

Characteristics of Munjal sheep

B.P. Kushwaha, Riyazuddin, R. N. Singh & S. Parthasarathy

Central Sheep and Wool Research Institute, Avikanagar Rajasthan, 304 501, India

Summary

Munjal is a mutton-type sheep found in some districts of the Haryana, Punjab and Rajasthan states. A sample survey was conducted in two districts of Rajasthan and one district of Punjab to record characteristics of Munjal sheep. Information was recorded on morphological characteristics, body measurements and body weight. Munjal sheep are quite big in size, tall, rectangular and massive with a dark brown face. Measurements were recorded of body length, height, heart girth, paunch girth, ear length and tail length. Adult body weights were also recorded. Wool samples were collected and analysed for their quality attributes. Wool from this breed is very coarse and hairy.

Résumé

La race Munjal est un type de mouton qui se trouve dans certains départements des états de Haryana, Punjab et Rajasthan. Une enquête sur échantillon a été conduite dans deux départements du Rajasthan et dans un du Punjab dans le but d'enregistrer les caractéristiques du mouton Munjal. On a noté les caractéristiques morphologiques, les mesures et le poids corporel. Le Munjal est un animal de grande taille, d'apparence rectangulaire et massif avec une tête de couleur brun foncé. Les mesures sur la longueur du corps, la hauteur, les circonférences du torax, la longueur des oreilles et de la queue ont été enregistrés, ainsi que le poids corporel adulte. On a ramassé des échantillons de laine qui ont été analysés pour évaluer leur qualité. La laine de cet animal est grossière et velue.

Key words: Munjal, Body weight, Wool quality, Punjab.

Introduction

The origins of Munjal sheep are not known exactly but it is supposed to have originated in India through the sheep breeders of Rajasthan, Punjab and Haryana breeding Nali with Lohi sheep (Basuthakur, 1988; Mason, 1988). The Munjal, a mutton-type sheep, is found in the Hissar, Ambala, Patiala, Karnal, Ganganagar and Bhatinda districts of the mentioned states. They are popular among the farmers for their heavy body weight. Farmers generally sell their surplus male lambs at the age of 8-10 months when weight is reported to be around 35 kg. Wool from this breed is very coarse and hairy. Traditional shepherds and landless farmers normally rear this type of sheep, which graze mostly in the outskirts of the villages, on stubble from the harvested crops, on canal banks and by the roadside. Information on population and distribution has not yet been documented and similarly, literature on Munjal sheep is scarce.

Materials and Methods

A sample survey was conducted on 76 farmers/sheep flocks of 24 villages representing five departments (tahsils) in two districts (Ganganagar and Hanumangarh) of Rajasthan and one district (Muktshar) of Punjab. In Rajasthan, a total of 66 farmers was surveyed, only 28 of whom kept Munjal sheep (mostly breeding rams) in their flocks. In the Muktshar district of Punjab all 10 farmers surveyed had Munjal sheep in



Figure 1. Munjal ram.

their flock with an average of 72 sheep per flock. Information related to morphological characters, body measurements and body weight was thus recorded from only 38 flocks, taking one or two animals from each flock. Wool samples were also collected and analysed for their quality attributes.

Results and Discussion

Morphological characters and body measurements

The animals of this breed are quite big in size, tall, rectangular and massive. They have a long head with a roman nose and narrow



Figure 2. Munjal ewe.

forehead. The face is generally tan or brown in colour which may extend up to the middle of the neck. Ears are long and leaf-like, hanging down beside the flat cheeks. Body fleece is generally white with a skin colour varying from pink to light blue. Legs are long and strong with brown to dark hooves. The tail is long. The udder is medium sized and well developed with medium sized teats. Both sexes are polled. The face is clear of wool and legs and belly are generally bare. Photographs of the animals of this breed taken during the survey are presented in figures 1, 2, 3 and 4.

Body measurements were recorded on 21 males and 49 females. Since most of the farmers keep only 1 or 2 rams in their flock

and rest of the males are disposed of at marketable age (8-10 months), males measured were mostly breeding rams.

Length, height, heart girth, paunch girth, ear length and tail length averaged 82.76 ± 1.07 , 78.71 ± 1.01 , 97.57 ± 1.51 , 99.47 ± 2.05 , 18.14 ± 0.64 and 44.85 ± 1.82 cm, respectively in males and 74.55 ± 0.83 , 68.73 ± 0.59 , 85.24 ± 0.72 , 89.20 ± 1.27 , 17.14 ± 0.44 and 39.13 ± 0.86 cm, respectively in females.

Body weight

Body weights were recorded on 15 males and 32 females. Adult body weight in males ranged from 50 to 83 kg with an average of 65.93 ± 2.43 kg. In females it ranged from 35 to 55 kg with an average of 45.37 ± 0.99 kg.

Table 1. Wool quality parameters

Diameter (μ)	Hetero (%)	Hairy (%)	Medullation (%)	Staple length (cm)	Crimp (per cm)	Tenacity (g/tax)	Extension (%)
51.18 ± 0.97 (90)	11.71 ± 0.859 (90)	52.65 ± 1.414 (90)	64.37 ± 1.414 (90)	9.05 ± 0.534 (90)	0.47 ± 0.795 (89)	4.68 ± 0.707 (82)	13.97 ± 1.149 (81)

The number of observations are between parenthesis.



Figure 3. Munjal lamb.



Figure 4. Munjal flock grazing at a roadside in Punjab.

Generally farmers sell their surplus ram lambs to the local butchers at the age of 8 to 10 months of age, body weight at this age varies from 30 to 40 kg.

Wool yield and quality

Flock owners were interviewed to collect information on wool production. Wool is coarse and hairy and is around 1.5 kg per shearing with two shearings a year in March/April and Sept./October. Wool samples were collected on 90 animals and were analysed for their quality attributes. Results are presented in table 1. The average fibre diameter, medullation and staple length of six-monthly growth were $51.18 \pm 0.97 \mu$, $64.37 \pm 1.41 \%$ and 9.05 ± 0.53 cm, respectively. Similar staple length was also reported by Basuthakur (1988). The diameter is very high, indicating that these fibres may produce only very coarse yarn. Medullation being very large it may be very difficult to produce even coarse yarn. However, these wools can be

blended with finer wools to improve the quality of the blends. Such blends will be useful for manufacturing carpet, dhurries, coarse blankets etc. The staple length is quite satisfactory or even better because of coarseness. Tenacity and extension are low because most fibres are of a hairy type. This was also observed when the fibres were combed to parallel them and weigh the fractured fibres after testing for tenacity fibres which were loosely packed or single rather than being a small cohesive mass. Crimps are low again due to the hairiness of the wool samples.

Reproduction and breeding

It is customary among the farmers to keep breeding rams in the flock all times. Rams are given utmost care and are supplemented with concentrate throughout the year. In the farmer's flock, age at first mating is reported to be around 12 to 15 months in females. Males are generally used for breeding at around 18 months of age. Ewes normally have single births and twinning is rare (about 5%). Basuthakur (1988) reported that the animals of this breed can start breeding quite

early in life and are known for good rate of fertility and milk yield. Ewes are generally not milked.

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Conservation of livestock breed diversity

J.S.F. Barker

*Department of Animal Science, University of New
England, Armidale, NSW 2351, Australia*

Summary

Mankind uses some 40 species of animals as domestic livestock to meet our needs for food, clothing, power, etc. Within these species, there are in total some 4,500 breeds that are referred to as the global animal genetic resources. Each breed comprises a unique set of genes. More than 30% of breeds are estimated to be at risk of extinction, and many more, particularly in developing countries, are threatened by inefficient utilization. The Food and Agriculture Organization of the United Nations has been mandated by its member nations to manage the global animal genetic resources, and major progress has been made in the last few years. However, resources are limited, and priorities will have to be set for breed conservation, for breed development programmes and for evaluation studies. Breeds that are taxonomically distinct should be favoured for conservation, the objective being to maintain maximum genetic diversity of each livestock species. Genetic distances and phylogenetic diversity provide the best available objective criterion, and microsatellites are the current markers of choice for obtaining the genetic data. Microsatellite-based genetic distances will describe breed similarities due to common ancestry, but cannot account for consequences of artificial or natural selection. Phylogenetic trees for 11 water buffalo populations in southeast Asia, constructed using 25 polymorphic protein coding loci or 21 microsatellite loci, show differences in both topology and branch lengths, but the microsatellite tree is a better representation of the similarities due to common ancestry. Thus

phylogenetic diversity, based on microsatellite loci, should be used as an initial guide in making conservation decisions for livestock breeds.

Resumen

El Hombre utiliza unas 40 especies animales como ganado doméstico para satisfacer sus necesidades de alimentación, ropa, tracción, etc. Dentro de estas especies, existe un total de 4 500 razas conocidas como recursos genéticos animales globales. Cada raza comprende un grupo único de genes. Se estima que más del 30% de las razas están en peligro de extinción y muchas más, sobre todo en los países en vías de desarrollo, están amenazadas por una utilización ineficaz. La Organización para la Alimentación y la Agricultura de las Naciones Unidas ha sido encomendada por sus naciones miembros de gestionar los recursos genéticos animales globales. Se han hecho grandes progresos en este sentido en los últimos años, sin embargo, los recursos son limitados, y será necesario establecer prioridades para la conservación de razas, para programas de desarrollo de razas y para estudios de evaluación. Las razas taxonómicamente diferentes deberían ser favorecidas para la conservación, ya que el objetivo es de mantener la máxima diversidad genética de cada especie ganadera. Las distancias genéticas y la diversidad filogenética proporcionan el mejor criterio objetivo disponible y los microsatélites son actualmente los marcadores elegidos para obtener los datos genéticos. Las distancias genéticas basadas en microsatélites describirán las similitudes entre razas debido a sus antecedentes comunes pero no podrán

explicar las consecuencias de la selección artificial ni natural. Árboles filogenéticos para 11 poblaciones de búfalos de agua en el sudeste de Asia, elaborados utilizando 25 loci polimórficos codificadores de proteína o 21 loci de microsatélites, muestran diferencias tanto en topología como longitudes de ramas, pero el árbol de microsatélites es una mejor representación de las similitudes debidas a antecesores comunes. Por consiguiente, la diversidad filogenética, basada en loci de microsatélites, debería utilizarse como una guía inicial para tomar decisiones sobre la conservación de razas ganaderas.

Key words: Conservation priorities, Biodiversity measurement, Microsatellite, Phylogenesis.

Introduction

The total global biodiversity most likely includes tens of millions of species. Of this vast number, one species - our own, uses some 40 other animal species to meet our demands for food (meat, milk, eggs), clothing (wool and other fibres, skins), draft power and manure, to serve as a "bank" or hedge against hard times, and to satisfy various cultural, religious and recreational purposes. For these domestic livestock species, conservation at the species level (in the sense of preventing their loss) clearly is not an issue; what is of concern is conservation of diversity within each species.

The diversity within domestic livestock species is perceived generally in terms of differences among sub-groups that are referred to as breeds, where "breed" has been defined (Turton, 1974) as "a homogeneous, sub-specific group of domestic livestock with definable and identifiable external characters that enable it to be separated by visual appraisal from other similarly defined groups within the same species, or a homogeneous group where geographical separation from phenotypically similar groups has led to general acceptance of its separate identity". While generally appropriate, breeds often are not distinguished in the developing world. Local populations may have different names,

but without change in phenotype; a change in phenotype may occur without change in name; or all populations may have just one name and be phenotypically similar. In the broad context of global animal genetic resources, the term "breed" is used to include strains and populations, the members of which are distinguished from other such groups in local, national or regional usage. That is, a breed is a cultural entity, recognized as such by the community where it is found.

Animal Breeding and Conservation - A Conflict?

The aim of animal breeding is to change the genetic makeup of domestic animals so that they better meet our needs. Such improvement in production, product quality or the efficiency of production is sought by either or both of selection within breeds or use of differences among breeds through cross-breeding, grading-up to a superior breed by repeated back-crossing, or formation of a synthetic population. Thus future improvement is dependent on genetic variation - both the variation within breeds, and the variation between breeds, and loss of variation will restrict the options available to meet unpredictable future requirements.

Loss of variation within breeds is continually countered by the introduction of new variation through mutation (Franklin, 1981; Hill and Keightley, 1988), but the variation among breeds cannot be readily regenerated. Each breed is the product of mutation and genetic drift, as well as separate adaptation and evolution, with differing selection pressures imposed by climate, endemic parasites and diseases, available nutrition and criteria imposed by man. Each breed thus comprises a unique set of genes.

Yet many breeds have become extinct, and many more are at risk. The global animal genetic resources almost certainly comprise some 4 500 breeds, although the true number is not known. For seven mammalian species (ass, buffalo, cattle, goat, horse, pig and sheep), FAO (1995) lists 2 944 breeds as

Table 1. Numbers of breeds of each of seven major species of domestic livestock that are recorded in the FAO Global Databank for Animal Genetic Resources, and the numbers estimated to be at risk.

Species	Numbers of breeds			Per cent at risk
	Recorded	With population size data	At risk*	
Ass	77	24	9	37.5
Buffalo	72	55	2	3.6
Cattle	787	582	135	23.2
Goat	351	267	44	16.5
Horse	384	277	120	43.3
Pig	353	265	69	26.0
Sheep	920	656	119	18.1
Total	2 944	2 126	498	23.4

*Estimated from breeds with available population data

recorded in the FAO Global Databank for Animal Genetic Resources, of which 498 are considered to be at risk (Table 1). Extinctions of past breeds and this potential loss of more breeds is due to the demand for increased animal production, with economic pressures (primarily in developed countries) and political and social pressures (primarily in socialized economies and less-developed countries) causing some breeds to be considered unsuitable for today's needs or those of the immediately perceived future. Yet some of these breeds, and particularly those that have evolved in and become adapted to stressful environments, are likely to carry valuable genes and gene combinations controlling specific behavioural, physiological, and disease and parasite resistance traits. The genotypes of some of these breeds could be crucial to the development of sustainable animal production systems in the future.

Thus there is an apparent conflict, which will be countered only by active and effective management of all animal genetic resources.

Conservation History

The realization of the need for conservation of animal genetic resources is not new, and in fact has been on the international agenda for some 50 years (Barker, 1994). Translation of this realization into action has been slow, although there have been notable achievements and recent developments are encouraging. In the developed world, organizations such as the Rare Breed Survival Trust in the UK, Safeguard for Agricultural Varieties in Europe, and the American Livestock Breeds Conservancy in the USA have instituted effective programmes (see Alderson, 1990) for the conservation of rare and endangered breeds.

However, no such organizations and programmes exist, or are likely to be developed in the near future, in the developing world. In any case, the problems there are rather different. Many breeds are endangered, but others that are not numerically small and that are being used for production, are threatened - primarily by being cross-bred with imported breeds that are perceived (often wrongly) to be superior. But these native breeds are likely to be

well-adapted to the traditional husbandry systems. Thus primary emphasis needs to be given to more effective use and genetic improvement of these breeds within the prevailing and generally sustainable production systems.

FAO has for some 25 years taken a major role in promoting awareness of the significance to mankind of the global animal genetic resources (e.g. FAO, 1984, 1992). There is now a clear recognition (FAO, 1993) that "in the global management of animal genetic resources, the fundamental distinction is **not** between those breeds that are endangered and those that are not, but between those that are perceived to have little or no current utility and those which do have current utility or seem likely to have in the immediate future. For each of these latter categories, the necessary actions are then **preservation** (as live animals or frozen storage of embryos or semen) or **utilization** (including development of breeding programmes for genetic improvement)." Given this recognition, the apparent conflict between animal breeding and conservation is resolved; successful management of animal genetic resources must incorporate both utilization and conservation.

In November 1995, the FAO Conference of member governments made two major decisions in relation to animal genetic resources: (i) it provided an intergovernmental mechanism for animal genetic resources by broadening FAO's long-established Commission on Plant Genetic Resources to a Commission on Genetic Resources for Food and Agriculture, and (ii) it supported as a priority activity for FAO a Global Strategy for the Management of Farm Animal Genetic Resources. Most importantly, the Global Strategy is being designed to harmonize fully with the UN Convention on Biological Diversity, the international law which is now ratified for use by more than 170 countries. FAO is funding the essential core activities of the Strategy (coordinating and facilitating regional and national programmes, maintaining the Global Databank and early warning system,

developing technical guidelines for use by countries in establishing cost-effective action and reporting on all activities), although very substantial funding from sources external to FAO will be required for full implementation of all aspects. Nevertheless, with the direct involvement of individual countries, other international agencies, including the International Agricultural Research Centres, and non-governmental organizations including farmer associations, implementation of the Strategy has been initiated. Its success will be vital to the future of livestock breed diversity.

Defining the Problem

Ideally, consideration of the conservation of animal genetic resources would start with complete information on all existing breeds - numbers, distribution and population structure, trends in numbers (increasing, stable or decreasing), productive performance and adaptive characters. That ideal is not even within reach - the best information available is that there are some 4 500 breeds, of which some 30% are estimated to be at risk of loss (FAO, 1995). For most breeds, even basic data on population numbers and trends are not available. Of the 2 944 breeds of seven mammalian species that are listed in the FAO Global Databank, 818 (28%) do not have any population data. This proportion of 28% is certainly an underestimate of the global situation, as breeds not yet listed are primarily from developing countries where census data is less likely to be available (FAO, 1995).

Clearly the first problem is lack of information, so the identification and characterization of all breeds of livestock has high priority in the FAO global strategy, and must also have high priority for all national livestock development programmes (Barker, 1992). Once available, this documentation of existing resources would identify those breeds at risk of extinction. However, census data alone will not provide a basis for the rational choice of breeds for development programmes. Identification at the global level

Table 2. *F*-statistics for swamp and river buffalo estimated using 25 polymorphic protein coding loci and 21 microsatellite loci.

	F_{IS}	F_{ST}	F_{IT}
<u>Protein Coding</u>			
Swamp	-.004(.062)	.182(.041)	.181(.083)
River	-.068(.048)	.108(.036)	.048(.059)
<u>Microsatellites</u>			
Swamp	.047(.027)	.168(.018)	.207(.034)
River	.031(.028)	.038(.008)	.068(.029)

Table 3. Correlation coefficients among genetic distances estimated from data on 21 microsatellite loci or 25 protein coding loci.

	Microsatellites			Protein Coding		
	Nei D	D_A	Delta mu	Reynolds	Nei D	D_A
Reynolds	.921	.911	.748	.831	.773	.798
Nei D		.991	.890	.754	.774	.772
D_A			.897	.748	.771	.783
Delta mu				.738	.797	.772
Reynolds					.929	.965
Nei D						.937

All significant, $P < 0.001$

of priority breeds for immediate development was one of the major questions addressed by an FAO Expert Consultation (FAO, 1992). The criteria for choice of such breeds were specified as:

1. the breed possesses one or more highly desirable attributes in terms of productivity and/or adaptation,
2. the breed is endangered, or is not being utilized efficiently,
3. the breed should be one whose improvement could have the potential to influence large populations, either of the same breed in one or more countries, or other very similar breed types.

Again, there is an assumption of information being available with regard to "desirable attributes", but for many breeds, particularly in developing regions, this will be true, and pragmatic and subjective decisions will have to be made.

In relation to the total global biodiversity, animal production encompasses a small and finite universe - only some 4 500 breeds across some 40 species, and the total genetic variation within each species. There is a critical need to develop breeding programmes to improve the production and productivity of a selected set of breeds that have major utility now or which seem likely to have in the immediate future. As already noted, selection of these breeds must be somewhat *ad hoc*, and the best choices may not be made. Thus breed evaluation studies are needed to compare performance, and the underlying genetics and biology, so that future choices will be more soundly based. Further, with increasing emphasis on sustainable production systems, on animal welfare and on pollution, future breeding objectives may differ quite dramatically from those now

considered most important. Thus there is the need to prevent loss of breed diversity (i.e. conservation of endangered breeds).

But given all of these needs, the relatively small and finite universe of animal production is simply not manageable. On both country and global scales, financial and other resources are limited; it will not be possible to maintain every breed that is in danger of extinction, nor to develop breeding programmes for all breeds considered suitable for improvement, nor to set up evaluation studies of the many breeds that might contribute to future breeding programmes.

For each of these different aspects of animal genetic resources conservation, priorities will have to be defined in choosing those breeds to be included.

Setting Priorities for Conservation

In the context of setting priorities for conservation, Miller (1977) suggested that the only rational criteria are the likelihood of extinction of a breed and the degree to which it possesses unique genes. Further, he suggested that immunogenetic and other biochemical polymorphism data should provide the basis for determining whether a breed is sufficiently unique (i.e. sufficiently different) from other breeds.

With emphasis on the need for planning of comparative evaluation studies, Barker (1980, 1985) suggested that the genetic relationships among breeds within each species of livestock should be determined, so that the breeds could be grouped into sets that are genetically similar, with one representative from each set then included in an evaluation study.

Both of these suggestions relate to different aspects of what is now broadly interpreted as conservation, and the concepts of genetic uniqueness and genetic relationships have become accepted as the basis for setting priorities for conservation (FAO, 1993; Barker, 1994). Inherent in this is the practical realization that breeds that are taxonomically

distinct should be favoured for conservation, and that the objective is to minimize loss of genetic diversity.

An objective quantification of the magnitude of the genetic differences among a set of breeds can be obtained from allele frequency data for each breed, estimating genetic distances between each pair of breeds, and by constructing from these pair-wise distances a diagram that best represents all relationships among the populations, i.e. a phylogenetic tree. The topology of the tree shows the patterns of relationships, while branch lengths indicate the magnitude of the differences between breeds. The problem then is how to use this information to ensure maintenance of maximum genetic diversity, or realistically to ensure minimum loss of genetic diversity, given economic, social and other constraints. For non-domestic species, the analogous problem of optimizing reserve selection so that the maximum species diversity is preserved has been considered recently by several workers (see Witting and Loeschcke, 1995). Methods based on phylogenetic relationships, on genetic divergence or on both have been developed, and these have been compared by Krajewski (1994). He shows that the different measures of taxonomic diversity agree in identifying the species that contribute the most and the least to overall diversity, but disagree at intermediate levels. Although no consensus has emerged as to the relative merits of these measures, some of the complications in dealing with sets of species that are outlined by Krajewski (1994) are not relevant to the breed conservation issue. Here all breeds in one species is the set to be considered, and the diversity is specified in terms of genetic differences, i.e. allele frequencies translated to genetic distances. Thus a method combining topology and divergence information is likely to be preferred. In addition, as the objective is to minimize loss of genetic diversity in each species, within-breed genetic variation must be considered, perhaps by being incorporated into a diversity measure as suggested by

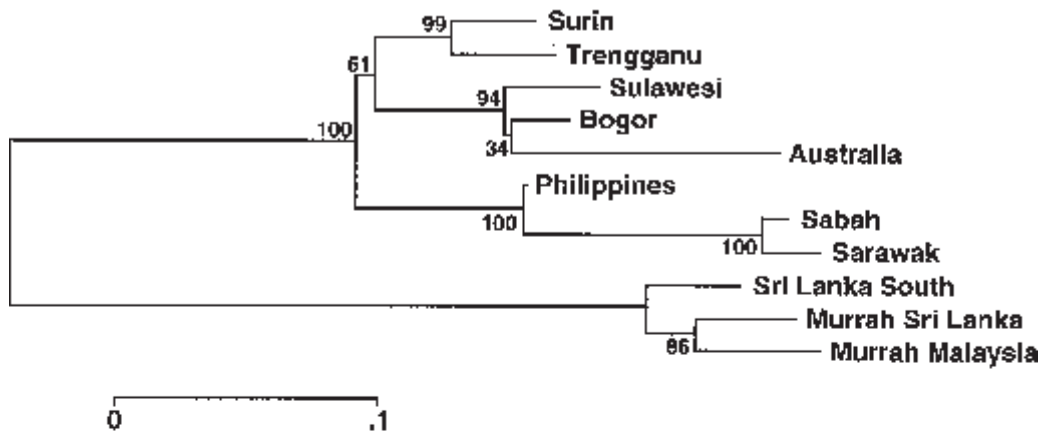
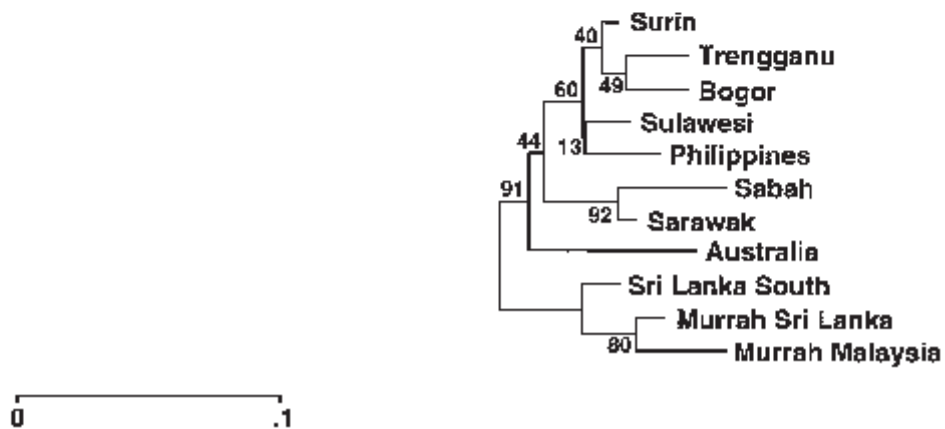
(A) Microsatellites**(B) Protein coding loci**

Figure 1. Neighbour-joining trees constructed using the DA distance measure for (a) microsatellite loci and (b) protein coding loci.

Krajewski (1994). However, even without such incorporation, the breed with highest average heterozygosity should be preferred in choosing among breeds that otherwise have equal priority.

In setting conservation priorities for livestock breeds, genetic distances and phylogenetic diversity will provide the best objective criterion. However, distance measures cannot account for consequences of

artificial selection on morphological or economic traits, nor for natural selection on fitness, and thus will give only the first (albeit essential) guide in making conservation decisions. Where decisions regarding conservation are to be made among a set of rare or endangered breeds, phylogenetic diversity will be the major criterion. In the choice of breeds for development programmes or for comparative evaluation studies, final decisions should also take into account any available data on traits of

economic value, specific adaptive features, presence of unique genes or genotypes, local or regional importance of a breed in production systems, and availability of resources and infrastructure in the region where a breed is located (FAO, 1993).

However, before any priorities can be set, we first need the distance estimates. Some 100 studies of genetic distances among livestock breeds have been made (Barker, 1994), but these are not sufficient to provide a global overview that would be a basis for conservation decisions. Hence FAO, as part of its Strategy for the Management of Farm Animal Genetic Resources, has planned a global research initiative to characterize genetic diversity in each livestock species.

In 1993, an FAO Working Group concluded that a global project for estimating genetic distances among the breeds of each species of domestic livestock was feasible, and the design and procedures were outlined (FAO, 1993). Another FAO Working Group, supported by some 20 international experts, has now developed the details of this global project for the measurement of domestic animal genetic diversity, referred to as the MoDAD project (FAO, 1996). All 4 500 breeds clearly cannot be included, and a two-phase strategy is proposed, with appropriate selection of breeds in phase 1 to evaluate the range of diversity within each species. Phase 2 for each species would depend on results obtained in phase 1, but could for example, include analyses of additional breeds from regions showing the greatest diversity.

Measuring Diversity

Many phylogenetic studies have used allele frequencies of biochemical polymorphisms (e.g. Nei, 1987 - Table 9.3). However, microsatellite markers are being used increasingly in population and evolutionary genetics (Bruford and Wayne, 1993). They have essentially replaced biochemical polymorphisms as the markers of choice for

such studies, because their higher average per locus heterozygosity and potentially many more loci are expected to provide higher resolution discrimination among closely related populations of a species.

Microsatellites are the markers of choice for gene mapping studies in livestock species, so that many loci will be available for use in phylogenetic studies, and some studies of relationships among livestock breeds already have used microsatellite markers, e.g. cattle - MacHugh *et al.* (1994), sheep - Buchanan *et al.* (1994), pigs - van Zeveren *et al.* (1995) and buffalo - Barker *et al.* (1997b). They are to be used in the FAO MoDAD project.

While microsatellites have apparent advantages as markers for genetic distance studies (Meghen *et al.*, 1994; Hall and Bradley, 1995), our knowledge of their evolution is inadequate to be certain that they are representative of the genome. Most are in non-coding regions, and subject to genetic turnover mechanisms (Amos and Hoelzel, 1992), mutation mechanisms are not clear and may differ for different types of microsatellites (Estoup *et al.*, 1995), loci with large numbers of alleles may be subject to high mutation rates and show departures from Mendelian segregation, while undetected non-amplifying (null) alleles (Pemberton *et al.*, 1995) would cause errors in allele frequency estimates and hence in estimated genetic distances.

The question then is whether microsatellite markers will give the same phylogeny as a set of real genes. In particular, would they give the same phylogeny as one (impossible to obtain!) based on allele frequencies at the larger set of genes controlling important productive, reproductive and adaptive traits? In fact, they may not, and it should not be expected that they would because two different questions are being addressed. When genetic distances are estimated and used to construct a phylogeny of breed relationships, the aim is to describe similarities that are due to common ancestry. Thus the markers used should be selectively neutral. In contrast, the genes controlling traits of interest to animal

breeders will not be selectively neutral, and breeds may be genetically similar at these loci because of convergence due to similar selection pressures, or dissimilar because of differential selection. As emphasized earlier, distance measures describing similarities due to common ancestry should be used only as an initial criterion in making breed conservation decisions.

An Example

Nevertheless, it is of interest to determine if microsatellite markers will give the same phylogeny as a set of real genes. A possible approach to this is to compare phylogenies based on biochemical and microsatellite markers, as has been done for water buffalo populations in southeast Asia (Barker *et al.*, 1997a,b). Seventeen populations (12 swamp type, 2 river (Murrah breed) and 3 Lankan buffalo (genetically river type)) were sampled and a total of 801 animals assayed for 53 protein coding loci, 25 of which were polymorphic. A subset of 261 animals from 11 of these populations were genotyped for 21 polymorphic microsatellite loci. Only the results for the 11 populations that were assayed for both protein coding and microsatellite loci will be discussed here, with results based only on the 25 polymorphic loci for the former.

F-statistics estimates (Table 2) show no significant departures from Hardy Weinberg expectation for either buffalo type, whether based on protein coding loci or on microsatellites. All estimates of F_{ST} (population differentiation), however, were significantly greater than zero, and for swamp buffalo (8 populations), estimates from protein coding and microsatellite loci were very similar. For river buffalo, the F_{ST} estimated from protein coding loci was about three times that from microsatellites, but not significantly different.

For both protein coding and microsatellite loci, the standard genetic distance of Nei (1978), the D_A distance of Nei *et al.* (1983) and Reynolds' distance (Reynolds *et al.*, 1983) were estimated, while for

microsatellite loci only, the $(\delta\mu)^2$ distance of Goldstein *et al.* (1995) also was estimated. Correlation coefficients among these measures (Table 3) were all highly significant ($P < 0.001$), although the correlations among measures using microsatellites only or protein coding loci only were higher than those between microsatellites and protein coding loci.

Neighbour-joining trees (Saitou and Nei, 1987), constructed using the D_A distance measure for each of microsatellites and protein coding loci (Figure 1), show differences in both topology and branch lengths. In both trees, some of the nodes are not strongly supported and although the numbers of loci used are not small (21 microsatellite and 25 protein coding), assay of larger numbers of loci could well change the patterns of relationships. Clearly it is not possible to confirm which tree is a better representation of the true genetic relationships among these populations, but the microsatellite tree does accord better with the geography of the populations and the known history of the Australian population, which descends from a small number of animals imported from Timor some 160 years ago. The microsatellite tree is most likely a better representation of the similarities due to common ancestry, while the protein coding loci tree is distorted, reflecting additional effects due to bottlenecks in some populations and selection at some loci.

Thus these results provide empirical support for the view that phylogenetic diversity based on microsatellite loci, as in the proposed FAO MoDAD project, will provide the best objective criterion for making initial conservation decisions for livestock breeds.

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The development of a system of linear measurements to provide an assessment of type and function of beef cattle

G.L.H. Alderson

Rare Breeds International, Avenue Q, N.A.C., Stoneleigh Park, Warks CV8 2LG, UK

Summary

Linear measurements have been used as indicators of weight in cattle. Withers height has been used most commonly, but measurements of White Park cattle show that it is of limited value. This paper explores alternative measurements and indices, not only to provide a superior guide to weight, but also as indicators of type and function of beef cattle. A complex index is recommended for breed characterisation, while hip width or rump length are shown to be the preferred single measurements for evaluation of individual animals or within-herd groups.

Resumen

Las medidas lineales se han usado como indicadores del peso en el vacuno. La alzada a la cruz ha sido la variable utilizada más comunmente, aunque sus valores en la raza White Park Cattle se han mostrado de utilidad limitada. Este artículo explora variables alternativas e índices, no sólo para proveernos de una mejor guía del peso, sino también de un indicador del tipo y de la función del vacuno de carne. Se recomienda un índice complejo para la caracterización racial, mientras que la anchura de la cadera y la longitud de la grupa se muestran como las variables simples más adecuadas para la evaluación de animales individuales o de grupos dentro del rebaño.

Key words: *Body measurement, Linear measurement, Cumulative index, White Park cattle.*

Introduction

Morphological descriptions of beef cattle have been used either to indicate breed origins and relationships through the medium of head measurements (Jewell 1963), or to indicate size and weight through measurement of height at withers. EAAP and FAO used withers height as a prime indicator of type (Simon and Buchenauer 1993). More recently rump height has been preferred to withers height, especially for describing cattle in beef show classes. In addition, girth circumference has been used as a basis for the calculation of weight. Since 1994, a group within the International Committee for Animal Recording has been established to study conformation recording, but its work has been directed mainly at dairy cattle (Stoll *et al.*, 1996).

Height, at either withers or rump, has limited value as an indicator of weight, and it was evaluated as a preliminary exercise in this study. Similarly, the accuracy of girth as an indicator of weight is low, and Schwabe used a more complex formula involving girth, height and body length measurements (Schwabe and Hall 1989). The limited value of both height and girth as single measurements, and the lack of a tested empirical alternative, has restricted the ability of breeders to assess type in beef cattle and their value as potential breeding stock, and has limited the opportunity to provide potential purchasers with a reliable evaluation of animals. This paper is concerned with measurements associated with production characteristics. The development of a new system has been explored to enable earlier assessment of breeding animals and, by

establishing a standard format, to enable comparison of individual animals against a breed standard. The study determined the value of each measurement, and devised indices of type and function.

Method

Eight separate measurements were used for females, and nine for males. The common measurements were:

Height at withers, height at rump (tuber coxae), body length (withers to pins), length from withers to hips (tuber coxae), rump length from hips (tuber coxae) to pins (tuber ischii), width of hips (tuber coxae), width of pins (tuber ischii), width of chest (widest point of shoulders) and depth of chest (thorax) immediately behind forelegs.

The extra measurement for bulls was scrotal circumference.

The equipment was a measuring stick (as used for horses) to measure withers height, rump height, body length and length from withers to hip; a measuring stick modified with sliding caliper to measure hip width, pin width, chest width, chest depth and rump length; and an adapted metal tape to measure scrotal circumference.

The measurements were taken by the same fieldsman using a standard form; a separate form was prepared for each animal. The measurements from the standard form were transferred to a master sheet which calculated the appropriate indices for each animal and the mean, SD and coefficient of variation for the group of animals included in the study. Two measurements were not used in subsequent analyses. Length from withers to hip was intended initially as a check on body length and rump length measurements, but it proved unreliable. Width of pins was measured on the points of the bone rather than the outer dimension, and again this proved unreliable.

The calculated indices were: weight, height slope, length index (2 indices), rump length index, balance, width slope, depth index, foreleg length and cumulative index (3 indices). In all cases the results for individual animals were indexed against the average for the group. The calculations are reported in table 1.

The system was tested on White Park cattle in the United Kingdom in 1994-5, and was repeated in 1997. Both sexes were included, comprising 315 cow records and 29 bull records. Some animals were included in both phases of the study. The ages of the females ranged from 15 months to 201

Table 1. Results of the calculations for individual animals indexed against the average for the group.

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- Weight: $\text{Body length} \times \text{girth depth} \times [(\text{hip width} + \text{chest width})/2]/1050$
 - Height slope: $\text{rump height} - \text{withers height}$
 - Length index ⁽¹⁾: $\text{body length}/\text{chest (thorax) depth}$
 - Length index ⁽²⁾: $\text{body length}/\text{withers height}$
 - Rump length index: $\text{rump length}/\text{withers to hip length}$
 - Balance: $(\text{hip width} \times \text{rump length})/(\text{chest depth} \times \text{chest width})$
 - Width slope: $\text{hip width} - \text{chest width}$
 - Depth index: $\text{chest depth}/\text{withers height}$
 - Foreleg length: $\text{withers height} - \text{chest depth}$
 - Cumulative ⁽¹⁾ index : $(\text{weight}/\text{breed average weight}) + [(\text{length index 1} + \text{balance})/2]$
 - Cumulative ⁽²⁾ index : $(\text{weight}/\text{breed average weight}) + [(\text{length index 2} + \text{balance})/2]$
 - Cumulative ⁽³⁾ index : $(\text{weight}/\text{breed average weight}) + \text{length index 2} + \text{balance}$
-

months, and of the males from 12 months to 133 months; almost all animals were in unfitted (i.e. not Show) condition.

Results

The results were expressed as:

1. mean, SD, coefficient of variation and range for each linear measurement
2. graphs to show the development with age for each linear measurement
3. coefficient of correlation matrix for linear measurements, weight and cumulative index
4. histogram profile charts for individual animals and for individual animals with sire and dam for linear measurements, weight and cumulative index.

Evaluation of measurement of height at withers and rump was undertaken as a preliminary analysis. The measurements were easy to apply and showed high repeatability. Height at withers was correlated most closely with length of foreleg (0.760), but both height at withers and rump had a lower correlation with weight and cumulative(3) index than any of the other linear measurements. Height was an unreliable guide to weight, and lacked value as an indicator of type or functionality, except possibly at extremes of the frequency

distribution curve. It was determined that the identification and assessment of alternative indicators was necessary.

The results indicate that White Park cows reach their maximum weight at approximately nine years of age, but that they reach 98-99% of maximum size (linear measurements) by five years of age. The results for mature cows were calculated from data relating to animals of 60 months of age or more. The measurements (Table 2) and indices (Table 3) show the averages for the breed and indicate the typical structure of White Park cattle.

Each measurement developed at a different rate at different ages (Table 4). Rump height developed most rapidly, reaching 93-94% of full size by 24 months of age. Chest depth developed more slowly, reaching 97.8% of full size by 60 months of age. Most other measures progressed at a similar rate (86-90% at 24 months, 92.5-94.5% by 36 months, circa 96% by 42 months, and 99% by 60 months). The development of hip width was unusual. It developed most slowly to 24 months of age, but reached 99.4% by 60 months of age. Leg length (calculated by deducting chest depth from withers height) reached full size by 12 months of age. Chest width was the most variable measurement

Table 2. Linear measurements of mature cows over 60 months of age.

Measurement	Mean (cm)	S.D.	Cof. V.	Max (cm)	Min (cm)
Withers height	131.13	5.31	4.05	145	121
Rump height	131.91	5.12	3.88	146	120
Length of body	147.57	6.62	4.49	169.5	131
Rump length	55.41	3.57	6.44	68	47
Width of hips	59.66	3.81	6.39	72	51
Width of chest	51.37	5.94	11.57	71	41
Depth of chest	75.36	3.46	4.59	88	62

Table 3. Indices of mature cows over 60 months of age.

Index	Mean	SD	Cof.V.	Max	Min
Weight (kg)	619.43	96.13	15.52	957	399
Length 1	1.97	0.09	4.36	2.08	1.72
Length 2	1.11	0.05	4.31	1.26	0.96
Rump length	0.59	0.05	7.73	0.83	0.49
Balance	0.86	0.08	9.08	1.11	0.66
Depth	0.56	0.03	4.72	0.64	0.49
Foreleg length (cm)	56.31	4.09	7.26	66	45
Cumulative 1	2.47	0.15	6.28	2.89	2.09
Cumulative 2	2.04	0.16	7.84	2.55	1.69
Cumulative 3	3.88	0.17	4.45	4.37	3.38

Table 4. Development of cows at 42 and 60 months of age relative to full size measured by two methods (a. and b.)

Measurement	42 months of age			60 months of age		
	a.	b.	av.	a.	b.	av.
Wither height	96.2	96.9	96.55	98.8	99.1	98.95
Rump height	98.1	98.1	98.10	99.4	99.3	99.35
Body length	95.8	94.2	95.00	99.1	97.4	98.25
Rump length	96.1	95.2	95.65	99.5	97.4	98.45
Hip width	95.5	93.9	94.70	99.4	99.3	99.35
Chest width	95.4	92.1	93.75	98.9	97.9	98.40
Chest depth	94.5	93.9	94.20	97.8	98.2	98.00
Weight	86.1	82.2	84.15	95.2	94.4	94.80

a) total sample development curves

b) age group direct comparisons

Table 5. Development of cows at 42 and 60 months of age relative to conformation of mature cows.

Index	42 months of age			60 months of age		
	a	b	av	a	b	av
Weight	102.8	98.2	100.50	101.6	100.9	101.25
Length 1	101.4	100.3	100.85	100.8	99.3	100.05
Length 2	98.7	97.2	97.95	99.4	98.3	98.85
Rump length	102.5	101.7	102.10	101.3	99.2	100.25
Balance	103.4	103.2	103.30	101.9	100.8	101.35
Depth	95.9	96.9	96.40	98.9	98.9	98.90
Foreleg length	100.2	100.9	100.55	100.1	100.6	100.35
Cumulative 1	101.6	99.9	100.75	101.1	100.3	100.70
Cumulative 2	100.5	98.9	99.70	100.1	100.2	100.15
Cumulative 3	101.1	100.4	100.75	100.5	100.1	100.30

(coefficient of variation of 11.57%) and this reflected the sensitive response of chest width to changes in the fitness (condition) of an animal. Other measurements had a coefficient of variation between 3.88% and 6.44%.

The linear measurements were used to calculate indices, which show the structure and proportions of each animal. The indices for all females in the study (Table 3) show the highest coefficient of variation for balance, rump length index, and foreleg length, and the lowest for both length indices, depth index and cumulative(3) index. Weight was markedly variable (coefficient of variation 15.52%) and this again reflected the variety of environmental effects and the condition of each animal. Indices remained relatively constant at each stage of development from 12 months of age (younger animals were not included in the study). A detailed comparison of indices (Table 5) in 42 month and 60 month animals, compared with fully mature animals, showed that only length(2) index and depth index varied with age, and this resulted from the slower development of chest depth (Table 3). All other indices were within 1.7% of the expected norm at 60 months of age and within 4.1% at 42 months of age.

Both linear measurements and indices for different age groups (Tables 4 and 5) were calculated by two methods. The first (a.) was derived from a best curve based on data of the total study sample; the second (b.) was calculated from averages for each age group (42 month - 40-44 months; 60 month - 58-62 months). The results for indices were tested against coefficient of regression data. In all cases the slope of the regression line was negligible (<0.06% per month of age). The steepest slope was for depth index, followed by length(2) index. Cumulative(3) index and balance showed no regression.

The coefficient of correlation was calculated between each linear measurement and weight and cumulative(3) index (Table 6).

The results were also produced on histogram profile charts, either for individual animals or for an animal in conjunction with

its sire and dam, incorporating linear measurements and weight and cumulative(3) index.

Discussion

The linear measurements and, more particularly, the indices, established norms for breed type and conformation. They showed that White Park cows are short-legged animals with a good girth; long-bodied with good rump length; and are active, grazing beef animals. They have the proportions of beef animals (Table 7), although not typical of either the traditional British beef animal such as the Beef Shorthorn or Aberdeen Angus, or continental breeds such as the Charolais or Limousin. They are efficient grazing animals, adapted to rough grazing, and the non-breeding animals produce high quality beef, with excellent flavour, low fat and good marbling (Alderson 1997).

It was not possible to demonstrate the degree of variation within breed due to genetic effects. Blott (1997) indicated a relatively high level of homozygosity in the breed, but Royle (1983) showed relatively high heterozygosity, and anecdotal opinion suggests different types in the breed. For example, breeders claim that the Dynevor type based on Dynevor Raven is long-bodied and 'scopy', while the Chartley type based on Dynevor Samson is more compact, and the linear assessment results do confirm some differences. There were specific differences - for example mature Dynevor type cows stand as high or higher at the rump than at the withers, whereas mature Chartley type cows are the opposite (Table 8) - but other indices, such as depth, width slope and balance, which seem to indicate variation, probably are more a reflection of environmental effects and the more fertile grazing available to the Chartley herd. Indices for length did not show significant variation. An undefined proportion of the variation for each measurement or index was due to human error or to environmental effects of management systems.



Figure 1. These two cows are the same weight and have the same chest depth, but the difference in withers height is 11 cm.

Table 6. Correlation matrix for primary measurements, weight and cumulative(3) index: results for all cows above diagonal, and for cows over 60 months of age below diagonal.

	Weight	Withers ht	Rump ht	length	Rump lg	Hip width	Chest wi	Chest de	cum ind
Weight		0.693	0.661	0.862	0.815	0.918	0.849	0.924	0.6
Withers ht	0.566		0.902	0.721	0.627	0.644	0.399	0.707	0.4
Rump ht	0.621	0.903		0.652	0.632	0.613	0.431	0.655	0.4
Length	0.726	0.616	0.569		0.708	0.771	0.551	0.771	0.6
Rump Length	0.745	0.469	0.535	0.522		0.779	0.636	0.795	0.6
Hip Width	0.861	0.424	0.496	0.535	0.654		0.751	0.837	0.6
Chest Width	0.864	0.259	0.369	0.396	0.632	0.761		0.711	0.5
Chest Depth	0.861	0.594	0.628	0.528	0.683	0.644	0.668		0.5
Cum 3 Index	0.818	0.446	0.481	0.805	0.781	0.809	0.561	0.611	

Cumulative(3) index is the preferred measure of the overall value of an animal, although it does not distinguish between different types of conformation. It has a neutral correlation with age, and thus can be used as a measure in young animals to predict mature rating. It is a superior measure to weight because it incorporates measures of desirable conformation, namely length and balance. The results of coefficient of regression calculations reinforced the value of cumulative(3) index on young animals as an indicator of mature type and conformation. It is influenced to some degree by management, but to a much smaller degree than weight.

However, it is a complex index requiring five measurements on each animal. Simpler alternatives are provided by single measurements. Results for cows (Table 6) show that body length, rump length and hip width have the highest correlation with cumulative(3) index. Correlation with weight shows that hip width and chest depth are the best measures. Thus, hip width and/or rump length are the preferred measures. The results

(Table 9) suggest that rump length and hip width in particular are more difficult to measure than withers height, but the differences are small (3% and 2.2% respectively). Both measurements are influenced by management of young cattle. Analyses of within-herd results confirm the superiority of these measures compared with height, but indicate that hip width is more reliable than rump length.

A limited study of bulls showed a different pattern of results. In a very small sample of mature bulls, body length was significantly the best indicator of cumulative(3) index, followed by rump length and scrotal circumference, while chest depth was the best indicator of weight. In the full sample of bulls, rump length and chest depth were the best indicators of cumulative(3) index, while all linear measures had a high correlation with weight. Results for linear measurements of young bulls, together with weight and cumulative(3) index, were presented in histogram profile charts, and these were used



Figure 2. This heifer was reared on a low-input, non-intensive system. Linear assessment identified her type and quality at a young age.

in conjunction with GCI (effective founder number) data (Alderson 1992) to identify superior bulls. The results for each bull were also presented with the results of their sire and dam.

Limitations

Cumulative(3) index is the best measure of functional value of an animal, but it requires five linear measurements. It has value in detailed studies and analyses of breeds of cattle, but it is too complicated to operate on a routine herd basis. The measurements of hip width or rump length, ideally combined in a rump area index, offer simpler alternatives, and are superior to height as indicators of cumulative(3) index or weight.

Consistency of measurements was influenced to some degree by human error. There seemed to be greater difficulty with some measurements; but all were within a 5%

limit of variation. The employment of one operator was designed to minimise this problem.

Environmental influence also confused the genetic effect, especially in young animals. For example, sire referencing demonstrated that animals raised on Salisbury Plain varied significantly from their half-sibs on Oxfordshire pastures, and the effect was noted even on indices, particularly weight, length(2) index, balance and depth index (table 10) in these two herds. A wider study of five herds confirmed the environmental effect on weight, length(2) index and depth index, but not the effect on balance. All the linear measurements except withers height and rump height were susceptible to environmental effect.

Different calculations are necessary for different breeds, and this is indicative of varying conformation between breeds. These differences were not tested fully, but

Table 7. Indices of conformation in different types and breeds of cattle.

Breed	Type	Index	
		Length/height	Length/girth
White Park	Beef	1.095	0.72
British White	Beef	1.089	0.72
Gloucester	Dual-purpose	1.056	0.71
Ayrshire	Dairy	1.053	0.68
Friesian	Dairy	1.039	0.68

Table 8. Indices of conformation in mature cows in two herds of White Park cattle

Herd	Ht slope	Index			
		Length	Rump lg	Depth	Balance
Dynevor	2.07	1.99	0.58	0.55	0.9
Chartley	-1.51	1.98	0.57	0.57	0.88

Table 9. Variation of measurements compared with previous measurement on same cow by same operator.

Cow	Age (m)	% change						
		Withers ht	Rump ht	length	Rump lg	Hip width	Chest wi	Chest de
A	144/180	1.21	1.21	2.17	3.81	3.69	2.38	2.82
B	132/156	1.55	0.76	1.36	0.91	6.03	10.42	2.67
C	111/144	2.86	1.57	3.89	3.51	0	2.68	5.63
D	108/132	1.53	1.52	1.02	1.96	5.26	7.45	2.61
E	96/132	0	2.99	1.36	9.43	0	9.78	4.11
F	91/118	1.45	1.76	4.05	1.82	6.67	2.04	1.32
G	86/122	1.18	1.61	4.12	9.57	3.71	2.33	0
Average		1.397	1.631	2.567	4.43	3.623	5.297	2.737

Table 10. Progeny results for a bull in two herds under contrasting systems of management. Results expressed as % difference from breed average.

Herd	Index						
	Weight (kg)	Length(1) index	Length(2) index	Rump index	Balance	Leg length	Cum(3) index
1 (17 daughters)	-11.3	3.2	-0.1	-3.5	0.2	5.6	0.5
2 (6 daughters)	9.8	1.3	1.6	1.4	4.2	3.9	4.2
Sire's own rating	12.2	2.1	9.1	-10.8	1.4	-0.1	4.6

preliminary results were obtained from Red Poll, Irish Moiled and Traditional Hereford cattle.

Linear assessment is only one factor in selection procedures. It takes no account of maternal qualities, and the use of linear assessment in the absence of breeding records or evaluation of temperament could be misleading.

Conclusions

Height at either withers or rump has limited value as an indicator of weight, and negligible value as an indicator of type and function. The value of weight is limited without some qualification of associated type and conformation. Cumulative(3) index is a useful indicator of overall morphological merit, as it combines values of weight and structure, and provides an accurate portrait of typical breed type. It is relatively constant throughout the life of an animal and can be used on young animals to predict mature merit. It is influenced by environmental effect (although significantly less so than weight), and it is complicated, requiring five linear measurements. Thus cumulative(3) index has potential application in breed studies to establish type and function, although its application by individual breeders is less attractive.

Single linear measurements are more relevant for on-farm within-herd use. Hip width or rump length, individually or

combined, are the preferred measurements. They have a high correlation with cumulative(3) index and weight, and are significantly superior to height in both cases. They are influenced by environmental effect, and are of limited value in between-herd comparisons.

The study demonstrated the value of linear assessment in general, and specific measurements in particular, with White Park females, and identified further potential areas of study to evaluate and refine the proposed system, namely:

1. repeat the study with a significant sample of bulls to assess the validity of indices for both sexes of White Park cattle
2. relate linear measurements to production characteristics other than weight (e.g. meat quality, KO%, maternal qualities, longevity)
3. study the effect of compensatory growth on linear assessment in animals reared under different systems of management
4. apply the system to other breeds to compare them with the White Park, and to test cumulative(3) index as an indicator of function in different breeds.

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A programme for the inventory, characterisation, evaluation, conservation and utilisation of European rabbit (*Oryctolagus cuniculus*) genetic resources

G. Bolet¹, M. Monnerot², C. Arnal³, J. Arnold⁴, D. Bell⁵, G. Bergoglio¹⁴, U. Besenfelder⁶, S. Bosze⁷, S. Boucher⁴, J.M. Brun¹, N. Chanteloup⁸, M.C. Ducourouble⁹, M. Durand-Tardif¹⁰, P.J. Esteves¹¹, N. Ferrand¹¹, G. Hewitt⁵, T. Joly¹², P.F. Koehl¹³, M. Laube⁹, S. Lechevestrier⁹, M. Lopez³, G. Masoero¹⁴, R. Piccinin¹⁵, G. Queney², G. Saleil¹, A. Surridge⁵, W. van der Loo¹⁶, J. Vanhomerig¹⁵, J.S. Vicente¹⁷, G. Virag¹⁸ & J.M. Zimmermann⁴

¹Institut National de la Recherche Agronomique, S.A.G.A., P.O. Box 27, F31326 **Castanet-Tolosan** Cedex, France

²Centre National de la Recherche Scientifique, C.G.M., Avenue de la Terrasse, F91198 **Gif sur Yvette** Cedex, France

³Universidad de Zaragoza, Facultad de Veterinaria, Miguel Servet, 177. 50013 **Zaragoza**, Spain

⁴Fédération Française de Cuniculture, 28 rue du Rocher. F75008 **Paris**, France

⁵University of East Anglia, School of Biological Sciences, NR4 7TJ. **Norwich**, Great Britain

⁶Interuniversitäre Forschungsinstitut Für Agrarbiotechnologie, Konrad Lorenz Strasse 20, A3430 **Tulln**, Austria

⁷Agricultural Biotechnology Center, Institute for Animal Science, PO Box 411, **Gödöllő** H2101, Hungary

⁸Institut National de la Recherche Agronomique, P.A.P., F37380 **Nouzilly**, France

⁹Centre d'Enseignement Zootechnique, Ecole d'Aviculture, Parc du Chateau, F78120 **Rambouillet**, France

¹⁰Bureau des Ressources Génétiques, 16 rue Claude Bernard, F75231 **Paris** Cedex 05, France

¹¹Faculdade de Ciências do Porto, Departamento de Zoologia-Antropologia, Praça Gomes Teixeira, P4050 **Porto**, Portugal

¹²Institut Supérieur d'Agriculture Rhône Alpes, 31 Place Bellecour, F69288 **Lyon** Cedex 02, France

¹³Institut Technique de l'Aviculture, 28 rue du Rocher. F75008 **Paris**, France

¹⁴Istituto Sperimentale per la Zootecnia, Via Pianezza, 115. 10151 **Torino**, Italy

¹⁵Entente Européenne d'Aviculture et de Cuniculture, Rabbit Section, Wilhelminastraat 8. 6351 GN **Bocholtz**, The Netherlands

Summary

In Europe, more than 60 breeds are described by the national associations of rabbit breeders. However, these breeds are scarcely used in the commercial production of rabbit meat in Europe, which is based mainly on commercial strains. A European programme, coordinated by the I.N.R.A., has been initiated to realise the inventory of all these breeds and to evaluate the zootechnical value and the genetic characteristics of some of them.

Through the European association of rabbit breeders and the FAO national focal points, all the European countries have been asked to fill out a questionnaire describing their populations of rabbits. A data bank is being set up, which will be included in the FAO (DAD-IS) and EAAP data banks. A sample of 10 breeds has been chosen (Flemish Giant, French Lop, Belgian Hare, Vienna White, Champagne Argente, Thuringer, Fauve de Bourgogne, Chinchilla, Himalayan, British). Their zootechnical value (reproduction, growth and carcass traits) is being evaluated



Figure 1. Flemish Giant rabbit.

on three experimental farms, in comparison with a control breed. At the same time, their genetic polymorphism and the genetic distances between these 10 breeds are calculated on the basis of microsatellites, mitochondrial DNA, other genetic markers and protein polymorphism. Finally, a bank of frozen embryos from these 10 breeds is being constituted.

Résumé

En Europe, plus de 60 races de lapins sont décrites dans les standards des Associations nationales d'éleveurs. Cependant, ces races sont très peu utilisées pour la production de viande, qui est basée essentiellement sur des animaux croisés provenant d'un faible nombre de races ou souches. Un programme européen, coordonné par l'INRA, a été mis en place pour recenser ces races et évaluer le potentiel zootechnique et les caractéristiques génétiques de certaines d'entre elles. Par la voix de l'Entente Européenne de Cuniculture et des points focaux nationaux de la F.A. O.,

tous les pays d'Europe ont reçu un questionnaire destiné à décrire leurs races de lapins. Une banque de données est en cours de réalisation, elle sera ultérieurement intégrée dans les banques de données de la F.A.O. (DAD-IS) et de la F.E.Z. Un échantillon de 10 races a été choisi (Géant des Flandres, Bélier Français, Lièvre Belge, Blanc de Vienne, Argenté de Champagne, Chamois de Thuringe, Fauve de Bourgogne, Chinchilla, Russe, Papillon Anglais). Leurs performances zootechniques (reproduction, croissance et caractéristiques de la carcasse) sont évaluées dans 3 fermes expérimentales, en comparaison avec une souche témoin unique. A partir du polymorphisme de microsatellites, de l'ADN mitochondrial, de marqueurs génétiques et de protéines, la variabilité génétique au sein de ces races et les distances génétiques entre elles sont calculées. Enfin, une banque d'embryons congelés est en cours de réalisation.

Key words: Conservation, Rabbit data bank, Breed characteristics, Reproductive traits, Genetic diversity.

Introduction

Western Europe contributes some 60 per cent of the world's commercial production of rabbit meat. This production is sometimes based on pure-bred animals, but mainly on cross-bred animals derived from very few specialised strains disseminated through pyramidal systems. Pure-breeding is decreasing and local populations, used in traditional backyard farming, are currently nearly extinct. Additionally, these populations have hardly been surveyed (Arnold and Rochambeau, 1983). Depending on the extent of selection, one can distinguish local populations or breeds, defined by standard (more than 60 in Europe) or commercial strains, extracted from a few breeds and strongly selected for production traits. Besides rabbit breeders for meat production, there are fancy breeders. The former are predominant in France, Spain, Italy, Hungary,... where rabbit meat consumption is popular. The latter are particularly active in Germany and Switzerland, but also in France, Italy, Belgium

and the United Kingdom; most of their national associations are federated into a European Association (Entente Européenne d'Aviculture et de Cuniculture), including 15 countries and 66 breeds, most of them being present in various countries.

At the present time, profits obtained from rabbit husbandry are insufficient to encourage the development of this industry. An inventory of existing genetic resources could allow a better knowledge of the abilities of breeds rarely used today because of their low level of production under standard conditions. It could lead to the development of new activities with higher profits for breeders. Owing to the great variability in body size, diversification of carcass weight is one approach. The patterns of production could be diversified, and, with more adapted breeds, lead to a more extensive way of rearing rabbits for a part of the production. This inventory could also lead to the utilisation of breeds showing a good resistance to some diseases, which would reduce the use of chemicals to the benefit of the breeder and the consumer. It could also lead to the utilisation of animals with a better



Figure 2. French Lop rabbit.



Figure 3. Belgian Hare rabbit.

feed efficiency which would help decrease effluents produced by animal husbandry (particularly the nitrogenous waste), and hence help protect the environment. Finally, a more thorough knowledge of the different breeds, particularly from an immunological point of view, would develop the production of rabbits for laboratories, producing more homogeneous or more sensitive groups of animals better suited to users' needs.

Characterisation and Conservation: Current Status

Some efforts have already been made to characterise European rabbit breeds.

- Most national associations of fancy rabbit breeders have made a primary phenotypic characterisation of the breeds they manage (national breed standards). The European Association, mentioned above, has published a European standard of breeds (Anonymous, 1995), which tries to synthesise the national standards. It gives

a detailed description of the shape, conformation, size, fur coloration for a total of 66 breeds.

- A European network of interested laboratories has been working together on the characterisation of genetic polymorphism in several wild and domestic populations from Portugal, Spain and France (Monnerot *et al.*, 1994; Van der Loo *et al.*, 1991, 1999; Ferrand, 1995).
- A research network on rabbit production in the Mediterranean area was founded in 1987 with the support of the International Centre for Advanced Mediterranean Agronomic Studies (CIHEAM). It includes 8 countries (including Spain, Italy and France) and is working on the identification and characterisation of local populations and breeds (Rouvier, 1994; Khalil, 1998). So far, mainly southern Mediterranean populations have been considered.
- A European concerted action ("Germplasm banking"), in which the rabbit was used as a model animal, allowed the defining of the technical basis for cryoconservation of rabbit embryos. Embryos from some commercial cross-bred strains and from 3 small-size endangered strains were collected and frozen (Joly *et al.*, 1994, 1996).

In spite of these efforts, important points are lacking concerning European breeds :

- The rabbit is missing from the FAO / DAD-IS, <<http://www.fao.org/dad-is/>> and the European Association for Animal Production (EAAP) (Hannover) data banks on domestic animal breeds.
- Most previous work was devoted to selected strains or cross-breeding (see Rochambeau, 1988, for a review), and comparative studies of native breeds are badly lacking. Only some zootechnical evaluations so far have concerned a few breeds treated separately (Pilandon *et al.*, 1986; Chevalier *et al.*, 1986; Lopez *et al.*, 1992, Pagano Toscano *et al.*, 1992, Koehl and Van Der Horst, 1998), and some

cross-bred products of these breeds were compared (Ouhayoun and Poujardieu, 1978).

- There is no systematic collection of rabbit genetic resources, as exists in most domestic animal species. Their preservation is currently performed *in situ* by either professional or fancy breeders, but without any consistent programme such as that of the "Conservatoire National des Animaux de Basse-Cour" which worked in France between 1978 and 1985 (Arnold and Rochambeau, 1983) and no longer exists.

So far, different parts of a conservation programme have developed more or less independently, and do not constitute an integrated and coherent project. For these reasons, an ambitious programme was proposed and approved within an EC framework (Regulation No 1467/94 on the conservation, characterisation, collection and utilisation of genetic resources in agriculture). The objective of this paper is to describe in detail this programme, which began in 1997.

Creation of a Data Bank

The first phase involves the definition of a rabbit data bank. The rabbit has not, to date, been included in the FAO and EAAP data banks. Our project will allow a data bank to be created with information from the European countries involved in the project. The first source of data will be the review of 66 breeds registered by the above mentioned European Association of Rabbit Breeders which proposes only a phenotypic description of the breeds and very little zootechnical data. Detailed propositions for the organisation of a rabbit data bank have already been made by Lukefahr (1988) and by Khalil (1993). On the basis of these different sources, we assembled a questionnaire (Annex 1) which was sent to national rabbit breeders associations and to FAO European national focal points. This questionnaire is available in English, French, Spanish, Italian, German and Russian. So far, more than 100 national breeds were registered, from twelve countries. The questionnaire may be obtained from the first

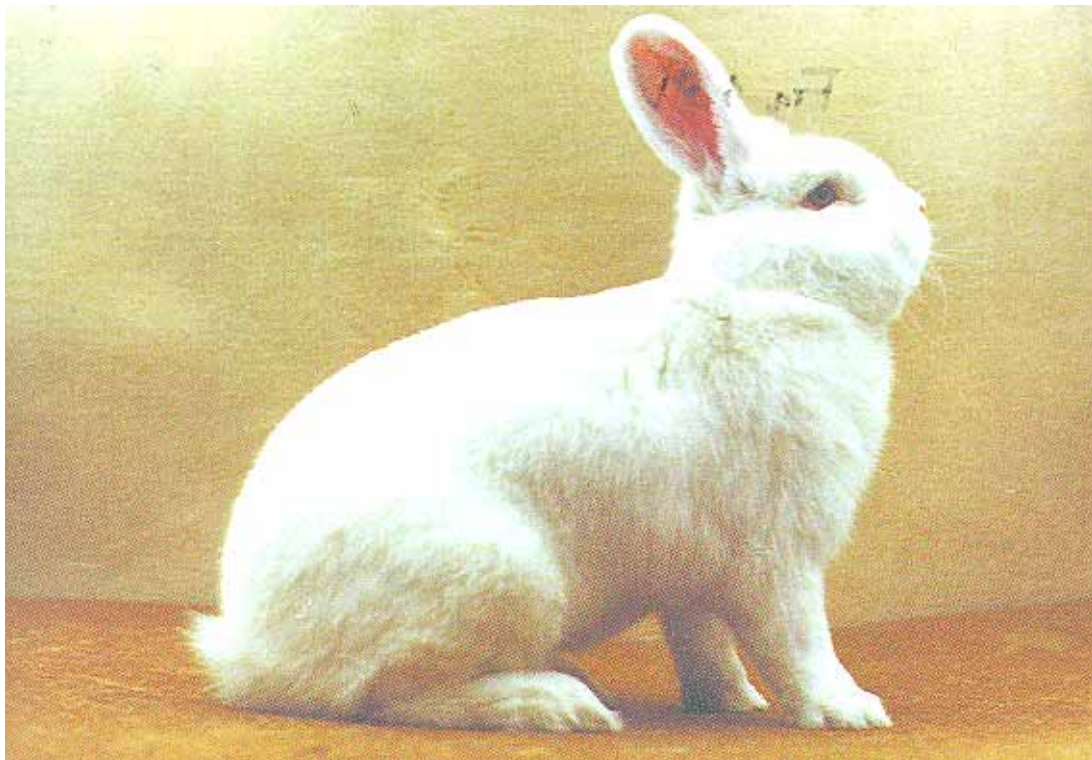


Figure 4. Vienna White rabbit.

author of this paper. The construction of the computerised data bank is now in progress and a first draft will be available in 1999 (Ducourouble *et al.*, 1999). It will be maintained by participants and incorporated simultaneously, in FAO and EAAP data banks, as soon as possible.

Detailed Characterisation of a Sample of 10 Breeds

Choice of the 10 breeds

As it is not possible to make a detailed characterisation of all the censed breeds, for economical reasons, we decided to work on a sample of 10 breeds. Figures from 1 to 10 show these breeds.

These breeds were chosen on three criteria:

- They are presumed to be among the oldest; some breeds which are known to originate from recent cross-breeding of the oldest ones.
- They are present in various European countries; some breeds, which are present in only one country and whose

preservation is relevant of a national programme, were discarded in spite of their potential interest.

- They have a potential zootechnical interest. The 10 chosen breeds were :
- Two heavy breeds : Flemish Giant and French Lop
- Five average-sized breeds : Belgian Hare, Vienna White, Champagne Argente, Thuringer, Fauve de Bourgogne
- Three small-sized breeds : Chinchilla, Himalayan, British (Papillon).

Zootechnical characterisation

The evaluation of the breeds takes into account the following points :

- On-farm characterisation concerning reproductive performances and genealogies.
- Zootechnical evaluation, in controlled management and environmental conditions including growth, feed efficiency, carcass traits and muscular fibre characterisation.

For the latter, the average size of a sample from a population is expected to be around 50 females and 20 males whose dam and sire are known, as unrelated as possible. Young are bought in farms at weaning or at birth. When bought at birth, they have to be nursed



Figure 5. Champagne Argente rabbit.



Figure 6. Thuringer rabbit.

by a synchronised female on the experimental farm. This technique is now well known and used for introduction of rabbits in farms.

On each experimental farm, comparison is made between a control strain and one or more breeds at a time, according to the number of available cages. The control strain will be the 9077, from INRA (France), which has been kept without selection, as a control line, for 20 years. Conditions will be standardised as much as possible, but in agreement with biological abilities of each breed.

The parameters which will be measured are the following.

Reproductive traits

Reproductive performances of females will be studied during a period of 6 months to one year, i.e. an average of 4 litters, according to the reproduction rhythm chosen (in rabbits, mating is performed either the day after littering, 5 to 12 days after, or even after weaning in traditional systems). Ovulation of

does is induced by coitus (or by an injection of exogenous gonadotrophins in artificial insemination) (Bolet *et al.*, 1992).

In all cases, fertility rate, litter size and weight of young at birth will be recorded. In some cases, components of litter size, measured by laparoscopy, namely number of ova shed and number of embryos alive, will also be recorded. Both are easily counted by laparoscopy at 12 days of gestation without any damage to the female or the foetuses (Santacreu *et al.*, 1990). Male semen composition and quality will be recorded by semen collection using an artificial vagina, a technique routinely used in rabbits.

Growth and feed efficiency

Adult body weight differs dramatically between rabbit breeds, but little is known about growth rates, except in "standard" strains. First and second litters of does compared for reproductive traits will be used to establish growth curves: a sample of them will be weighed from birth to adult weight.



Figure 7. Fauve de Bourgogne rabbit.

To measure appetite and feed efficiency, animals will be fed ad libitum during growth, and feed consumption of groups of siblings after weaning will be measured.

Carcass traits

To study the carcass traits, a sample of young from 3rd and 4th littering will be slaughtered around 2, 2.3 or 2.6 kg. These weights correspond to classical slaughter weights and to potentially heavier weights more adapted to cutting. The carcass composition will be studied according to classical criteria defined and normalised by Blasco *et al.* (1993), including a reference carcass dissection and prediction of carcass composition (via meat/bone ratio estimated by hind leg dissection). Components of quality such as muscular pH and colour will be measured. When possible, organoleptic qualities of meat will be analysed by trained panels.

The above assessment of quality will be completed by further analysis of muscular fibres using established techniques (the

avidin-biotin complex method and the ATP-ase method). On samples from the same animals, lipids, energy, protein and magnesium content of muscle will be determined using a near infrared spectroscopy (NIRS) method on freeze-dried samples of muscle (Masoero *et al.*, 1994).

Detailed Characterisation of Genetic Diversity

A number of different markers will be used to evaluate different breeds and different geographical populations within each breed, to establish diversity within and between breeds. All of them have proved to be useful criteria for this purpose in preliminary works. The final objective is to measure the degree of specificity of each breed. This will also allow definition of the best possible sampling strategy for measuring and conserving biodiversity at all levels.

Diversity in maternal lineage: mitochondrial DNA characterisation

Mitochondrial DNA (mtDNA), which is almost exclusively maternally inherited, is an essential tool to assign animals to a precise maternal lineage. Early studies on several natural populations and three breeds has led to the recognition of 22 types organised within two well differentiated and geographically structured maternal lineages (Monnerot *et al.*, 1994). Sequence analysis of various domains of mtDNA belonging to these different types has allowed the genetic characterisation of animals whatever their degree of relationship. Two regions of mtDNA are assessed: part of cytochrome b gene for distantly related animals and part of the main non-coding domain for closely related animals. Various pairs of primers specific for these two regions define mtDNA portions of different lengths and phylogenetic signals. Once amplified by PCR, these portions are analysed either by sequencing or by RFLP (Hardy *et al.*, 1995; Monnerot *et al.*,

1996; Mougel, 1997). Comparisons with data previously collected will then allow the animal under study to be assigned to one of the 2 mtDNA groups already described.

Allelic diversity of immunoglobulin loci

The antibody diversity in the rabbit is fundamentally different from that of other species. The rabbit Ig loci are highly polymorphic (with alleles that show up to 40 % amino acid differences). Most polymorphic are the a locus encoding the predominantly expressed variable region gene and the b locus encoding the constant region of the Kappa light chain. There is strong evidence that in the rabbit species, allele diversity at the Ig loci is a crucial component of population fitness (Van der Loo and Verdoodt 1992, Van der Loo 1993). While contributing to the characterisation of populations, the monitoring of the Ig genotypes is important to avoid accidental loss of allele diversity in races.



Figure 8. Chinchilla rabbit.



Figure 9. Himalayan rabbit.

food available to pups up to the age of 21 days. RFLP of the rabbit κ -casein gene has been observed in DNA isolated from New Zealand rabbits and digested with Hind III (Baranyi *et al.*, 1996). It was shown that in this breed the κ -casein B allele is less frequent than the κ -casein A allele and that differences between the two alleles include part of the LINE sequences in the first and the fourth introns (Hiripi *et al.*, 1998). The polymorphism of κ -casein gene will be evaluated after DNA amplification of the first intron, using primers located in the bordering exons. The diversity of α s2 casein will be examined with isoelectric focusing of milk samples (Virág *et al.*, 1996).

Haplotypic diversity of the Major Histocompatibility Complex (MHC)

In all species, MHC is the best 'identity card' of individuals, possibly playing a role in individual recognition. Rabbit class I and class II MHC gene haplotypes were described (Marche *et al.*, 1989). One class I and 4 class II loci (DQ, DR, DP, DZ/DO) are identified and used in this programme.

Casein polymorphism

In milk the four major caseins, namely β -, α s1-, α s2- and κ -casein exist in the form of casein micelles. Studies on the physicochemical characteristics of bovine, goat and ovine milk have shown that the genotype has a significant effect on casein, fat content and micelle characteristics. Whereas the bovine, ovine and caprine are of major importance to the dairy industry, rabbits are principally bred as meat animals. Nevertheless, the level of lactation in rabbit does is important since doe milk is the only

Diversity of various proteins

Genetic variability between populations will be estimated from the analysis of protein polymorphism. Around 25 variable loci will be studied. The following established techniques will be used: conventional electrophoresis, electrophoresis in denaturing conditions, isoelectric focusing in pH gradients, isoelectric focusing in immobilised pH gradients, isoelectric focusing followed by immunoblotting or enzyme blotting. Enzymes will be visualised with specific staining methods and non enzymatic proteins with current staining methods. (Ferrand, 1995).

Diversity of alleles at microsatellite loci

Microsatellites occur commonly in eukaryotic genomes and consist of stretches of mono, di or tri nucleotide motifs which are randomly repeated, dispersed throughout the whole genome and usually flanked by unique sequences. They are becoming the markers of choice for molecular population genetics because they represent an important source of polymorphic genetic markers which are easily and rapidly scored. Differentiation of very closely related populations is possible based

on allele frequencies as well as diagnostic alleles. A set of 20 to 30 microsatellite loci already identified and available will be used (Rico *et al.*, 1994; Mougél *et al.*, 1997; Surridge *et al.*, 1997; Van Haeringen *et al.*, 1997). Some of them have already been shown to be useful in characterising wild and domesticated populations (Vachot, 1996; Mougél, 1997; Surridge, 1997). They will provide an essential tool for the identification of breeds and testing individual genetic relatedness in combination with the other markers presented above. In the future all the nuclear markers could be useful in identifying quantitative trait loci (QTL) for breeding for zootechnical characteristics.

Conservation

The conservation actions will be as follow.

Constitution of a bank of frozen embryos

It is our intention that embryos and possibly semen of each breed should be stored in at least 2 places for a matter of security, according to recommendations concerning management of frozen germplasm. When sampling and collecting this material, the objectives are to avoid any shift in gene frequencies between original population and cryoconserved sample population. To reduce the initial genetic drift, three variables must be taken into account: sample size (Joly *et al.*, 1999), choice of animals and breeding system. The efficiency of the method has already been investigated (Joly *et al.*, 1996).

In situ preservation by breeding the selected populations in farms



Figure 10. British rabbit.

Following the data produced by this project, *in situ* preservation of breeds of reduced genetic variation or at particular risk of extinction will be proposed in private farms. These will be supported technically by breeders organisations and supported financially, in order to manage their stock according to some defined rules (mating plan, number of bucks and does, exchange between farms,...).

Conclusion

The situation of European rabbit breeds among domestic mammals is unique: there is still a great diversity of breeds, but they are mainly owned by fancy breeders who have more interest in their phenotype than their zootechnical and economical value. These genetic resources may be important for rabbit meat production if rabbit breeders can take advantage of this diversity. The inventory of all the breeds and the detailed characterisation of a sample of 10 breeds will provide valuable information on economical value of this diversity. This programme will collect and disseminate such vital information, and may have important consequences for the management and conservation of European rabbit genetic resources for the future.

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The Peel-Neck chicken of Belize and Guatemala, Central America

J.G. Mallia

Department of Population Medicine, Ontario Veterinary College, University of Guelph,
Guelph, Ontario, Canada N1G 2W1

Summary

A previously undescribed heavy, soft-feathered population of chickens characterised by a partially featherless portion of the neck known in Belize as the "Peel-Neck" was studied. It was also widely present in Guatemala. This population of chickens was said to have a dual purpose, raised for meat and eggs. The eggs were tinted, and the hens were sitters, also caring for the young until independent. The birds were active and independent foragers. The plumage colour was variable, but body weight and conformation were consistent across all specimens, as was the comb type and dimensions, and location of the featherless area on the neck. These chickens were kept under backyard rearing systems in both countries, although usually they were allowed to scavenge, at which they were said to excel. This population was not considered threatened, although apparently no attempt was made to breed pure specimens.

Key words: Genetic resources, Chicken, Belize, Guatemala.

Résumé

Nous décrivons une population nouvelle de poule Bélizienne de grande taille au plumage doux, mais chez laquelle le cou est dépourvu de plumes, soit au "cou pelé". Cette population se retrouve aussi au Guatemala. C'est une race à viande et à production d'oeufs teintés brun clair. Les poules sont

couveuses, protégeant leurs poussins jusqu'à leur indépendance. Elles sont aussi d'excellentes fourrageuses. Leur plumage est de couleur variable, mais leur masse, leur conformation, la forme de leur crête et l'emplacement de la partie du cou dépourvu de plumes sont semblables chez tous les spécimens. Ces poules sont élevées dans un système au sol. La population n'est pas menacée; par contre il n'y a aucun effort pour assurer l'élevage de race pure.

Introduction

The naked neck (Na) is an autosomal dominant gene responsible for the complete absence of feathers and down in the neck region of chickens (Davenport, 1914; Warren, 1933; Hertwig, 1933), mapped on chromosome 1 (Stevens, 1991). Several breeds exhibiting the naked neck trait have been described, including the "Cou Nu du Forez" from France, the "Malay Game" from Malaysia, the "Shingangadi" from Zaire, and the "Transylvanian Naked Neck" from Hungary and Romania (Merat, 1986). The "Transylvanian Naked Neck" is said to have been brought over into Europe during the Turkish occupation (Bodo *et al.*, 1990). Breed characteristics and production data are available for the European populations of chickens with the naked neck trait, for example France (Zein-el-Dein *et al.*, 1984; Pesti *et al.*, 1996), and Hungary (Bodo *et al.*, 1990). The naked neck trait was also said to be present in several regions of the world, generally those with a hot and humid climate (Merat, 1986), although breed descriptions

were not available. The purpose of this report is to bring attention to, and provide a description of a population of chickens in Belize and Guatemala exhibiting the naked neck trait.

Materials and Methods

Participants included local inhabitants raising and selling fowl in Belize and Guatemala in January 1994, and January 1998, identified by visiting the towns on their market day, and by the presence of free-ranging fowl, and chickens kept in enclosures adjacent to homes. A questionnaire was administered to the participants in English (Belize) or Spanish (Guatemala). Information on population data, description of the breed, its uses, management conditions and performance were collected. A version in English of the questionnaire is reported in table 1. Photographs were also taken to show body conformation, face and neck characteristics, and plumage.

Breed Description and Uses

The Peel Neck chicken was present throughout Belize and most of Guatemala, usually in mixed flocks also having chickens with normally feathered necks. Information on the Peel Neck was collected on 38 males and 114 females examined by the author, and additional information was gathered by means of a breed-information questionnaire based on that used by Mallia (1998). The body was large and compact with a "heavy breed" conformation, superficially similar to the Rhode Island Red or Sussex. The back was broad and flat, and the breast was prominent, broad and square (prevalence, $P=100\%$). On average, males weighed 3.95 kg (standard error, 0.10 kg), and females weighed 3.1 kg (standard error, 0.06 kg). The legs of the Peel Neck were proportionately longer than the fore-mentioned heavy breeds, devoid of feathering, and with prominent well spread toes ($P=100\%$). The wings were of medium size, carried high, horizontally, and close to the body, and in the male the wing tips were

Table 1. Peel Neck Fowl: questionnaire for growers and breeders in Belize and Guatemala (adapted from Mallia, 1998).

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- Q1. How many birds, males, females, young, do you have, and where they kept ?
 - Q2. How many females are ideally kept for each male ?
 - Q3. Do they forage, do you feed them, or both ?
 - Q4. From where do you obtain new stock ?
 - Q5. Do you keep the chickens with ducks or turkeys ?
 - Q6. If Q5.is in the affirmative, do you perceive any problems ?
 - Q7. At what age do the males and females mature ?
 - Q8. What weight do the males and females have at maturity ?
 - Q9. What colour are the eggs, does the hen incubate the eggs, how many does she lay annually ?
 - Q10. What is the morbidity and mortality of the young, and if so, mainly at what age ?
 - Q11. What is the morbidity and mortality of the adults?
 - Q12 What are the main uses of rearing chickens ?
 - Q13. Is there a particular feather colour preference for Peel Necks ?
 - Q14. Do you breed Peel Necks with other fowl ?
 - Q15.What are the main uses of rearing Peel Neck chickens ?
 - Q16. Any management or production advantages of the Peel Necks with respect to other fowl ?
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Figure 1. Male (to the left) and female (to the right) Peel Neck; (Belize).

usually obscured by the abundant shackle (P=100%). The tail was small or medium sized, carried upright at an angle of around 45° (P=73.4 %). The sickles in the male were only occasionally well-developed; usually they extended to only slightly beyond the rest of the tail, and were not markedly curved (P=73.4 %). Some males, particularly those in Guatemala, however, had an upright, well-developed tail with prominent sickles (P=26.6%). The head was of medium size with prominent, alert amber eyes and a medium-sized curved beak. There was no presence of white skin in the face or ear lobes (P=100%). The rest of the head was also devoid of feathering, aside from a small, well-defined tuft at the ears, and a “cap” of feathers extending around the blade of the comb (P=100%). The unfeathered area extended to about half way down the neck; an area with sparse feathering was present, corresponding to the anterior extremity of the keel; however, the rest of the body was covered with normal feathering (P =100%).

The plumage-type was soft-feathered in all specimens observed; feather colouring was very diverse: white, black, brown, red, partridge, speckled, silver cuckoo and wheaten colour phases were observed. The skin on the featherless areas was bright red, and usually with a fairly irregular texture (P=83%). Folds of skin were also occasionally present, particularly at the base of the posterior aspect of the wattles, giving a “double-wattled” appearance (P=78%). Despite the irregular appearance of the skin of the featherless areas, no evidence of follicles was present (P=100%). The comb in all specimens was single, upright, well-developed, deeply serrated and with 5-6 points in both the male and female; the free part of the blade was usually well-distanced from the contour of the skull (P =100%). Many of the physical characteristics of the Peel Neck chicken are illustrated in figures 1-3. The birds were very gregarious, and interacted well with other fowl and also humans. They actively foraged

around houses, gardens, ditches and fields during most of the daylight hours, roaming considerable distances. The hens laid tinted or light brown eggs ($P = 100\%$), and were easily trained to deposit their eggs in a convenient location for collection. They were also said to be excellent sitters, and several hens with broods were observed the hens being cautious and defensive when with young. The young were also very alert and independent, exploring various sources of food, for example ground coconut left out to dry. The long-legged appearance, bare head and neck areas of the young mirror those of the adults. The dorsal parts of the body were unevenly feathered or naked, from a young age, however the ventral parts, especially the abdomen, were thickly covered with feathers.

The questionnaire showed that despite their markedly wide distribution, there was no indication given by poultry growers of the Peel Neck having superior carcass or

egg-laying traits. Although they were considered to be good foragers, and the hens good sitters and mothers, they were not considered better than the fully-feathered varieties. Hens commenced laying eggs between seven and eight months, and laid between 40-50 eggs per year; these values are comparable to those found by Cook *et al.* (1997) for other backyard poultry raised in the Yucatan, Mexico. When reared in enclosed backyard compounds, Peel Necks were said to be about as productive as chickens with feathered necks: production of eggs was said to be linked to ration quality and quantity, rather than presence or absence of neck feathers, despite the predominantly hot and humid climate. The prevalence of Peel Neck chickens per backyard within a village varied substantially (e.g. from 0-80% in Monkey River Town, Belize). When present in a village, the overall prevalence of Peel Neck chickens was usually of 30-50%, although



Figure 2. Female Peel Neck with young; (Belize).



Figure 3. Female Peel Neck scavenging in village; (Guatemala).

these estimates are only approximate due to the difficulty in identifying all chickens within a population.

Discussion and Conclusion

It has long been hypothesised that chickens with the naked neck trait have better production traits compared to normal feathered chicks when raised in hot climates

(> 30°C); an excellent review is given by Merat (1986), and studies examining the possible production advantages of naked neck trait chickens are still ongoing (Pesti *et al.*, 1996). This study has not specifically attempted to assess the productivity of the Peel Neck chicken. However, it is interesting to note that although no advantage of raising Peel Necks was identified by those who raise them, these chickens are widely kept in both nations, and possibly also other Central American countries.

Some authors have suggested that the Na gene is incompletely dominant, and homozygous chickens (Na Na) can be distinguished from the heterozygous chickens (Na na) because the former genotype has markedly reduced or no feathers on the front of the neck (Crawford, 1976; Scott and Crawford, 1977), and lack of feathers on the ventral face of the thighs and breast (Merat, 1986). The featherless areas in the chickens observed in this study were fairly consistent across the population, consistent with the Na gene being fully dominant as stated by Stevens (1991). The Na gene is on chromosome 1, which also carries

the gene for pea comb (P), and blue egg (O), however, no significant linkage was said to occur (Bitgood *et al.*, 1980). In this study, Peel Neck chickens consistently had single combs and tinted or light brown eggs. Most known populations of fowl having the naked neck trait are present in parts of the world that have a hot and humid climate (Merat, 1986). The Peel Neck is another example of fowl with this trait being raised under tropical conditions. Further studies are necessary to ascertain whether these chickens have any production-trait advantages over normally feathered chickens when kept in hot and humid conditions. This is of particular

relevance for chickens that are raised under challenging situations, for example as scavengers or in backyard systems.

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