	10			1	
Denmark	3				1
France	18	2	15	18	33
Germany	29	6	7	10	5
Greece	7				1
Hungary	3		1		
Ireland			1		3
Italy	22		5	24	15
Netherlands					1
Norway	11	5	1		
Poland	5	2		5	1
Portugal	1				
Romania	3		3		
Spain	12		12	8	2
Sweden	4			1	
Switzerland	2	1	4		11
UK	5	2	4	7	8
Yugoslavia	2		3	5	
former USSR	22	6	20	21	31
Australia	2		1		1
New Zealand				1	1

[1] In addition, there are four extinct breeds of ass in Italy and one extinct breed of ass in Spain. In total, breeds extinct since 1892 are: ass 5, buffalo 0, cattle 228, goat 26, horse 90, pig 126, sheep 142. Grand total worldwide: 617.

Utilisation of indigenous animal genetic resources

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Introduction

Indigenous livestock are well adapted to tropical conditions. They have a high degree of heat tolerance, are partly resistant to many of the diseases prevailing in the tropics and have the ability to survive long periods of feed and water shortage. These properties are genetic and have been acquired by natural selection over hundreds of generations. They are all essential for successful animal production in the tropics. Indigenous stock represent a genetic resource which should not only be conserved for future use, but should also be fully exploited for short-term benefits.

However, it is quite obvious that the potential for milk and/or meat production is poorly developed in most of the livestock indigenous to the tropics. The challenge to the breeder is to improve this potential to a satisfactory level, without sacrificing adaptational qualities. The problem can be approached in basically two different ways:

i) Improvement by selection within the indigenous stock.

ii) Introduction of genetic material from outside by crossbreeding.

Improvement by selection

Most populations of indigenous livestock have been subjected to little or no deliberate selection for productivity. Considering the impressive results that have been achieved by selection in many temperate breeds, there should also be good prospects for improvement by selection in the tropics.

Genetic improvement per generation from selection depends on the variability of the traits considered, their heritability and the intensity of selection. Variability, in terms of the coefficient of variation, is often higher in tropical than in temperate populations, although the variation in actual units is less. As to heritability, few studies based on sufficient amounts of data have been reported, but most estimates fall within the same range as those for temperate breeds. Intensity of selection is restricted by the reproductive rate of the species and is further influenced by the rate of early mortality, which is often high under tropical conditions. In cattle, 50 to 80% of female progenies surviving to breedable age are needed for replacement in order to maintain herd size, and this leaves little room for selection. The situation is slightly better in small ruminants, particularly in populations where twinning is common. In both cattle and small ruminants, rate of genetic progress from selection is further reduced by the long generation intervals.

Traits which can be recorded in live animals of both sexes at an early stage of life, e.g. growth rate, can be improved relatively easily by selecting individuals for breeding on the basis of their own performance (individual selection, mass selection), provided there is a

reasonable amount of genetic variation in the population. For traits which cannot be recorded until the animal is dead (carcass quality, longevity), sex-limited traits (milk yield, maternal ability) and traits with very low heritability (fertility, survival rate), more sophisticated selection procedures are required if a satisfactory rate of progress is to be achieved. The impressive results obtained in modern dairy cattle breeding programmes in temperate countries can, to a large extent, be ascribed to efficient use of progeny testing: accurate progeny testing of bulls; intensive selection among progeny-tested bulls; and extensive use of the selected bulls. These conditions can be fulfilled only in large breeding units, with tens of thousands of breedable females, widespread recording and artificial insemination (AI).

In most tropical countries, the large populations of recorded animals needed to support such schemes do not exist. In addition, AI services might not be available, or they are irregular and unreliable. Because of this, a breeding programme might have to be established in a single herd or in a group of cooperating herds. In order to make progeny testing worthwhile—even strictly on genetic grounds—several hundred females of breeding age would be needed. Still, the high costs involved in such a programme might not make it attractive. But if the herd serves as a nucleus—where males are also provided for breeding outside the herd—the benefit of genetic progress will, in turn, be transmitted to a much larger number of animals. This might be justified in order to maximise genetic progress, despite the high costs. In this case, use of advanced reproduction technology, like embryo transfer, to speed up genetic improvement might be justified. A rather small breeding scheme can have a tremendous impact if properly organised and operated.

Would intensive selection for increased productivity lead to a deterioration in adaptational traits? The question seems appropriate, although our present knowledge might not allow for a clear-cut answer. It may be speculated that increased production would require higher feed intake, which means an increase in the heat load. Further, if the animal tries to reduce heat load by restricting feed intake or feed availability is insufficient to meet nutritional requirements, this will lead to a depletion of body reserves and an increase in nutritional stress, which in turn will have an undesirable influence on disease resistance, fertility and viability. With dairy cattle in temperate conditions, higher genetic potential for milk production has been found to be associated with increased frequency of metabolic disorders and slightly lower conception rates. This happens because it is almost impossible to meet the nutritional requirements of a high-yielding dairy cow in the first part of lactation. In the tropics, feed quality is usually poorer and nutritional stress would occur at a much lower production level.

Introduction of inheritance from outside

Some temperate livestock breeds have been selected for increased productivity over many generations and have reached a much higher genetic level than most tropical stock. This superiority of exotic stock can be combined with the desirable properties of tropical livestock through crossbreeding. In temperate countries, crossbreeding has been widely used in some species, particularly pigs and poultry, to exploit both breed differences and heterosis (hybrid vigour). Crosses between temperate and tropical stock have often shown large amounts of heterosis, which might be expected because of the large genetic distance between the two types. There is also some evidence that heterosis is more important under a suboptimal than optimal environment.

In species like cattle, sheep and goats, the choice of crossbreeding method is restricted by the low reproductive rate of the females. In general, only two methods are feasible: formation of a synthetic (or composite) population and rotational crossbreeding.

Synthetic population

A synthetic population is formed by combining the inheritance from two or more breeds. The new population can be established from any number of breeds and with any proportion from each breed. The amount of heterozygosity will, in general, increase with increasing number of breeds, according to the formula $H = 1-\Sigma p_i^2$, where p_i is the proportional contribution from the i-th breed. For n breeds, each contributing equally (1/n) to the new population, the formula simplifies to: $H = 1-1/n = (n-1)/n$.

This assumes that all breeds are equally different from one another in terms of gene frequency. In crossbreeding between temperate and tropical livestock, this is most probably not the case. It seems likely that the genetic difference between two temperate breeds is much less than the difference between a temperate and tropical breed. This has also been verified in studies on blood groups and other genetic markers in various breeds. The extra heterozygosity achieved by adding a second temperate breed is therefore slight. The same argument applies, of course, to the second tropical breed.

In a two-breed synthetic, the proportion of F_1 heterozygosity retained equals $H = 2pq$, where p and q denote the proportions of the two breeds ($p + q = 1$). This reaches its maximum of 1/2 at intermediate levels of the two breeds, but a large proportion is retained even if the ratio is 3:1.

A synthetic population can be established in several ways. The most straight-forward procedure is to produce males and females carrying the desired proportion from the two breeds and then start *inter se* mating. If the new population is to have equal proportions of the two breeds, the population is established by mating males and females of the first crossbred generation. When more exotic inheritance is desired, *inter se* mating can start after one or two generations of backcrossing to the exotic breed.

One disadvantage of this method is the decline in performance from the base generation to the first generation from *inter se* mating, because of the expected decrease in heterozygosity. This decline is most pronounced if the synthetic population is established by *inter se* mating of F_1. An alternative procedure is to upgrade to the desired level of exotic inheritance by repeated backcrossing to males of that level. The genetic benefit from the exotic inheritance will be achieved more slowly in this way, but the decline in performance in the first generation from *inter se* matings will be avoided. It also gives livestock keepers more time to adjust their management to the needs of more productive animals. The ultimate result will be the same in both cases.

In many cases, it might be more convenient to apply both procedures in the same scheme. As an example, a nucleus herd of animals with the desired level of exotic inheritance can first be established. Bulls produced by *inter se* mating in this herd can then be made available for upgrading local stock outside the herd.

An objection which is often raised against intermating of crossbred animals is that segregation of genes will lead to excessive variation among the progenies. This is true for some external traits, like coat colour, which are often controlled by a single pair of genes. Most traits of economic importance in animal breeding, such as milk yield and growth rate, are influenced by a large number of genes. Moreover, these traits are affected by many non-genetic effects which will tend to inhibit the various genotypes. Therefore, no observable genetic segregation should be expected. This has been verified in crossbreeding experiments.

A common question in connection with crossbreeding is how many generations of breeding it takes before a synthetic population is stabilised and can be considered a new breed. Actually, the population is already stable in the first generation produced by *inter se* matings. From this stage onwards, the genetic structure will remain constant, except for the effect of selection.

The synthetic breed strategy has many attractive features:

i) Heteroris is exploited in individual, maternal and paternal traits.

ii) Once established, the population is self-contained and needs no outside breeding material.

iii) All individuals in a herd will be of the same breed composition, making mating arrangements easy.

Rotational crossbreeding

In rotational crossbreeding, crossbred males are not used for breeding. The crossbred females are mated to males of various pure breeds—the breed of male alternating from one generation to the next. As for the synthetic population, any number of breeds can be used, but in the present context, little is gained by using more than one exotic breed and one native breed. When two sire breeds are alternating (sometimes termed criss-crossing), the genetic composition of the crosses will converge towards 2/3 from the breed of sire and 1/3 from the other breed. Two thirds of maximum heterosis (F_1 heterosis) will be retained in the crosses.

If more exotic inheritance is desired, this can most conveniently be achieved by using males of the exotic breed in two successive generations and males of the native breed in the third. The proportion of exotic inheritance would stabilise at 5/7, 6/7 and 3/7 in the various generations, and would average 2/3. The average proportion of maximum heterosis retained would be 4/7.

At a given level of exotic inheritance (an average for all generations) rotational crossbreeding retains slightly more individual and maternal heterosis than a synthetic population. It is also easier to exploit genetic progress made in the parental breeds in their home countries. The main disadvantage is that the breed composition of the animals, and their production ability, will fluctuate from generation to generation. In a species with overlapping generations, the herd will consist of females differing in breed composition. As a consequence, males of two (or more) breeds are needed at any time, and the generations have to be separated for breeding (if the males run with the females). Therefore, the method requires a reliable system of identification and pedigree recording.

It is doubtful that the slightly larger heterosis retained by rotational crossbreeding than in a synthetic population is sufficient to outweigh larger management problems. Even if the F_1 heterosis for milk yield were, say, 500 kg per lactation, the difference in average lactation yield between the two strategies would be less than 100 kg. This is not enough to justify keeping an extra bull, unless the herd is rather large. With the present state of knowledge, it seems that the synthetic population is the most practical way to exploit heterosis in dairy cattle.

Choice of strategy

The best way to exploit indigenous genetic resources would depend on climatic conditions, level of management and type of production (and probably other factors as well). Beef cattle and other classes of livestock kept mainly for meat production utilise natural pasture and are often subjected to serious nutritional stress. Fertility and viability are more important than the growth rate of individual animals. Moreover, the superiority of exotic breeds in growth potential is generally small. It seems logical to try to improve indigenous stock by selection rather than crossbreeding.

In milk production, most indigenous cattle are quite inferior to temperate dairy breeds. The introduction of some exotic inheritance seems necessary in order to achieve a reasonable production level. The optimum proportion of exotic genes depends on climatic

conditions, disease prevalence and management level. In most cases, at least 50% exotic inheritance seems to be needed. Crosses with less than 50% *Bos taurus* genes have been found to be poor dairy animals.

The first cross between exotic and indigenous breeds (F_1) has usually performed well, but the next generation of halfbreds (from F_1 x F_1) has often been disappointing. A deterioration from F_1 to F_2 could be expected because of the reduced amount of heterosis (50% of F_1 heterozygosity is lost in F_2), but it seems that this alone cannot explain the poor milk yield of F_2. Backcrosses to the exotic breed (75% exotic genes) have usually been on par with F_1 in institutional herds. At this level of exotic inheritance, the deterioration from the first to subsequent generations is much less than at the 50% level.

In a rotational crossbreeding system (criss-crossing), the generation sired by indigenous bulls (1/3 exotic breed) would probably be unsatisfactory as dairy animals. As has been stated, the system is also rather complicated and requires reliable identification and recording. It is doubtful that this is a feasible strategy of breeding in the field at the present stage of development.

The potential contribution of biotechnology in breed characterisation

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Introduction

The classical description of breeds: coat colour, horns, humps, etc., is based upon phenotype. However, an organism's phenotype is principally a manifestation of its genotype. Thus, the near ultimate description of an organism is a description of the sequence of nucleotides that comprise its genome.

To date, there is a poor understanding of how this sequence governs the phenotype. Describing differences and similarities in the DNA of two animals can provide a superb "fingerprint" but it cannot yet provide a useful description of what the animal looks like and how it will perform. This has been compared to understanding the letters that make up a book and understanding the plot, but not knowing how to relate the two.

This paper will discuss the ways in which the DNA of an animal or a breed can be characterised. However, it should be stressed at the outset that as biotechnology stands today, this is a blind description. It is a methodology of great power but it is helpless unless used in partnership with traditional ways of describing breeds. In some special cases, given good phenotyping and good genotyping data, we hope to be able to make a connection between a trait and a piece of DNA sequence. However, this will represent only a tiny fraction of all that goes into making a living animal.

The genome of a mammal comprises about $3x10^9$ bases. Most of this is "nonsense" sequence; that is, it has no product (it should not be assumed however that it has no function). Even in the DNA which encodes proteins, there is a great deal of redundancy. The 20 common amino acids are defined by codons of three bases. Since the genetic code has four bases, it is able to form 64 unique codons. Some codons are used as control sequences, but in a piece of DNA which encodes a protein, there are a number of different codons which translate into the same amino acid. In many cases, exchanging the last base of a codon for any other base will have no effect on the protein produced. For these reasons, most DNA polymorphisms are silent; they have no effect on an animal's phenotype. Therefore, DNA contains many times more polymorphisms than all the proteins of the animal combined. Furthermore, they all exist in a single and extremely robust chemical form.

In recent years, our ability to study DNA has improved enormously. One technique has transformed our ability to examine DNA sequences—the polymerase chain reaction (PCR). The PCR is a method of exponentially amplifying specific DNA sequences. Described by Mullis and Faloona (1987), the implications of this method are still reverberating through the field of molecular biology, into forensics, archaeology, phylogenetics, diagnostics, immunology and many other disciplines. Given two short pieces of sequence (say 20 bases each), the PCR allows an essentially unlimited amount of the intervening sequence to be generated from as little as one single template molecule. Every

approach described here makes use of the PCR. Some approaches would not be possible without the PCR and all are made easier and cheaper by it.

DNA collection

Because of PCR, DNA is very easy to collect. Before PCR, to compare sequences of mitochondrial DNA, for instance, it was necessary to collect large quantities of tissue (a piece of liver or large volumes of blood) and go through an expensive and tedious purification procedure to allow RFLP (restriction fragment length polymorphism) analysis. Raw sequence analysis required a further complex series of procedures. Today, 10 ml of blood preserved in a number of simple ways provides enough DNA to allow any of the PCR-based procedures to be performed an unlimited number of times. If necessary, it is even possible to recover useful amounts of material from an old microscope slide or a single hair root.

Methods of examining DNA polymorphism may be divided into two broad categories. The first, site-directed polymorphism, consists of techniques for searching known sequences or genes for polymorphism. The second, anonymous polymorphism, contains methods which reveal arbitrary polymorphism, that is, polymorphisms which are developed on a purely random basis.

Site-directed polymorphism

Sequence polymorphism

All methods of describing differences between the DNA of animals depend upon detecting differences in the nucleotide sequence. However, they do not all require that the sequence be explicitly determined in each case. Generating sequence is still a relatively expensive and time-consuming process. However, given the technological advances flowing from the PCR, it is now feasible for a single scientist to determine the sequence of 500–1000 bases of a specific part of the genome from a few tens of animals in a few weeks.

It is only in special cases that this approach is used. It is usually more efficient to determine the sequence of a specific gene in a small number of animals and use this information to construct assays for polymorphism based on one of the techniques described below.

One important exception to this is in the study of mitochondrial DNA. The sequence of the 16 kb of circular DNA which is found in the mitochondria is of interest to those studying breed relationships. The sequence of mtDNA changes at a faster rate than genomic sequence and provides a “biological clock” which allows estimates of degree of relationship between species and races on the basis of their sequence divergence. For this application, raw sequence data is often used. The PCR makes it possible to obtain mtDNA sequence from museum specimens or from small blood samples. This approach can be applied to address such questions as the origin of trypanotolerant breeds.

It is important to note that the cost of sequencing DNA is almost certain to fall dramatically. The human genome project, which has the goal of sequencing the entire human genome, is putting much effort in developing new, more efficient sequencing strategies. When costs fall, it will be cost-effective and powerful to characterise an animal by simply sequencing a few megabases of DNA.

Restriction enzyme polymorphism

There exists a large battery of restriction enzymes which cut DNA at specific sequences; these recognition sites may be four to eight bases long. Therefore, they provide an indirect

means of examining a particular sequence. If an enzyme cuts the DNA of some but not all animals at a particular site, then a polymorphism may be inferred in at least one of the bases in the recognition site.

Until recently, such restriction fragment length polymorphisms were the only form of DNA polymorphism readily detectable. The original method of applying RFLPs was to digest whole genomic DNA with an enzyme, electrophorese the resultant sample, transfer it to a membrane and probe it with a radioactive piece of DNA complementary to the gene of interest. A polymorphism was then detected by a shift in apparent size of the labeled DNA. This is a clumsy and expensive technique largely superseded by PCR-based approaches.

PCR-based RFLPs rely on amplifying a specific piece of DNA and digesting it with an enzyme. If the enzyme site is polymorphic, then the PCR product of some animals will be cut and others will not. This is revealed by simple non-radioactive agarose electrophoresis. This is a particularly powerful means of screening large numbers of animals for polymorphisms which were originally detected by sequencing two or three individuals. It may also be performed "blindly"; the PCR products of a panel of animals may be digested with a large number of randomly selected enzymes and those which reveal polymorphisms become useful typing tools. However, with advances in technology this is becoming less attractive than simply sequencing to locate RFLPs.

Sequence-specific oligonucleotides

An alternative means of revealing polymorphism in a rapid and simple assay is by use of sequence-specific oligonucleotides (SSO). These are sets of PCR primers which function in an allele-specific manner. In order to function as a specific PCR primer, an oligonucleotide must have good complementarity with the target sequence, particularly at its 3' end. It is possible, therefore, to design primers which will produce a product from one allele but not from another. This approach has been widely exploited in the well characterised polyallelic systems of the human major histocompatibility system. It is an elegant assay when developed but requires considerable experimentation to initially set-up for each polymorphism.

A related approach is to use labeled sequence-specific oligonucleotides to hybridise to a PCR product which has been generated in a non allele-specific manner. When used in this fashion, they are often termed "allele specific oligonucleotides", or ASOs.

Conformational polymorphisms

The final group of techniques used to detect polymorphism in specific locations relies upon detecting sequence-specific mobility differences of PCR products under electrophoresis. One way of doing this is by use of a denaturing gradient gel electrophoresis—a technically demanding approach. A simpler method detects "single-stranded conformational polymorphism" (SSCP) in which DNA is denatured and the separated strands are allowed to form sequence-dependent secondary structures which affect their mobility on a polyacrylamide gel.

The methods outlined above can contribute to the study of breed characterisation. They may be considered the molecular biology equivalents of the classical biochemical polymorphisms. Indeed, they provide direct replacements for many of them. However, it is in the exciting new areas of anonymous polymorphisms where molecular biology can very quickly bring new power and simplicity to breed characterisation.

Anonymous polymorphism

Minisatellites

The discovery that mammalian genomes contain scattered islands of short sequences which are repeated a highly variable number of times led to the first "DNA fingerprint". These minisatellites may be detected by labeled probes which reveal a complex pattern of bands caused by variation in the number of times the core motif is repeated at many different loci in different individuals.

Minisatellites have been extensively developed for use in forensics; however, they have been largely superseded in livestock research by other methods.

Microsatellites

Microsatellites, like minisatellites, are regions of repetitive DNA. They comprise much shorter repeat motifs, most commonly two nucleotides in length. They are also highly polymorphic in terms of the number of repeats present at each site. However, their major advantage over minisatellites is the ease with which they are exploited in a locus-specific manner. Microsatellite markers are being intensively developed by a number of laboratories working on gene maps in several species. They are exploited by obtaining sufficient sequence information from their flanking region to design specific PCR primers. They may then be amplified from genomic DNA and their polymorphism revealed by high resolution electrophoresis. Each microsatellite marker initially requires some sequencing data, but once in place is easily and rapidly exploited. The extreme polymorphism of microsatellites makes them ideal tools in gene mapping studies.

RAPD markers

The most recently described polymorphic markers have been termed RAPDs (random amplified polymorphic DNA) (Williams et al, 1990). These are the simplest group of polymorphisms to detect and are based on the PCR amplification of random DNA segments with single, short (10 base) primers of arbitrary sequence. The resulting pattern of bands is highly polymorphic and is simply revealed by agarose electrophoresis with each random primer producing a different pattern of bands and each effectively revealing many different polymorphisms. The polymorphism is believed to be due to differences in spacing between primer binding sites and also to point mutations which allow or abolish primer binding.

The drawbacks of this technique are the relative complexity of the resultant fingerprint and the fact that the heterozygote cannot be distinguished from the homozygote. These problems are more than outweighed by the ease with which RAPDs are exploited. Many hundreds of polymorphic loci may be detected by a small number of randomly chosen primers and no prior sequence information is required.

It was recently demonstrated (Michelmore et al, 1991) that the use of RAPD markers to analyse pooled DNA samples of the extreme phenotypes from an F_2 population segregating for a trait is a powerful tool for mapping a trait. A marker associated with a trait is polymorphic between pools while unlinked markers appear monomorphic. This has important implications for the research teams presently searching for markers associated with quantitative traits (e.g. ILRAD's work with trypanotolerance). Surprisingly, the RAPD technique is relatively insensitive to rare alleles in a pool of DNA. If an allele is present in less than approximately 10% of the contributing animals, it is generally undetectable. The advantage of this is that it sets convenient limits to its sensitivity. A single recombinant between marker and trait in a pool of 10 animals will not mask the linkage.

The use of pooled DNA samples in combination with RAPD markers could also have great value in breed characterisation studies. If large numbers of RAPD markers are tested upon pools of DNA, one pool from each breed under study, then breed-specific markers might quickly be found with minimal effort. Here the implications of the system's insensitivity are rather different. A band polymorphic between two breed pools would not necessarily be a true breed marker; it may simply be relatively rare in one population and frequent in the other. However, by using initial pools containing large numbers of animals, many thousands of potential markers might be rapidly screened. Candidate markers might then be followed-up with more and smaller pools and eventually with unpooled DNA.

Having located an anonymous RAPD marker of a breed or trait, it is relatively straightforward to assign it to a part of the chromosome which will allow the process of locating the responsible gene to begin.

Conclusions

The techniques outlined above are potential means of assisting in the process of breed characterisation. They could play a role in two main areas. The first is in understanding breed relationships by calculating genetic distances. Almost any of these approaches could be used for this purpose. There are ways to compare specific genes of interest between breeds or to use anonymous polymorphisms to measure many more variables. Second, molecular biology is capable of providing tools for defining breeds. To locate and apply markers which are useful in characterising breeds is now a straightforward task.

Any group which is expending effort upon characterising breeds must consider the role that molecular biology may play now or in the future. Since the raw material, DNA, is cheap and simple to collect and bank, it would seem wise to collect samples from populations under study. Once prepared, DNA keeps indefinitely at room temperature. If the technology continues its fast growth in power, the value of a sample prepared today can be expected to grow at a similar rate.

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Discussion

Q: Can you explain why RAPD causes problems? What is the rethink you are doing here?

A: It is part of the strategy—to generate a gene map. If we have a pooled analysis, there is no need for linkage information.

Q: Which of the two options—estimation of genetic distances or characterisation of breeds using fingerprinting—would you deem most appropriate for ILCA?

A: Both options could be undertaken simultaneously, except in those cases where you wished to home in on breed markers. That would be a different exercise. The two

options use the same basic technologies. The important question is, what do you want to do?

Q: How different are the options in terms of handling samples?

A: The advantage of PCR techniques is that you can use almost anything as a sample—including a single hair root. It is pretty hard to destroy DNA.

SESSION II

Case studies

Chair: A. Lahlou-Kassi

Breed characterisation: The IEMVT/CIRAD experience

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Introduction

When they landed on the African continent in 1819, one of the main activities of the first French veterinarians was to describe the animal populations they saw. For several decades, IEMVT/CIRAD (Institut d'élevage et de médecine vétérinaire pays tropicaux/Centre de cooperation internationale en recherche agronomique pour le developpement) has contributed to these descriptions by setting up a comprehensive mechanism for characterising animal breeds in their production environment.

How to characterise

IEMVT/CIRAD work in this field focuses on cattle, small ruminants, camels and, of late, fish. Breed characterisation can assume different forms depending on the particular animal or production system targeted.

Knowledge of animal performance, including understanding the livestock production system, is a central component of our institutional approach. All the species mentioned above are dealt with using this approach which puts as much emphasis on the production environment—which we know plays a vital role in trait expression—as on the performance of an animal population.

Characterisation exercises based on quantitative criteria such as body measurements or different phenotypic data have been conducted on many livestock populations for a long time. They show that unlike what is generally assumed, within-population variability can sometimes be greater than between-population variability. The use of such data when no complementary data sources are available can be confounding. That is why IEMVT/CIRAD has managed to keep a very extensive data base. More recently, condition-scoring under different and well-described husbandry conditions has been added to the list of measurements.

Another aspect of IEMVT/CIRAD work has been the development of a better knowledge base of animal hereditary resources based on quantitative and factorial genetics. With the use of modern techniques and tools like genomic studies on cattle and small ruminants, our current competence has been extended to cover all areas of study dealing with animal genetic resources.

Geographical distribution

Traditionally based in West Africa, IEMVT scientists have contributed to the characterisation of local breeds in several countries of this zone. For cattle, work has been focused in Mali, Burkina Faso, Côte d'Ivoire and Cameroon along with the French departments in America and the territory of New-Caledonia in the Pacific Ocean.

For small ruminants, characterisation studies have been carried out in Senegal, Côte d'Ivoire, Cameroon, Niger and Chad. Cameroon, Niger and Chad fall under the regional small ruminants research programme. Important work has also been carried out on local breeds in the West Indies.

Characterisation work on camel breeds has also been conducted for several years in Sudan.

Methodological approach

Depending on the level of knowledge one is looking for, the amount of available data or the time and means available, different methods for breed characterisation can be used. Three levels of description, varying from the general to the specific, can be considered.

The first level, MACRO, uses a survey methodology developed about a decade ago by IEMVT/CIRAD. A relatively rapid tool based on the use of a sizeable amount of standardised data, this technique allows for swift implementation as well as for the use of large animal populations. Thus, the initial lack of clarity of a situation gives way to a rapid and sufficiently accurate appraisal. Information thus provided can be labelled point-specific.

The macro approach has been used by applying a standardised methodology at close intervals of time in different countries. Data recorded become more valuable and can be validated by comparisons and development of simulation studies. Thus, the study of the age structure of an animal population shows, among other things, the probable trend in its development and may guide the choice of subsequent decisions aimed, for instance, at preserving an endangered breed.

The second level, META, is based on a monitoring of on-farm husbandry activities. Whatever the tool used, this method requires data of the highest quality. On the other hand, it compels research teams that use it to embark on a continuous data collection process. Two to five years will often be necessary to obtain the data needed to qualify a population independently from time or geographical contingencies. Based on an individual recording system for performances of identified animals, the method facilitates monitoring of trends in the animal's capabilities and career. Data bases developed along these lines are an invaluable source of information both for scientists/developers and livestock producers, all of whom play an important part in the complex environment of livestock production systems.

The third level, MICRO, is based on selected methods that can be used to gain knowledge of the genome of individual animals within a population. It uses statistical modelling methods and quantitative genetics and/or tools for measuring factorial genetics that require both a high level of investment and technological input. In general, only a small number of animals can be covered by this method due to the high cost of the method and the difficulty involved in analysing appropriate biological samples using advanced techniques in adequately equipped laboratories, only a few of which are presently available.

When considered alone, each of these methods can no doubt provide valuable data to breed characterisation exercises; however, it is only when used together that each reaches its highest level of effectiveness and that the international community's objective to inventory animal genetic resources can be met.

The IEMVT/CIRAD data bases

An outline of current IEMVT/CIRAD activities is provided below.

At the MACRO level, our data base covers about 10 countries and includes information about 300,000 on cattle, 60,000 sheep, 90,000 goats and 40,000 camels. These survey results, which were conducted using the same methodology, are part of a bank to be created by IEMVT/CIRAD in 1992, for use by the international community after each of the countries concerned has been supplied with relevant data.

In terms of the on-farm monitoring method (META level), IEMVT/CIRAD has been mobilising substantial resources for a number of years to gain better knowledge of existing production systems and of livestock performance in different production situations and cropping practices. Currently, in about 10 countries, 8,000 cattle, 11,000 sheep and more than 8,000 goats are regularly monitored. Some of them have been monitored for the last 10 years or so. While involving heavy investment, these long-term monitoring activities have paved the way for efficient partnerships, thereby enabling decision makers who want to move quickly in the field of African animal genetic resources development to save a great deal of time.

Finally, at the MICRO level, although our research over the last few years has focused on cattle (N'Dama, Baoulé and some Zebu breeds have been characterised from a genomic point of view), a similar research project is being launched on small ruminants. In 1992, results from 20 years of cattle research will be published along with the evaluation of genetic distances between the populations concerned. Work carried out on the Creole goat has also made it possible to launch a programme on genetic resistance to cowdriosis. This programme will guide the research programme planned on resistance to internal parasites.

What tools?

It makes little sense to carry out work on such a scale without developing, from the experience gained, specific tools that are well-suited to the approach selected. While we do not claim to be the only institution capable of showing effectiveness in this field, it may be worthwhile to stress that all these tools have been developed on the basis of considerable field experience and that they have been utilised by different teams, who have faced many constraints in the geographical zones in which we are working.

All our surveys were run on a software called KALAO. The basic principle of this software is a rapid collection of data using three standard sheets. On average, it takes one month of survey work and two months of analysis work to obtain the information needed and to present it in the form of a detailed report.

Two software package (PANURGE and PIKBEU) have been developed to collect and manage on-farm monitoring data. In theory, the former is more applicable to small ruminants and the latter to cattle. Recent developments make it possible to use either one of the two softwares in any management system interchangeably, depending on whether one is focusing on research or on development. Based on individual identification of monitored animals, a central demographic module records all events occurring in the herd. Because of satellite modules, particular types of data (e.g. pathology, feeding, herd management, husbandry practices etc.) can be managed as needed. Automatic outputs allow for global information processing. Work files are developed for any livestock production analysis required.

Quantitative characterisation of individual animals is carried out with softwares designed for calculation of productivity indices in situations where the animals are not kept on a breeding farm (ARAS software). Thus, in situations where on-farm performance evaluations are rigorously carried out, an estimate of sire genetic value can be obtained.

Finally, the in-house expertise of IEMVT/CIRAD in blood types, blood proteins and milk analysis is used to develop knowledge on local breeds.

Conclusion

The relevance of a particular animal population, i.e. its chance for survival, is dependent on the availability of an environment that it helps develop, on a livestock production system in which it is managed or on specialised output that it helps generate. This is why IEMVT/CIRAD has developed a comprehensive system for characterising animal populations using modern prospective tools such as simulations. Results from previous studies indicate the existence of substantial animal variability, unlike in other continents where within-breed variability is quite low. Indeed, some populations have almost disappeared, while others have evolved in the face of constraints.

Genetic resistance of Guadeloupe native goats to heartwater

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Abstract

Goats were imported from Africa about two centuries ago. While these animals had a number of special features, they also developed problems with heartwater—a disease that can easily be transmitted to most of the American continent. Antigua, Guadeloupe and Martinique are all affected by heartwater, although the disease is not officially recognised. Experiments were carried out in Guadeloupe to look at heartwater and examine resistance and survivability.

Rate of resistance to *Cowdria ruminantium* infection of different populations of the same breed of Creole Guadeloupean goats varied greatly, depending on the history of heartwater exposure. After experimental infection of goats removed decades ago from endemic areas, the observed rate of resistance was found to be 25%; 54% of the population receiving no exposure for the last ten years had developed resistance. Resistance reached 78% for a flock that was actually exposed to heartwater.

Resistance to heartwater appeared to be genetically controlled and determined by a number of effects. For instance, it was found that paternal effect was an important factor that helped explain resistance in a group of 198 kids of a flock tested under controlled conditions. Rate of resistance varied greatly (20-83%) depending on the sire, with an estimated heritability of 0.26 for half-sibs and 0.55 for full-sibs. CLA specificities could be connected with the genetic determinism of resistance.

From these results, it can be stated that in areas endemic with heartwater, each population (each flock) will be resistant up to a definite limit – depending on age and level of past and present exposure to the disease – by natural selection of resistant lineages. Populations removed from heartwater exposure will progressively lose their ability to resist by an increase in the frequency of susceptible breed stocks.

The study concluded that there is better resistance for animals before weaning and if born in August–September. If the hypothesis of a genetic basis for resistance proves correct, it should be easy to achieve selection in order to improve resistance of the Guadeloupe goat breed to heartwater and to identify susceptible animals early.

Discussion

Q: Regarding differences observed pre-post weaning and kidding, please comment on the similarity of results. Could this be a reflection of nutritional status?

A: Yes. Looking at nutrition, we have the same indicators. Immunity also appears to be transmitted from dam to progeny.

Q: Could you mention the parameters used to define resistance?

A: Animals not in contact and those infected. Observe their reaction; if the animal dies, perform an autopsy to identify cause of death. We also look at seroconversions (e.g. epidermic stage). If the animal survives, it is considered resistant.

Q: You indicated on a slide that the heritability of susceptibility is higher than the heritability of resistance, and followed this with a question mark. Please explain.

A: Sixty percent of the animals mated responded similarly. Therefore, either they are both resistant or susceptible. We have not yet decided if one is stronger than the other. Thus far, our results are based on experiments only.

C: What is important here and should be developed is immune response as a criterion to determine resistance/susceptibility of a population.

A: This has been done a bit in Europe with cattle. We do not know if this is linked to a certain type of disease or to a specific environment.

C: The chair of Group A should take stock of these points so that they may be further discussed in the working session.

Biometrical characterisation of Nigerian cattle, sheep and goats: A case study

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[The presentation was exclusively based on results already published (Hall, 1991) in *Animal Production* 53(1):61-70. Full abstract and title are reproduced below.]

Body dimensions of Nigerian cattle, sheep and goats

Abstract

One hundred and thirty-six multiparous cows, 63 goats and 71 sheep were measured in breeding flocks and herds in Nigeria. The humped cattle breeds, and the large-bodied, humpless Kuri, are narrow-bodied and tall in relation to their length when compared with British breeds. Pelvic dimensions are small. The sheep and goats native to the coastal and middle belts (the West African Dwarf breeds) are miniature versions of those found in the north. Neither appears to be achodroplasic but dwarfing seems to have proceeded differently in the two species in that the adult West African Dwarf goat is similar in its relative body proportions to the adult northern goat, implying a proportional miniaturization. The West African Dwarf sheep appears to be a neotenous form with body proportions similar to those of an immature sheep.

Discussion

Q1: You spoke of the Adamawa Gudali breed. There are three distinct strains. Which one are you referring to?

Q2: You spoke about size differences between the WAD and the Northern breed of sheep and implied clear-cut distinctions. What about the Djallonke? As you move across geographical regions, one finds gradations in size. How does this relate to your hypothesis?

A1: The Adamawa Gudali is close to the Red Bororo. What I observed was the Northern type. A proper genetic study should be done to distinguish among them.

A2: Regarding the sheep, there are no published results linking area to size. As I understand it, there are distinct breeds although the Enkasa may be an intermediate breed. I would not wish to make conclusions based on measurements from such a small sample size. This reinforces the importance of undertaking studies on genetic distance to identify differences and to sort out one type from another.

Q1: The use of individual measurements to characterise animals, particularly those on-farm, seems problematic. Nutrition is clearly an important factor.

Q2: There is a continuity between breeds but how do we separate these breeds? On what basis does one seriously decide which breed is which?

A1: One needs to look at the males and females. Differences that are noted tend to be more acute in males.

A2: There are difficulties in making clear distinctions.

C: As we talk about population characteristics, once we delve into the intricacies of phenotypes or a phenoytype of a particular polyphormism, then we may have to go to that level to see population differences. Linear measurements are “quick and dirty”. We want to be careful about combining these methods and techniques. The working groups need to be thoughtful about the type of data to be collected.

C: Even if body measurement cannot be used accurately for breed characterisation, it is still important. For instance, size of body/legs is most important in terms of production. Size, then, should be taken into account.

Characterisation of trypanotolerant cattle: A case study

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Introduction

Much consideration is being given to the use of domestic animal breeds that possess the ability to survive and be productive in tsetse-infested areas without the aid of trypanocidal drugs. This trait, termed trypanotolerance, is generally attributed to N'Dama and West African Shorthorn cattle as well as to their sheep and goat counterparts.

Formal characterisation of trypanotolerant livestock started in the late 1970s when ILCA, the Food and Agriculture Organization of the United Nations (FAO) and the United Nations Environmental Programme (UNEP) worked with researchers in 18 West and Central African countries to build up general relationships between trypanosomiasis risk and animal performance (ILCA/FAO/UNEP, 1979). They used all available information from the many individual projects previously undertaken in these countries and found clear relationships between risk level and animal performance.

Most work in the 1980s was carried out on the N'Dama, thought to be the most important of the trypanotolerant cattle breeds. Much was accomplished within the African Trypanotolerant Livestock Network, by national researchers in many West and Central African countries. This work supported the belief that ability to control both the level of parasitaemia and the development of anaemia are key indicators of the trypanotolerance trait, and that these processes, although controlled genetically, are not necessarily genetically linked to each other (Murray et al, 1990).

In field studies, the degree of anaemia can be easily quantified by measuring packed (red) cell volume (PCV) percent. This has allowed progress to be made in relating control of anaemia development to animal productivity (Trail et al, 1991b), in evaluating a field test for anaemia control in young N'Dama cattle to help in choosing replacement animals (Trail et al, 1991a) and in investigating the possibilities of genetic selection for trypanotolerance based on PCV measurements (Trail et al, 1991c).

In contrast, the degree of parasitaemia is not so easily quantified and has depended on demonstration of trypanosomes in peripheral blood by parasitological techniques. The most sensitive practical field approach has been to detect the presence of trypanosomes by the dark ground/phase contrast buffy coat method (Murray et al, 1977) and quantify the intensity of the infection as a parasitaemia score (Paris et al, 1982). However, a high proportion of infections go undetected as many infections fluctuate markedly and may be below the limit of detection by this technique. Thus, at the end of the 1980s, it seemed possible to plan improvement programmes based on the anaemia control component as measured by PCV when infected, but not on actual infection data as measured by the buffy coat technique.

In 1990, field work started using recently developed antigen-detection enzyme immunoassays (antigen-ELISA) for the diagnosis of *Trypanosoma vivax, T. congolense* and

T. brucei infections (Nantulya and Lindqvist, 1989; Nantulya, 1990). The assays are based on monoclonal antibodies which recognise trypanosome antigens specific for the three trypanosome species. The antigen-ELISA has been shown to be more sensitive than the buffy coat technique in monitoring *Trypanosoma congolense* infection in cattle (Masake et al, 1991). This is because the buffy coat technique detects only trypanosomes present in the peripheral blood circulation. The number of trypanosomes is often too small for detection by this technique, despite the fact that there may be trypanosomes in other body organs such as the spleen, liver and lymph nodes. The antigen-ELISA, on the other hand, detects soluble antigens released by dying trypanosomes wherever they may be. Thus, sensitivity of this test does not depend upon parasite numbers in peripheral circulation; hence, the high sensitivity even when there may be no detectable parasitaemia. Results from this recent and still ongoing work (Trail et al, 1992a; Trail et al, 1992b), indicate that we now have the potential to greatly increase the efficiency of selection of trypanotolerant N'Dama cattle under tsetse challenge in the field.

What follows are the various steps that have been taken in the characterisation of N'Dama cattle from 1977 to 1992.

ILCA/FAO/UNEP survey of trypanotolerant livestock

In 1977, ILCA began planning a study on the use and potential of trypanotolerant livestock. FAO and UNEP were also planning a survey of West African trypanotolerant cattle breeds. To avoid duplication, the three organisations initiated a joint study to survey the status of trypanotolerant livestock of West and Central Africa, appraise existing information on their productivity and present comparisons between trypanotolerant and non-trypanotolerant livestock maintained under comparable conditions. This would allow plans to be prepared for the conservation of trypanotolerant cattle breeds which were in danger of absorption or extinction, for the most effective use of trypanotolerant breeds and crosses in livestock development schemes in the humid and semi-humid tropics and for further research on trypanotolerant animals and trypanotolerance. Eighteen West and Central African countries were included in the study. These were the coastal countries from Senegal to Zaire, and three landlocked countries, Mali, Burkina Faso and the Central African Republic.

The final report of the joint study was completed in 1979. It was entitled *Trypanotolerant livestock in West and Central Africa* and appeared in two volumes, one of general studies and one of specific country studies. The general studies covered the environmental background pertaining to, and the classification, populations, distribution, descriptions, performances, etc. of, trypanotolerant livestock throughout the study area. Research and development centres and the activities being undertaken by them were identified and classified. Suitable indices of productivity were developed and presented in detail for the main cattle groups, and, in less detail, for sheep. Preliminary comparisons were carried out between groups wherever possible.

Productivity of trypanotolerant livestock

In each country section, whenever sufficient information was available, estimates of the main production traits required to build up a productivity index were given. In the case of cattle, the traits evaluated were reproductive performance, cow and calf viability, milk production, growth and cow body weight. These were then used to build up the index of the total weight of calf and liveweight equivalent of milk produced per cow per year and per unit weight of cow maintained per year. The latter index was considered the most reliable method for comparing the actual productivities of the wide range of cattle types involved. Its merit lay in relating all the more important production traits to the actual

weight of breeding cow that had to be supported, this being closely connected with maintenance costs.

The study emphasised the importance of trypanotolerance by indicating that trypanotolerant breeds were at least as productive as other indigenous African breeds in areas of zero to low tsetse challenge and that in areas where tsetse challenge was substantial, only trypanotolerant breeds could survive. It was known that as tsetse challenge increased, the resistance of trypanotolerant livestock to trypanosome infection diminished, resulting in stunting, wasting, abortion and death. Similarly, stress factors—such as overwork, pregnancy, parturition, lactation, poor nutrition and intercurrent disease—had been identified as affecting the susceptibility of trypanotolerant animals to infection.

It was apparent that more precise research information would have to be obtained in order to achieve a better understanding of genetic resistance, acquired resistance, environmental factors that affect susceptibility and the efficacy of control measures available, and to ensure optimal application of research findings. In the 18 countries, preliminary enquiries were made with government stations and institutions, universities, commercial ranches, village groups, etc. with suitable facilities and programme intentions, concerning their willingness to cooperate in further work on the use and potential of trypanotolerant livestock. Many localities were identified where relevant work was in progress, but in nearly all cases, additional input was needed before conclusive results could be produced.

The joint report (ILCA/FAO/UNEP, 1979) was used to interest donor agencies to support situations which could handle specific aspects of the overall research requirements. Between 1980 and 1984, sites in Zaire were established through Administration Generale de la Cooperation au Developpement (AGCD), Belgium; in Gabon through partial funding from France; in Côte d'Ivoire and Togo through Deusche Gesellschaft für Technische Zusammenarbeit (GTZ), Federal Republic of Germany; and in The Gambia and Senegal through the European Development Fund (EDF).

Relationships between trypanotolerance criteria and cattle performance

The first comprehensive evaluation of the links between factors related to trypanosome infection and animal performance was carried out at Mushie Ranch, Zaire, where calving interval records were built up from N'Dama cows maintained for 3.5 years under high natural tsetse–trypanosomiasis challenge. Monthly blood samples were examined by the buffy coat method to detect the presence of trypanosomes. The species of trypanosome was identified and the intensity of infection quantified as a parasitaemia score. The degree of anaemia was quantified by measuring PCV. Attempts were made to control other possible causes of anaemia; ticks by weekly dipping and internal parasites through a pasture management system involving extensive grazing conditions, no night paddocks and regular burning of pastures (Trail et al, 1991b).

The comparative influences of time detected parasitaemic, parasitaemia intensity representing control of development of parasitaemia and PCV value representing control of development of anaemia, were measured on cow productivity (weight of weaner calf per cow per annum) using least squares mixed model procedures. Significant findings included that cows detected parasitaemic for a short time were 15% more productive than their contemporaries that were parasitaemic for a long time. The effects of parasitaemia intensity were not significant. In contrast, animals maintaining a high PCV value had a 24% superior cow productivity over those maintaining a low PCV value. Thus, control of anaemia development, as measured by average PCV value, appeared to be the criterion of trypanotolerance most closely linked to overall cow productivity in this production system where attempts had been made to systematically control other possible causes of anaemia.

Repeatabilities between calving intervals for the three trypanotolerance criteria and the three performance measures, all expressed as traits of the cow, were computed. Traits with significant repeatabilities were calf weaning weight (0.35), average PCV over the calving interval (0.33) and time detected parasitaemic during the calving interval (0.23). The repeatability of PCV value was reasonably high and almost equal to that of calf weaning weight. Thus, the ability to control development of anaemia, as indicated by PCV value, might well be a useful criterion of trypanotolerance with which to identify more trypanotolerant individual animals.

Simultaneous evaluation of the relative effects of criteria of trypanotolerance, in both the preweaner calf and its dam, on calf performance (weaning weight) showed that calf PCV values were at least as important as dam PCV values. Thus, evaluation of criteria of trypanotolerance in an animal might be feasible before it reached maturity, but would need to be sufficiently long after weaning for the preweaning influence of the dam to have disappeared.

A field test for trypanotolerance in young N'Dama cattle

The Zaire study suggested that investigations into practical field tests for trypanotolerance should focus on the use of post-weaners, maintained for varying lengths of time in as high natural tsetse–trypanosomiasis challenge situations as possible. Three such tests were carried out in which a total of 436 one-year-old N'Dama cattle were maintained for 12, 18 and 24 weeks under a medium tsetse–trypanosomiasis challenge at the Government Ranch (OGAPROV) in Gabon (Trail et al, 1991a).

Every four weeks in the first and every two weeks in the second and third tests, blood samples were examined by the buffy coat method to measure infection criteria. The degree of anaemia was estimated by measuring PCV. Attempts were made to control other possible causes of anaemia. On the last day of the first and second test, all animals were treated with Samorin (isometamidium chloride) at the rate of 1 mg/kg body weight by intramuscular injection, to evaluate the recovery of PCV values. In all three tests, ability to control anaemia development had a major effect on daily weight gain four times that of the ability to control parasitaemia. Above-average PCV values, as a measure of anaemia control, resulted in a 44% superior daily weight gain over below-average PCV values.

Post-test recovery of PCV values after trypanocidal drug treatment was evaluated to see how quickly recovery from such a test could be achieved. At the completion of the first test, as an example, trypanosome prevalence was 30%, and the PCV values of groups that had been detected parasitaemic for varying percentages of the 12-week test period ranged from 33.1% for those never detected as parasitaemic to 18.8% for those parasitaemic for 80% of the period. Coefficients of variation, indicating the amount of variation in PCV values within each group, ranged from 15.9% in animals never detected as parasitaemic to 26.5% in animals parasitaemic for 80% of the test period. On the last day of the test, all animals were treated with Samorin at the rate of 1 mg/kg of body weight. When PCVs were measured 30 days later, major recovery of PCV had taken place; even those parasitaemic for 80% of the test period had a PCV value of 34%, and the coefficients of variation within all groups were reduced to 8.7%. In the second test, 73% of the recovery achieved one month after the trypanocidal drug treatment had been reached in nine days. Thus, normal PCV levels could be reached rapidly after a three-month field test.

Genetic aspects of control of anaemia development

Blood typing for parentage determination allowed genetic parameters of measures of control of anaemia to be evaluated (Trail et al, 1991c). The heritability of body weight at the start of the test when animals averaged 50 weeks of age was 0.49 (s.e. 0.32). This is

within the normally reported range for this trait. The large standard error could be a reflection of the small number (five) of progeny available per sire. When all environmental and parasitaemia information was taken into account, the heritability of growth over the test period was 0.39 (s.e. 0.32), again within the expected range for growth over a three month period. The heritabilities of both PCV measures were higher than the corresponding heritability of growth, being 0.64 (s.e. 0.33) for average PCV and 0.50 (s.e. 0.32) for lowest PCV reached. The genetic correlation between average PCV and growth was 0.70 (s.e. 0.42) and between lowest PCV reached and growth, 0.28 (s.e. 0.55). These values, coupled with the higher heritabilities of the PCV measures, indicate some possibility of selection on PCV values for control of anaemia development.

Cow lifetime data on trypanosome infection

Data on trypanosome infection detected by the buffy coat technique over the reproductive lifetimes of cows became available (Wissocq, 1991). At Mushie Ranch, Zaire, data from 186 N'Dama cows had been recorded monthly over an average of five years (range three to seven years) under an average monthly trypanosome prevalence of 10%. Findings were that under this challenge level, all N'Dama cows would be expected to be infected during their reproductive lifetimes. There was a major difference in *T. vivax: T. congolense* infection ratios between young calves and their dams grazing together. Significant effects of the number of infections per unit of time on the average PCV were found, and *T. vivax* and *T. congolense* had different effects on average PCV. It was clear that accurate trypanosome species identification in detected infections was essential if clarification of linkages between infection, anaemia and animal performance was to be achieved.

Antigen-detection test for more accurate assessment of trypanosome infection

In an attempt to measure infection more precisely, antigen-detection enzyme immunoassays developed by Dr. V. Nantulya at ILRAD (International Laboratory for Research on Animal Diseases) were used for the diagnosis of *T. vivax, T. congolense* and *T. brucei* in the same group of N'Dama cattle in Gabon that were used for the heritability estimates (Trail et al, 1992a). An average of six assays per animal were carried out over a 92-day period. Of the animals detected parasitaemic by the buffy coat technique, 90% were positive to the antigen test. More importantly, 40% of the animals with negative parasitological findings were also found to be antigen positive.

The proportion of animals with mixed species infection (*T. congolense* and *T. vivax*) over the six occasions when each animal was antigen-tested was 27% compared to 17% found by the buffy coat technique. Additionally, on an individual sample basis, while it was extremely rare for a buffy coat examination to reveal a mixed species infection, 13% of all individual antigen tests did. It is possible that the difference reflects relative sensitivities of the two methods.

When antigen positive, parasite negative animals were classified as having more ability to control parasite growth than parasitaemic animals. A significant sire effect suggested some possibility of a degree of genetic control being involved, the heritability estimate for parasite control being 1.08 (s.e. 0.50) compared with 0.33 (s.e. 0.47) for growth and 0.57 (s.e. 0.49) for average PCV. Thus, the ELISA might offer a practical possibility for selection of trypanotolerant animals based on infection criteria.

Antigen-ELISA and efficiency of selection of N'Dama cattle

Further work was then set up to more accurately evaluate relationships between trypanosome infection as measured by antigen-ELISA, anaemia as determined by average

PCV and animal performance as assessed by daily weight gain. A total of 99 N'Dama cattle in Gabon were exposed to natural tsetse challenge at 11.5 months of age and recorded 14 times over a 13-week period (Trail et al, 1992b).

T. congolense infections had significant deleterious effects on animal growth while *T. vivax* infections did not. In animals with mixed infections, the regression of daily weight gain on the number of *T. vivax i*nfections in the mixed infection was -1.0 (s.e. 3.3) g/day, while the regression of gain on the number of *T. congolense* infections in the mixed infection was -6.2 (s.e. 2.9) g/day. When the species effect was ignored, the overall regression of gain on the total number of infections was -3.6 (s.e. 2.1) g/day. This shows the importance of accurate trypanosome species identification in this region of Central Africa.

The same picture has been confirmed with recent analyses of trypanosome species effects on cow reproductive performance in Gabon.

Current situation

It appears that tools are now available that will allow us to increase the efficiency of selection of N'Dama cattle under tsetse challenge in the field. By October 1991, a great deal of effort had been put into assembling a large group of N'Dama post-weaners in a high natural challenge site in Zaire to try to tie together the various aspects discussed in this paper. Unfortunately, socio-political problems have delayed the work. It is hoped that work will start soon. There we have good numbers of half-sib groups, antigen testing and strategic antibody testing alongside the normal field buffy coat and PCV measurements. Historical blood and buffy coat slides have been prepared to refer back to and DNA has been stored for planned work using a candidate gene approach for the identification of genes involved in trypanotolerance.

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Discussion

Q1: PCV was used to determine antigenic control in characterising breeds. But PCV is also related to the nutritional status of the animal.

Q2: Are you trying to determine other genetic factors, such as the relationship between BoLa (bovine lymphocyte antigens) and health?

A1: PCV is affected by nutrition. All these aspects have been looked at by the African Trypanotolerant Livestock Network. I was focusing on one aspect today.

A2: Studies on the relationship betweein BoLa and health and performance have yielded disappointing results. We are now using DNA technology and are expecting clearer results.

Q: The response of N'Dama differed depending on parasite species. There is evidence of a differing response between tsetse challenge and animal species. How important is this in terms of characterisation? Do we need to attend to both species of parasite and species of the host?

A: Both are likely to be equally important and should be taken into account. Field tests were not accurate enough to distinguish the species, particularly in mixed species infections.

C: Evidence from work with other species suggests that regardless of parasite infection, there are similar results regarding within- and between-breed differences. Thus, differences in response to parasite infections between host breeds may not be expected.

SESSION III

African animal genetic resources: On-going and planned breed characterisation projects

Chair: K. Agyemang

The Global Data Bank for Domestic Livestock

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Introduction

To work for the preservation or promotion of animal genetic resources, it is essential that we first know what resources exist. The Global Data Bank for Domestic Livestock aims to document and characterise the different populations of domestic livestock found throughout the world.

Current status

The Global Data Bank in Rome contains information on 1,974 breeds (and varieties of breeds) of buffalo, cattle, goat, horse, pig and sheep. All areas of the world are covered with the exception of Europe, but including the former USSR (Table 1). The regional data bank for Europe is based in Hannover, Germany and, as of September 1991, included 665 European entries. In the European data bank, each entry refers to a single breed or breed variety *within a country* whereas the Global Data Bank in Rome allows one entry per breed even if the breed is found in more than one country. The book, *World dictionary of livestock breeds* by (Mason, 1988), was used as the primary source of information on breeds and breed varieties for the data bank. This book provides breed names and synonyms, indicates where breeds are found and gives a basic description of the origin, physical appearance and main uses of each breed.

Table 1. *Number of breeds or breed varieties per geographical region in the data bank.*

	Buffalo	Cattle	Goat	Horse	Pig	Sheep	Total
USSR	1	50	20	59	27	135	292
Africa	8	175	59	35	8	133	418
N & C America	1	67	12	41	35	48	204
South America	2	45	11	22	17	17	114
Asia,	63	200	147	88	142	232	872
Oceania	0	21	6	2	6	39	74
Total	75	558	255	247	235	604	1974

Not all entries in Mason (1988) were included. For example, those referring to a cross between breeds, a hybrid between two species or to a group or collection of breeds were excluded. On the other hand, all varieties or strains of breeds as well as wild or feral species were included. Of the 1,974 entries in the data bank, 455 are described by Mason as a variety, subvariety or a strain and 75 as wild or primitive.

Mason does not provide estimates of population size (other than to occasionally indicate that a breed is nearly extinct, rare or declining in numbers) or of production characteristics for the breeds cited. To find this information, a wide range of literature sources in FAO Headquarters was consulted:

- *FAO Animal Production and Health Papers (*about 20 are relevant)
- *Animal Genetic Resources Information* booklets (seven in total)
- *World Animal Review* (1972 to date)
- Reports on individual countries (mainly carried out for FAO) and a selection of books from the library of the Animal Health and Production Division, FAO

After inputting this data, it was found that information on population size was available for 26% of all entries in the data bank (Table 2). In most cases, however, this information consists of only an overall figure for total population size or a description of the breed as rare, disappearing or almost extinct.

Table 2. *Number of breeds or breed varieties for which there is some information on population size.*[1]

	Buffalo	Cattle	Goat	Horse	Pig	Sheep	Total
USSR	1	30	11	48	14	54	158(54)
Africa	1	50	12	1	1	23	88(21)
N & C America	0	13	4	9	5	9	40(20)
South America	0	19	0	1	4	5	29(25)
Asia	4	48	27	16	18	85	198(25)
Oceania	0	0	1	1	1	4	7(9)
Total	6(8)	160(29)	55(22)	76(31)	43(18)	180(30)	520(26)

[1] The figures in brackets represent % of all entries in the data bank (Table 1).

Thirty percent of the entries in the data bank include some information on production (Table 3). This may consist of data on adult size or weight, birth weight, milk traits, fleece weight or litter size. Eighteen percent of the entries have information on both population size and production (Table 4).

Table 3. *Number of breeds or breed varieties for which there is some information on production.*[1]

	Buffalo	Cattle	Goat	Horse	Pig	Sheep	Total
USSR	1	28	9	30	14	53	135(46)
Africa	1	51	21	0	1	46	120(29)
N & C America	0	3	0	1	0	7	11(5)
South America	0	15	3	0	2	4	24(21)
Asia	24	61	61	12	27	112	297(34)
Oceania	0	1	1	0	0	0	2(3)
Total	26(35)	159(28)	95(37)	43(17)	44(19)	222(37)	589(30)

[1] The figures in brackets represent % of all entries in the data bank (Table 1).

Table 4. *Number of breeds or breed varieties for which there is some information both on population size and on production.*[1]

	Buffalo	Cattle	Goat	Horse	Pig	Sheep	Total
USSR	1	26	7	30	14	51	129(44)
Africa	0	38	11	0	1	17	67(16)
N & C America	0	2	0	0	0	5	7(3)
South America	0	11	0	0	2	3	16(14)
Asia	2	34	18	0	11	71	136(16)
Oceania	0	0	1	0	0	0	1(1)
Total	3(4)	111(20)	37(15)	30(12)	28(12)	147(24)	356(18)

[1] The figures in brackets represent % of all entries in the data bank (Table 1).

Information stored in the data bank

Information relating to each entry in the data bank is divided into seven main sections. The information stored is, in most cases, the same for all species, although it is obvious that particular questions refer to some species and not to others, e.g. wool type refers only to goats and sheep. The printout for the Curraleiro cattle breed is given as an example in Appendix I.

General information

- Species (ass, buffalo, cattle, goat, horse, pig, sheep)
- Whether the entry refers to a breed variety
- Where the animals are found plus the country (or area) code relating to this region
- Local names, synonyms and international name (as described by Mason, 1988) of the entry
- Sources of information for the entry

Origin and development of the breed

- Origin of the breed
- Whether the breed is wild or primitive
- Whether immigration of animals from other breeds or countries has taken place in recent years
- Description of population size, in detail or in simple terms (including reference)
- Usage of artificial insemination and storage of semen and embryos

Description of breed

- Coat colour
- Presence of horns
- Hair and/or wool type
- Adult size and weight
- Genetic characteristics of the breed e.g. marker genes, chromosomal aberrations, etc.

Uses and qualities of the breed

- Main uses of breed
- Special qualities of breed, e.g. resistance to trypanosomiasis

Management conditions

- Type of management, housing period, feeding

Production record

- Two ways of describing the performance record are possible: a) giving figures for the traits in Table 5 (including reference) *or* b) comparing the breed to a standard breed (preferably one that is very common) for a range of production traits

Genetic distances and breed conservation

- Genetic distances to other breeds
- Conservation programmes for the breed

Table 5. *Performance record sheet.*

	Buffalo Cattle or Horse	Goat or Sheep	Pig
Milk yield per lactation (kg)			
Lactation length (days)			
Milk fat percent (%)			
Milk yield per year (kg)			
Birth weight (male) (kg)			
Birth weight (female) (kg)			
Daily gain (male) (g)			
Lean meat (%)			
Litter size (n)			
Fleece weight (female) (kg)			

Computer software

The program for the data bank were written with a standardised software package, dBASE III PLUS. The original program were written at the Institute for Animal Breeding and Genetics in Hannover, Germany with European breeds and conditions in mind. Consequently, it was necessary to make some changes to the programs to make the data bank more suitable for breeds from developing countries. Among the changes made were the simplification of the section on production data and the addition of references for population or production data. These changes were made while ensuring that the data stored in the data banks in Hannover and Rome would remain compatible.

Questionnaires

From Tables 2 to 4, it is obvious that essential information is missing for the majority of breeds. To rectify this, contacts have been made with parties in Asia, South and Central America, Africa and the former USSR asking them to:

- Confirm that the entries in the data bank relating to their country or region are a true representative of the animal genetic resources in their area.
- Complete short questionnaires for those breeds for which there is no information on population size in the data bank and, if possible, to do the same for those breeds for

which there is *some* information on population size. For these questionnaires, it was emphasised that information on population numbers was of primary importance.

Extinct breeds

The 1,974 breeds or breed varieties in the Global Data Bank represent populations known to be in existence around the world today. A parallel data bank has also been set up containing information on 205 extinct populations that Mason (1988) described as being recently extinct or that were important to the origin of certain breeds in the Global Data Bank.

Future work

The first phase of the project has been completed. A rough list of animal genetic resources has been drawn up, and, following a relatively brief literature survey at FAO Headquarters, information on population numbers and production data has been collected for a small fraction of these genetic resources.

The next phase of the project should have two objectives: first, to update the entries in the data bank by confirming the existence of the breeds or breed varieties already in the data bank and the addition of genetic resources not yet documented or included in the data bank; and second, population (of primary importance) and production data should be collected for those breeds lacking this information and updated in those cases where some information already exists. The completion of questionnaires by individuals throughout the world concerning genetic resources in their own region should fulfill both requirements.

Once the completed questionnaires are received, the data must be thoroughly checked before they can be entered into the data bank. It is especially important that no breed be entered more than once. This is a danger since the same breed may have several names.

Currently, breeds and breed varieties of only six domestic species (buffalo, cattle, goat, horse, pig and sheep) are present in the data bank in Rome. Expansion is planned to include asses, camelids and poultry as they also represent important animal genetic resources. Mason (1988) provides information on breeds of asses that can readily be included in the data bank while some data on camelids in South America have already been collected through the group in Hannover.

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Discussion

Q: There seems to be little information on breeds in the US.

A: I have concentrated my efforts on developing countries.

Q: Can you comment on your figures regarding population size? Are they accurate? Usually such figures tend to be underestimated.

A: True, this does happen. I make reference back to my sources.

Q: Some countries are not included on the list. I know there are unique breeds (e.g. in Swaziland). Are these intentional omissions?

A: Questionnaires have been sent out asking for verification of the list provided on breed/breed varieties and for additional information on population size. Seventy-four percent of the breeds have been verified and/or updated.

Q: You have only one entry per breed and none on breeds that are the same but distinct.

A: If they are distinct, they are listed as separate entries.

Q: Since you only have one entry, how do you obtain population trends?

A: You get this information from individual countries and include it in the section on population size.

Q: Could you have a line in the data base saying where the breeds are found?

A: We do that already. Most entries are unique to specific countries.

Background to ILCA's AGR characterisation project, project objectives and agenda for the Research Planning Workshop

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Introduction

The rich diversity of life-forms on our planet—genes, breeds, species and ecosystems—provides an abundant supply of essential goods and services which has for too long been seriously undervalued and/or taken for granted. Diversity flourished under the care and influence of our ancestors and (plants and) animals developed genetic resistance to pests and diseases. Some animals developed the ability to live and produce in particular environments, e.g. arid, humid, etc. In general, biological diversity has previously succeeded in adapting and evolving to cope with environmental change. But the current rate of change, resulting mainly from the sheer size of the human population and its capacity to transform the world around it, presents a new serious challenge.

The term Animal Genetic Resources (AGR) is used to include all animal populations, species, breeds and strains, particularly those of economic, scientific and cultural interest to mankind in terms of agricultural production for the present or in the future. Indigenous livestock in Africa (and the rest of the tropics) are being threatened by the need for higher animal production. It is often argued that radical improvements in animal production can be achieved through the use of improved strains or breeds and animal management. Indeed, improvements in veterinary care, nutrition and husbandry in African livestock production systems do generate opportunities for using exotic breeds known to be highly productive in high-input production systems. Such trends already exist in Africa, especially in regard to cattle, and are resulting in widespread importation of improved exotic breeds and extensive (and sometimes indiscriminate) use of imported germplasm in crossbreeding. The population of pure indigenous breeds is likely to diminish as a direct result of crossbreeding or neglect. There is an urgent need to ensure both improved production and the conservation of these breeds which represent unique AGR. Otherwise, by losing diversity, we will lose options for future livestock development.

Conservation of AGR incorporates *preservation, maintenance, improvement and sustainable utilisation* (FAO, 1986). Conservation and management of AGR have been topics of discussion in many fora since the UN Conference on the Human Environment (Stockholm, 1972). The concept of regional AGR data banks for developing countries was proposed by FAO/UNEP in 1983. As part of the development of AGR conservation methodology, FAO (1986) published a comprehensive dictionary of genetic characteristics (descriptor lists) which is expected to form the basis for the data base. The purpose of descriptors is to facilitate valid comparison, classification or enumeration of breeds within a species in the context of the environments existing in different countries and regions.

Breed or species conservation requires characterisation. *Characterisation* means the distillation of all available knowledge, both published and unpublished, which contributes

to the reliable prediction of genetic performance in a defined environment. It does not imply mere accumulation of existing reports or individual findings on genetic performance (FAO, 1984). The exercise includes a clear definition of the genetic attributes of an animal species or breed which has a unique genetic identity, and the environments to which species or breed populations are adapted or known to be partially or not adapted. Characterisation is for purposes of documentation for present and future utilisation. *Documentation* is simply the collation of existing data. *Evaluation* is a contemporary comparison of performance records of two or more breeds under the same environmental circumstances. Thus, breed evaluation or comparison should provide characterisation information for two or more breeds.

Since 1987, FAO has cooperated with the European Association of Animal Production (EAAP) in developing a Global Data Bank for breeds of domestic livestock with the aim of documenting and characterising different breeds and varieties found throughout the world. The Data Bank is based in Hannover, Germany and Rome, Italy. FAO is responsible for the acquisition of necessary data. The purpose of the Data Bank is to provide a comprehensive and accessible description of the characteristics of each livestock breed (and crossbred) population together with characterisation of the environments to which the breed or cross is adapted.

Two important meetings—the FAO/UNEP Joint Expert Panel on AGR Conservation and Management Meeting (Rome, October 1983) and the OAU/IBAR Second Expert Committee Meeting on AGR in Africa (Bulawayo, November 1983)—identified ILCA as being in a position to potentially play a significant role in the design and creation of the African AGR Data Bank in collaboration with FAO/UNEP, OAU/IBAR and national agricultural research systems (NARS) in Africa. In taking this challenge, ILCA recognises that it cannot succeed without substantial collaboration with NARS colleagues.

In November 1990, the Ninety-eighth Session of the FAO Council recommended that FAO prepare a programme for the sustainable development of animal genetic resources on a global level. The specific objectives of the programme are to establish and operate a global system to serve the interests of national governments and to support their efforts to describe, evaluate, develop and preserve AGR. It was also recognised that, to achieve these objectives, it was necessary "to reinforce national activities and initiatives; to provide opportunities for linkages with national programmes; and to provide technical support services at a regional and global level" (FAO, 1991). As a centre with a regional mandate covering sub-Saharan Africa (SSA), ILCA is in a position to provide the opportunity for linkage between the donor community and FAO on the one hand and NARS in SSA on the other.

Main issues

In order to make decisions about how to protect genetic diversity, one has to know the structure of genetic variation in the population. Without this knowledge, the safest strategy is to conserve virtually everything. However, this is not a feasible option.

Even if only some aspects of the distribution of genetic variation are known, that information, while incomplete, can help guide the development of useful conservation strategies. Thus, for genetically uniform breeds, sampling for conservation can be based on relatively few populations and small samples would cover the available genetic variation.

Indigenous livestock have, through natural selection, developed characteristics which make them well-adapted to the environmental conditions under which they live and produce. Thus, indigenous breeds form a valuable genetic resource which needs to be maintained and improved as the basis for national livestock breeding programmes and policies. This is both an economic and a moral issue.

Several important African breeds are spread over a number of countries (e.g. the East African Zebu; the Boran in Ethiopia, Kenya and Somalia; the Nguni or Nkone in Swaziland, Zimbabwe and Botswana; and the Djallonke sheep in several West African countries). It would be interesting to test whether some of these "breeds" are actually different. On the other hand, there are many "breeds" which look similar but have different names across countries. It would be equally important to investigate whether indeed these are different breeds. It may be possible to employ DNA technology, not only to estimate genetic distances between such populations, but also to improve them by identifying which genes are responsible for their outstanding merits.

Needing special consideration will be those breeds adapted to very specific environments and which play a major role in rural economies (e.g. the N'Dama and other trypanotolerant breeds in tsetse-infested areas). Generally, in hot, humid areas and other harsh tropical environments, it may not be possible to improve animal health care and feeding and management practices to levels that would allow high-yielding temperate animals to be used. The need here is to design appropriate breeding programmes based on native livestock populations adapted to such environments.

Ex situ conservation (of semen and embryos) is a topical issue today in debates concerned with biodiversity. Whether or not ILCA is involved in *ex situ* conservation, the issue of sustainable use is of direct relevance to the Centre. The high cost of collection for *ex situ* conservation is a key concern, especially in view of the fact that the exercise is not associated with short-term quantifiable output. The issue of intellectual property rights and related legal instruments is also a concern echoed constantly in relation to germplasm conservation.

Project objectives

The project objectives are to:

- Characterise indigenous breeds in terms of physical characteristics, productive parameters and adaptive characteristics, including a description of environmental conditions under which performance has been measured. Consideration will first be given to those breeds for which required information can be obtained from the literature. Systematic characterisation will then be undertaken for other breeds and to fill information gaps identified in the literature. This objective will address several more specific questions: which breed/strain/population exists and where? What are the characteristics of the breed and similarities to others? Does the same breed exist in other countries/regions? Is the population stable or decreasing?
- Identify the main problems preventing utilisation and improvement of animal genetic resources at national and regional levels and determine how these problems may be solved. Particular attention should be directed towards how existing national and regional organisations may be strengthened for this purpose.
- Develop inventories of animal genetic resources in Africa, starting with cattle and small ruminants. Such data bases will be shared with the Global Data Bank and other interested parties, and may form the basis for an African Data Bank of AGR.

Workshop objectives

The workshop objectives are to:

- Assess the importance and relevance of the proposed project and to determine the feasibility of implementation.
- Set priorities in terms of breeds to be characterised and characteristics to be measured, considering the limited resources.

- Streamline procedures for extraction, compilation and summary of results from the literature. Specific questions to be answered will include: how far back one needs to go in the literature; determination of authenticity or reliability of published results; combination of results of different studies (on the same breed) conducted at different periods; etc.
- Work out standard research methodology to facilitate comparison of results from different studies. Specific issues include: on-station vs on-farm; animal sources and sampling procedures, including numbers; animal management (supplementation for maximum expression of genetic merit vs evaluation using available feed resources in the system, i.e. pastures only); possibility of pooling data from different studies; etc.
- Identify breed evaluation programmes in NARS which may be strengthened, with modest input, to provide the required characterisation data.
- Discuss the possibility of using DNA technology to study genetic characteristics of livestock in Africa, especially to determine which breeds are truly different. This could be extremely useful in future conservation efforts. Germplasm preservation could be made significantly cheaper if it were shown that several breeds shared a common DNA heritage and thus are practically genetically identical. ILCA could, through collaborative arrangements, obtain biological material from NARS partners and channel them to laboratories of collaborating international agricultural research centres (IARCs) or other institutions.

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General discussion

C: The descriptors used in the FAO Global Data Base were developed by J. Hodges. They are very detailed. What we are using at FAO is a short summary developed by FAO and the EAAP. We do not use Hodges descriptors. We want to shorten the list without losing substance.

C: When we start looking for breed characterisation data, we should look at the genetic variance of certain traits which are of interest to us. In the literature, one tends to find only a number, usually a mean. Information on phenotypic variance tends to be lacking.

C: Yes, we need to quantify variation as part of the characterisation process.

Q: How is ILCA's proposal different from what FAO does? ILCA's main interest is on breed characterisation. FAO goes beyond that—into preservation. Should we be doing one thing at a time?

A: You cannot begin the process of preserving germplasm without first knowing population sizes, the dynamics of the population, etc. Characterisation helps set priorities for conservation.

C: There is a natural sequence of action: documentation (what is it you are dealing with) then interventions (which may include improvement programmes, husbandry research, genotypic intervention, cryopreservation for endangered breeds, etc.). ILCA has targeted the first stage. There are many common elements between FAO and ILCA. The two organisations should align themselves better to one another.

C: We are talking about characterisation for preservation and utilisation. This is an open plan. The question before us is, where is ILCA's comparative advantage? One of the issues to be examined is how to describe a breed. Hopefully, this information will be teased out of the discussions to be held during the course of this week.

Q: Why does ILCA avoid the issue of conservation? We have been talking about utilisation and preservation, but what about conservation? We can preserve and better utilise some breeds through management or land tenure assistance. ILCA should take policy/management issues into consideration when talking about animal genetic resources.

A: Conservation by preservation *(ex situ)* is part of the workshop topic but is somewhat peripheral to our discussion. There are sequences of action that need to be followed.

C: We have published and documented accounts of endangered breeds. In these cases, we cannot wait for characterisation. We need some action plans for conservation of these breeds. Conservation efforts can proceed at the same time as characterisation. ILCA should include conservation in its mandate.

Q: I agree. To improve utilisation and conserve at the same time, could breed characterisation include constraints to productivity?

A: Identifying problems in utilisation and improvement includes *in situ* conservation. I would avoid a commitment to *ex situ* preservation without additional donor funding.

C: We return to our countries and our politicians ask, conserve for what? The issue here is when you speak of utilisation, characterisation, preservation and conservation, there is a need to look for characteristics that improve productivity and are adaptive to particular environments. If we say that a breed has adaptive characteristics, adaptive to what? What are our terms of reference? We need to convince policy makers that there are animal species that are useful and productive.

C: Some of this is a moral issue—do we conserve a breed simply because it is unique and possibly useful in the future? It is important to address the question, how do we combine conservation with improved production and, therefore, utilisation?

C: In discussions thus far, we have been talking about characterisation. But the real value of animal genetic resources, and what should be characterised, is, for instance, milk composition of breeds (to promote the maximum range of dairy products), growth rates, carcass characteristics, ability of breeds to control parasitism, ability to digest indigestible foods, oestrus sychronisation through nutritional manipulation to control/influence reproductive traits. These issues are of wider scope; characterisation becomes a tremendously important means of capturing the diversity of animal genetic resources in Africa.

C: We need to characterise before we can begin thinking about preservation. How do you preserve *ex situ* without *in situ*? We should focus on indigenous breeds because bringing in exotics, etc., tends to upset the process.

C: It tends to be the case that if scientists cannot justify immediate objectives to policy makers, no money may be forthcoming. There are also donor agencies and their agendas to consider. However, characterisation studies should not preclude other activities.

Relevant on-going programmes at CRTA

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Introduction

The CRTA was created in 1972. The founding members were France (IEMVT and Ministry of Cooperation), Germany (GTZ and BMZ) and Burkina Faso (Ministry of Agriculture).

The Centre is located in Burkina Faso in Bobo-Dioulasso, 360 km south-west of Ouagadougou, in the subhumid zone of West Africa. Its location makes it possible to survey livestock populations across different ecological regions: Zebu cattle originating from the Sahelian North, trypanotolerant Baoulé in the southern areas and several breeds of small ruminants either of Sahelian type or of the trypanotolerant Djallonke type and crosses. Level of tsetse challenge also varies from light to heavy. Devoted to the study of trypanotolerance in West African taurines, the CRTA has concentrated its efforts on the Baoulé breed: its characterisation and the expression of its resistance in comparison with Zebu cattle under natural and artificial challenge.

Research activities of the CRTA focus mainly on:

- tsetse control through nonpolluting techniques (use of traps, screens and other targets associated with olfactory attractants, sterile insect technique);
- trypanotolerance to identify, through bioassays, the most resistant animals to be included in selection and multiplication schemes.

An immunogenetic programme for characterisation of cattle breeds has been on-going at CRTA for more than 10 years. A programme in animal husbandry was more recently implemented. Work reported on immunogenetics is primarily under the leadership of Dr. R. Queval. Results of his work are presented below.

Work to date

As part of the characterisation exercise, immunogenetic profiles have been obtained for 20 different cattle populations in West and Central Africa. These populations include: trypanotolerant taurines (N'Dama, Lagune, Baoulé), trypanosusceptible taurines (Kuri), different taurine crosses (N'Dama x Baoulé, N'Dama x Jersiais, N'Dama x Abondance, N'Dama x Simmental) and Zebus (Azawak, Choa, Foulbe, Sudanese Fulani). The following criteria were studied: blood types (11 systems) plasma protein polymorphism (albumin, transferrin), enzymic systems polymorphism (hemoglobin, nucleoside phosphorylase (NP), phospho- gluco-mutase 3), MHC BoLa-class I-antigens-typing for Baoulé and Zebus.

The main results of these studies were:

- Differences in allele frequencies for albumin, hemoglobin and PGM3 were significant for NP.
- In a field experiment, one third of the West African Shorthorn cattle were susceptible to trypanosomiasis under high natural tsetse challenge. When susceptible and resistant sub- populations were compared, the difference of allele frequencies was highly

significant ($P < 0.01$) for albumin, significant ($P < 0.05$) for hemoglobin and non significant ($P > 0.05$) for NP and PGM3.

Among other results, it was observed that:

- In the heartland of N'Dama and Baoulé breeds and in areas of high tsetse challenge, the animals were homozygous for genes A for hemoglobin and F for albumin.
- The frequency of gene F for albumin showed significant variability between the sub-populations of resistant and susceptible Baoulé.

The programme on MHC antigens or BoLa typing was done by Drs. Queval and Maillard. A large set of antisera of the different specificities was prepared in cooperation with ILRAD, INRA and AFRC (Edinburgh). As an example, the different gene frequencies of BoLa class I specificities were studied in a population of 1,016 Baoulé cattle in Pays Lobi in Burkina Faso.

The main conclusion of this study was that BoLa typing adds to the hemoglobin AA-albumin FF combinations. Thus, it can be used to confirm breed differences. However, BoLa typing does not add anything to the study of plasma proteins or blood groups.

Two years ago, a livestock production research unit was implemented at CRTA, first by Dr. Salas, and now by Drs. Godet and Bassinga. Observation of cattle in natural conditions is done in different sites around Bobo-Dioulasso. For example, in Pays Lobi, 1,960 animals in 57 herds (mainly Baoulé) are studied; in Sideradougou, 1,160 animals in 25 herds (mainly Zebus) are monitored. Management systems have been identified. Health and performance records are being collected on a regular basis. Data are now being analysed by a micro-computer-based animal performance recording and analysis package (PANURGE) from IEMVT.

Two additional programmes on the reproduction of cattle should be mentioned. First, a semen bank has been set up by Mr. Cloe and D. Thombiano for Baoulé, N'Dama and Zebu bulls; more than 9,000 doses are now available at CRTA. Second, a new research programme on the superovulation of cows has begun, to improve embryo transfer technology for better breed conservation and diffusion.

Conclusion

Research in breed characterisation will continue at CRTA, and the Centre will maintain the existing close links with national institutions and international centres. The Centre will also work closely with the CG-funded centres (e.g. ILRAD, ILCA etc.). To reinforce these linkages, a strong mechanism of cooperation needs to be established. For instance, special projects prepared with the CG centres and submitted for funding to different donors should be developed. A good example is the special project recently set up with ILCA, ITC and CRTA which, it is hoped, will be funded by the EEC.

Discussion

Q: Has any work been done on the connection between hemoglobin type and the mechanism of trypanotolerance?

A: We do not say that for trypanotolerance, you need purebreds that are AA for hemoglobin. There is no correlation between hemoglobin and trypanotolerance. There may be some between albumin and trypanotolerance because there is variability in allele frequencies in this population.

Q: What is the objective of the semen storage? Is it only for storage or for breeding activities as well? What is the purpose of the embryo transfer (ET) work.

A: Semen is being used in Mali, Burkina Faso and Côte d'Ivoire to study, under village conditions, the use of AI and the impact of AI in terms of trypanotolerance and productivity.

Q: You have three breeds. Are you using them in some breeding plan?

A: Yes, we have Zebu, Baoulé, West African Shorthorn and we hope to get N'Dama shortly.

Q: In an earlier Centre report, it was shown that with crossbreeding, trypanotolerance broke down.

A: According to the work of Dr. Queval, trypanotolerance is absolutely correlated with purebreds. In crossbreeding with Zebus, trypanotolerance does appear to break down.

Q: Will the work at CRTA include other diseases?

A: Yes. In our new mandate, we will go to other vector-transmitted diseases (tick-borne diseases). We are already working on internal parasites.

Q: Is trypanotolerance in West Africa unique? Have there been attempts to characterise trypanotolerance in other breeds?

A: ILCA's activities focus mainly on the N'Dama. We are now discussing with colleagues in NARS and regional institutes the possibilities of undertaking collaborative studies to examine other trypanotolerant breeds and to look at the effects of crossbreeding (N'Dama x Zebu). The same criteria will be used to determine their importance in terms of trypanotolerance and effect on performance. We are, at present, also working on Djallonke sheep.

A: There are some trypanotolerant breeds in Eastern Africa as well.

Q: What are you attempting to conclude from the differences in allele frequencies? The literature suggests that there are pitfalls with this type of analysis. Also, if you are using animals of different sizes, you may get spurious results if you are suggesting that differences in allele frequencies are related to trypanosusceptibility.

A: Dr. Queval is trying to limit the characterisation of the breed. No attempt has been made to link trypanotolerance to this marker.

Q: We had a presentation from ILRAD and many others on trypanotolerance. Is this work coordinated or being carried out independently?

A: Linkages between FAO and ILCA are strong and coordination is good. We have tried to coordinate within our Network. ISCTRC (International Scientific Council for Trypanosomiasis Research and Control) is quite involved as well. It is one of the most important areas for coordination. The donor community is pushing for more collaboration.

The National Sheep Improvement Programme (PNSO) in Côte d'Ivoire

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Introduction

A sheep improvement programme was started in Côte d'Ivoire in 1984. Its aim is to increase sheep productivity by improving body weight and growth rates of Djallonke sheep through the selection and distribution of Djallonke rams to farms supervised by SODEPRA (Socíete de développement des productions animales). The open nucleus scheme includes three phases: pre- selection of lambs on- farm; selection of rams on-station; and distribution of rams on-farm. The nucleus holds 10,000 ewes with an output of 300-350 rams per year. The programme intends to consolidate progress already achieved in the field (performance testing and distribution of selected animals) and to develop research agendas (use of data and genetic evaluation of selected animals).

Improvement scheme

Phase I: Pre-selection of lambs on-farm

After performance testing, lambs from foundation farms are pre-selected based on weight at 80 days of age (only lambs weighing above 13 kg are selected). At this stage, additional factors, such as season of birth, type of birth, parity and technical skills of the farmer are used to help fine- tune selection criteria. Dams for future breeding are also identified from the foundation stock during this phase. Pre- selected lambs are bought from the farmers and transferred to the station at Bouaké (project headquarters) for individual testing.

Phase II: Selection of rams

In Bouaké, lambs are maintained under optimal conditions (zero-grazing) to allow expression of their potential. After control testing, mass selection, based on weight at 180 days of age, is practiced. Rams ranking highest in terms of body weight and body conformation are selected.

Phase III: Distribution

Selected first category rams (weights greater than 35 kg at 365 days of age) are distributed only to participating (foundation) farms for breeding, according to a mating management system. Outstanding individuals in the first category (weight greater than 40 kg) are multiplied through controlled mating in farms where adequate facilities are available.

Second category rams (30-35 kg) are bought by outside farmers who are advised to use them for a two-year period. To avoid inbreeding, rams are later exchanged among farmers of this category, with due regard to health precautions.

Testing design

Performance testing includes:

- Testing on productive and reproductive traits
  - Fertility
  - Fecundity
- Prolificacy
  - Abortion
  - Neonatal mortality
  - Lamb mortality at 80 days
  - Number of 80 day old lambs per ewe
  - Weight of 80 day old lambs per ewe
- Early maturity testing in lambs

On the basis of three weighings per lambing (20,000 to 30,000 weighings per year), information is obtained on weight at 80 days of age and average daily weight gain from 0–80 days.

Progress and results

Foundation stock

From 1984 to 1990, the number of ewes in the foundation stock increased from 3,000 to 10,000 animals spread over 86 farms throughout the country. During this period, 2,955 lambs were pre-selected on-farm. Annual average weights at 80 days of age ranged from 13–15 kg; average market weights ranged from 15–16 kg. The target is to test 12,000 ewes and pre-select about 900 lambs per year.

Production of selected rams and dissemination of genetic progress

Overall, the project produces 300–350 rams per year. PNSO has a stock of 250 selected first category rams within 14 male breeding lines which are used to service the foundation stock. Breeding proceeds according to a mating management system (45 days) by male line in order to keep inbreeding under control as much as possible.

In addition to the 10,000 ewes in the nucleus flock, the project monitors from 10,000 to 11,000 ewes in other flocks covered by the project.

In 1988, PNSO, in collaboration with CNA (National Sheep Centre) and CNIA (National Artificial Insemination Centre) supplied, on request, selected genetic material (rams, ewes and fresh semen) to Togo. Another consignment will be supplied this year.

Future prospects

For the future, PNSO hopes to decentralise performance testing and distribute rams to each SODEPRA area. Increased participation of farmer groups now being trained in the sheep genetic improvement process is planned as well. Finally, the role of research and development will be expanded to include economic and genetic evaluation of animal performance with a view to maximising the overall improvement scheme.

Discussion

C: The project presented is the only documented case in Africa where an indigenous breed is being improved through an open nucleus scheme. This is important. It reflects

utilisation of improved indigenous stock. When we break into groups, we need to look at the kinds of programmes underway that fit into our workshop objectives.

Q: How did selection increase numbers from 3,000 to 10,000?

A: The institution we work with had about 50,000 sheep; among these, we used about 10,000 for selection.

A: In the process of developing the programme, PNSO started out with small numbers. Through selection and multiplication, numbers have been built up.

A: We began activities in central Côte d'Ivoire. Work has now spread to the whole country.

Q1: Is this project totally funded by the government?

Q2: Is there any evidence of a selection response from 1984–1991?

A1: The project was financed by Côte d'Ivoire and the French (through a cooperative assistance fund). Funding from France stopped in 1990. For the past three years, money has been provided by the EDF (European Development Fund). This money is only for ensuring programme continuation. Funds are almost exhausted. We need more to assure the proper functioning of this scheme.

A2: We are beginning analysis. But based on some findings, farmers have noticed that their animals weigh more at birth and at market age.

Q1: Regarding results on rams, you say that mean body weight was 36.1 kg in 1984 and increased to 36.37 kg in 1990. This is an improvement of about 15 g/year. Does this represent genetic improvement to you?

Q2: Do you have problems identifying performing rams?

A1: The weights from 1984–1990 are the weights at which the animals were selected, not the gains made in the selected population. What is now occurring is that the African Small Ruminant Research Network is negotiating to provide funds to do actual evaluation and analysis of data and to see if there has been any change as a result of selection.

A2: The first grade rams were selected on weight after one year. It is only now that we will be able to determine genetic progress made.

Q1: What is the average herd size of the farmers you are dealing with?

Q2: How do you ensure that progress is not diffused at the farmer level?

A1: We are speaking of about 80 lambs/farmer. Some have more lambs. It is when we work out gross numbers that the figure becomes 10,000.

A2: The dilution will not occur because we are working at two levels. We use strict selection methods. If there is a decrease in numbers of lambs, we will go back to farmers. Farmers receiving second grade rams out of the nucleus are those who are sufficiently skilled to be able to use a ram that would improve their animals.

C: Another aspect of this is the environment in which selection is done. It is exactly the same as would be found on-farm. No interventions are being proposed at the farm level.

A: Our objective is to provide farmers with animals that can produce on-farm. We keep the same conditions on-station so that when rams go on-farm, their management is not different.

End of Wednesday, 19 February 1992 session.

Breed evaluation and characterisation work in The Gambia

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Introduction

The major livestock species in The Gambia are cattle, sheep, goats and equines (horses and donkeys). It is estimated that there are 300,000 cattle, 150,000 each of sheep and goats and 50,000 equines. An estimated 95% or more of the cattle are N'Dama while the remaining are crosses between Zebu and N'Dama, with a few Zebus found at the fringes of tsetse-free areas of the country. The small ruminant (sheep and goats) population consists mainly of the Djallonke breed. Virtually all cattle and small ruminants are held by smallholder farmers and are managed under traditional husbandry practices. Whereas cattle are kept for milk, meat and draught, small ruminants are mainly kept for meat, although it is reported that goats may be milked for short periods. As a rule, equines are used only for draught purposes.

Since 1985, scientists at the International Trypanotolerance Centre (ITC) in The Gambia have been investigating the performance of N'Dama cattle in terms of milk production, growth, carcass characteristics and resistance to diseases (trypanosomiasis, helminthiasis and tick-borne diseases). Over 4,000 village cattle and 1,000 station-managed animals have been monitored. Data from these investigations have provided a unique opportunity for characterising the N'Dama and evaluating its potential as a multiple-purpose breed. Similar but limited work is being carried out on Djallonke sheep and goats.

Livestock research and development

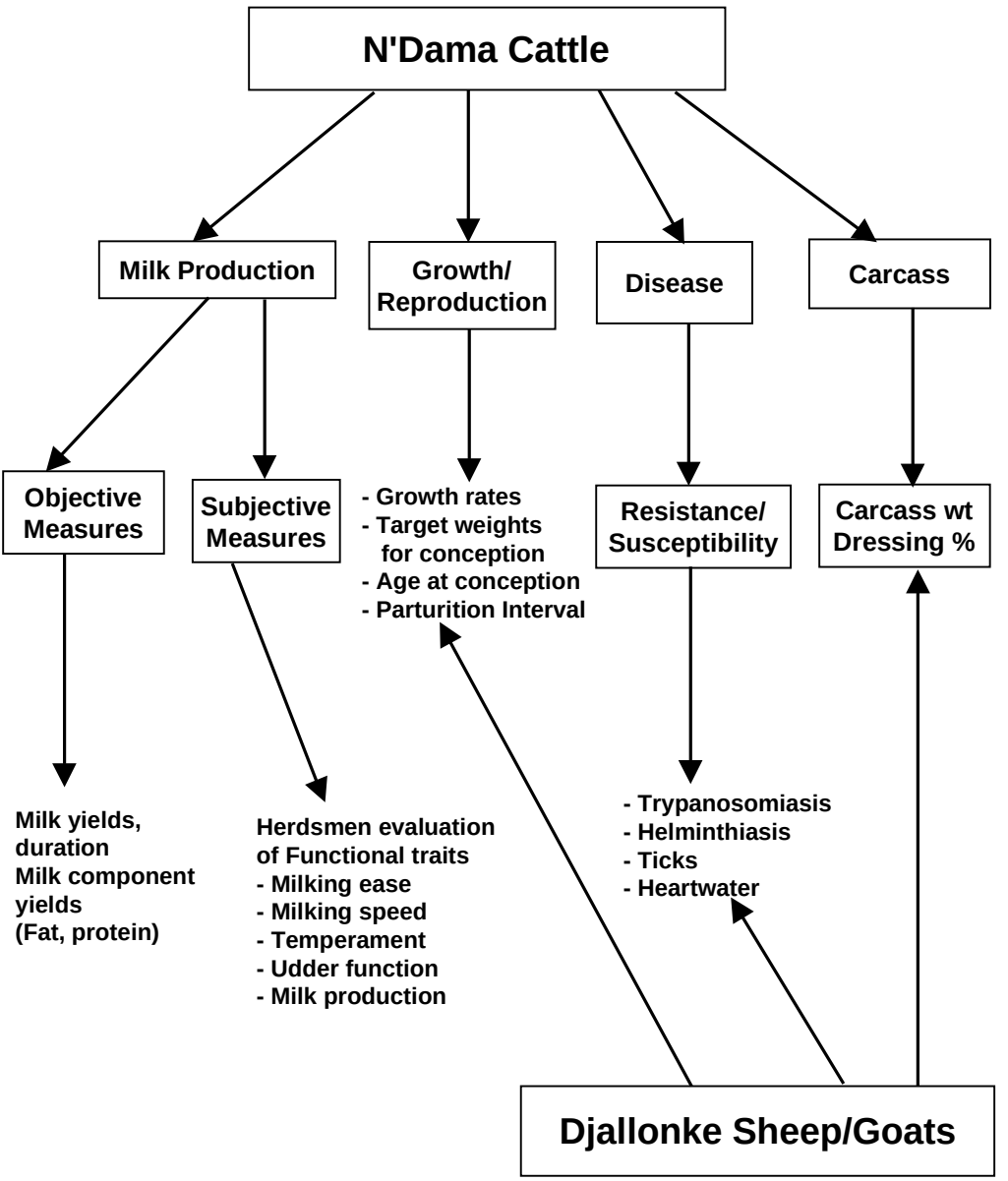
Livestock development in The Gambia is the responsibility of the Government's Department of Livestock Services (DLS). A research unit under DLS undertakes research on small ruminants in the areas of nutrition and management. Under special arrangement, major research on cattle is entrusted to the ITC which also has responsibility for developing livestock and related infrastructures in selected areas of the country. ITC also does research on small ruminants. Research on N'Dama cattle production at the ITC is done on-station and on-farm (village). On-station work, mainly implemented under the African Development Bank- funded Livestock Development Project (LDP), produces high quality N'Dama breeding stock for export and the local market. Nucleus herds have also been established through the purchase of outstanding village animals, constituting them into herds and testing and culling mediocre animals based on production characteristics.

The on-farm work funded by the European Economic Community (EEC) was initially executed jointly with the International Livestock Centre for Africa (ILCA) and the International Laboratory for Research on Animal Diseases (ILRAD) and later (during 1991) by ILCA. The ILCA/ILRAD project conducted research to support work undertaken by the LDP. One of the major objectives of this project was to evaluate the productivity of N'Dama cattle, subjected to varying levels of disease risk, under village

conditions. From these two programmes and other associated projects at the ITC, such as the Swiss Government/University of Berne Helminthiasis Project (UBP), characterisation of N'Dama cattle and Djallonke sheep and goats has taken the form summarised in Figure 1.

Figure 1.

Summary of livestock breed evaluation and characterisation work in The Gambia.



Milk Production

Nearly 1,500 cows spread over 45 village herds have been monitored in a milk recording scheme during a five-year period to determine quantity of milk extracted for human use, lactation length and fat and protein concentration. Over 2,500 lactations have been recorded and individual cow and herd variations quantified. For example, over a 14-month lactation period, milk extracted for human use averaged 404 kg (SD 183 kg); milk fat and

protein percents of 5.1 (SD 1.0%) and 3.2 (SD 0.3%), respectively, have been recorded (Agyemang et al, 1991). The use of multiple records has allowed for estimation of repeatability of milk offtake. Predictions of breeding values and estimation of annual genetic progress is being attempted.

Additionally, about 150 station-reared cows have been monitored on a daily basis for three years for milking characteristics. A first-phase herdsmen subjective evaluation of functional or workability traits for 650 village and 60 station-managed cows has been completed. These traits included milking ease, milking speed, temperament, udder function and milk production. Repeatability of evaluation by multiple herdsmen has been estimated. The philosophy behind this exercise is that with the diminishing range of feed resources in the region, some intensification of cattle production is anticipated and cattle will be expected to produce more output/unit of animal. Milk extraction for human use would also assume even greater importance; traits that interfere with the proper functioning of milking should be identified. It is our conviction that when it comes to identifying animals with undesirable functional traits, herdsmen know best. By allowing them to evaluate the animals, we will ultimately be able to identify and cull parents with multiple offspring possessing undesirable traits.

Growth and reproduction traits

Nearly 2,000 ear-tagged calves in village herds have been weighed on a monthly basis from birth onwards. Approximately half are females and weighings have continued until conception and parturition. Similar records have been kept on animals in the station nucleus herds. The objective is to characterise the growth curve parameters of N'Dama in both sexes and to establish target weights for puberty and conception. Available results from on-farm research indicate that heifers attain a target weight of 180–200 kg at about 42 months, whereas heifers on-station reach this weight about 10 months earlier.

Disease resistance

A group of 20 N'Dama bulls have been repeatedly inoculated artificially with known quantities of cloned *Trypanosoma congolese* in comparative studies also involving Zebus. Bulls have subsequently been exposed to natural tsetse challenge in medium to high tsetse-density areas. Superior bulls, in terms of repeatable anaemia and parasitaemia control, are selected for breeding. Studies have been extended to sheep and goat flocks on-station. N'Dama cattle of different ages and physiological status have been fed known quantities of strongyles larvae in combination with inoculations of *T. congolese*. Individual animal responses to challenge have been monitored in terms of faecal eggs shed, anaemia and parasitaemia control for eventual selection of more resistant animals.

Tick loads and patterns of attachment to cattle have been monitored in a comparative study with N'Dama and Zebu cattle exposed to tick challenge (Claxton and Leperre, 1992). N'Dama yearlings have been subjected to artificial challenge of ticks and responses to development of heartwater disease monitored.

Carcass characteristics

Nearly 2,000 carcasses of N'Dama cattle have been evaluated for weight and dressing percentage over different seasons of the year in a preliminary study to characterise slaughter attributes of N'Dama and how these could be related to factors such as condition score, working status, age and sex. Results show that the average dressing percentage is 43% and was significantly higher during the late rainy season and early dry season than in the late dry season and that dressing percentage was not influenced by condition score. Similar studies are being planned for Djallonke sheep and goats.

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Discussion

Q: What type of herdsmen are you evaluating?

A: They are either herdsmen who are on-contract to milk or those who herd. We designed a questionnaire asking them to describe the animals in terms of specific traits (milking ease, milking speed, temperament, udder function and milk production). We provided options for response: poor, average or good.

Q: Do you know about the level of crossbreeding that has occurred between the N'Dama and Zebu? Are there many Zebu herds here?

A: In those cases where we suspected crossbreeding, herdsmen were asked to identify where the animals came from and if they thought the animals were crossbreds.

Characterisation and evaluation of Sanga and West African Shorthorn on the Accra Plains

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Introduction

Together, the West African Shorthorn and the Sanga account for about 95% of the cattle population in Ghana. These and other indigenous breeds also account for well over 95% of the domestic milk and meat production. Except for isolated records on government ranches, a few private ranches and university research stations, there is little information on the productive potential of these breeds.

Examples from other parts of the world highlight the importance and value of using indigenous breeds in development schemes to improve national milk and meat production. Thus, the characterisation and evaluation of the Sanga and West African Shorthorn represent important and necessary steps in the design of genetic improvement programmes aimed at sustainable increases in milk and meat production in Ghana.

Objectives

The objectives of this project are to:

- identify and define physical characteristics of the Sanga and West African Shorthorn in Ghana;
- characterise reproductive and other performance traits of each breed;
- develop improvement programmes for meat and milk based on breed characteristics.

Work programme

The study will take place on-farm in three phases. In Phase I, a literature review of relevant information on the Sanga and West African Shorthorn will be carried out. In Phase II, a rapid survey, in questionnaire form, will be carried out on smallholder farms to obtain general information about the farms, particularly the breeds kept and herd characteristics. Based on survey results, farms will be identified to participate in the breed characterisation project. Phase III will involve sampling the farms keeping these breeds and measuring various production parameters. Data to be collected would include information on the following characteristics.

External features:

- horns
- dewlap
- umbilical fold
- ears
- coat colour

- heart girth
- wither height

Reproduction parameters:
- age at first calving
- calving intervals
- oestrus cycle

Pre-weaning calf mortality

Milk production:
- milk offtake
- composition of milk
- lactation length

Growth data:
- liveweight at birth, 3, 6, 9, 12, 18, 24 and 36 months
- mature weight

Carcass data:
- slaughter weight
- dressing %
- backfat thickness
- longissimus dorsi area
- carcass yield, etc.

Progress to date

Some literature has been compiled on the West African Shorthorn, the Sanga and other indigenous breeds. Even though the Sanga are believed to be the most numerous breed of the estimated 200,000 head of cattle on the Accra Plains (20% of the national herd), there is relatively little information on their production characteristics. The West African Shorthorn appears to be the most studied breed, possibly because it is the most numerous in Ghana, representing 79% of the cattle population. This is followed by the N'Dama. A few studies have also been reported on the Gudali and White Fulani which are relatively few in numbers.

The rapid survey by questionnaire has begun. Thus far, the questionnaire has been administered to 13 farms on the Accra Plains. Sanga and West African Shorthorn were found on eight of the 13 farms.

Expected output

The folowing outputs are expected from this project:
- the Sanga and West African Shorthorn will be quantitatively and qualitatively characterised;
- promising cattle breed(s) for further genetic improvement will be identified and selected;
- appropriate indigenous breeds for dairy/beef production will be recommended to farmers;
- the basis for cattle breed standardisation in Ghana will be established;
- Ghanaian scientists and technicians will be trained;
- Extension bulletin for farmers will be produced.

Discussion

Q: You found that Sanga and West African Shorthorn breeds were on eight farms. How have farmers kept the two breeds from crossing?

A: Most of the bulls were either Zebu, N'Dama, White Fulani or Gudali and then the Shorthorns. So, you have a mixture. The Sanga could be a Gudali x N'Dama cross or a White Fulani x Shorthorn cross. It is difficult to tell. But they are the most numerous. Farmers like the Zebu bulls. The Sanga is not really a breed but a common type.

C: You have a nondescript situation. In most cases with no clear geographical boundaries between the Sanga and Zebu, you have intermediates.

C: Aren't the indigenous breeds better known from their physiological characteristics (e.g. water intake, heat tolerance) that make them uniquely adapted to the environment? Perhaps it is these features that should be studied in depth.

C: Drought is important and should be considered in the evaluation. Time-scale and financial requirements should be examined because of the proposal to carry out work on-farm.

Animal genetic resources and breed characterisation work in Ethiopia

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Introduction

Ethiopia has diversified topographic conditions with altitudes ranging from extremes of 4500 m asl in the Semen mountains to areas below sea level in the Danakil depression. Within this diversity, climatic conditions vary from arid, tropical, sub-tropical and temperate. Ethiopia has an estimated 27 million cattle, 23.2 million sheep and 17.3 million goats—ranking them first, second and third, respectively, in Africa. For all of Africa, 17%, 12%, 11% and 49% of the cattle, sheep, goat and equine population, respectively, is found in Ethiopia (Table 1). Given its diversified topographic and climatic conditions, the huge livestock population size, the different types of animals, which have evolved over time and adapted to the ecological conditions of their habitat, and, to some extent, been influenced by the production system of their owners, Ethiopia can be considered a centre of diversity for animal genetic resources.

Table 1. *Estimated livestock population of Ethiopia.*

Livestock type	Number ('000)	Rank in Africa	% Share in Africa
Cattle	27,000	1	17
Sheep	23,200	2	12
Goats	17,300	3	11
Camel	1,000		
Equine	7,000		49
Poultry	50,000		
Pigs	13		

Source: FAO, 1987

Ethiopia is considered the home of some of the most important cattle breeds in eastern and southern Africa. The indigenous breeds, as described by Epstein (1957), originated from the migration of Hametic Longhorn from Egypt along the Nile Valley and the humped Zebu from India through the Horn of Africa. Interbreeding between the Hametic Longhorn and the Zebu resulted in a third breed, the Sanga, which spread to the southern part of the continent. Among some of the strains and varieties of the Sanga are the Nilotic of the Sudan, Ankole of Uganda, Tonga of Zambia and Tuli and Mashona of Zimbabwe. A second invasion of Zebu cattle is believed to have led to the displacement of the Sanga and, in some areas, interbreeding with the Sanga to form the intermediate Sanga/Zebu type.

Classification of Ethiopian livestock

The livestock population is primarily of local origin and not characterised as belonging to specific breeds. However, the local breeds are generally named after the area they occupy. Even amongst these identifiable types, there has been large inter-mixing, resulting in a dilution of breed characteristics. Thus, a large proportion of the population is nondescript.

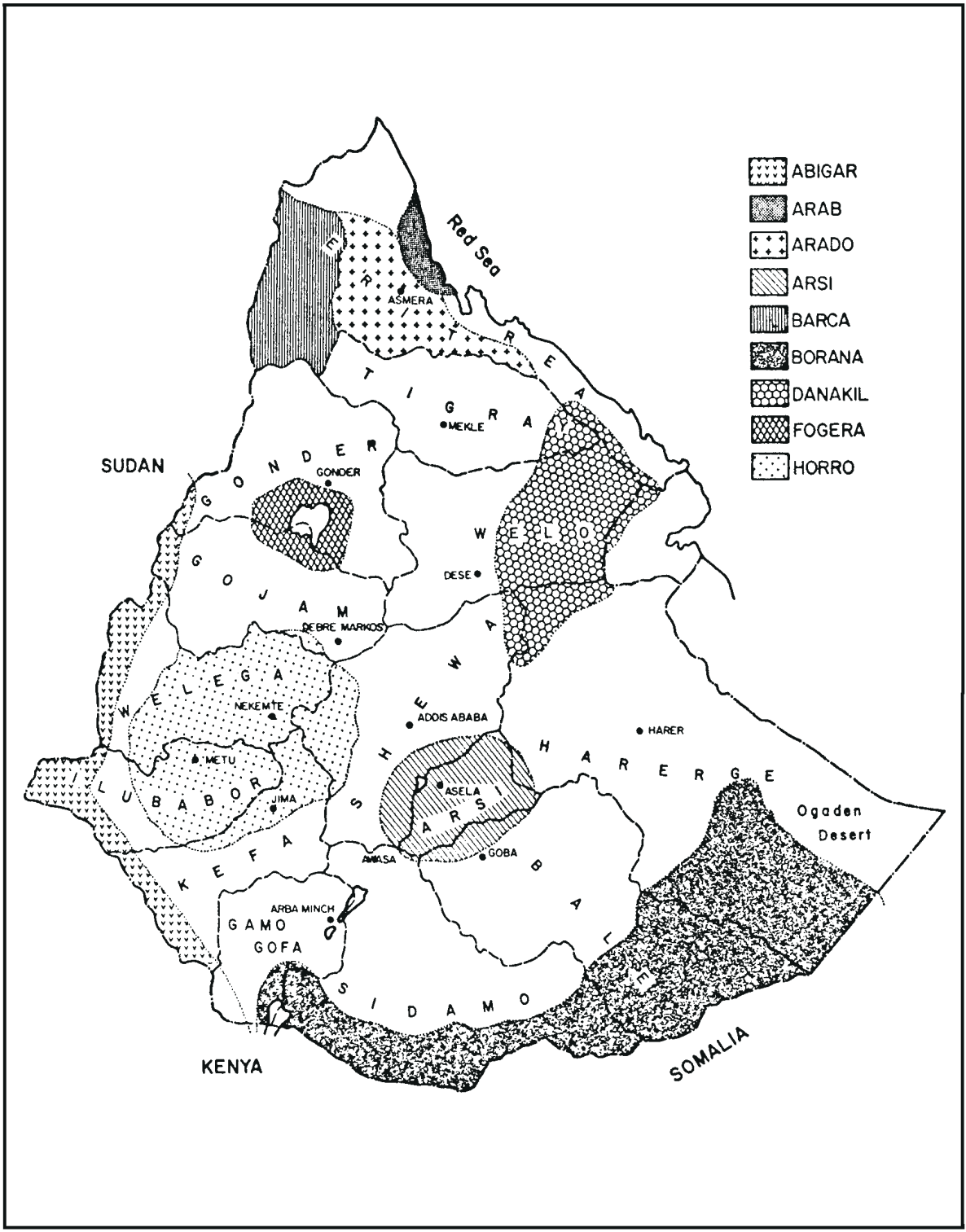
Little effort has been made to comprehensively describe the indigenous livestock populations of Ethiopia. Alberro and Haile- mariam (1982a; 1982b) attempted to identify and classify some Ethiopia cattle types by compiling available literature and gathering information from field trips and Ministry of Agriculture provincial offices. Cattle were classified into four broad categories: the humpless Hametic Longhorn and Shorthorn, the Zebu, the Sanga and the intermediate Sanga/Zebu (Table 2). Geographical location and distribution was also provided (Figure 1). All of these cattle types were described as having considerable adaptability to harsh climate, poor nutrition and diseases endemic to their respective areas. Alberro and Haile- mariam also attempted to describe some of the specific characteristics by which each of the types could be differentiated. For instance, the Boran and the Danakil can withstand prolonged droughts; the Abigar and Fogera are able to withstand periodic flooding while the Abigar has some trypanotolerant traits.

Table 2. *Classification of the indigenous cattle of Ethiopia.*

Class	"Breed" or "Population"
I. Humpless	
Brachyceros	Sheko (Mitzan,Goda)
Hametic	
Longhorn	Kuri (Kouri)
II. Zebu	Arsi
	Barka (Begait)
	Borana (Boran)
	Arab (Adeni,Berbera,Bahari)
	Shorthorn Zebu (Harer)
	Highland Zebu (Bale)
	Black Zebu (Jem-Jem)
	Small Zebu (Jijjiga)
III. Sanga	Danakil (Adal,Raya,Keriyu,Afar)
	Raya Azebo (Galla-Azebo)
	Abigar (Nilotic)
IV. Intermediate Sanga/Zebu	Horro
	Fogera (Wagera)
	Arado
	Jiddu
V. Other	Fellata (Red Bororo)

Source: Alberro and Haile-mariam (1982a)

A number of organisations have also attempted to characterise some of the well-known indigenous cattle and sheep breeds through on-station breed evaluation and improvement programmes. Amongst these are the Ministry of Agricultre (MOA) ranches for breeds like the Boran, Fogera and Arsi; research programmes for the Horro, Barka and Boran breeds initiated by the Institute of Agricultural Research (IAR); and research/teaching



Areas with no shading, except for Ogaden Desert, are populated with several varieties of Abyssinian Zebu.

Source: Alberro and Haile-mariam, 1982a.

programmes with the Boran, Barka and Fogera types developed by the College of Agriculture at Alemaya University. In all these efforts, major emphasis was placed on assessing the production potential of the breeds for meat and milk under improved feeding and management conditions and to study their potential for crossbreeding. Purebred strains of indigenous cattle were kept in all cases as were records for such characteristics as birth weight, weaning weight, mature weight, age at first calving, calving interval, lactation milk yield and lactation length. Results, in general, indicated that productivity of indigenous cattle breeds is low. Usually, cows do not produce their first calves earlier than three to four years of age and the calving interval is about two years. Milk production is low and lactations are short: 224 kg in 148 days for Arsi type (Schaar, 1990); 494 kg in 155 days for Boran; and 559 kg in 285 days for Horro (IAR, 1972).

In addition, very little work has been done to identify and characterise Ethiopian sheep and goat breeds. The Ministry of Agriculture has classified indigenous sheep breeds into four broad categories: the Hairy Thin Tailed, Wooled Thin Tailed, Fat Tailed and Fat Rumped. Accordingly, attempts have been made to group some of the well-known types into these different categories (Table 3). Five major goat types have also been identified and are classified as Nubian, Highland, Adal, Somali and Long Tailed Gishe. Additional goat classes have been proposed (Werkneh Ayalew, 1991): the white Digodi (Somali) in Borana; the coloured Gugi in Borana and Sidamo; the red Tsemay in north Omo; and the black and brown Konso in north Omo. Farm Africa, a British-based NGO, in collaboration with the Ministry of Agriculture and the Alemaya University of Agriculture, has started a national goat survey programme. So far, the survey work has covered central, eastern, southern and south-eastern parts of the country but the results have not been published.

Table 3. *Classification of the indigenous sheep breeds of Ethiopia.*

Class	"Breed" or "Population"
I. Hairy Thin Tailed	Hamele (Eritrea) Barka (Eritrea) Horro (Western Ethiopia)
II. Wooled Thin Tailed	Arrit (Eritrea)
III. Fat Tailed	Menz (Northern Shoa) Arsi (Arsi and Bale) Akele Guzai (Eritrea) Rashidi (Eritrea) Tucur (Wello)
IV. Fat Rumped	Black Head Ogaden (Southeast Ethiopia) Adal (Northeastern lowlands)

Source: MOA, 1975.

On-station breed evaluation work of some well-known sheep and goats types has also been undertaken by different institutions. These include the IAR evaluation programme on Adal, Black Head Ogaden, Horro and Menz sheep and Adal goats and the MOA improvement programme on Menz and Black Head Ogaden sheep. Major emphasis in all of these studies was on meat, milk (goat) and wool (Menz sheep) production. Results indicate that the average mature Ethiopian sheep (rams) weighs 26-35 kg; wool production is about 0.5 kg per head.

Planned projects on breed characterisation

Establishment of a centre for animal genetic resource conservation

As part of FAO's programme to establish a global system of animal genetic resources conservation, Ethiopia was chosen to be one of seven regional animal genebank centres in the world. The Centre is expected to represent the English-speaking African countries. It will organise regional animal genetic resource activities and facilitate the receipt, processing and cryogenic storage of endangered breed germplasm. It will also be responsible for organising regional training courses on the identification, characterisation and evaluation of endangered breeds and the collection and processing of embryos. The Centre will be expected to coordinate the flow of genetic information in the region as well as globally.

The Ethiopian National Artificial Insemination Centre of the Ministry of Agriculture has taken responsibility for establishing the Centre. So far, FAO has donated a small amount of money to the AI Centre to undertake initial studies for the establishment of the genebank; a budget has also been submitted to FAO for the purchase of materials and equipment to activate the envisaged embryo transfer programme. Governments of English-speaking countries in the region have been approached and asked if they wish to participate in the programme; nine countries have already responded positively. Initial preparations regarding training activities have been undertaken. It is envisaged that ILCA and other regional organisations will assist in these activities.

As a member of the animal genetic resource conservation programme, Ethiopia has also taken the initiative to lay down its own groundwork for breed identification and characterisation of indigenous breeds. To that effect, a task force has been formed to prepare some guidelines.

Strengthening existing animal breeding ranches and establishing new ones

As part of the efforts to develop a new strategy for livestock improvement in the country, the MOA intends to establish new ranches and rehabilitate existing ones for some of the well-known Ethiopian cattle and sheep breeds. These ranches will provide information on important breed characteristics. Amongst the cattle breeds to be included in the programme are the Boran, Barka, Arsi, Horro, Fogera and Abigar.

A similar programme is also envisaged for small ruminants and farms for some of the well-known sheep and goat types will be established. In addition, the goat survey programme will cover areas not included in the previous survey.

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Discussion

Q1: I heard about this genebank programme about 5–6 years ago. What is its status?

Q2: Have we properly looked at these breeds in order to say they are distinct? Perhaps they are only strains or crosses.

A1: Five to six years ago, expectation was high that freezing technology (e.g. embryo freezing) would play a greater role than it has in conservation efforts. Over time, concern over the viability of freezing embryos, particularly in the long term and the costs involved led to a rethinking about these centres.

A2: Little work has been done in terms of broad/systematic classification. As part of a genebank, we hope to work closely with indigenous breeds. There is a task force looking at the list of descriptors to do a more thorough study on these breeds.

Characterisation and evaluation of indigenous cattle breeds in their natural breeding environment in Cameroon

D.A. Mbah

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Introduction

Cattle represent approximately 43% of the livestock population in Cameroon and provide 61% of the meat consumed in the country. Yet, because of a deficit in meat production, there has been an increase in meat imports since 1983.

There are 13–15 cattle breeds found in four ecological zones across Cameroon. In these zones, approximately 24% of pasture land remains unexploited. However, there is little or no reliable information available on most, if not all, cattle breeds in the country. Attempts to reduce the meat deficit by increasing domestic production have been frustrated by lack of information on production characteristics of the indigenous breeds. Available information suggests that indigenous cattle are characterised by poor growth, late maturity, poor milk yield and high mortality. Recent surveys in Adamawa and North-West provinces have revealed the presence of numerous unproductive females in herds, high bull/cow ratios, uncontrolled breeding and low offtake. Lack of improved breeding stock, unorganised production systems and poor management practices (e.g. increasing the cattle population on rapidly degrading pastures, use of little or zero inputs) only adds to the problem.

Earlier attempts to provide improved stock through importation of exotic breeds were unsuccessful because of animal susceptibility to local diseases and resulting high mortality. It is hoped that selection within indigenous populations or selective crossbreeding will be good alternatives to previous efforts aimed at improving stock in Cameroon.

Objectives

The project aims to provide information on indigenous cattle breeds which will enable cattle breeders and policy makers to make appropriate, timely and profitable decisions. This information will help IRZ choose a few breeds for improvement and to pursue discriminate crossbreeding activities to maximise breed viability and adaptability. The information will also be used to help develop means of conserving valuable breeds that are on the verge of extinction. Specific objectives of the project are to:

- Determine physical characteristics of indigenous cattle breeds
- Evaluate milk and meat potential
- Evaluate reproductive performance
- Determine adaptive characteristics of indigenous breeds in their natural environment (e.g. in terms of disease, heat tolerance, nutrition and socio-cultural stress)

Methodology

On-station work

Current breed evaluation will continue on-station. However, at least two breeds on-station will be evaluated for purposes of characterisation and comparison (under the same conditions). Sixty breeding females per breed will be constituted at each station. Herds of breeding females will be randomly constituted from samples which are as homogeneous as possible (in terms of age and physiological status). Breeding will be by natural service and year round in order to simulate on-farm conditions. At least three calf crops are expected; calves will be weaned at around six months of age. Bulls not manifesting sex drive will be eliminated. The mating plan is two breeds (Gudali and White Fulani) in a straight breeding procedure.

Parameters to be measured include: external characteristics (heart girth, wither height, hinds, horns, coat colour, etc.); reproduction characteristics (e.g. age at first calving, calving interval, oestrus cycle, etc.); milk production; growth; environmental characteristics such as climatic information (e.g. rainfall, temperature, humidity) and diseases (ticks and tick- borne diseases, trypanosomiasis, dermatophilosis, etc.); and mortality.

On-farm work

A minimum of 28 herds, with an average of 30 females per herd, will be used for on-farm performance evaluation. Animals will be sampled from Adamawa and North-West provinces. On-farm visits will be made on a monthly basis and growth and dairy performance measured.

Linkages with existing projects

The proposed project will be integrated with on- going cattle breed evaluation projects at four experimental stations: Wakwa, Bambui, Yagoua and Bangangte. Cooperation with the following research and development projects is also anticipated: IRZ/GTZ (for on-farm research activities); MINEPIA Third Meat Plan, Heifer Project International, World Bank Livestock Monitoring Project envisaged in North Cameroon, the Northwest Development Authority (MIDENO) and the Cattle Research Network.

Conclusion

It is hoped that through this project, indigenous cattle breeds will be qualitatively and quantitatively analysed; that promising indigenous breeds will be identified and selected for further genetic improvement; appropriate cattle breeds for milk and meat production will be recommended to farmers; and that a model for standardising comparison of indigenous cattle breeds will be developed.

Discussion

Q: Can you use culled animals for carcass evaluation?

A: We have used only males for carcass evaluation.

Q: Why are indigenous crossbreds being used?

A: We are not using indigenous crossbreds. This is a straight breeding project. Crossbreeding is not planned on- station.

A: While we do not plan crossbreeding projects, this is actually occuring on-farm. Farmers were asked why they were crossbreeding between the White Fulani and the

Gudali. They suggested that White Fulani had high dairy potential and the Gudali is the breed of choice. The Gudali also has the ability to travel long distances.

General discussion

Q: To Dr. Mbah, you say that exotics were imported for crossbreeding and the outcome was disastrous. What were they crossed for—meat, milk?

A: Importation took place in the early 1930s. The animals were brought in for meat and milk. They were introduced as purebreds. But the management required was not acceptable to farmers. Later, Brahmans were imported from the US. Productivity was superior to locals by 10-15%, but the problem of dermatophilosis emerged.

Q: After listening to the case studies, it is clear that we have a reasonable idea regarding some genetic populations—we can actually put names on them. Are these populations unique or are they part of a larger landrace that crosses national boundaries? Are we aware of the discrete populations of cattle, sheep and goats that need to be characterised/inventoried or is there still a piece of work to be done country-by-country to develop a list. I am worried we may not have a complete list of discrete populations and now we are going into a priority setting process of characterisation without passing through the first step. Is that first step needed?

C: The speaker is correct. There are outstanding problems and some things we do not know. Perhaps this problem can be dealt with country-by-country. Information is adequate in some countries but suspect in others.

C: A list of all available populations would be a logical first step. But this is a large undertaking.

Q: I do not know how quickly we could get information on characterisation of breeds. As well, how quickly could we get to know the parameters that are important for breeds in different countries?

C: Regarding the overall objectives of this meeting, I think that the issue is more complex than genetic improvement. We need to be aware of country needs—how to use existing resources to meet these needs and how to characterise breeds to achieve these needs. The work we are embarking on will require a great deal of money. By the end of the day, we should be aware of our objectives. Work in central, west or eastern/southern Africa may demand different methodologies because genetic expression will be different depending on different environments. We need to define our strategy and what we want to produce for farmers.

C: As we go into the different working groups, I hope we will consider the objectives of this exercise. Our objective is to get to know and gather information—make it more succinct. Are we confusing knowing what is there with productivity? The focus of this exercise is not so much on what has been done, but has it been done adequately? Are we talking about characterisation or improved productivity? We need to focus.

C1: Regarding the different case studies, there is a mixture of objectives—from utilisation to characterisation. There are existing productive breeds in- country. But they are not being utilised for human requirements. If that is the problem, what are we trying to do? In other cases, there are breeds with outstanding merits. Here, can we breed to maximise output for human consumption?

C2: It is important to know the merits of breeds so they can be incorporated into breeding plans or productive processes. Characterisation takes a long time. We should select a few breeds rather than go through them all.

C: We should examine the objectives of this workshop. The workshop is on African animal genetic resources—their characterisation, preservation and utilisation. Utilisation is an important aspect and ties back into characterisation.

C: One of the issues to be raised by Group A is to recommend priority breeds. But, do we know enough about the breeds in order to provide a priority ranking? How does one prioritise without having sufficient information about breed populations?

C: One way to begin is to ask people (country-by- country), do you know breeds that might be endangered? Are there other populations which are not clearly breeds, but thought to be so? Are there breed mysteries in your country? Are there suspected indistinct breeds that need to be characterised and separated out to determine distinctiveness?

C: We can, as a starting point, take Mason's breed list and add/delete as needed.

C: It is not a definitive list (and, in some cases, not authenticated) but may be a catalyst for building a better one.

SESSION IV

Group meetings and presentations

Introduction

Prior to breaking into individual workgroups, participants met to discuss terms of reference for each group. The workshop coordinator circulated the handout entitled,*What is a breed* (Appendix II) to participants. His instructions to the group are designated by CC (coordinator comments).

CC: Group A, which is expected to work on priority setting, should tell us the priority characteristics we should measure on the breeds we characterise. From the discussion earlier today, perhaps it is important to talk about the breeds before discussing characterisation. The first issue should be to determine the breeds to focus on. Here, there are two ways of discovering the necessary information:

- Go country-by-country to identify breeds and determine if they are priority breeds. However, not all countries are represented at this workshop.
- Begin with Mason's list and build upon it.

Comments?

C: It is a good idea to start with "which breeds" and define those to be listed. To do this, we need to clearly state the objectives of characterisation. Do we address preservation, characterisation, utilisation? Otherwise, we will be spending a great deal of time listing breeds. How many of the objectives do we wish to address?

C: The speaker is correct. To define a breed, you need to define its characteristics. How do you do this? We need to determine if we are concerned with utilisation, preservation, etc.

C: In terms of conservation and utilisation, are we conserving endangered breeds or are we utilising breeds that are widespread and will have national impact? When we speak of conservation, we are often thinking in terms of localised breeds. If we are speaking of utilisation, we are speaking about broader usage. Therefore, it is important to think more in terms of widely utilised breeds.

C: Group A should identify endangered breeds. If you just identify priority breeds, there must be a reason for identifying them as a priority. From these discussions, it is clear that endangerment has been identified as an important criterion to be used in establishing priority ranking.

C1: Group A is expected to talk about characterisation, not conservation or improvement schemes. We need to spend some time talking about "what is a breed". It is not feasible to go through a list of all breeds in Africa and classify them as endangered, etc. It is beyond both our terms of reference and our ability. We would need more information than is available to the group.

C2: I do not think we are in a position to classify according to importance or endangerment. But we can speak in terms of priority of different characteristics that needs to be noted, whether it is production characteristics or particular adaptabilities. We should take this shortened set of descriptors that John Ruane presented yesterday and see if the information is practical for our purposes and appropriate for African conditions.

C3: We also need to debate the possibility of using new technologies, such as those presented by Kemp, to underpin this work.

C: In the interest of time, perhaps the groups should clarify their own terms of reference.

C: Looking at the terms of reference now may make it difficult for work to progress. For example, Group A has been asked to prioritise breeds to be characterised. This is too big a task. The group should, instead, decide on the parameters needed in order to characterise.

CC: The objectives of Group A are, first, to put forth a clear definition of breeds. This will provide a working definition for the future. The second objective is to recommend priorities for measurement in order to have a complete definition of a breed. This should include information from Ruane's presentation. Third, the group should discuss the possibility of using biotechnology for characterisation. Any additional issue they think is important should also be included.

Q: What species should we focus on?

A: The species for ILCA are cattle and small ruminants. But we are not saying that other species (e.g. pigs) should be excluded.

C: ILCA is mandated to work on cattle and small ruminants. The Centre has restricted its focus because of limited resources. However, the status of ILCA's resources and midterm goals should not limit present discussion. I suggest we focus on domesticated animal genetic resources—all of which are part of ILCA's broad mandate.

CC: For Group B (Utilisation of published results), their terms of reference are clear.

Q: Regarding the terms of reference for Group B, how do you define authenticity?

A: That is for the group to decide.

Q: The title of the workshop and the way you have divided the groups suggests a movement away from the theme. Here we are talking about priority setting, utilisation of published results, methodology and identification of on-going projects. Where do we address conservation and utilisation?

A: If we draw a matrix with characterisation, conservation and utilisation, you will find that they fit into all groups.

CC: For Group C (Research Methodology), it is essential that you come back with a minimum essential data set.

C: Group C, rather than Group A, may want to look into biotechnology issues.

CC: Biotechnology is with Group A because the question to be considered is, does biotechnology have a role in characterisation?

C: Group C should include phenotypic versus genetic characterisation. Members should provide guidance on where they would place emphasis and how they would go about doing it.

CC: Terms of reference for Group D (Identification of on-going or planned projects in NARS) are clear.

At this point, participants broke into individual work groups. They were asked to reconvene in full session at 10:15 on 21 February 1992.

End of Thursday, 20 February 1992 session.

Group A: Priority setting

Presenter: E.P Cunningham

Group Members: E.P. Cunningham (Chair), A. Lahlou-Kassi, K. Agyemang (Rapporteur), G. Matheron, B. Rey, G. Duvallet, R.O. Mosi, A. Oya, Y.N. Hadzi, E. Kaluba, J. Ruane

Our group had a rather easy task and clear terms of reference—essentially, to debate what was necessary for appropriate characterisation of breeds and consider what new technology can offer in that regard. The conclusions of Group A follow.

What is a breed?

The term "breed" is used here to indicate a separately identified (or identifiable) population or group of interbreeding domestic animals.

Identification will usually be based on common physical characteristics such as colour, size, shape, and also on shared genetic and historical origins. A breed can vary in numbers from tens or hundreds up to millions of animals. It is usually associated with a particular ecological zone, geographical area and farming system. Some breeds may, however, be present in several countries. Established crosses between two or more breeds may be recognised as a separate breed, but shifting or transitional crossbred groups are not.

Priority elements in breed characterisation

The following list of seven broad categories of breed descriptors selected are from a longer catalogue used in compiling the FAO Global Data Bank. This subset is regarded as an essential assembly of information for the initial characterisation of a breed.

The objective should first be to secure a reliable set of information corresponding to these seven descriptors. This should be followed by the addition of further levels of information, as specified in the complete FAO list, and covering such factors as the genetic relationship to other breeds, DNA-level data, information on storage, conservation programmes, etc.

Priority elements include the following seven points.

1. General identification consisting of: country (and source of data); species, breed or population and location within country where breed is found.
2. Population size during the reporting year broken down into number of breeding females, number of males of service age.

   Indication of number of purebreds in mating group and changing trends in breeding females up to the reporting year.

   Average herd size during the reporting year.

   Average age of animals used for breeding by sex.
3. Physical characteristics including coat colour giving details of special colours and colour combination, horns shape and size (by sex); presence or absence of hair/wool and other specific visible traits (e.g. fat tail, hump).

4. Measures of adult size and weight including wither height, liveweight, body length (for each sex) with indication of precision: number of records, standard deviation and range.

5. Current uses (purposes) as indicated by producers and ranked by priority.

   Possession of special or unique adaptive traits such as resistance to major diseases and to climate.

6. Qualitative description of predominant management system (stationary, transhumant, nomadic; housing, feeding, etc.).

7. Biological performance. Important traits applicable to dairy, meat or dual-purpose breeds, giving indication of variation:

   (i) milk yield or offtake

   (ii) milk quality

   (iii) liveweight traits (birth, weaning, yearling)

   (iv) early measures of reproduction (e.g. age at first parturition)

The place of new technology

A range of recent innovations in molecular biology offers the prospect of contributing significantly to the aims of characterising, conserving and developing African animal genetic resources. Rapid methods of DNA amplification (PCR) and sequencing permit extensive comparisons at the DNA level. The discovery of highly variable regions (VNTRs) should greatly increase the precision of individual and group characteristics. Randomly amplified polymorphic DNA (RAPD) may speed up and reduce the cost of both group discrimination and the search of associations between given DNA sequences and disease resistance or production traits.

While these techniques are still evolving, their present value is such that they should be utilised in the programme to characterise African animal genetic resources. Few institutions in Africa have developed the capacity in personnel and equipment to undertake this work. Existing capacity should be strengthened, with emphasis on concentration of resources at relatively few centres. In the meantime, opportunity exists to undertake those studies in collaboration with IARCs or institutions abroad with the required capabilities.

The immediate objective of the work will be to characterise at the DNA level the common genetic heritage, as well as the inherited differences which are to be found in African populations. The longer-term aim is to contribute to the location and use of specific genes related to useful traits.

A further group of technologies is relevant to breed characterisation and improvement for disease resistance traits. These include precise diagnostic methods and the use of DNA probes for identification of strains of parasites and infective agents.

In addition, the measurement and enhancement, through breeding, of specific adaptive traits (e.g. heat tolerance, unusual water or energy metabolism), will require the use of sophisticated measures of animal physiology. The objective of this study of the biological functioning of specific African breeds is to clarify and better exploit their individual potentials.

Discussion

Q: When listing the mininum data set for breed characterisation (passport data and general descriptive data), you did not include a measure of a biological specimen. Did you figure to use blood or semen?

A: We did not consider that in detail. FAO has a record of blood/semen taken and stored. We talked about the minimum set. This is a first wave. Perhaps it is not appropropiate to take, at the first stage, samples with no purpose in view.

Q: Some cattle and other related livestock are a source of energy, for example, traction. Did you not think energy potential was important as a trait?

A: This was brought up in the group—whether some measure of animal traction power was to be included. Perhaps another member of the group would like to comment.

C: The question was indeed raised. We had problems with the issue of quantification. If there are suggestions from the floor on how traction power could be quantified, we could add it to our summary report.

C: Muscle physiologists might provide the answers.

Q: With limited resources for this initial inventory/description, did you, in terms of priorities, get into the issue of which breed(s) to deal with first?

C: We did not attempt to prioritise which should be looked at first or second. The group's answer was, all breeds in all countries. We are talking in the order of about 1,000 breeds. Our objective should be to document them all. However, in terms of *ex situ* preservation, only endangered breeds should be considered. Still, the problem is how to determine risk of endangerment in the absence of breed population data.

C: The social importance of some breeds may not be in this descriptor list. Since we are talking about conservation, this aspect should be considered.

Group B: Utilisation of published results

Presenter: J.S. Kasonta

Group Members: O. Syrstad (Chair), G. H. Kiwuwa, W. Thorpe (Rapporteur), A. Said, Beruk Yemane, G. Aboagye, C. Banga, J.S. Kasonta, A. Zimba, L. Tawah

Introduction

The group closely followed their terms of reference, but recommended that the title of this topic should read: "Utilisation of published results and available data."

The group considered that the major objectives of reviewing published results were to characterise breed performances with the ultimate aim of:

- identifying information gaps
- screening breeds for conservation
- improving the possibility of exploiting breed resources through the ranking of breed performances

With this in mind, the group considered in turn the four headings on the agenda. As many of the issues had already been addressed and resolved in the handout entitled, *Extraction and preparation of data*[1], the discussion makes reference to specific excerpts in the handout.

Identification of sources

The group endorsed the list on page 1, section 2, reproduced below:

- published scientific papers
- papers presented in conferences with or without proceedings
- specific reports or case studies
- annual reports (by livestock stations, research centres, government departments, etc.)
- theses, graduate and undergraduate, and
- stores of unpublished data

The list was considered comprehensive. The group emphasised the importance in sub-Saharan Africa of the latter category, the identification and utilisation of unpublished data. The analysis and reporting of such studies may well reduce the need for further experimentation.

How far back in the literature should we go?

The group disagreed with the arbitrary cut-off date of 1960 recommended in the handout (page 4, point 7). It is recommended instead that any reliable, informative source, regardless of year, should be used.

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1 In: FAO (Food and Agriculture Organization of the United Nations). 1986. *Animal genetic resources data banks 2. Descriptor lists for cattle, buffalo, pigs, sheep and goats.* FAO, Animal Production and Health Paper 59/2. FAO, Rome, Italy.

Criteria for inclusion, including authenticity judgement

The concept of a reliability score (handout, page 4, point 1) was endorsed. Specifically,

> The authenticity of the data in the source needs to be judged and a value between 1 (most reliable) and 5 (least reliable) be given. Various factors such as statistical results (number of observations, standard deviations), management system, feeding standards and clear presentation of experimental design or model will serve as indicators.

Criteria to be included in developing a reliability score were recommended to be, in order of importance:

- number of observations per breed group
- experimental design, including contemporaneity
- appropriate statistical analysis
- possible biasing introduced through data editing

If a report does not name the specific breed, but uses a general term such as "local" or "native", then the results will be included if the breed can be identified through the location and period of the study.

The group disagreed with the recommendation (handout, page 6, point 1) that states the first source reporting a study should be utilised. If there are two reports from the same study, then the later source of information may report results from a larger number of observations. Also, second and later reports may give more comprehensive descriptions of the study. Obviously, the report with the most complete information should be used in the data base.

Combining results from different sources

Should we take what seems to be the most reliable? Should we combine data from different sources? If so, how?

The group recognised the importance of combining results from different sources, particularly to assist in the ranking of breed performances. It was recommended that all results should be included in these combined analyses, but that each study would be weighted by reliability score, the number of observations or the standard errors.

If appropriate, the sources can be classified by, for example, production level as determined by lactation yield or parturition rate. If possible, the individual production traits should also be combined for analyses of productivity indices.

How does one treat breed evaluation results on which other treatments may have been superimposed at some point?

In these studies, the breed x treatment subclass means should be entered in the data base, and the same principle applied to any other experimental treatments imposed on two or more contemporary breed groups.

Incomplete statistics from a source

The data should be included in the "slave record" but will not be included in the combined analyses requiring weighting of sources by the number of observations or standard errors.

Access to the data base

The group recommended that the published results should be entered into the FAO data bank, and that NARS and individual researchers should have access to the data for review and analysis. The group stressed the need for mechanisms to facilitate that access.

Discussion

Q: Commenting on your aim, screening breeds for conservation, please clarify. Screening the literature is necessary for identifying breeds that are rare or declining. However, because breeds become endangered by being poorly adapted to the requirements of modern husbandry practices, the criteria for commercial merit should not be used in selecting breeds for conservation. The breeds may appear unfavourably in tests being conducted today but have characteristics that may be important tomorrow.

C: When utilising published results, we note for example the population size. If there is a decrease in numbers of the breed in question, it will be so indicated with a statement of need for measures of conservation.

Q: How do you combine results from different sources? You say you want to use a reliability score. How do you define reliability? Does it include, for example, frequency of measurements, accuracy of measurements? How do you obtain the information for it? Or does it include statistical methods used for analysing the data? What do you have in mind for this score?

A: The group acknowledged the difficulty in developing a clear-cut method for determining reliability. In the handout, there was a reliability scale. We recommended that perhaps it is better to develop criteria, which we did. Four such criteria have been proposed. Still, it might be difficult to score, particularly when information is missing.

Q1: In combining data in the way you have recommended, if the reliability score is not sufficiently reliable, you introduce more error by combining. You may have one good study and one bad study. If you combine, you create, rather than remove, noise. Perhaps if you identified one reliable source and used that?

Q2: I do not understand your comment that "if a report does not name the specific breed, but uses a general term such as local or native, then the results will be included if the breed can be identified through the location and period of the study." Please elaborate.

Q3: Regarding your comments on how one treats breed evaluation reports, you say that breed x treatment subclass means should be entered in the data base. Please clarify.

A1: If you are looking at a breed and have a comprehensive study, you should use it. If you use several sources, you may obtain a different picture and the data may become diluted. We felt that we should use as complete information as possible for the data base.

A2: We felt that if locality was known and if only one breed existed, then it would be safe to assume we are dealing with that particular breed.

A3: Regarding the use of information from superimposed treatment, one should clearly indicate, by building subclasses, what happened in the experiment in order to interpret the data more efficiently. If there are several experiments with results provided, it might be good to combine information.

Q: Since we are describing breeds more or less in their natural environment, would it be useful to use subclass control as the one that approaches the animal's situation under its natural environment?

C: Where interactions are important, they should be included in the slave report.

Q: In terms of combining data from different sources, I am not sure how different the sources really are. Are we combining sources from different experiments (e.g. from three to four countries)? If we combine this kind of data, we may lose the genotype x environment interactions that are unique to certain countries/localities.

A: We did not think in terms of combining sources from different countries, but, rather, within country.

C: We need to differentiate between breed and population. If results are relevant to populations, then there is no problem. If we are consolidating results on breeds from different populations, then, perhaps, there is a problem.

C: In some cases, I would be concerned if you were not pooling data from across populations. Useful information can be gathered.

C: It is mainly a question of the number of treatments or locations you are referring to. If you have information on one breed in only two locations and there is no overlap with other breeds, I would hesitate combining results. If we have information on several experiments where breeds have been treated differently over several environments, treatment and environment can be considered random factors. Here there is no problem combining results.

C: The problem we should be addressing is not just combining results, but how we handle subclass means and how we evaluate breeds in their environments.

C: In terms of combining information from different sources, the data may have been taken at different times. If there is improvement in breed performance over time, the issue of a genetic trend is raised. If the data are combined, you regress to a mean which underestimates current breed performance. Also, in the software being referred to by the Group, you need to include as part of the data base, the source of the information.

A: The group did not suggest that information should be combined before being entered into the data base. Data should be entered individually but combined later for summarisation. In terms of the question raised on subclass means, this information helps us understand the type and level of management.

C1: A number of important points are coming out of this discussion. First, the value of synthesising available information in the literature. The value is that it brings together information, that by itself may not be convincing, but, when combined, leads to conclusions and recommendations for future action. It is important to recognise that a literature review represents the testing of an hypothesis. The reviewer, therefore, has a great responsibility. He/she is no longer an objective experimenter, but judge and jury.

C2: Second, for a literature review to meet its full potential, the individual scientist needs to provide the type of information that can facilitate good syntheses. At this workshop we are hearing frustration that the material is often lacking (e.g. in terms of design, results, etc.). My frustration with authors, and more so, with editors, is that information reported is often at a bare minimum. Descriptions are where the full value lies. There are some techniques being developed to synthesise large volumes of information, i.e. META analysis.

C3: Third, we are here to design a major new initiative on African animal genetic resources. As we design the work, we must design it in a systematic and consistent fashion where we can combine information. Our ability to synthesise will be key for providing us with an overall picture of what is happening with animal genetic resources.

Q: Regarding an earlier question on the use of a reliability score, is there an alternative?

A: I was not questioning the reliability score. Often, the number of studies is all you have to generate the score. You usually do not have standard deviations, etc. If you combine results by using reliability score and number of observations, you end up using the number of observations twice. Variance is also a critical consideration when combing results. You should not combine, for instance, on-station and on-farm results where

you may have considerable variance. I would rather see something more sophisticated that takes into account number of observations and variances.

C: The problem we are addressing is one that is highly amenable to simulation. Is it possible to find out the possible degree of deviation from the mean from a large population (the breed) by using a smaller sample, analysing it differently? It would mean we would introduce different sampling variation in the data set and compare in some way.

C: It is a complicated issue to speak about combining results. Before, we were talking about combining means from different studies. In some cases, we may have individual data and could analyse and combine, and use an overall model of analysis. But this assumes equal variances. The degree to which the mean of a sample deviates from the true population mean is indicated by the standard error of the mean. So you could get a sense of where you are with the sample. When you combine results, you get more information. You assume however, that the definition of a variable is the same across studies. Clearly, there are many definitional problems involved.

C: In terms of definition across sites where data have been gathered, I refer to the feed x breed interactions. Did Group B decide on the form of information to be entered? Were supplements, etc. considered? The issue is quite complex.

C: The slave record requires a very comprehensive description of feeding.

C: In the FAO data base, we can put in 16 traits. Productivity, socio-economic, climatic data, etc. can be entered. Data can be put in and references are given (usually from one or two sources). Afterwards, you can calculate your reliability score.

Group C: Research methodology

Presenter: R.L. Baker

Group Members: R.L. Baker (Chair), K. Peters, H.A. Fitzhugh, E. Bruns (Rapporteur), J. Trail, S.J.G. Hall, Alemu Gebre Wolde, G. d'Ieteren, Beyene Kebede, O. Mwai, B.Y. Abubaker

The research methodology with respect to characterising, conserving and utilising African animal genetic resources can be defined at three different levels, as shown below:

Macro	Phenotypic characterisation, conservation
Meta	Phenotypic characterisation
Micro	Penotypic and genetic characterisation

I. Macro level

The macro level consists of on-farm surveys similar to studies carried out by IEMVT/CIRAD and reported by G. Matheron at this meeting. The survey, based on a stratified sampling procedure, collects information about herds and animals. It asks basic information about the location, village identification of the herd, as well as animal details such as type or breed, sex and age and some simple measurements such as body height and hair root samples (for DNA analysis). Additional historical information about the farming system and herd production can be collected based on direct questioning of the farmer. These studies do not need to be carried out in all countries, but should be done where there is a clear lack of information. They may also be undertaken in conjunction with other on-going livestock operations such as vaccination. It is seen to provide information about the approximate size of a population, its breeding structure and age distribution and the type of environment in which the breed is kept.

This survey procedure was not seen to be a census, but could provide some approximate estimates of relative proportions of breeds. If some breeds were shown to be in particular danger in terms of low numbers, this should lead to conservation action and/or a more detailed census. It has been suggested that the approximate numbers which indicated that a population is endangered are for sheep and goats, 1,500, for cattle and horses, 500 and for pigs, 250. However, conservation action should also be discussed for populations which, though larger, are agreed to be declining.

II. Meta level

For phenotypic characterisation of breeds, a more detailed on-farm monitoring exercise can be carried out which allows comparing breeds with respect to the mean and the phenotypic variance of the performance. For sampling farms and animals within farms, a stratified random sampling procedure is seen to be most appropriate. The number of farms and individuals within farms to be sampled is a function of the following factors:

- variability among farms
- variability among animals within farms

- breeding structure within farms, in particular, the number of sires being used per year or breeding season

With these factors, it is possible to define the necessary numbers of farms and animals within farms to be sampled for any particular required precision. The minimum number of farms should not be less than 40 and preferably farms should be sampled that are using two or more sires. The total number of animals per breed should not be below 400. But, it has to be recognised that the precision of on-farm breed comparisons is less than on-station comparisons unless farms are being sampled which have animals of two or more breeds.

The duration of those on-farm studies and the frequency of measurements depend on the variables under consideration. The following list gives some indication of a minimum data set that is desirable.

Variable	Time and frequency of measurement
1. Physical traits	
– linear measurements	across the herd structure
– condition score	seasonal
2. Performance traits	
– milk yield	monthly
– body weight	weaning,post-weaning,mature
– fertility:	
calving interval	two or more calving dates
number born	two or more
number weaned	two or more
– viability	young and mature
– fleece weight	once
3. Health	
– abortion	two or more calvings
– blood samples for disease monitoring	several, depending on
– faecal samples	disease and season
– tick infestation	
– DNA extraction	once
4. Environment	
– location	farm or village by map reference, local goverment area
– climate	
temperature	seasonal
rainfall	seasonal
humidity	seasonal
– feed resources	
feed type	seasonal
feed availability	seasonal
– management	
shelter/housing	once
herding practice	once
watering frequency	seasonal
supplementation	seasonal
health intervention	seasonal
– herd structure	
animal movement in/out of a herd	seasonal and dates
– breeding structure	
number of males	once
number of females	once
castration practice	once
use of AI	once
age distribution	once

III. Micro level

A detailed phenotypic and genetic description of selected breeds can be done under on-station and under well-controlled on-farm conditions. The phenotypic description includes comparing breeds with respect to the mean and the phenotypic variance of the performance. The genetic description includes comparing breeds with respect to genetic parameters such as genetic variances and covariances. The precision of the estimated breed differences and genetic parameters within breeds is a function of the sampling procedure and the family structure within the sample. The sampling should follow a stratified random sampling procedure assuring as broad a genetic sample from as many different farms as possible and not more than one sire per farm. For detecting breed differences of approximately 10% of a mean, a total of 200 breeding females and 10 males per breed is required. For estimating genetic parameters, at least 20 sires, each mated to 20 dams, are required. It is important to note that these numbers can be built up over time. These are the required numbers in the final data set to be analysed. Additional numbers of sires and dams may have to be used to allow for reproductive and survival losses. If genotype-environment interactions are to be studied, the given numbers relate to those required per genotype- environment subclass.

The detailed characterisaton studies can complement on-farm studies and the same parameters can be measured in both. There is scope for more detailed measurements, such as:

- carcass traits
- feed and water intake
- digestibility
- ability to withstand feed and water shortages
- physiological measurements, e.g. hormone analysis
- behavioural traits, e.g. libido and ease of milking
- birth weight

These more detailed characterisation studies provide the opportunity for between- and within-breed strategies, e.g. estimation of heritabilities lead to breeding values of sires and dams and development of selection strategies. The information might also be used for extension work.

Supporting documentation for the preceding presentation can be found in Matheron and Planchenault (this proceedings); E. Bruns, *Synthesis of research methodology* (Appendix III); and ILCA's *Livestock systems research manual (1990)*.

Discussion

Q: You did not have a preamble, unlike other groups, concerning terms of reference. One of the terms of reference is, where do you get the animals you wish to use—particularly at the micro level.

A: To quote from the text, "The precision of the estimated breed differences and genetic parameters within breeds is a function of the sampling procedure and the family structure within the sample. The sampling should follow a stratified random sampling procedure assuring as broad a genetic sample from as many different farms as possible and not more than one sire per farm." The appendix to be developed by E. Bruns will provide further information. It is a difficult problem. You want to get as broad a genetic sample for these 200 females and 10 sires. You have to sample them from the farms and villages that are out there. Perhaps we should have said, as broadly geographically spread as possible.

You could get this information from direct questioning of farmers. There is no one answer. What you are looking for is, basically, a broad genetic sample.

Q: Assuming you are working on-station, are you recommending that animal management should simulate on-farm conditions?

A: That is one we did not discuss. My view is that you should, as close as possible, simulate the general environment unless you wish to set up a genotype–environment interaction study.

Q: When doing on-station experiments, we usually try to simulate the on-farm environment. Extensive on-farm surveys are needed in advance to understand details of the environment.

A: We discussed it briefly. The only problem is that as soon as you start comparing/testing breeds under a well-controlled environment, this created environment might be useful and applicable to one breed but not to another. Here is where adaptation problems arise. In that respect, we need to somehow look at genotype–environment interactions.

C: That would only be the case if you were doing breed comparison. If you are doing breed characterisation, you do not need two breeds at the same site.

Q: Could you define the distinction between breed comparison and breed characterisation?

A: In order to characterise, you do not need two breeds. If you are comparing breeds, the issue is different.

C: If we are talking about characterising a breed, presumably we are speaking of phenotypic characterisation. The environment in which you are measuring specific traits probably becomes as important as the genotype of the breed you are dealing with. Priority should be given to characterisation of most traits typical to the environment. The thought of justifying the use of expensive experiment station facilities to characterise a breed seems problematic. An experiment station should be used for experiments.

C: This information would be generated from appropriately designed meta- and macro-level studies.

C: With 400 or less animals, the precision of heritability estimates and genetic correlation estimates would be so low, it would not be very useful. These two estimates should be omitted. Emphasis should, instead, be placed on breed comparison.

C: I disagree. You can generate good breed comparison information. You identify unique characteristics. In due course, we would need to know these estimates. If you were talking about body weight, etc., I might agree. But there are some unique characteristics we need to better understand.

C: The point is, we cannot guess heritabilities of new traits we are interested in. This is the smallest distribution of animal numbers we think is practical and will give us useful ideas regarding the genetic parameters we want.

C: One of the factors we considered was utilisation. Eventually, some of the stations can be used for selection purposes where farmers can get elite animals from these herds. It is not a futile exercise—at least to obtain genetic parameters.

Q: You are suggesting 200 females per breed. That is a large number to be identified anywhere. Are you talking about individuals or accumulated numbers of individuals over time?

A: These numbers can be built up over time.

C: Perhaps this needs to be specified—that this is a final data set and you can get there anyway you wish.

C: If you are accumulating this data over time, it is important to ensure that sires overlap across time.

Q: When we speak of on-farm characterisation and talk about these numbers, would it be appropriate to have a number of small samples geographically isolated or to have a herd of 200 females in one location?

A: The immediate question that comes to mind is genotype-environment interactions. If I had a sense that this was important, I would probably avoid a geographical spread. If I thought it was not too important, it would not worry me.

A: From the point of view of breed structure, geographical distribution would be dealt with in your first survey.

A: You need to remember the purpose of the meta study. Its aim is to phenotypically describe for a breed or breeds the mean performance and variance with respect to certain parameters. The other aim may be to get as close as possible to the true genetic value of a breed. If that is an aim, then we need to reduce the environmental impact on mean performance. Thus, our samples need to be as widespread as possible to cover a range of environmental conditions. This will also help avoid localised selection problems with breeds.

C: If not careful, we will get an environmental factor confounded in our measure of phenotypes. This has great impact on how the project might go about designing the activities that would characterise some of these land races spread widely. Do you want to spread available resources in one or many sites?

A: Assuming we were focusing on the Djallonke, spread across West Africa, what we would wish to do would be to look across environments to see if there are differences. If the information is the same, it can be combined. This would be sampling a very narrow range of what is available.

C: I have a problem with the word, breed. We need to define populations in a regional and an ecological context and evaluate/characterise a population within that setting.

Q: Are we going to do just characterisation or also compare breeds for efficient use? How much do we lose by having smaller populations spread over several areas and increase the number of breeds for comparison?

A: When you are talking about meta level studies, the wider the sample, the better. At the micro level, you are asking a different question. Here, you can still do a wide sampling. These levels represent a progression. The easiest to do is the macro level. The next level is the meta, and quite a lot has been done already. Interesting results from this level will lead to micro level studies. Precision is different at different levels.

Q: Coming back to the issue of selection and estimating genetic parameters for characterisation. Could you comment.

A: As soon as we talk about populations under selection, we are sampling randomly. What you will find in the animals in your data set is that the problem of selection is gone after awhile. If you have different breeds and you want to compare them and one breed is under strong selection and the other is not, then you run into problems and will encounter different parameter estimates. Normally, selection is not that strong so you will unlikely face this problem.

C: I thought that if there is selection, it should be taken into account. At some level, selection does have an effect. There are methodologies available to take account of selection.

A: If we have a population under selection, we can get around it by random sampling.

C: As soon as you start sampling, what information do you have? You sample on-farm, breed on-station. You may not have information about parentage, etc. As soon as you begin speaking of populations which are being bred by companies where you apply strong selection, the situation is different and you can take selection information into account.

C: Most of the populations we will encounter will have gone through some selection, but not strong selection. If you have strong selection, then it needs to be taken into account.

Q1: On your recommendation of 40 farms as a minimum, given our experience, the great limiting factor preventing us from covering this number is money, particularly if we are speaking of cattle. Can we get approximate information from fewer numbers?

C: Concerning estimates of heritability, if selection is important, this information is important. If we do not have these estimates, progress we make in the process of selection may be overestimated.

A: The numbers can be worked out by you, given the average reproductive rate of your herd or flock. Forty farms was seen as giving reasonable precision.

A: Twenty farms may be sufficient given your acceptable standard error. With on-farm situations, variance between farms is roughly 30–40%; between-sire variance is 5–10%. From that ratio, you can immediately see you need 3–4 times as many farms as you need sires. The size of variance between farms is so large, you will need a large number of farms, otherwise the exercise is useless.

Q: Stressful environments will have an effect on your parameter estimates. But here you are talking about indigenous animals in indigenous environments. What would the stress be? Why should we assume that parameters would be affected?

A: For heritabilities, the question is wide open. Evidence in the literature suggests it can vary. I agree with your point that for indigenous breeds, there may be no stress.

C: I do not think there is much genetic variation between breeds found in one area. I suspect they would have the same genetic parameters. When it is more or less correlated, I would rather use the aggregate values you can get from various sources and use this for breed characterisation. There are many problems, I agree. Is this really a burning issue at this moment?

Q: Are you saying there is not much genetic variation within African genetic breeds, or between breeds? Or are you talking about within-breed genetic parameters?

A: Between breeds.

C: Heritabilities and genetic correlations are likely to be similar across breeds and these values can be found in the literature. This group is saying that there are a number of traits in African breeds where estimates of genetic parameters have not been made, in particular, indicators of resistance to certain diseases. If you are going to put together a population and put effort into measuring, you should use that population to find out if there is additive genetic variance.

C: You can also obtain heritability estimates from parent-offspring correlations without sacrificing the accuracy of breed comparisons. This is almost as efficient as half-sib estimates.

C: I agree, but you need information on the performance of the parents.

A: I think that half-sib analysis might be easier.

C: I agree that you can use estimates of heritability from the literature. Yet, in the long-run, we should get estimates from the population, despite the potential problems.

C: We have many on-going selection programmes on African breeds without estimates on heritabilities. Do we need those estimates for selection programmes? We all agree there are large genetic variations, but perhaps we are overplaying this.

C: I agree if you are talking about certain characteristics, but there are some interesting traits we do not have a handle on, for instance, disease resistance.

C: This point should be emphasised in the working group report.

C: We have emphasised the characterisation process. Heritabilities come in later.

C: If we identify objectives and find some economically important traits for adaptation, then heritability estimates are important.

C: Normally we do not know size of variance; when you begin speaking in terms of utilisation, breeding objectives need to be defined. Before, these objectives have been very simplistic (e.g. more milk or more meat). Perhaps we need to broaden. Here then you would need genetic correlations and heritability information.

C: Let us take disease resistance, for example. When Brahmans were introduced into Cameroon, the population was dessimated by dermatophilosis. Resistance to the disease was found to be inherited. In response, a selection process for resistance to dermaphilosis was initiated. Yet, the disease reappeared in the same herd that had been selected. This example emphasises the need to have prior estimates of heritability to avoid such problems.

C: When we spoke of the farm component, we ignored the possibility of using dam–offspring analysis for parameter estimation. We need to think about this. Second, estimates of heritability by sire–offspring regression may be another option. This should be added as an appendix as another possibility to be considered.

Q: In terms of using 40 farms to get 400 animals, are you speaking of farms spread over the whole country where the animals exist?

A: We are talking about 40 farms spread over an area where the population is found. That can be countrywide, regional, etc. depending on how widespread the animal population is found or how you define the population.

C: From personal experience, in characterisation, we first identify the farms, then set our priorities.

Group D: Identification of on-going or planned projects in NARS

Presenter: S. Lebbie

Group Members: M. Mgheni (Chair), J. Smith, S. Lebbie (Rapporteur), E. Olaloku, J. Kategile, P. Osuji, E. Rege, D.A. Mbah, F. Adebambo, D. Vilakati, A. Fall, L. Setshwaelo

Terms of reference

Identification of relevant on-going or planned projects in NARS (discussion to be based on write-ups submitted by representatives from different countries)

- country or region
- reasons for selection
- available infrastructure and other resources
- suitability of experimental design
- contact(s) and addresses

The group discussed the terms of reference before commencing its deliberations and observed:

- that the committee was expected to decide which country projects were relevant to the AGR project and which, therefore, merited consideration for collaboration,
- that the group did not have any guidelines or criteria for judging the relevance of the presented projects, and
- that since only a few countries presented project reports or plans during the workshop, it was premature to carry out effective identification.

The group therefore decided to modify the terms of reference as follows:

Establish the project selection criteria that will meet the objectives of the African animal genetic resource characterisation, conservation and utilisation exercise.

Project selection criteria

In recognition of the diverse country needs and priorities, the numerous African genetic resources and financial constraints, the following criteria are recommended for consideration by workshop participants:

1. The project objectives must be clearly stated, must be relevant to the global AGR project objectives and must address at least one of these themes: characterisation; conservation; or utilisation.
2. The species addressed by the project must be the African indigenous livestock, mainly cattle, goats, sheep, pigs and poultry.
3. Since characterisation is a prerequisite for ascertaining the importance of a population, it is envisaged that eventually all populations will be characterised. However, priority will be given to populations that are known to be of economic importance and/or endangered.
4. The project must have national/institutional support.

5. Priority will be given to projects that will strengthen the capabilities of NARS in Africa.
6. Projects with potential for complementarity and efficient use of resources will also be given priority.
7. It is desirable that projects should have a multi-disciplinary approach.
8. Project methodology (design, analysis, etc.) should be scientifically sound, implementable and capable of contributing to the realisation of the objectives the project has set out to achieve.
9. The collaborating institution should be able to contribute in physical, human and material resources and provide a conducive environment necessary for the execution of the project.

General recommendation

Existing institutional mechanisms/machineries (networks, regional programme liaison offices) and procedures (protocol formats, research grant agreements) should, as far as possible, be used for project development, implementation and management.

Discussion

C: We discussed whether the word "economic" should be deleted from project objective number 3 which states, "However, priority will be given to populations that are known to be of economic importance and/or endangered." Some species or populations may be important, but not in an economic sense. Also, we should have attached a list of projects submitted at the workshop, that we are aware of, or are in a planning stage.

C: Since we took no action on the projects presented here, it was decided that this list would not be included.[1]

Q: For those of you who presented case studies at the workshop, how well do these criteria for project selection fit?

A: I am in general agreement with the criteria. In reference to the comments on economic importance, in fact, the Cameroon government would not be supportive of a project that did not have economic importance.

A: We thought ILCA could go through the projects now and select ones for collaboration based on the criteria put forth.

C: The criteria you have laid out are useful and could be presented to project leaders for comments on how well on-going projects fit within these criteria. Are there particular concerns you might wish to raise at this point?

A: Now that I know the criteria for selection, I may wish to resubmit. For instance, the criterion on institutional support. There is presently none. But I might wish to pursue options in this regard.

C: In addition, we should look at recommendation number 9. There are aspects where the nation/institution is expected to provide some support.

C: The concern over funding in NARS is a real one. It raises the issue of what will end up getting funded. For instance, the World Bank is funding projects. However, i f you do not link into utilisation and extension services (and only do characterisation/ documentation of breeds), money may be hard to obtain. It will be difficult to get

1 Editor's note: Projects submitted during the workshop but not formally presented are found in Appendix IV.

projects such as these funded unless there is a good argument on their merits—including potential economic impact.

C: In this age of concern over biodiversity, there are funding sources. For some, if you talk about utilisation of livestock, the issue of environmental degradation is raised and there seems to be no money. If you speak about AGR for biodiversity, money is available.

Q: I have a concern regarding project methodology. Would on-farm research design meet these criteria?

A: The important point is simply that the methodology should be scientifically sound, whether it be on-station or on-farm. Group C addresses the issue of design.

Concluding remarks

J.E.O. Rege

I have learned much from this workshop and consider it a success. I owe this to my colleagues who responded to my invitation and came with open minds and a willingness to contribute. I thank everyone for their attendance and participation.

The question before us is, where to go from here? Proceedings of this workshop will be out shortly. In the next few months, we will spend time looking again at the literature, considering the deliberations and points raised in the last few days. By the end of the year, we hope to get back to you, through respective networks, and inform you of progress made. It might be possible, initially, to set up 2–3 pilot projects. Simultaneously, efforts will be made to find funding for a larger and more comprehensive effort. My hope is that resources at ILCA can be targeted for the smaller efforts.

Q: What role will the networks play in these projects?

A: Group D's presentation provided some guidelines on how, in the longer-term, we might be able to select projects, but did not identify how to get those projects. ILCA works very closely with several networks and we believe they will be the primary mechanism for receiving projects. In this regard, we will need the cooperation of network coordinators, steering committees and members. The exact form of implementation will depend on a number of things.

H.A. Fitzhugh

The task ahead is so substantial, it calls for close collaboration with African scientists, who will be at the forefront, and with scientists/institutions outside Africa. We want to be careful not to compete for available funds. If we can assist other institutions, scientists, etc. to be more effective, that is our goal. To that end, we have had productive talks with Dr. Cunningham regarding future collaboration with FAO. Funding is a serious problem. While FAO does not have the funds to undertake some of the activities that have been recommended, the organisation is hopeful that fundraising efforts will be effective in terms of a global programme. There is a recognition of the importance of African genetic resources. We have agreed to coordinate our efforts and not to overlap.

There is a consensus that one of the real needs is to channel resources to African scientists so the work will reflect credit back to them and their institutions. The real success of research in Africa will depend on the success of national scientists and the support they receive from their national governments. These politicians need to appreciate the value of research in the national institutions.

A particular opportunity for ILCA is to help in the coordination and mobilisation of funding and assist with the synthesis of results coming in from many sites. We do believe there is a role for an international centre such as ILCA to play, but we will call attention to the efforts of the national scientists and be sure to inform policy makers that it is their scientists who will make the difference.

We are enthusiastic, the time is right. Some of us have been deliberating on genetic resources for over 20 years. As interest in biodiversity is on the rise, this is an opportunity

to do something substantial. The human resources are there. Over the next five years and through the decade, we are optimistic and enthusiastic about the opportunities ahead.

Appendices

Appendix I

Curraleiro
FAO/EAAP-Global Data Bank for domestic livestock[1]

A) General Information

1	Country:	BRAZIL
2.	Species:	1.1 = Buffalo, 1.2 = Cattle, 1.3 = Goats, 1.4 = Sheep 2.1 = Horses, 2.2 = Ass, 3.1 = Pigs
3.	Breed or population	
3.1	Local name: CRIOULO NORDESTINO, GOIAS, PE DURO, SEPTANEJO, CORRAL OR HARD HOOF CRIOLLO, CURRALEITO	
3.2	International name: CURRALEIRO (see MASON's dictionary)	
4.	Main location of breed	
4.1	Region within country: N.E. BRAZIL (STATES OF PIAUI , MARANHAO, GOLAS).	
5.1	Main organization concerned with the breed (normally Breed Society: name, address)	
5.2	If not 5.1 (Breed Society), please complete University/State institution/Others	
5.3	An 'X' on this line indicates that this entry is a breed variety	
6.	Preparation of replies	
6.1	on page 1 to 3 by (NAME, ORGANISATION):	
6.2	on page 4 to 7 by (NAME, ORGANISATION):	
6.3	Date of preparation: (Month) (Year)	

B) Origin and development of breed

1	Origin		
1.1	Breed was mainly established out of the following breeds: (if breed is wild, feral or primitive, let year = 1111) DESCENDS DIRECTLY FROM THE BEIROA TYPE OF MIRANDESA		
		year around	0
1.2	Breed was mainly imported from country		
	breed	in	0
	and from country		
	breed	in	0
1.3	Breed is known by its local name	since	0
1.4	Herdbook established	in	0
2.	Immigration has taken place in the last years: for cattle, buffalo and horses since 1950, for sheep and goats since 1960 and for pigs since 1970 . (1: < 5%, 2: 5-20%, 3: > 20% estimated of % matings) year		

1 This is a revision of a printout of information stored in the data bank.

	0 from breed	country	in	0
	0 from breed	country	in	0
	0 from breed	country	in	0
	0 from breed	country	in	0
3.	Breeding population numbers in 1988			
3.1	Females (numbers being bred)	3.1.1 total		
		3.1.2 in herdbook		0
3.2	Percent females being bred pure (mated to males of own breed)			
3.3	Number of males total in service			
3.4	Out of the above males, the number in AI-service			
3.5	Changes in numbers of females:			
	(1 = increasing, 2 = stable, 3 = decreasing)			
	until 1988 3	since 1988		
3.6	Average herd size 1988	3.6.1 total		
		3.6.2 in private herds		0
		3.6.3 in other herds		0
3.7	Total Population Size	> 300(F80), 500(F66)		
3.8	Reference of Population Data	F80-124, F66-23, 167		
4.	Average age of animals used for breeding (months)			
	females males			
5.	Storage of semen and embryos			
5.1	semen: II	number of males		0
5.2	embryos: II	number of sires		0
	number of dams			0
5.3	Additional information on storage or on population data			

C) Breed description

1.	Coat colour	Black grey blue red brown yellow white blond			
1.1	predominantly unicoloured:_____				
1.2	colour combinations as follows:_____				
1.3	special colour characteristics (e.g. spotted, saddle, white head, etc.)				
2.	Comments on colour: RED, FAWN, DUN. PALE BELLY AND ESCUTCHEON				
3.	Horns		4	2	0
3.1	typical number of horns	male:	II	IXI	II
	(please mark with 'X')	female:	II	IXI	II
3.2	knobs only (spurs) (please mark with 'X')			II	
3.3	remarkable horn shape (or size)			II	
	which? SHORT HORNS				
4.	Hair and/or wool? (only sheep and goats)				
4.1	hair (please mark with 'X')				
4.2	wool (1= fine, 2= medium/crossbred, 3= coarse/carpet, 4= mixed) code:				
5.	Adult size and weight				
5.1	wither height (cm)	males	116	females	108
5.2	live weight (kg)	males	337	females	229
6.	Other specific visible traits, e.g. fat tail, hump				
	Please describe: SIMILAR TO TROPICAL DAIRY CRIOLLO				

7.	Genetic peculiarities	
7.1	Chromosome aberrations:	
7.2	Typical marker and/or major genes	gene-frequency
7.3	Other	
7.4	Additional information on genetic peculiarities can be obtained by the following institution or person:	

D) Qualification of breed

1.	Present main use		
1.1	Milk	2	
1.2	Tractive power	3	
1.3	Meat	1	
1.4	Wool	0	please indicate lst, 2nd and 3rd
1.5	Fur	0	rankings according to
1.6	Vegetation management	0	present importance
1.7	Sport, hobby	0	
1.8	Other (state below)	0	

2. Are there other uses which are of importance - please specify

3. Breed has special qualification (other than stated above) in the following fields (please mark with 'X')

3.1	quality of product for human consumption	II
3.2	resistance against specific pathogenic agent specify:	II
3.3	adaptability to climate specify:	II
3.4	fertility (e.g. twinning, long breeding season) specify:	II
3.5	adaptability to marginal land (e.g. mountain, marsh, wetland, semi desert) specify: Thrives on low quality grazing	IXI
3.6	Other specify:	II

3.7 experimental results in the above fields have been published

3.7.1	by	for field	I	I *)
	in (reference)	for field	I	I *)

3.8 Additional information on above qualifications can be obtained from the following institution or person:

for field	I	II	I *)
for field	I	II	I *)

*) Field number (3.1 to 3.6) for which additional information can be obtained.

E) Management conditions

1 Type....1	2 Housing period....	3 Feeding of adults.
1 = stationary	1 = no housing	1 = total grazing
2 = transhumant	2 = up to 2 months	2 = grazing+ fodder
3 = nomadic	3 = 2 to 6 months	3 = mixed
	4 = over 6 months	4 = concentrate
	5 = total housing	5 = total concentrate
		6 = grazing+ concentrate

4. Special conditions, e.g. lack of water supplyspecify:

F) Summary performance record

1. Standard breed for comparisons within country

The performance of breed (B) in specific traits is to be compared with the performance of a standard breed (SB), same trait, same measurement; preferably one of the most frequent breeds should be used as standard breed:

Buffalo:

Cattle : H. Friesian, Simmental, Jersey, Hereford, Charolais

Goats: Malta, Saanen, Toggenburg, Alpine

Sheep: Border-Leicester, Merino, Suffolk, Texel, Scottish Blackface, East Friesian, Finsheep

Horses: Arab, Thoroughbred, Halfbred, Fjord, Percheron, Quarter Horse

Ass:

Pigs: Landrace, Large White, Pietrain, Duroc

If none of the above breed is present in the country, the most popular breed should be used as standard breed.

1.1 Name of standard breed chosen: CURRALEIRO

1.2 approximate production of standard breed within country

trait			buffalo/cattle
1.2.1	milk yield per year	kg	0
1.2.2	milk fat percent	%	0.00
1.2.3	daily gain (males)	g	0
1.2.5	lean meat	%	0
1.2.6	milk yield per lactation	kg	
1.2.7	birth weight (male)	kg	19.3
1.2.8	birth weight (female)	kg	17.2
1.2.10	lactation length	days	

1.3 Reference for production data and/or adult size and weight

F80-218, F66-169

2. Relative comparisons

The absolute production level of breed B in comparison to the standard breed is

1 = very lower	(–51 to –100 %)
2 = much lower	(–16 to –50 %)
3 = lower	(–6 to –15 %)
4 = about equal	(–5 to + 5 %)
5 = higher	(+ 6 to + 15 %)
6 = much higher	(+ 16 to + 50 %)
7 = very much higher	(+ 51 to + 100 %)
8 = higher, more than factor 2	(+ 101 to + 200 %)
9 = higher, more than factor 3	(> + 200 %)

in the following traits (please enter codes in table):

Trait	Buffalo + cattle
2.1	milk yield 0
2.2	% fat 0
2.3	%protein 0

2.4	pulling power	0
2.5	milkability	0
2.6	daily gain	0
2.7	muscularity	0
2.8	calving rate	0
2.9	calving ease	0
2.10	calf mortality	0
2.11	calving interval	0
2.12	handling ease	0
2.13	age at sexual maturity	0

3. Validity of comparisons

The production conditions for Breed B (the one in question)

3.1 are about equal with the conditions for standard breed SB in above trait number(s)
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

3.2 are probably not as good as for the standard breed SB in above trait number(s)
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

3.3 are probably better than for the standard breed SB in above trait number(s)
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

G) Additional information on the breed

1. Genetic distance:

Estimates of genetic distance to the following other breeds are available:

1.1 (Breed)	1.2 (in country)
1.1.1	1.2.1
1.1.2	1.2.2
1.1.3	1.2.3
1.1.4	1.2.4

1.3 Additional information on genetic distance can be obtained by

2. Storage of genetic material in a “gene library”

Please mark “X” if genetic material of the breed such as DNA-sequences was entered in a gene library

Additional information on this kind of storage can be obtained by

3. Activities to conserve live animals of the breed

3.1 The following specific programs exist for live animal conservation (please indicate number of males and females, location, sponsor, etc.), excluding individual breeders who are part of and overall program:

3.2 Additional information on conservation of live animals of the breed can be obtained from:

Appendix II

What is a breed?

H.A. Fitzhugh

The concept of a breed, in which all members have a pedigree tracing their ancestry, was developed primarily in Western Europe during the eighteenth century. In its strictest sense, a breed designates a closed population—mating pairs are drawn only from within the population and relationships among individuals are documented by recorded pedigrees for all animals. Its members share certain recognisable phenotypic characteristics, such as color, horn shape, and body type, that designate their breed identity.

Members of a breed have developed under the same selection pressures and share a common ancestry. For example, the Holstein breed of dairy cattle, developed from the Dutch Black Pied breed, have been selected to produce large quantities of low-fat milk, while the Jersey breed of dairy cattle, from the Channel Islands, has been selected to produce smaller quantities of rich, high-fat milk.

The term *breed* as a formal designation often has little meaning outside areas of Western influence, where pedigree recording is often nonexistent. For the purposes of these discussions, the term *breed* means any recognizable interbreeding populations within a livestock species. A degree of mixing may occur among different breeds where mating is not strictly controlled. However, recognizable, regional stocks or populations exist worldwide that are analogous to Western breeds.

Appendix III

Synthesis of research methodology

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Introduction

Discussions held at the workshop identified three phases for breed characterisation. First, a macro study (survey type) gives some overall figures on the distribution and phenotypic performance of populations. Second, a meta study, seen as an on-farm performance study, gives more precise information about the phenotypic performance of a population. Third, a micro study is a detailed study measuring the performance of a population under controlled and standardised, but population-typical environmental conditions and allows for precise phenotypic and genetic evaluation of the population. The following remarks summarise the workshop discussions with respect to sampling animal sources and sample size, but provide more technical details with respect to statistical methods from which the conclusions are drawn.

Macro study

For surveying livestock populations in a country or region, one needs a quick and sufficiently accurate picture. IEMVT (1989) has developed a reliable and rapid survey method for studying livestock and production systems which might be applicable for breed characterisation studies. The method is based on a theory of surveys involving quotas. An analysis from this type of survey will give information about the general composition of herds specifying the animal breed, age, sex and usage. Reproduction and production parameters are also available from the analysis. This survey method was used by IEMVT in a number of countries, including Guinea and Chad, and covered about 300 herds per ecological zone within each country.

Meta study

Sample size

If animals to be sampled are kept and performance-tested under on-farm conditions, the most likely data structure with respect to breeds and farms or herds is a hierarchical one with farms nested within breeds. This assumes, of course, that the regional distribution is such that no farm is keeping more than one breed of animal. With respect to farm size, it is assumed that the typical smallholder does not have more than 20 animals sired by not more than two sires.

Sample size calculations with respect to comparing the mean performance of breeds were carried out changing the formula 8.17 of Steel and Torrie (1960) to:

$$LSD = [2 (t_0 + t_1)^2 (\sigma^2_f/i + \sigma^2_s/ij + \sigma^2_a/ijk + \sigma^2_e/ijkl)]^{1/2}$$

where

LSD is the least significant difference (in units of the standard deviation)
t_0 is the t value for probability .05
t_1 is the t value for probability 2(1-.90) or .20
σ^2_f is the relative variance between farms
σ^2_s is the relative variance between sires ($1/4\ h^2$)
σ^2_a is the relative variance within sires ($3/4\ h^2$)
σ^2_e is the relative variance within animals
i is the number of farms
j is the number of sires per farm
k is the number of dams or progeny per sire within farm
l is the number of replicates per animal

For testing breed differences in mean performance, it is advantageous to have as many unrelated animals as possible coming from as many farms as possible. If there is a need for a genetic analysis based on field data, then a genetic structure such as a half-sib structure has to be in the data set and reduces the precision for testing differences of means. With on-farm performance data, the size of the least significant difference depends not only on the family structure in the data set, but also, and mainly, on the relative variance among farms. Of minor importance are the size of the true heritability of the variable under consideration and the number of replicated measurements per animal.

Depending on the size of differences between means to be detected, the optimal number of farms and animals to be sampled per breed can be determined (Table 1). Assuming a difference of about 35% of the phenotypic standard deviation has to be detected, which equals about 10% of the mean with a coefficient of variation around 30%, then not more than 200 unrelated animals (200 farms, one sire per farm, one dam per sire) are needed. As soon as related animals within farms are sampled, the number of animals to be selected and tested has to be increased. For example, data on 400 animals coming from 40 farms sired by one or two sires per farm will give the same precision as the 200 unrelated animals if the relative variance between farms is small. If the variance between farms is large, then 400 animals have to come from about 100 farms and sired by one or two sires per farm with very small half-sib groups (2–3 progeny per sire). Thus, the larger the variance between farms, the more farms that have to be sampled.

For estimating genetic parameters based on on-farm performance data applying half-sib analysis, data from multiple-sire flocks with some half-sib structure can be used. As shown in Table 2, estimating phenotypic means and differences between breeds and estimating genetic parameters from the same data set requires a compromise with respect to the optimal experimental design. A reasonable compromise should give more emphasis on the precision of estimating phenotypic parameters and less on the precision of estimated genetic parameters. The latter can be studied in micro studies under well-controlled, standardised conditions. A fair compromise seems to be a data set providing performance data on animals coming from 40 to 50 farms sired by two sires per farm if the relative variance between farms is small (10%). If the variance between farms is close to 40%, then the total number of animals to be sampled has to be close to 800 coming from 80 to 100 two-sire flocks.

The alternative method for estimating genetic parameters by daugther-dam regression is not advisable for on-farm performance data because of overestimating heritabilities due to environmental resemblance between daughter and dam kept in one herd.

- For estimating differences between breeds with respect to their mean performance, 200 unrelated animals per breed sampled from a total of 100 to 200 randomly selected farms (one to two animals per farm) are sufficient to detect differences between breeds of about 10% of the mean. Such a data structure does not allow for any genetic analysis.
- For estimating phenotypic breed differences and genetic parameters, a data set with a family structure has to be sampled. Depending on the size of the variance between

farms, the necessary number of farms and animals to be sampled can be determined. If the variance between farms is small (10%) then 400 animals from 40 to 50 farms sired by two sires per farm are sufficient. If the variance between farms is large (40%) then 800 animals from 80 to 100 farms sired by two sires per farm are sufficient.

- For estimating genetic parameters, a half-sib analysis is more appropriate than a regression (daughter-dam) analysis.

Table 1. *Least significant differences (* SD) for comparing breeds in on-farm studies.*[1]

no. of farms	no. sires	no. dams	σ^2_f = 10%		σ^2_f = 40%	
			h^2 = .16	h^2 = .32h	^{2} = .16	h^2 = .32
10	1	20	0.64	0.71	1.03	1.07
20	1	10	0.50	0.53	0.73	0.76
40	1	5	0.41	0.43	0.54	0.56
200	1	1	0.32	0.32	0.32	0.32
5	2	20	0.84	0.90	1.47	1.50
10	2	10	0.61	0.64	1.01	1.02
20	2	5	0.47	0.49	0.72	0.73
100	2	1	0.34	0.34	0.39	0.39
2	5	20	1.65	1.70	3.10	3.13
4	5	10	0.91	0.94	1.67	1.68
8	5	5	0.64	0.66	1.12	1.12
40	5	1	0.39	0.39	0.53	0.53
20	1	20	0.45	0.49	0.71	0.74
40	1	10	0.35	0.37	0.51	0.53
80	1	5	0.29	0.30	0.38	0.39
400	1	1	0.23	0.23	0.23	0.23
10	2	20	0.57	0.60	0.99	1.01
20	2	10	0.42	0.44	0.70	0.71
40	2	5	0.33	0.34	0.50	0.51
200	2	1	0.24	0.24	0.27	0.27
4	5	20	0.88	0.91	1.66	1.67
8	5	10	0.60	0.62	1.10	1.11
16	5	5	0.44	0.45	0.77	0.77
80	5	1	0.27	0.27	0.37	0.37
40	1	20	0.31	0.34	0.50	0.52
80	1	10	0.24	0.26	0.36	0.38
160	1	5	0.20	0.21	0.27	0.28
800	1	1	0.16	0.16	0.16	0.16
20	2	20	0.39	0.42	0.69	0.70
40	2	10	0.30	0.31	0.49	0.50
80	2	5	0.23	0.24	0.36	0.36
400	2	1	0.17	0.17	0.19	0.19
8	5	20	0.58	0.60	1.09	1.10
16	5	10	0.41	0.43	0.76	0.77
32	5	5	0.31	0.32	0.54	0.54
160	5	1	0.19	0.19	0.26	0.26

[1] Power of test = 90%; level of significance = 95%; three breeds to be compared.
no. of replicates per animal = 1.
h^2 = heritability.

Table 2. *Least significant differences (* SD) for comparing breeds and standard errors of heritabilities in on-farm studies.*[1]

no. farms	no. sires	no. dams	LSD σ^2_f = 10%	LSD σ^2_f = 40%	SE(h^2)
10	2	20	.59	1.00	.13
20	2	10	.43	.71	.14
40	2	5	.34	.51	.16
50	2	4	.32	.47	.18
67	2	3	.29	.41	.21
100	2	2	.27	.35	.28
20	2	20	.40	.70	.09
40	2	10	.31	.50	.10
80	2	5	.24	.36	.12
100	2	4	.23	.33	.13
134	2	3	.21	.29	.15
200	2	2	.17	.25	.20

[1] see legend Table 1.
LSD = as shown in Table 4a, averaged over two true heritabilities (0.16 and 0.32)
SE(h^2)= standard error of heritability, averaged over two true heritabilities (0.16 and 0.32)

Animal sources and sampling

With respect to the objectives in breed characterisation using on-farm performance data, the sampling process includes farms and animals within farms:

- The farms should be sampled at random from the most typical distribution area of the breed under consideration. Stratification can be a helpful tool for identifying regional differences.
- If animals sampled per farm are unrelated (have different sires) then only a phenotypic analysis of the data is possible.
- If animals sampled per farm are genetically related to each other (e.g. two half-sib groups, each group having four to 10 half-sibs) then a genetic analysis is possible provided the sires are identified.

Constraints in on-farm studies

Carrying out on-farm performance testing with respect to phenotypic and genetic characterisation of breeds will have the following constraints:

- Small farm size. Due to the small farm size, many (40–100) farms have to be sampled, probably best in a stratified way. This will create logistical problems and high costs, especially when farms have to be visited repeatedly.

  In addition, due to small farm size, many farms are single-sire farms which cannot be used for genetic evaluation because of the confounded effects of farms and sires. The assumption has to be made that multiple-sire farms which ought to be selected for genetic studies are a random sample of farms keeping a breed. One way to at least partly overcome the problem with the confounded effects of sires and farms is to cluster farms according to some factors, describing the production level of the farm (e.g. farm size, rainfall, location, production system, etc.). Those farm clusters may, to a certain extent, describe the effect of a farm and can replace the farm in the ANOVA. So, a paternal half-sib analysis can be carried out on a within-farm cluster basis.

- Unknown sire identification. Unknown sire identification is one of the common problems in on-farm studies making a paternal half-sib analysis impossible. However, if a dam has two or more offspring, then the genetic analysis can be based on a full-sib analysis. This, of course, will lead to biased estimates of heritabilities due to maternal and dominance effects. This bias can be considerable depending on the variable under consideration.

  If maternal half-sibs from different litters are available, assuming for each mating season different sires are used, then the estimated heritability will only be slightly biased due to environmental and maternal effects common to animals in subsequent litters. This bias is much smaller than the bias encountered in full-sib analysis. Therefore, recording and testing offspring from two or three subsequent pregnancies can be a way to circumvent the problem of unknown sire parentage.
- Incorrectly identified offspring. In on-farm studies, the sire parentage may be unknown. But even for maternal half-sib analysis it is important to correctly identify offspring. For paternal half-sib analysis, the effect of misidentified offspring on the estimated heritability was derived by Van Vleck (1970). For maternal half-sib analysis, the effect of misidentification can be derived from the half-sib correlation assuming two maternal half-sibs per dam, one of which may be misidentified. Then, the effect on the estimated heritability (h^2) depends on the number of dams with misidentified offspring (m) compared to the total number of dams(f):

  $h^2 = [(f-m)/f]\, h^2$

Table 3 shows the reduction in estimated heritability due to misidentified offspring and stresses the importance of correctly identifying offspring.

Table 3. *Reduction in heritability estimates (%) for various misidentification rates.*

misidentification rate	paternal half-sibs[1]	maternal half-sibs
0.05	10	5
0.10	19	10
0.20	36	20
0.40	64	40

[1] Total number of paternal half-sib families = 50.

Micro study

Sample size

The micro study is considered a detailed study measuring the performance of animals of selected populations under controlled and standardised, but population-typical environmental conditions allowing for a precise phenotypic and genetic evaluation of a population. The micro study is seen to be complementary to macro and meta studies for comparing and testing animal populations.

Sample size calculations were carried out to define the optimal data structure. Results as shown in Tables 4a and 4b were obtained by changing formula 8.17 of Steel and Torrie (1960) to:

$$LSD = [2\,(t_0 + t_1)^2\,(\sigma^2_s/i + \sigma^2_a/ij + \sigma^2_e/ijk)]^{1/2}$$

where

LSD	is the least significant difference (in units of the standard deviation)
t_0	is the t value for probability .05
t_1	is the t value for probability 2(1-.90) or .20

σ^2_s	is the relative variance between sires ($1/4\ h^2$)
σ^2_a	is the relative variance within sires ($3/4\ h^2$)
σ^2_e	is the relative variance within animals
i	is the number of sires
j	is the number of dams or progeny per sire
k	is the number of replicates per animal

For testing breed differences in mean performance, it is advantageous to have as many unrelated animals as possible, but that is a contradiction to estimating genetic parameters using, for example, a half-sib analysis. At least a family structure needs to be in the data set. For a given number of animals tested, the more sires or the smaller the half-sib groups, the smaller the least significant difference. Also, the size of the least significant difference depends not only on the family structure in the data set, but also on the heritability of the trait measured and on the number of measurements per animal. In general, the smaller the true heritability and the more measurements that are taken per animal, the smaller the least significant difference.

Table 4a. *Least significant differences (* SD) for comparing breeds in on-farm studies.*[1]

		no. reps/animal = 1		no. reps/animal = 3	
no. sires	no. dams	h^2 = .16	h^2 = .32	h^2 = .16[2]	h^2 = .32[3]
5	20	.70	.85	.59	.73
10	10	.57	.66	.46	.55
20	5	.51	.55	.38	.45
5	40	.61	.78	.55	.68
10	20	.47	.57	.40	.49
20	10	.40	.45	.32	.38
40	5	.36	.39	.27	.31
10	40	.41	.53	.37	.47
20	20	.33	.40	.28	.37
40	10	.28	.32	.22	.28
80	5	.25	.27	.19	.23

[1] power of test = 90%; level of significance = 95%; three breeds to be compared.
[2] repeatability = .2
[3] repeatability = .4

Depending on the size of differences between means to be detected, the optimal number of animals per breed can be determined. Assuming a difference of 30–40% of the phenotypic standard deviation (which equals about 10% of the mean with a coefficient of variation between 25% and 30%) has to be detected, then 200 animals per breed (20 sires bred to 10 dams each and one progeny per dam) are considered to be the minimum requirement. A total number of 300 to 400 animals per breed sired by 20 sires each mated to 15–20 females would be more secure. On the other hand, if variables are measured repeatedly, e.g. three times, then a sample size of 200 animals per breed might be sufficient. Repeated measurements are especially advantageous when the heritability of a variable is low.

If a completely unstructured sample of animals can be drawn, i.e. all animals sampled are genetically unrelated, then a much smaller sample will give the required precision (Table 4b). In fact, a minimum sample of 100–120 unrelated animals will give the required precision to detect differences of about 10% of the mean, whereas under a given family structure (20 sires, 10 dams) 200 animals will be needed to give the same precision.

Table 4b. *Least significant differences (* SD) for comparing breeds in on-farm studies (all animals unrelated).*[1]

	no. reps/animal = 1		no. reps/animal = 3	
no. animals	h^2 = .16	h^2 = .32	h^2 = .16[2]	h2 = .32[3]
10	1.51	1.51	1.03	1.17
20	1.04	1.04	.71	.81
40	.74	.74	.50	.57
60	.59	.59	.40	.46
80	.51	.51	.35	.40
100	.46	.46	.31	.36
120	.42	.42	.29	.32
140	.39	.39	.26	.30
160	.36	.36	.25	.28
180	.34	.34	.23	.26
200	.32	.32	.22	.25
300	.26	.26	.18	.21
400	.23	.23	.16	.18

[1] power of test = 90%; level of significance = 95%; three breeds to be compared.
[2] repeatability = .2
[3] repeatability = .4

For estimating genetic parameters, such as heritabilities and genetic correlations, applying half-sib analysis, the optimal family size depends on the true heritability of the variables under consideration (Table 5a) (see formulas 10.12 and 19.4 in Falconer, 1981). But a family size of 10 to 20 animals per sire is a good overall value which holds for low to medium heritabilities. Again, the total number of animals required depends on the size of standard error anticipated. If the standard error of the estimated heritability coefficient is smaller than 0.15, then at least 400 animals sired by 20 to 40 rams are needed. This sample size will give a standard error of an estimated genetic correlation of about 0.20. These values might be considered small enough for characterising breeds, but they are not small enough for comparing estimates of heritabilities and genetic correlations between breeds. Repeating measurements does not have a positive effect on the precision of estimated heritabilities and genetic correlations.

Another alternative for estimating genetic parameters is the estimation from the offspring on parents. If the sample is widely distributed, one may have sampled one dam per sire and data are available on dams and offsprings (usually one offspring per dam). If the data set is genetically structured, as shown in Table 5a, one may choose the regression approach for estimating genetic parameters on a within-sire basis. The precision of genetic parameters estimated by regression is about equal to the precision of the estimates from half-sib analyses (see Table 5b, based on formulas 10.8 and 19.4 in Falconer, 1981).

For example, with 100 offspring-dam pairs (200 animals tested), the standard error of the estimated heritability is 0.20, whereas a half-sib analysis of a data set with 20 sires and 10 dams per sire (200 offspring tested) gives standard errors of the estimated heritabilities between 0.18 and 0.22. The same conclusion can be drawn with respect to the precision of estimated genetic correlations.

Table 5a. *Standard error of genetic parameters (half-sib analysis).*[1]

		SE (heritability)		SE (genetic correlation)	
no. sires	no. offspring	h^2 = .16	h^2 = .32	r_A = .25	r_A = .50
5	20	.25	.34	.85	.68
10	10	.27	.31	.85	.68
20	5	.32	.35	.98	.78
5	40	.18	.27	.65	.52
10	20	.16	.22	.55	.44
20	10	.18	.22	.58	.47
40	5	.23	.25	.70	.56
10	40	.12	.18	.43	.34
20	20	.11	.15	.38	.30
40	10	.12	.15	.39	.31
80	5	.16	.17	.48	.39
opt. family size		25	12.5		

[1] no. reps/animal = 1.

Given a half-sib structure in the data set as shown in Table 5a, one may also choose the regression of offspring on sire to estimate genetic parameters (Table 5c). The most efficient design is to have as many half-sib groups (sires) as possible and to measure only very few offspring per sire. But even with half-sib groups of five to 10 offspring per sire, this procedure will give slightly more (10% to 15%) precise estimates of heritabilities and genetic correlations with respect to the standard error of the estimates. If both parents can be measured, regression on mid-parent gives an even better precision than regression on dam or sire.

Table 5b. *Standard error of genetic parameters (offspring-dam regression).*[1]

		SE (genetic correlation)	
no. offspring-dam pairs	SE (heritability)	r_A = .25	r_A = .50
10	.63	1.85	1.48
20	.45	1.32	1.05
40	.32	.94	.75
60	.26	.76	.61
80	.22	.64	.52
100	.20	.59	.47
120	.18	.53	.42
140	.17	.50	.40
160	.16	.47	.38
180	.15	.44	.35
200	.14	.41	.33
300	.12	.35	.28
400	.10	.29	.23

[1] no. reps/animal = 1.

Table 5c. *Standard error of genetic parameters (offspring-sire regression).*[1]

		SE (heritability)		SE (genetic correlation)	
no. sires	no. offspring	h^2 = .16	h^2 = .32	r_A = .25	r_A = .50
5	20	.27	.32	.86	.69
10	10	.23	.26	.72	.57
20	5	.22	.23	.66	.53
5	40	.23	.29	.76	.61
10	20	.19	.22	.66	.48
20	10	.16	.19	.51	.41
40	5	.15	.16	.45	.36
10	40	.16	.20	.52	.42
20	20	.13	.16	.42	.34
40	10	.12	.13	.37	.29
80	5	.11	.11	.32	.26

[1] no. reps/animal = 1.

It may also be recalled that assortative mating of parents increases the precision of the regression on mid-parent values due to the increase of the variance of mid-parent values (Falconer, 1981).

In on-farm and on-station studies, the parents used are often selected. Selection may be based on the variable for which genetic parameters are to be estimated or on some correlated variables. Selection causes the variances between parents to be reduced and consequently heritability estimates from half-sib analysis are biased downwards. The bias depends on the intensity of selection. Estimating variance and covariance components taking the selection into account by applying mixed-model techniques can overcome this problem in half-sib analysis. On the other hand, selection does not bias the regression of offspring on parents, either single parents or mid-parent values, but it does reduce the precision of the estimates. Selection can also improve the precision of the regression estimate if two groups of parents are selected, one with high values and one with low values, and offspring are reared only from the selected parental groups (Falconer 1981).

Summarising aspects of sample size, one may make the following conclusions:

- For estimating differences between breeds with respect to their mean performance, 200 animals per breed, progeny of 20 sires, are sufficient to detect differences of about 10% of the mean between breeds. If a sample of completely unrelated animals can be drawn, then only 120 animals are needed to detect differences of the same magnitude (about 10% of the mean). Repeated measurements will give an even higher precision.
- For estimating genetic parameters using half-sib analyses, at least 200 animals per breed, progeny of 20 sires, and a family size of 10 to 20 will give some indications on the genetic basis of variables. If data are available on parent and offspring, then the offspring-parent regression can be used to estimate genetic parameters. The minimum requirement with respect to sample size for the regression approach is 100 offspring parent pairs (i.e. 200 animals tested). For testing differences between breeds with respect to genetic parameters, more than 400 animals per breed are needed.
- Estimating differences between means of breeds can be done in a first phase. However, for estimating genetic parameters, the experiment has to be repeated with another sample of animals/sires at different times or locations.
- The numbers given above indicate the absolute minimum requirement that is needed for the final data set for analysis. In the planning stage, provision has to be made for animal losses, i.e. at the beginning of an experiment on breed characterisation, one should have at least 20% more animals than noted above.

Animal sources and sampling

With respect to the objectives in breed characterisation, one can sample animals in different ways:

- The animals sampled irrespective of the later statistical analysis (half-sib or regression) should be completely unrelated. This can best be assured by sampling from a large number, randomly selected village flocks and from many distinct villages.
- If a half-sib analysis has to be applied, then the animals selected will be the parents (e.g. 200 females and 20 males) which are kept and mated on-station to produce the required number of offspring which will be tested. Data on the offspring will allow phenotypic and genetic analyses. For some variables (e.g. fertility), a second generation is needed.
- If a regression analysis has to be applied, then the animals sampled should be pregnant females, e.g. 120 females. Also, some males (10) may be selected for future matings. The offspring born and tested on-station provide the information on mean and phenotypic variance of the animals' performance. For estimating genetic parameters, a second generation of animals has to be produced. For some variables (e.g. parturition interval), it may be necessary to repeat the matings with the females and males brought to station.
- Another procedure which allows for estimating breed differences and genetic parameters is to sample parental stock from station flocks. After selection, parents are mated to produce the required number of offspring per breed. Under station conditions, the parentage of all offspring and their parents should be known, taking into account the genetic relationship of the parents when estimating breed means and genetic parameters. On the other hand, artificial and natural selection as well as genetic drift may have caused genetic differences between the station flock and the population kept under village conditions.
- Sampling animals which are genetically unrelated to each other is advantageous with respect to estimating phenotypic population parameters such as means and variances. Fewer animals (about 40% less) are needed as compared to a study in which genetically related animals are used.
- For estimating genetic parameters, a regression (offspring-parent) analysis and/or a half-sib analysis can be applied. With respect to precision, expressed as the standard error of estimated genetic parameters, both analyses are about equal given the same number of animals tested. With respect to bias in the estimated genetic parameters, mainly due to common environmental effects such as maternal effects, the half-sib analysis is preferable because it provides less biased estimates.

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Appendix IV

The seven papers in Appendix IV were submitted to workshop participants for information and/or consideration for possible inclusion in ILCA's proposed project. They reflect the state of breed improvement programmes in a number of African countries and suggest research opportunities in the area of animal genetic resources. The papers included in this section are:

Proposed national animal breeding programmes in Nigeria

O.A. Adebambo

Characterisation of indigenous livestock breeds in Senegal

A. Fall

Characterisation of indigenous goats and sheep in Zambia

E.M. Kaluba

Identification of high milk-producing indigenous cattle in Uganda

G.H. Kiwuwa

Characterisation of livestock breeds in Botswana

L.L. Setshwaelo

The Swaziland national beef cattle breeding programme

D.D. Vilakati

Range performance testing of Malawi Zebu cattle: A summary

A.W.C. Zimba

Proposed national animal breeding programmes in Nigeria

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Introduction

Since the late 1960s, there has been indiscriminate importation of breeding stock into Nigeria. With the exception of poultry, these importations have made little impact on overall level of animal productivity, despite the massive foreign exchange involved.

Formulation of a National Livestock Breeding Policy has been in the pipeline since 1977. The policy was redrafted in 1991 and a final ratification from the National Council for Agriculture is awaited.

Most policies on livestock production have failed to achieve their goals because of poor implementation. There are few properly designed on-going livestock breeding projects in the country. In addition, data on breed evaluation have tended to be incomplete. Information is often based on small numbers and provides inadequate definition of traits or environments.

All of these problems have been magnified by economic hardships accentuated by the recently introduced structural adjustment programme in the country. Consequently, there is an even more urgent need to have in place good and effective national breeding policies and programmes.

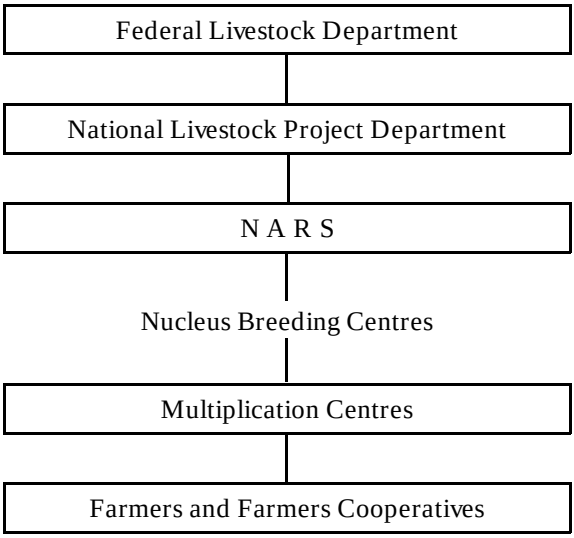
In order to attain self sufficiency in animal production, the thrust of national animal research is to be based on the exploitation and development of indigenous livestock species. Where necessary, crossbreeding with exotics will be judiciously applied under carefully defined conditions and clearly stated objectives. Characterisation of the different pure and crossbreds in specific environments—namely, their areas of origin—will be vigorously pursued.

Proposed national programmes

It is proposed that national breeding stations be established in different ecological zones of the country for the different livestock species. Cattle breeds, since they are multipurpose, must be characterised for specific purposes such as beef and dairy production. Small ruminants are to be evaluated and selected for both meat and milk production. In addition, the Red Sokoto is to be bred for its skin. The swine industry is to utilise indigenous pigs in selective breeding while foundation stock from exotic breeds under improved management will be addressed. Implementation of a nationally coordinated livestock breeding programme has been proposed along the lines shown in Figure 1.

Presently, research is underway with: milk-producing cattle utilising the Wadara, Bunaji and Sokoto Gudali breeds; beef cattle, utilising the Sokoto Gudali, Muturu and N'Dama breeds; sheep; goats; and pigs.

Figure 1. *Proposed flow chart of implementation.*



Breed improvement is to be launched as a campaign along with other components of the livestock development programme. It is envisaged that:

- a coordination centre for all national livestock breeding programmes will be established;
- record-keeping systems will be standardised;
- a national data bank will be created;
- national herd registers for breed improvement will be created;
- all nucleus and multiplication centres will be registered; and
- livestock shows will be organised.

Current dispensation

Out of 21 research projects funded by national livestock development projects during the Second Livestock Development Programme (which is to terminate in 1993), only one project on animal breeding was funded. This project is being stifled due to lack of funds.

Research on poultry breeding commenced in 1985 at the National Animal Production Research Institute, while selection of Yankassa sheep commenced in 1983. Work on purebred and crossbred Bunaji and Sokoto Gudali for milk production commenced in 1970. N'Dama cattle programmes are on-going at Fashola, Upper Ogun and Adada.

Major constraints to the expansion of breed improvement programmes have been:

- lack of funds and hence lack of continuity
- lack of proper extension organs
- lack of technical direction
- importation of exotic breeds that could not survive in these environments
- administrative and political problems
- low carrying capacity of existing paddocks
- insufficient numbers of animals used in breeding programmes

In addition, farmers' interests and needs have not been adequately incorporated into these programmes.

Animal breeds

Cattle

Eight widely known indigenous cattle breeds are present in Nigeria. Seven of these are highly localised while the Bunaji is widespread and singularly multipurpose. Other breeds are the Sokoto Gudali, Kuri, Jali, Muturu, Keteku, Wadara and the N'Dama.

Sheep

There are four sheep breeds in Nigeria. The Yankassa is the only breed that is widespread and intermediate in performance. Other breeds are the Balami, Uda and the West African Dwarf.

Goats

There are three goat breeds in Nigeria. All are restricted to their zone of origin.

Red Sokoto	–	NW of the country
Sahel	–	NE of the country
Dwarf	–	Southern part of the country

Others

Pigs in Nigeria could be classified based on their snout length into two types—long and short. Both are found in the southern part of the country. Several breeds of local chicken, ducks, turkeys and guinea fowls are also found in Nigeria and need to be characterised.

Conclusion

With such a wide animal genetic base and varying ecological niches, breed development should pose no problems in Nigeria. The human resources and ecological diversity make the country well suited for the development of a multi-directional and purposeful breeding programme that can benefit the continent.

Characterisation of indigenous livestock breeds in Senegal

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Introduction

In the past, attempts to characterise indigenous breeds in Senegal were based on the establishment of nucleus herds and/or flocks reared on-station for selection purposes. The main objective of these programmes was the production of improved breeding stock for distribution into villages. Along with these on-station programmes, extensive village herd monitoring schemes were implemented in different ecological zones. They were often components of larger research programmes aimed at the characterisation of livestock production systems in Senegal. These programmes focused mainly on ruminant breeds (cattle, sheep and goats) under either station or village management systems.

This presentation identifies past and on-going programmes intended to increase knowledge on the characteristics of local ruminant breeds under varying environments. Objectives, experimental design and progress are indicated.

Ruminant breeds in Senegal

Cattle

The cattle population in Senegal is made up of three main breeds: Zebu, N'Dama and Djakore. They are distributed along different climatic zones. The Zebu *(Bos indicus)* breeds are reared in the tsetse-free areas in the north of the country. They are of two types: the Peul or Gobra and the Maure. The Maure is limited in number and is located in the Senegalese river zone. The Zebu population is composed of 1,147,000 head.

The trypanotolerant N'Dama is distributed in the more humid soudanan and soudano-guinean tsetse-infested regions of the country. The population of N'Dama cattle is estimated at 644,000 head.

The Djakore genotype is a stabilised cross between N'Dama and Zebu and is found in intermediate areas between Zebu and N'Dama zones. The Djakore population is estimated at 409,000.

Small ruminants

The distribution of small ruminant breeds in Senegal follows climatic lines and the tsetse distribution noted above for cattle. The Djallonke sheep and goats are reared in humid tsetse-infested areas. The dry northern part of the country is populated by Sahelian sheep and goats. Three breeds of Sahelian sheep are present: the Touabir, the Peul-peul and the Warale, which is a cross of the first two breeds. Population numbers for sheep and goats are estimated at 983,000 and 1,967,000, respectively.

Programmes of characterisation of indigenous ruminant breeds

Table 1 shows the cattle breed evaluation programmes in Senegal.

Table 1. *Programmes of cattle breed characterisation in Senegal.*

Site	Ecological zone	Genotype	Manage-ment	Number of animals	Duration	Status
Kolda	Soudanan	N'Dama	Station	450	1972–1992	On-going
Kolda	Soudanan	N'Dama	Farm	1500	1985–992	On-going
Kolda	Soudanan	N'Dama	Farm	400	1988–1992	On-going
Dahra	Sahelian	Gobra	Station	600	1960s–1992	On-going
Dahra	Sahelian	Gobra	Farm	600	1988–1991	Ended
Sine Saloum	Soudano-sahelian	Gobra/ N'Dama/ Djakore	Farm	800	1983–1990	Ended
Ziguinchor	Guinean	N'Dama	Farm	400	1986–1990	Ended
Saint Louis	Sahelian	Gobra	Farm	NA	NA	

N'Dama cattle characterisation programmes: On-station

A herd of 450 cattle was established at the Kolda Centre de Recherche Zootechnique. The main objective of the programme is to produce and distribute improved breeding stock among village herds. Mass selection is applied to genetically improve the breed. An average of 250 breeding females are naturally mated to selected bulls. Male offspring are tested and ranked on body weight growth performances. Production data (reproduction, mortality, growth and milk offtake) are recorded. Linear measurements are also recorded. Results of this work have been reported (Fall et al, 1982). Data on milk yield is now available but not yet analysed.

N'Dama cattle characterisation programmes: Village herd monitoring schemes

Two village herd monitoring operations are run by the Centre de Recherche Zootechnique at Kolda. The first programme, begun in 1985, evaluates the productivity of N'Dama cattle under village conditions and includes the characterisation of traditional livestock production systems. Fifteen hundred head of cattle, in 15 herds at eight villages, are visited weekly. Data are collected on birth, death, exits, weight, milk offtake and diseases. Data pertaining to this on-going programme are not yet completely analysed.

The second programme is an ISRA/ILCA/ILRAD joint research project conducted in Senegal and The Gambia as part of the African Trypanotolerant Livestock Network. The objectives of the project are to evaluate the productivity of N'Dama cattle under village management and to assess the effect of factors such as trypanosomiasis risk, infection rates of trypanosomiasis and other parasitic diseases and nutritional status on animal productivity. About 400 head of village N'Dama cattle are being monitored on an individual and monthly basis. Data collected include body weight, reproduction, mortality, milk offtake and milk composition (fat, protein). Monthly blood and faecal samples are collected to detect blood and intestinal parasites. Trypanosomiasis risk is evaluated through monthly capture and dissection of flies as well as the identification of blood meal origin.

Nutritional experiments are being conducted in order to evaluate the effect of strategic supplemental dry-season feeding on the productivity of N'Dama cattle, particularly in

reference to the onset of oestrus after calving. This programme has been underway since 1988. Results have not yet been reported.

Gobra Zebu characterisation programmes

These programmes, dealing with the characterisation of the Gobra Zebu, are taking place at Dahra Centre de Recherches Zootechniques located in the northern part of the country. As with the N'Dama cattle, on-station and on-farm monitoring schemes have been implemented.

A breeding herd of about 600 head of Gobra cattle are reared on-station for selection purposes. Improved breeding stock is distributed to village herds after the application of mass selection, ranking young males according to their growth performance. Data collected are similar to those described above for N'Dama cattle on-station.

In the past, experiments were conducted on-station in order to evaluate the beef potential of the Gobra. Young males and females were shown to benefit from a high nutritional plane from birth to the age of two to five years with concentrate fed *ad libitum*.Growth, reproduction, milk and carcasses were evaluated and compared to a control group. Results have been reported (Redon, 1962; Denis, 1971; Denis and Valenza, 1971; Valenza et al, 1971; Denis et al, 1974).

An extensive breed characterisation programme was also implemented from 1983 to 1990 in the Sine-saloum region of Senegal. The area is populated by Djakore, N'Dama and Zebu breeds. About 800 head of cattle in 45 herds of 16 villages were regularly monitored. Demographic statistics, weight and milk offtake were recorded. Data are being analysed.

Small ruminant characterisation programmes

Most of the work undertaken to characterise sheep breeds was carried out on-station. Nucleus sheep flocks were established on the stations at Kolda and Dahra for breeding purposes. Results on the productivity of Djallonke and Sahelian sheep breeds have been reported (Fall et al, 1982; Sow, 1982).

Recently, an extensive monitoring of village flocks was started by a joint ISRA/IEMVT research programme named Productivite et pathologie des petits ruminants (PPR). The objectives of this comprehensive effort are to evaluate the productivity of indigenous sheep and goat breeds under traditional management systems and to evaluate the effects of different factors (breed, region, diseases and management systems) on productivity. Village flock monitoring operations have been underway since 1983 in various locations (Kolda, Dahra, Kaymor, Louga). Data have been collected on production traits (weight, reproduction), management systems and prevalent diseases (mainly helminthiasis). Experiments are also being conducted on-farm in order to assess the effects of deworming and immunisation on flock productivity (Faugere et al, 1988; Faugere et al, 1989).

Conclusions

The programmes described above are mainly oriented to the evaluation of breed productivity under different management systems. Work needs to be extended to include an examination of the physical characteristics of breeds in order to gain more comprehensive characterisations. There is also a need for further work on the adaptability of these breeds, especially in terms of resistance to diseases, heat tolerance, work capacity and roughage utilisation.

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Characterisation of indigenous goats and sheep in Zambia

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Introduction

Livestock are vital to subsistence and economic development in Zambia. They provide essential food products throughout the year, are a major source of government revenue and income to the millions of people in rural areas, contribute draught energy and manure for crop production and are the only food and cash security available to many rural people. In rural areas, the sale of livestock and their products, particularly during drought years, often constitute the only source of cash income with which farmers can buy consumer goods, improved seeds, fertiliser and other inputs to increase crop yields. The major livestock species in Zambia are cattle, sheep, goats, pigs and poultry.

Sheep and goats constitute the second most important form of livestock in Zambia after cattle and are a major source of meat in rural areas. Unlike cattle and pigs, they have an advantage of surviving over a wide range of environments. Sheep and goats are also generally easier to keep than cattle. Despite their importance and advantages, little is known about their physiological and productive characteristics. To improve and sustain the economic contribution of these livestock to the national economy, it is proposed that a project to quantify, characterise and conserve existing sheep and goat genetic resources be undertaken.

Objectives

The objectives of the project are:

- To quantify the available indigenous sheep and goats in the country and, if possible, group them into various phenotype/genotype groups.
- To identify the main traditional farming systems of sheep and goat-rearing and identify the main constraints preventing their utilisation and improvement.
- To characterise these breeds in terms of physical characteristics, productive parameters and adaptability.

Methodology

Field survey through administration of questionnaires to record:

- available sheep and goat numbers country-wide
- existing phenotypic groupings
- main farming systems of sheep and goat-rearing and utilisation
- main constraints within these systems preventing utilisation and improvement.

On-station research on randomly selected populations to characterise them in terms of:

- physical characteristics
- productive parameters
- special adaptations.

Records to be kept will include the following:

Field survey:

- location
- sheep and goat numbers
- type of phenotypic groups
- type of farming systems
- main uses
- major constraints.

On-station research:

- animal identification
- phenotypic group
- physical characteristics: coat colours, body weight at birth and maturity, wither height and body length.
- productive parameters: fertility, growth rates, weaning weights, milk yield, etc.
- special adaptations to heat and drought stress, disease challenge and nutritional stress.

Animal management will initially simulate the original environment and then subject animals to improved but affordable management levels for smallscale farmers.

Identification of high milk-producing indigenous cattle in Uganda

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Introduction

The high milk-producing exotic and grade cattle in Uganda, which numbered 150,000 before 1975, have been reduced to 25,000. They contribute about 15% to the marketed milk supply—mainly to urban areas. Similarly, the indigenous national cattle herd, previously numbering about 5.5 million head, has been reduced to 3.2 million. This decrease has been a result of destruction and reduced veterinary services brought about by the civil wars of 1979 to 1986. As a consequence, since 1976, Uganda has imported 28,296 tonnes of dried skimmed milk and 9,136 tonnes of butter oil—all worth US $52 million.

The national cattle herd consists of 63% East African Shorthorn Zebu, 20% Ankole (Sanga) and 15% Nganda type. Only 2% are exotic or grade cattle. Combined, these breeds contribute around 300 million litres of milk per annum to feed Uganda's human population of 16 million. From these figures, it appears that the bulk of consumable milk in Uganda is supplied by indigenous cattle.

Field surveys indicate that daily milk yields of the recently imported German Friesians and other exotic breeds averaged 9.4 and 9.3 litres, respectively. Yet the survey also revealed that a herd of 22 indigenous cows produced, on average, 10 litres of milk per cow per day. These figures suggest that, if properly identified for future breeding purposes, some indigenous breeds could produce at relatively higher levels within existing feeding and management practices found in Uganda. Therefore, the need exists to identify and propagate the more promising indigenous breeds for dairy or dual-purpose production and synchronise locally adapted breed resources with the feeding, management and economic resources most readily attainable by the average cattle farmer in Uganda.

Objectives

The proposed research seeks to explore the inherent potential of the top Ankole and Nganda cattle breeds under on-farm conditions and to create a directory for future breeding efforts with the aim of developing an adapted indigenous breed of cattle for dairy or dual-purpose production. In addition, the project will identify genotypes for multiplication through AI and multiple ovulation and embryo transfer (MOET) for breed improvement.

Work programme

Once field surveys have established the location and ownership of the most promising cows, on-farm data will be collected on the following: milk yield performance; butterfat and protein content of sampled milk tested over at least one complete lactation; body size estimates, voluntary feed intake, disease tolerance, blood typing and reproductive wastage.

Expected output

The project is expected to have the following benefits.

- Promote the utilisation of indigenous and environmentally adapted cattle breeds in order to improve the sustainability and supply of animal protein for human nutrition.
- Reduce dependence on imported milk/milk products.
- Match cattle breed resources to available feed and management resources to maximise productivity and income distribution.
- Gain information on milking potential of indigenous cattle to be used for genetic improvement.
- Initiate the establishment of an elite indigenous cattle breed association through the Elite Cow Directory membership and workshop training.
- Strengthen animal breeding manpower.

Characterisation of livestock breeds in Botswana

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Introduction

Indigenous livestock breeds in the tropics and subtropics are a valuable source of genetic material because of their adaptation to harsh climatic conditions, their ability to better utilise the limited and poor quality feed resources and their resistance to a range of diseases found in these regions. The fact that these breeds exist in relatively large numbers is also important because it implies that they will form the backbone of breed improvement programmes in these regions. Temperate breeds and their crosses are limited in their ability to survive and produce in tropical/subtropical environments, particularly during stressful periods of drought and disease outbreaks. Thus, emphasis in breeding livestock suited to tropical environments should be placed on the characterisation, conservation and genetic improvement of breeds indigenous to these areas in order to increase their production efficiency.

Evaluation of indigenous and exotic livestock breeds of cattle, sheep and goats and their crosses has been a major aspect of the livestock research programme in Botswana designed to meet the following major objectives:

- Evaluate locally available breeds to determine their potential for meat production with the aim of further improving their genetic potential through selection.
- Evaluate possibilities for utilisation of heterotic effects and their contribution in improving meat production efficiency.

Data on production parameters were collected over a 16-year period in several research stations covering the main ecological regions of the country. Information on reproduction, survival and growth was used to determine breed production characteristics in cattle, sheep and goats.

Beef cattle breed evaluations, 1970-1986

Beef cattle production in Botswana is based on the indigenous Tswana cattle which makes up a large proportion of the cattle population. Four other breeds widely used are the Africander, Bonsmara, Brahman and Tuli. Evaluation of these five breeds in pure or straight breeding systems was necessary in order to establish their potential as dam lines and to determine overall performance for production of slaughter stock (Table 1).

Because of their low reproductive rates, Africander and Brahman cattle had lower productivity values (160 kg and 185 kg, respectively) compared with the Tuli, Bonsmara and Tswana. Breeds with larger mature size, such as the Africander and Brahman, are likely to suffer more setbacks in reproduction when nutrition is limiting, thus canceling the advantages of high growth rates. Therefore, these breeds as pure lines are recommended for use when overall management and range conditions are high enough to allow them to

express their genetic potential. Because of its adaptation and high reproductive performance, the Tuli breed can be used for purebreeding or as a dam line in both communal areas and ranching situations. Although the Tswana cattle have not been improved like the other four breeds, they have shown great genetic potential for beef production as a pure breed. Their adaptation to this environment is their greatest asset.

Table 1. *Performance characteristics of the five pure breeds.*

Breed	Calving (%)	Mortality to 2 years (%)	Birth wt. (kg)	Weaning wt. (kg)	18 mo. wt. (kg)	Cow size (kg)	Wt.18 mo. calf/cow/ year (kg)
Tswana	80	11.8	31	180	294	415	207
Tuli	86	7.6	30	176	285	400	227
Africander	66	13.6	31	175	276	440	160
Bonsmara	84	15.8	31	199	307	445	216
Brahman	72	16.5	28	187	309	446	185

Selection of Tswana cattle for beef production

In view of the suboptimal production environment found in Botswana, the Tswana breed plays a major role in the agricultural sector, particularly in rural areas. Therefore, it is important that these cattle be genetically improved to increase their potential for beef production and thus raise the national herd performance levels.

Objectives

The objectives of the Tswana cattle selection programme are to:

- Increase the total genetic merit of Tswana cattle for beef production through improved reproductive rate, improved growth rate, improved maternal performance and improved calf survival.
- Increase rural income and the national herd average for traits of economic importance through development and distribution of genetically superior Tswana breeding stock.
- Provide an incentive for beef cattle producers to continuously improve and promote Tswana cattle to make them a more competitive breed in the beef industry.

Assembling the foundation herd

The base population was assembled using the different strains of Tswana cattle purchased from communal area farmers in the major agricultural regions of the country. The aim was to assemble a population with a broad genetic base to provide enough variability for the selection programme. Cows of varying age groups were purchased from Kweneng, Kgalagadi, Southern and Central regions. The regions were chosen because of the large numbers of Tswana cattle that are still present there. Due to some operational limitations, no animals were obtained from the Ngamiland region although a large number of what is believed to be a different strain of Tswana cattle is present there.

Planned selection criteria

A selection population of 600 breeding females and 20 males will be maintained per generation in two selection lines of 300 cows and 10 sires each. In Line 1 (Dikgatlhong), selection will be for weaning weight (adjusted to 210 $\pm$ 14 days). The aim is to improve maternal performance of the Tswana cow for increased pre-weaning growth. Line 2 (Morapedi) will be selected for 18 month weight adjusted to 540 $\pm$ 14 days. To improve reproductive performance in the two lines, all heifers which do not conceive at first breeding and cows which do not conceive for the second time will be culled. Selection in

both lines will be based on performance achieved under range conditions since the improved population will be expected to perform in similar conditions in communal areas.

Due to the low numbers of cattle available for the programme, there will not be any unselected control lines maintained. However, generation coefficients will be computed for each animal following the method used by Koch et al (1974). Intra-year regressions of offspring phenotype on offspring generation coefficients will then be used to estimate genetic progress per generation of selection.

Single stage selection will be done in both lines. The top 10% of the male progeny will be selected on their own performance for use as sires of the next generation. Fifty percent of the heifer progeny will be retained in each generation to serve as replacements in the cow breeding herd. The expected selection intensity per line will be approximately 1.78 in males and 0.835 in females, making an average of 1.307 for the two sexes. With the population size of 300 breeding cows and 10 males per line per generation, effective population size and expected increase in homozygosity (rate of inbreeding) are estimated at 39 and 0.012 per generation, respectively.

Management

Management and data collection in both lines will be similar to that of cattle in other APRU ranches except that sires of calves will be identified using chinball markers. Initial matings were started in January 1989, with 200 breeding cows per line. It is expected that the herds will be built up to 300 cows through retention of heifers in the first two calf crops.

Sheep and goat breed evaluations

The small ruminant breed evaluation work was aimed at comparing the production potential of Tswana and Boer goats, Tswana and Dorper sheep and their crosses for meat production.

Goat breed evaluations, 1976–1987

Shown in Table 2 are performance parameters of the two goat breeds and their crosses.

Table 2. *Performance of Tswana and Boer goats and their crosses.*

Breed type	Kidding (%)	Mortality to weaning (%)	Mortality to 18 mo. (%)	Birth wt. (kg)	Weaning wt. (kg)	18 months wt. (kg)
Tswana	121	9	30	2.8	13.4	34.5
Boer	127	25	46	3.2	14.9	36.5
Boer/Tswana	–	11	29	3.0	14.4	36.1

Weight of 18 month old goats produced per doe per year calculated from the figures in Table 2 was highest for the Tswana breed at 29.3 kg versus 24.5 kg for the Boer goat. This superiority mainly resulted from better survival rates for Tswana goats. Mortality in young stock was a major factor limiting productivity in both Tswana and Boer goats. On the western side of the country where tick infestations are low and the incidence of heartwater negligible, Boer goats and their crosses may be used with less reduced mortality due to heartwater.

Sheep breed evaluations, 1976–1987

High mortality experienced in the Dorper sheep offset the advantages due to the high growth rate of the breed. Weight of 18 month old lambs produced per ewe per year calculated from figures in Table 3 was highest for the Tswana at 12.0 kg compared to 10.3 kg for Dorper sheep. Results indicate that in the eastern side of the country where parasite infestations and disease incidence are high, sheep production could concentrate on the use of the adapted Tswana breed.

Table 3. *Performance of Tswana, Dorper sheep and their crosses.*

Breed type	Lambing (%)	Mortality to weaning (%)	Mortality to 18 mo. (%)	Birth wt. (kg)	Weaning wt. (kg)	18 month wt. (kg)
Tswana	86	11	30.2	3.2	17.1	34.1
Dorper	74	39	64	3.9	20.7	38.2
Dorper/Tswana	–	8	25.0	3.9	19.6	38.2

Selection of Tswana sheep and goats for meat production

Results obtained from the breed evaluation programme indicated the need to develop local breed types to improve their meat production efficiency through selection. Two selection projects were set up with the following objectives:

- To improve the local breeds of sheep and goats for meat production through increased pre- and post-weaning growth rates; increased reproductive rate; increased kid and lamb survival.
- To conserve local breeds that are most adapted to Botswana's production environment and yet may be at risk of being crossed out due to the widespread use of imported breeds.

Assembling the selection flocks

The flocks of purebred Tswana sheep and goats originally used in the breed evaluation programme were retained for this programme. Since available numbers were not large enough to be used in a selection programme, more animals were purchased from farmers in the communal areas to make up the numbers required. A total of 130 sheep and 150 goats were purchased to supplement flocks already in the ranches.

Selection procedures

Flocks of 300 breeding females each have been established at Sunnyside (goats), Morale (sheep) and Goodhope (sheep). Line 1 of sheep (Goodhope), will be selected for increased reproduction (fertility and litter size) and weaning weight to improve maternal performance. In this line, animals will be selected on their own records for weight at weaning and on the dam's record (covariance of parent and progeny 0.5) for litter size. These selection criteria will aim at improving the dam's potential for twinning and her ability to rear and wean the twin lambs. A selection index with equal weighting for both traits will be used to compute the aggregate breeding value of the progeny lambs. Only 10% of the top male progeny will be selected as sires of the next generation. With the female progeny, the top 40% will be used as replacements in the ewe breeding flock. The index used will be:

$$EBV = b_1 (LR_E - LR_P) + b_2 (WW_I - WW_P)$$

where LR = lambing rate
WW = weaning weight

E = ewe
P = population
I = individual
b_1 and b_2 = weightings used for all animals

Line 2 of sheep (Morale), will be selected for yearling weight to improve growth rate. Animals will be selected on their own performance at yearling age. The top 10% of the male lambs will be used as sires of the next generation and 50% of the female lambs will be used as replacements in the ewe breeding flock. Ewes not producing a lamb at the first breeding will be culled in both flocks. In the goat selection flock (Sunnyside), procedures will be as outlined above for Line 2 of sheep. However, in addition to increased reproduction, does failing to produce or to rear and wean a kid twice will be culled. All lines will be closed to outside introductions.

Data on growth, reproduction and survival will be routinely collected on all traits as is presently done in other APRU flocks. All lines will be evaluated after five generations of selection to determine whether any genetic progress has been made. Because of low numbers available for the selection programmes, unselected control lines will not be maintained. Thus, like for the Tswana cattle selection programme, genetic progress will be estimated according to Koch et al (1974).

Reference

Koch R M, Gregory K E and Cundiff L V. 1974. Selection in beef cattle. II. Selection response. *Journal of Animal Science* 39(3):459-470.

The Swaziland national beef cattle breeding programme

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Introduction

Swaziland has a national beef cattle breeding programme which was initiated in 1975 with a total of five government-owned cattle breeding stations. The stations are responsible for the production of superior breeding bulls for distribution to farmers and the provision of research information. There is also a Data Processing Unit (DPU) which was established for centralised record-keeping and analysis of data from the beef improvement programme. This unit is located at the Ministry of Agriculture and Cooperatives, headquartered in Mbabane.

Objectives

The objectives of the breeding programme are to:

- Provide superior performance-tested bulls of the Nguni, Brahman and Simmental breeds for distribution to group ranches and individual farmers throughout the country.
- Investigate the potential role of the recommended breeds for improvement of beef production.
- Evaluate the suitability of the various breed groups to the country's different ecological zones.
- Improve the indigenous Nguni through selection.

The breeding programme

The breeding programme was planned to cover the evaluation of three main breeds, Nguni, Brahman and Simmental, through performance testing to determine their potential and the exploitation of heterosis through crossbreeding. The Nguni is an indigenous Sanga type breed on which beef production in Swaziland is mostly based. The Brahman and Simmental are exotic breeds used for crossbreeding with Nguni. There is also a small Drakensberger herd which has been included in the programme for evaluation. It is an indicus-type beef breed which is indigenous to South Africa.

The five government breeding stations involved in the programme are Mpisi, Big Bend, Mahlangatsha, Balekane and Nsalitshe. The first three stations maintain straightbred Nguni herds and at least one Brahman and/or Simmental straightbred herd. They also carry out crossbreeding evaluations and are involved in the upgrading programme. Balekane breeding station is only involved in the upgrading of Brahmans.

Nsalitshe breeding station was established specifically for Nguni cattle breeding in order to facilitate research on the indigenous breed. The aim is to evaluate, improve and

conserve Nguni cattle. The breeding programme adopted for Nsalitshe is linebreeding. There will be at least six breeding lines with a herd of 300 breeding females. Rotational mating among the lines will be practised to limit inbreeding and to maintain a wide genetic base.

Animal management

Husbandry and management procedures employed on all breeding stations have been standardised in order to minimise environmental differences between stations and also between herds within stations. Cattle management is extensive at all ranches. Animals are raised almost entirely on range pastures. Some limited supplementary feeding of weaners and/or cows is occasionally used during dry years.

Calves are weaned at 210 $\pm$ 15 days. There is no milking of cows. All young stock of similar age and sex are run together irrespective of breed. Males are left entire until the completion of the growth performance test at 18 months of age.

Breeding cows of all genotypes and ages are kept in one group except during the 90 day service period. There is only one breeding season. Mating is by natural service. Heifers join the breeding herds after completing performance testing at the age of 18 months. Maiden heifer matings normally commence two weeks earlier. Cows which fail to conceive in two consecutive breeding seasons are usually culled.

Within each station, all cattle are weighed at similar times and/or dates each month. Cattle are kraaled the night before weighing. A newborn calf and its dam are normally weighed within 24 hours.

All cattle are vaccinated against diseases and treated for both internal and external parasites.

Data collected

The DPU uses a computerised system to assemble, validate, analyse and store data collected from the participating breeding stations. The following records are collected:

Calf birth records:	Completed immediately after birth for both live calves and still births. Submitted to DPU weekly.
Weight records:	All animals at each station are weighed monthly.
Mortality records:	Submitted weekly.
Abortions, treatments and removals:	Submitted weekly.

At the DPU, the data submitted by the breeding stations are processed and record files for calves, cows, bulls and mortality are produced. A calf record file consists of the history of each calf from birth to 18 months of age and includes station, calf identification, date of birth, sex, breed, pedigree, birth weight, weaning weight and weight at 18 months. A cow file has station, cow identification, date of birth, breed, pedigree and the complete calving history, including the weaning weights of all its calves. Mortality files have all the animal's basic information as well as date and cause of death.

In 1990, a comparative evaluation of the performance of breeds and crossbred cattle involved in the breeding programme was carried out at ILCA using data collected from Mpisi, Big Bend and Mahlangatsha breeding stations. Results of the study indicated that in general, straightbred Ngunis had the shortest calving interval, intermediate age at first calving, poor calf growth performance but good calf survival. Simmental genotypes were generally associated with older age at first calving, longer-than-average calving intervals,

poor calf survival but good calf growth performance. Drakensberger genotypes were best in terms of age at first calving. However, the growth performance of their calves was poor, calf survival intermediate and they had the longest calving interval. Brahman tended to be average in most of the traits but had poor calf survival.

Range performance testing of Malawi Zebu cattle: A summary

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Introduction

Problems associated with Malawi Zebu cattle for beef production in rural areas include inadequate numbers of high quality breeding males and females, uncontrolled mating leading to inbreeding, small body size associated with slow growth rates in an environment where feed resources are limited during most of the hot dry summer periods, decreased disease resistance and tolerance due to poor nutrition and increased mortalities accruing from these problems.

Objectives

The general objectives of the on-going programme on breed evaluation are to characterise the productivity of Malawi Zebu on-station and on-farm and to identify major constraints to increased production. Specific objectives are to select bulls (and cows) for sale to farmers based on their performance on the range in terms of growth and fertility; conduct progeny testing on-station and on-farm to identify superior bulls for subsequent use in AI schemes; and to form elite herds of Malawi Zebu from the available genetic resource of the breed.

Methodology

Malawi has six variable but small ecological zones: the lower shire, shire highlands, lakeshore areas, medium plateau areas, high plateau areas and plain areas. While evaluation of breeds in all of these zones might have been the most appropriate course of action, due to the small size of the zones, evaluation of cattle is done on regional (the country is divided into three administrative regions) and national levels. The initial animals in the study were obtained from all over the country and brought to one station. Evaluation/characterisation was done for the entire national sample—a sample which was later reallocated to two research stations, one in each of two regions. Additional animals were bought from surrounding villages.

Animals are regionally evaluated based on their individual performance in relation to their contemporary group—i.e. animals of the same age group or born within the same calving season are evaluated based on group performance. Feeding is usually divided into age groups. For example, if animals are weaners or cows/bulls, they are grazed separately as a group.

Herd management

Nutrition

Animals are grazed on average for eight hours daily on natural and established pastures (rhodes grass, *Chloris gayana)*. Supplementation with maize bran (9.3% CP; ME 4.0 kcal/g) is given only to sick or weak animals.

Disease control

Deworming is done for all cattle at the end of the rains and for weaners at the beginning of the rains. Adults are only dewormed once because of insufficient drugs. Animals are sprayed with supona 30 dip (organophosphate) once a week. Berenil and trypsin are occasionally utilised on cattle showing signs of trypanosomiasis and East Coast fever.

Breeding

Heifers are bred based on weight (mean 192.56± 44.38 kg) and conformation at about the age of 2–2 1/2 years. All females are bred in groups of not more than 35 per bull for three months.

Data collected

Data collected for males are scale weights from birth to three years which are adjusted for specific ages; weigh-band measurements alongside scale weights are collected for correlation analysis; scrotal circumference and semen are scored and evaluated to quantify their relationship and bull fertility. Condition-scoring is done to highlight changes at different times of the year. Semen is collected using an electro-ejaculator at least twice during a six month period. Cows are evaluated based on calf birth and weaning weights. Few data have been collected from on-farm studies because the work has just been initiated. Measurements on station cattle are done every month; on-farm data is collected when site visits are made by researchers—usually at least once every three months. Dip tanks are visited every month by veterinary assistants.

Progress made

To date, summaries of productivity of the Malawi Zebu during the initial evaluation have shown some major differences among animals from different regions. As well, characterisation has been done on growth and other reproductive characteristics of cattle at Mbawa Research Station (the plains area in the north) and Salima Research Station (the lakeshore area in the central part of the country). Elite herds of Malawi Zebu have been formed on-station and some bulls, selected for their performance on the range, have been sold to farmers.

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