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ANIMAL GENETIC RESOURCES INFORMATION

BULLETIN D'INFORMATION SUR LES RESSOURCES GÉNÉTIQUES ANIMALES

BOLETÍN DE INFORMACIÓN SOBRE RECURSOS GENÉTICOS ANIMALES

Food and Agriculture Organization of the United Nations
Organisation des Nations Unies pour l'alimentation et l'agriculture
Organización de las Naciones Unidas para la Agricultura y la Alimentación
UNEP
Initiative for Domestic Animal Diversity
Initiative pour la Diversité des Animaux Domestiques
Iniciativa para la Diversidad de los Animales Domésticos

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Editors - Editeurs - Editores:
S. Galal & J. Boyazoglu

Viale delle Terme di Caracalla 1, 00100 Rome, Italy

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FOOD AND AGRICULTURE ORGANIZATION OF THE UNITED NATIONS
ORGANISATION DES NATIONS UNIES POUR L'ALIMENTATION ET L'AGRICULTURE
ORGANIZACION DE LAS NACIONES UNIDAS PARA LA AGRICULTURA Y LA ALIMENTACION

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Editorial
The state of the world's animal genetic resources ?

Animal genetic resources (AnGR) contribute substantial inputs to and outputs from most food and agriculture production systems, and must be wisely used, developed and conserved, as part of efforts to achieve and sustain world food security and rural development. In view of this importance, and of the increasing pace of change, local, national and regional communities must be empowered to act based upon answers to such key questions as:

- Do we have essential baseline data and other information on the status of animal genetic resources to establish local community, country, regional and global priorities for their effective and efficient management over time?
- Do all communities and countries have the capacity to manage these resources, in an increasingly interdependent world?
- Do we have in place the appropriate methodologies and technologies to best understand, use and develop, conserve and access these resources, in a sustainable manner?
- Are AnGRs capable of increasing production and productivity, or at least productivity alone, whilst also maintaining the levels of product quality demanded by the consuming communitity, identified and deployed to the farmers of each of the full range of important production environments ?
- Do we have sustainable intensification programmes in place for those AnGR currently being used by farmers?
- Do we have an adequate understanding of the status of breeds that are currently not of value to farmers, and of wild relatives of the domesticated animal species, to provide the foundation for an Early Warning System for Animal Genetic Resources at risk of being lost, and to identify opportunities for the future use of these resources?
- Are we in a position to be able to identify situations where an emergency response could be considered to prevent the loss of animal genetic resources at risk?
- Do we have in place at the local, country, regional and global levels sustainable policies for wise use of AnGR?

The answer to these questions collectively seems to be no! This presents a real challenge for all those concerned with agricultural sustainable development and food security; whether they be farmers, researchers, educators, policy makers or administrators; and particularly if they are simply members of the consuming community; even more so if they are tomorrow's decision-makers, our children and theirs!

Through the help of its Member Governments and other national and international organizations, FAO has been assisting countries to establish breed databases, in DAD-IS, and publish two editions of the World Watch List for Domestic Animal Diversity that with analysis provide substantial amount of data on AnGR globally. But this data is far short from providing the information implied in the above questions which is needed for planning and implementing sound and sustainable management of our countryies'AnGR.

The issue of the State of the World's AnGR (SoW-AnGR) now and regularly updating this to monitor AnGR development, is now a topic of discussion by country delegations in FAO governing body sessions. It was an important item on the agenda of the FAO Commission on Genetic Resources for Food and Agriculture that convened during April 1999 with delegations from over 140 countries and organizations. Delegations

resolved that FAO should lead and coordinate the development of a country-driven Report on the State of the World's Animal Genetic Resource as funds become available.

The SoW-AnGR Report, will specfically establish essential baseline information in major areas: the state of animal diversity; the state of country capacity to manage animal genetic resources; the state of the art, the available methodologies and technologies to assist farmers, breeders and scientists to better describe, use, develop, conserve and access animal genetic resources, and thereby contribute to global food security and sustainable rural development.

The SoW-AnGR Report will establish the critical baseline data and information required to enable cost-effective AnGR Management activities to be planned and implemented at the local, country, regional and global levels. It will also provide the first reliable global outlook to examine potential future roles for animal genetic resources, and help project likely developments.

Finally, the first SoW-AnGR Report will help stimulate sustainable intensification of food and agriculture production of the broad range of production systems in countries, regions and globally.

The Editors

Editorial
Quel est l' état des ressources génétiques animales dans le monde?

Les ressources génétiques animales (AnGR), contribuent de façon importante autant qu'elles recueillent de la plupart des systèmes de production agricole et alimentaire. Elles doivent donc être utilisées avec précaution et développées et conservées, ceci dans le but d'atteindre et de maintenir la sécurité alimentaire et le développement rural dans le monde. Etant donné cette importance et le déroulement des changements en cours, les communautés au niveau local, national et régional doivent être en mesure d'agir en faisant face aux questions suivantes:

- Avons-nous les données de base essentielles et autres informations nécessaires sur la situation des ressources génétiques animales pour pouvoir établir les priorités, au niveau des communautés, des pays, des régions et au niveau mondial; quelle sera la gestion effective et efficace dans le futur?
- Est-ce que toutes les communautés et les pays possèdent les modalités nécessaires pour gérer ces ressources étant donné une toujours grandissant interdépendence mondiale?
- Avons-nous sur place les methodologies et technologies appropriées pour mieux comprendre, utiliser et développer, conserver et accéder à ces ressources de façon durable?
- Est-ce que les AnGR sont vraiment un moyen pour augmenter la production et la productivité, ou tout au moins seulement la productivité, tout en conservant la qualité des produits demandés par les consommateurs; identifier et déployer ses principes vers les agriculteurs de chacun des secteurs de production les plus importants?
- Avons-nous sur place des programmes d'intensification durables pour ces AnGR utilisées normalement par les agriculteurs?
- Possédons-nous une connaissance adéquate de la situation des races qui actuellement ne sont pas d'intérêt pour les agriculteurs, ainsi que des parents sauvages de ces espèces domestiques, pour jeter les bases pour un Système d'Alerte Rapide pour les AnGR qui sont en risque de disparition, et pour identifier les opportunités d'une utilisation future de ces ressources?
- Sommes-nous en position de pouvoir identifier les situations dans lesquelles une réponse urgente doit être prise en considération pour prévenir la perte de ressources génétiques animales à risque?
- Disposons-nous sur place, au niveau local, de pays, de région et au niveau mondial, de politiques durables pour une utilisation prudente des AnGR?

La réponse à cet ensemble de questions semble être non! Ceci représente un enjeu réel pour tous ceux concernés par le développement agricole durable et la sécurité alimentaire; aussi bien s'il s'agit d'agriculteurs, de chercheurs, d'enseignants, de politiciens ou d'administrateurs, et en particulier s'il s'agit simplement de membres de la société de consommateurs, encore plus si demain ils deviennent les "décideurs"!

A travers l'aide fournie par ses Gouvernements Membres et d'autres organisations nationales et internationales, la FAO a porté son aide aux pays pour établir des bases de données sur les races, DAD-IS, et a publié deux éditions de la Liste Mondiale de Surveillance pour la Diversité des Animaux Domestiques, qui, à travers son analyse, fourni un nombre important de données sur les AnGR au niveau mondial.

Cependant, toutes ces données sont bien loin de répondre aux questions posées précédemment, et qui sont nécessaires pour mettre en oeuvre et plannifier une gestion appropriée et durable des AnGR de nos pays.

La question de l'Etat Mondial des AnGR (SoW-AnGR) aujourd'hui et sa mise à jour régulière pour contrôler le développement des AnGR, est actuellement un thème de discussion durant les séances au sein des délégations des pays membres de la FAO. Il s'agissait d'un des points importants de l'agenda de la Commission pour les Ressources Génétiques pour l'Agriculture et l'Alimentation qui s'est réunie au mois d'avril 1999 avec les délégations provenant de plus de 140 pays et organisations. Les délégations ont conclus que la FAO devrait diriger et coordonner le développement d'un rapport-guide pour les pays sur l'Etat des Ressources Génétiques Animales (SoW) selon la disponibilité de fonds.

Le rapport SoW devra établir spécifiquement les bases d'information essentielles pour les thèmes principaux: la situation de la diversité animale; la situation de chaque pays à gérer les ressources génétiques animales; la situation actuelle, les méthodologies et technologies disponibles pour assister les éleveurs, les améliorateurs et les chercheurs à mieux décrire, utiliser, développer, conserver et accéder aux ressources génétiques animales, et ainsi contribuer à la sécurité alimentaire mondiale et au développement rural durable.

Le rapport SoW-AnGR établira les données guides indispensables et l'information requise pour permettre que les activités de gestion AnGR à plannifier et à mettre en oeuvre au niveau local, de pays, régional et au niveau mondial aient une bonne relation coût/efficacité. Ce rapport représentera aussi la première perspective fiable au niveau mondial pour examiner les futurs rôles potentiels des ressources génétiques animales et pour aider les projets de développement.

Finalement, le premier rapport SoW-AnGR servira à stimuler une intensification durable de la production alimentaire et agricole à large échelle dans les systèmes de production des pays, des régions et au niveau mondial.

Les Editeurs

Editorial
Cual es el estado de los recursos genéticos animales en el mundo?

Los recursos genéticos animales (AnGR) contribuyen en parte importante a los insumos y las producciones de la mayoría de los sistemas agroalimentarios. Deberían ser aprovechados, desarrollados y conservados prudentemente como parte del esfuerzo aunado para conseguir y sostener la seguridad alimentaria mundial y el desarrollo rural. Dada esta importancia, y debido al ritmo creciente de los cambios, las comunidades locales, nacionales y regionales deben tener la facultad para actuar basándose en las respuestas a preguntas clave como:

- Disponemos de datos fundamentales y de información adicional sobre el estado de los recursos genéticos animales para poder establecer prioridades en las comunidades local, nacional, regional y a nivel mundial para su gestión efectiva y eficiente a lo largo del tiempo?
- Todas las comunidades y países, tienen la capacidad de gestionar estos recursos en un mundo cada vez más interdependiente?
- Están puestas en práctica las metodologías y tecnologías apropiadas para entender, aprovechar y desarrollar al máximo los AnGR y para conservar y acceder a los mismos de una manera sostenible?
- Los recursos genéticos animales, son capaces de aumentar la producción y la productividad (o al menos esta última), manteniendo a la vez los niveles de calidad de los productos, exigidos por la comunidad de consumidores, identificados y puestos a disposición de los productores en cada parte del espectro de los medios importantes de producción?
- Existen en la práctica programas sostenibles de intensificación para los recursos genéticos animales utilizados actualmente por los ganaderos?
- Tenemos suficientes conocimientos sobre el estado de las razas que hoy día carecen de valor para los ganaderos, y de las especies salvajes relacionadas con las razas domesticadas, para establecer la base de un Sistema de Alerta para los AnGR en peligro de extinción, y para identificar las oportunidades para el aprovechamiento de dichos recursos en el futuro?
- Estamos preparados para identificar situaciones en las que una respuesta de emergencia sería necesaria para impedir la pérdida de recursos genéticos animales en peligro?
- Se están aplicando, a niveles local, nacional, regional y mundial, políticas sostenibles para un aprovechamiento juicioso de los recursos genéticos animales?

La respuesta global a estas preguntas parece ser negativa, lo cual presenta un verdadero desafío para todos los implicados en el desarrollo agrario sostenible y para la seguridad alimentaria, sean agricultores, ganaderos, investigadores, educadores, políticos o administradores; especialmente si son miembros de la comunidad de consumidores; más aún si son responsables políticos, y sobre todo ¡si de nuestros hijos y los suyos se trata!.

Mediante la ayuda de los Gobiernos de sus estados miembros y otras organizaciones nacionales e internacionales, la FAO ha estado ayudando a países a establecer bases de datos de razas, en DAD-IS, y ha publicado dos ediciones de la Lista Mundial de Vigilancia para la diversidad de animales domésticos, la cual ofrece bastantes datos sobre los recursos genéticos animales en el mundo. Pero estos datos están lejos de proporcionar la información implicada en las preguntas anteriores, necesaria para planificar y poner

en práctica una gestión firme y sostenible de los recursos genéticos animales de nuestros países.

La cuestión del Estado Mundial de los Recursos Genéticos Animales (SoW-AnGR) ahora, y su actualización periódica para hacer un seguimiento del desarrollo de AnGR, es actualmente tema de debate durante las sesiones por parte de las delegaciones nacionales de los países miembros de la FAO. Ha sido una cuestión importante en el orden del día de la Comisión de la FAO sobre los Recursos Genéticos para la Alimentación y la Agricultura que se convocó durante el mes de abril de 1999, con delegaciones proveniente de más de 140 países y organizaciones. Las delegaciones decidieron que la FAO debía liderar y coordinar el desarrollo de un informe impulsado por los países sobre el Estado Mundial de los Recursos Genéticos Animales a medida que vaya habiendo disponibilidad de fondos.

El informe SoW-AnGR establecerá específicamente cuál es la información fundamental en zonas principales: el estado de la diversidad animal; la capacidad de un país de gestionar recursos genéticos animales; la situación actual, las metodologías y tecnologías disponibles para ayudar a los ganaderos, mejoradores y científicos para mejor describir, utilizar, desarrollar, conservar y acceder a los recursos genéticos animales y así contribuir a la seguridad alimentaria global y al desarrollo rural sostenible.

El informe SoW-AnGR establecerá los datos fundamentales críticos y la información necesaria para permitir la planificación y puesta en práctica de actividades de gestión de AnGR a niveles local, nacional, regional y global. También proporcionará la primera visión global y fiable para examinar los papeles potenciales para los recursos genéticos animales en el futuro y para ayudar a proyectar posibles desarrollos.

Finalmente, el primer informe SoW-AnGR ayudará a estimular la intensificación sostenible de la producción agroalimentaria en el amplio espectro de sistemas de producción en los países, en las regiones y en el mundo.

Los Editores

Contribution to 25th Issue of AGRI from the Founder Editor

Animal Genetic Resources Information Bulletin (AGRI) was established jointly by FAO and UNEP in 1983 as a new global journal. Funds for the first four years were provided by UNEP while development, editorial and publication tasks were undertaken by FAO.

To understand the reason for the start of AGRI it may be recalled that a mere 15-20 years ago the conservation of domestic animals was a novel idea that, for many people, ran counter to the aims of livestock improvement. The concept of conservation as an important component of agricultural biodiversity surfaced at the first UN Conference on the Environment in Stockholm in 1972 as a result of which UNEP was created.

FAO worked closely with UNEP and in 1980 they convened a Joint FAO/UNEP Member Country Expert Consultation in Rome on "The conservation and management of animal genetic resources" under the independent chair of Dr. Helen Newton-Turner of Australia. This Consultation was not for experts in their own right. Participants were nominated by their governments and came as representatives of the member countries of FAO and UNEP. Thus, the recommendations were directed to FAO and UNEP from the member countries. I represented Canada at this Consultation.

Until that time, the thrust of FAO's support to governments for livestock improvement had been to increase production and productivity. A major component of the FAO and of some government bi-lateral programmes had been the provision of semen from Black and White cattle to developing countries. This practice was later judged to be misplaced from a production point of view and was discontinued. Further, the practice was diluting the gene pools of indigenous cattle.

Little was known about the numbers, condition and genetic parameters of indigenous breeds at that time in either developed or developing countries. Documentation was sparse, often unpublished, poorly classified and inaccessible. The 1980 Consultation recommended that FAO and UNEP should co-finance and that FAO should establish:

1. Classification criteria for endangered breeds;
2. Technical methods and standards for live and cryogenic conservation;
3. Methods of conservation;
4. Regional data and gene banks;
5. Comprehensive documentation of livestock breeds in China and the USSR;
6. Training in conservation methods;
7. A series of technical publications on animal conservation;
8. A Newsletter.

Based upon these recommendations, UNEP provided funds and FAO undertook the tasks by adding them to the existing livestock improvement responsibilities of the Senior Officer for Animal Breeding in the Animal Production and Health Division (AGA) without at that time, it might be added, any increase in human resources. I was appointed to the enlarged position in 1982, thereby becoming the Founder Editor of AGRI and serving until 1990. All the recommendations of the 1980 Consultation were either completed or launched during the 1980s.

The Newsletter was intended to support the increasing number of individuals, NGOs and a few governments throughout the world that were beginning to work on the conservation of animal genetic resources. These people were isolated, frequently lacked technical direction, experience and funds. The Consultation urged that the Newsletter should be sent free of cost to all who were interested. There were two special aims:

1. To provide all those involved in Animal Genetic Resources Conservation and Management with information;
2. To offer a specialized journal for publication of papers on Animal Genetic Resources Conservation and Management, since this topic was often viewed as irrelevant at the time by some of the major animal science journals.

25 issues and 16 years later it seems strange that this major field of animal genetics should have been so late in developing.

The Newsletter was enthusiastically supported from the start by a growing number of contributors and readers and, under the present Editorship, has continued to expand and to contribute meaningfully to the conservation of animal genetic resources. In my view, it has been a significant factor in changing the perspectives of scientists, governments and development practitioners to include both livestock utilization and conservation as essential partners in livestock improvement now and in the future.

Dr. John Hodges
Founder Editor of AGRI

Past, present and future

Is issue 25 of a journal of any particular importance? At least in this case it means 16 years of interactions and some 2 000 pages of inputs. It all started at a time when people interested in the conservation of Animal Genetic Resources (AGR) were *a minute minority*, euphemistically speaking *a species on its way to extinction*. Today, seven years after the Rio de Janeiro Summit, the terms *AGR* and *Biodiversity* are truly *a la mode*.

The extraordinary development of science and technology these past decades was particularly marked by the progress of biotechnologies, the extent of their actual application and the potential and dangers they could introduce in the future. Thus, the many crises we had to address these past couple of years oblige us to renewed attention in the relationship Biosciences-Society. Ethics are now again *news* and questioning the advances of science, the benefits and implications, the successes and the challenges is today integral part of any daily exercise, actions and reactions. In this complex, new but fundamental thinking, biodiversity becomes a master-card.

It is known that indigenous AGRs are well adapted to the marginal regions and extensive difficult grazing territories of the world and are mostly linked to the manufacture and availability of traditional products of animal origin. Their conservation must thus be seen as a mission of local and regional collective interest. They must be fully incorporated as one of the decisive factors of the prevailing livestock production systems.

Having said that and having been directly and actively involved with AGR conservation and use since 1960, I can dare wonder if we have not been in recent years overstating sometimes the *specific importance* of this field of animal agriculture. AGR should be dealt within the overall context of the Animal Production Sector, including Livestock Systems and Global Rural Biodiversity, not as a mystified study field apart.

The Animal Genetic Resources Information Bulletin (AGRI) launched in the early 80s by John Hodges, stopped appearing in the late 80s because of cutbacks in the FAO Regular Programme Budget. As soon as this problem could be solved, around 1991 with UNEP's further meaningful support, it seemed indispensable to resume this publication medium through which colleagues from around the world and in particular those from developing countries could share their information and know-how on farm animal breeds without the constrains of a too sharp formalism. This is also true for the great number of interested people who are not directly concerned with research, such as breed associations, NGOs, INGOs and hobby breeders.

The new AGRI was designed and developed as a support for the circulation of results, reviews, point of views and opinions that a strictly scientific publication would not publish.

It is necessary to underline, at this stage, that this bulletin is one of the most cost-effective venues of its sort and is partially run on a voluntary basis.

There are three distinct periods in AGRI's life (figure 1). The first one can be called the *birth and first difficult steps* (1983-1987) followed by two years of no activity due to financial constraints and the departure of the founder and first editor, John Hodges. The second period, (1991 to 1995; Co-Editors: Daniel Chupin and Jean Boyazoglu) corresponds to a time of *growth and worldwide*

Figure 1. Number of pages published per year.

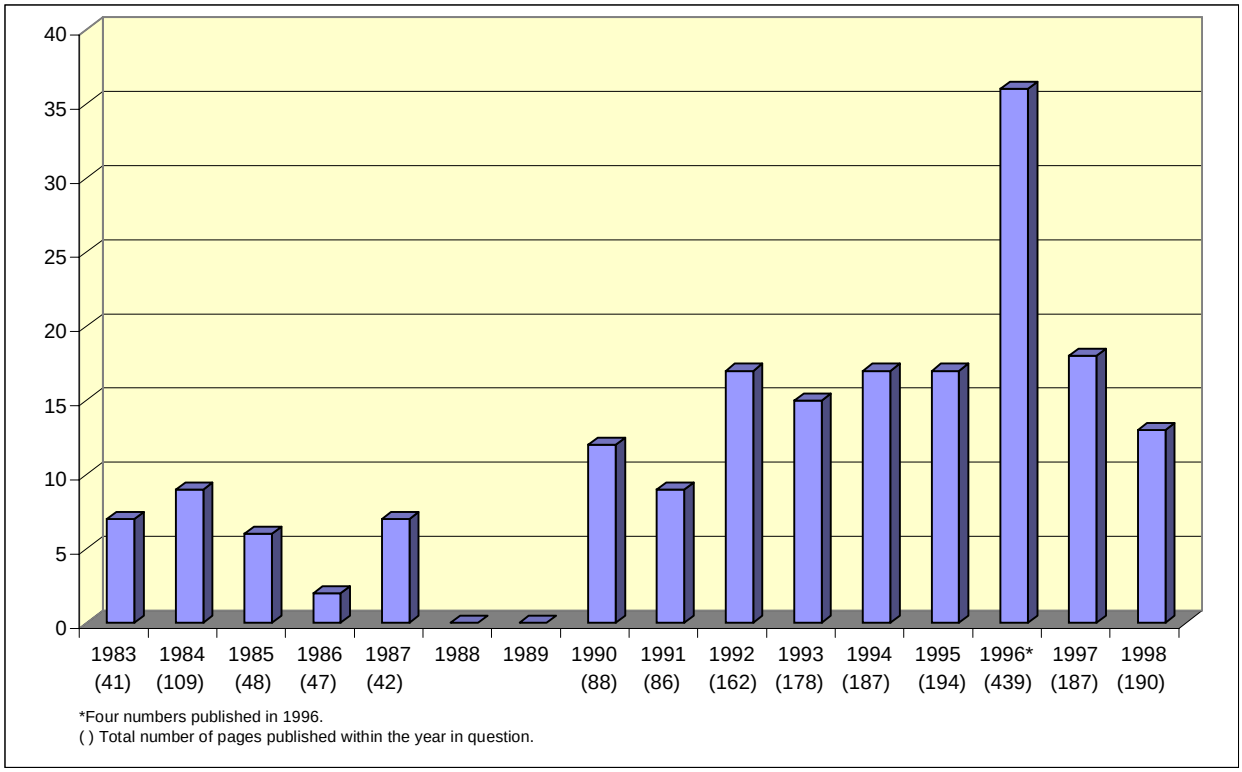


Figure 2. Number of articles published from different regions of the world.

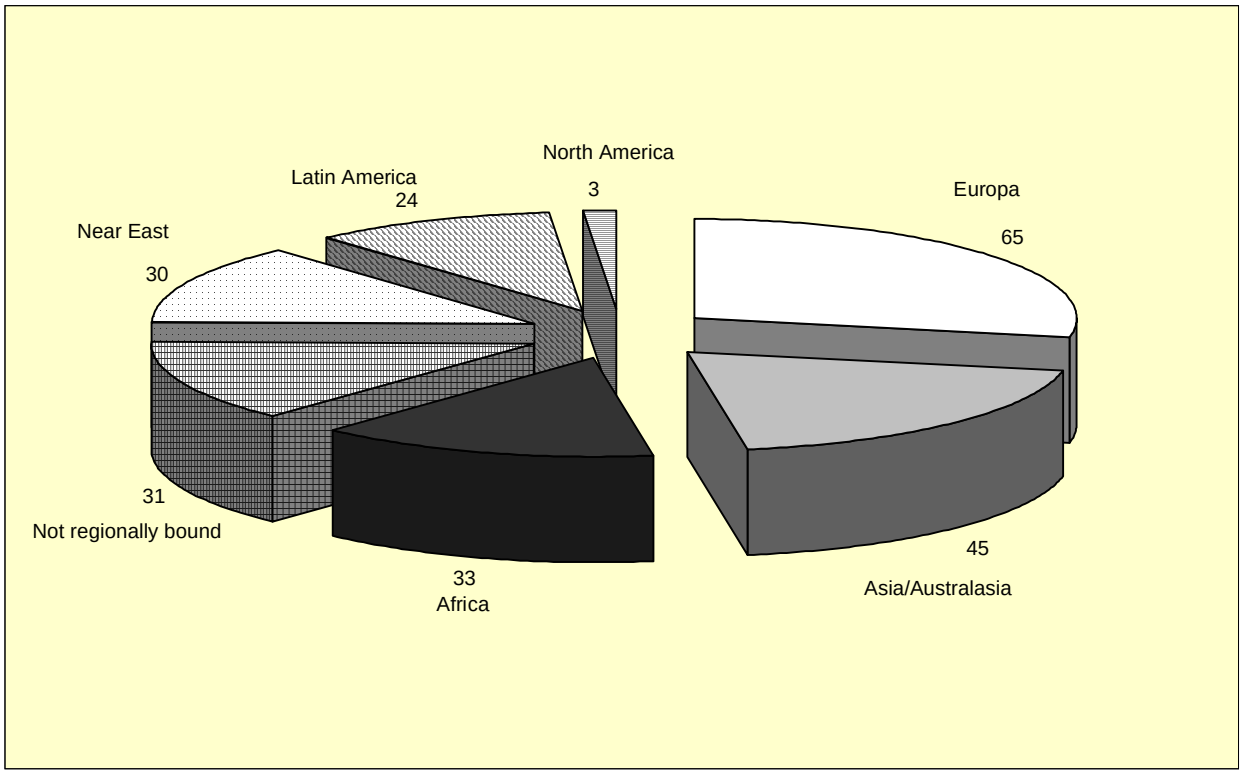
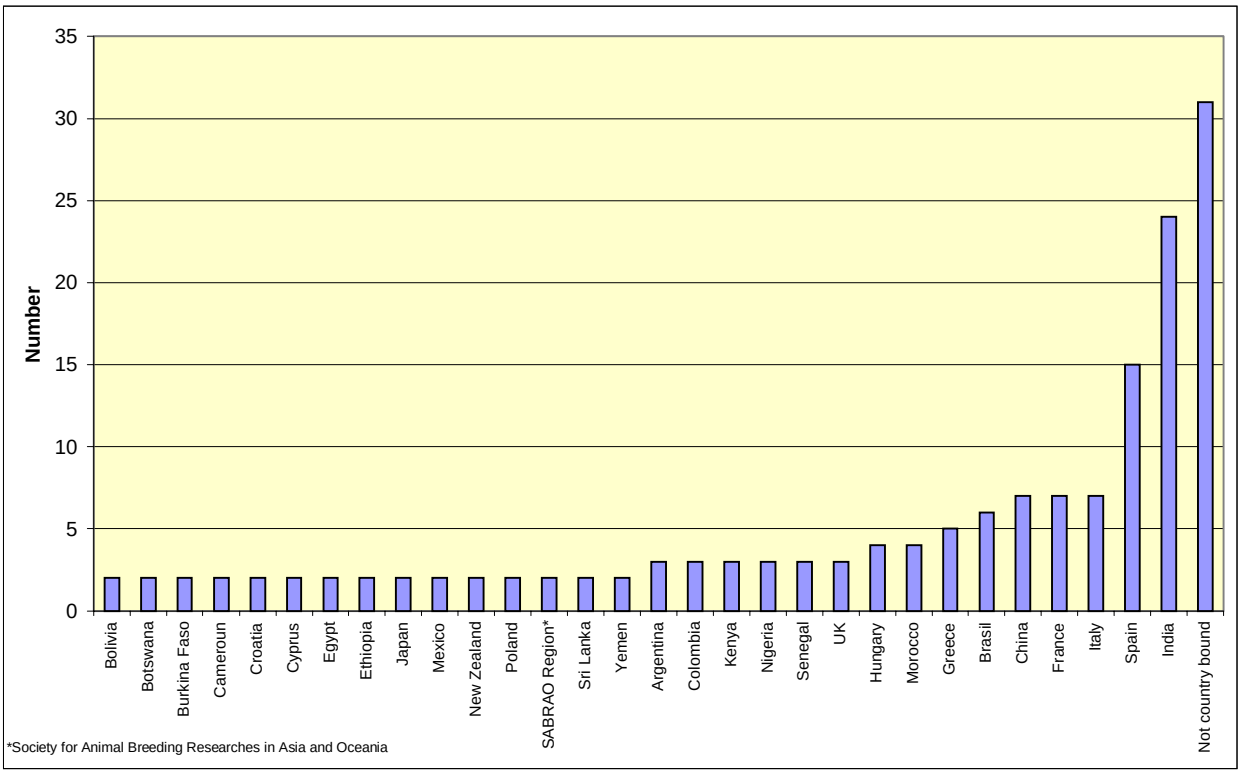


Figure 3. Countries with more than one paper published in AGRI.



recognition of the bulletin's value. The third period (1996 to date; Co-Editors: Salah Galal and Jean Boyazoglu) is one of *enhancing the journal's status, important changes in format and presentation, much more selective choice of the material published and the electronic publication on the Internet and in a CD ROM.* This period also correspond to the development of FAO's Global Strategy. While in the early years we had to struggle to obtain manuscripts, and in many cases had to rewrite them completely to meet linguistic and technical standards and needs, today we can be more discriminative: from 61 papers received since AGRI no. 19, 45 manuscripts were published or accepted for publication, while 5 are pending; thus a rejection rate of around 20%.

We mostly try to publish two issues per year, though there are some exceptions such as the year 1996 with four issues and 439 pages published; we had to find extra funding to meet the need of clearing the backlog of manuscripts. The average number of pages published per issue was around 50 in the 80s, moving up to 100 in the 90s. The issues dated 1990 correspond to the backlog of articles that were received during the 1987-1989 period; they were edited for publication in early 1991.

The 201 articles published in the 25 issues (figure 2) originated from Europe(33%), from Asia/Australasia (24%), from Africa (16%), from Latin America (12%), from Near East (4%) and from North America (2%); the remaining articles (19%) did not concern a specific region of the world. In particular, the geographic origin (country/subregion) of the material analysed in the published papers is given in figure 3 and table 1. The distribution of the articles shows that papers concerning the main ruminants (cattle, sheep and goats) and horses are in the great majority (figure 4) although the interest goes from pigeons to rabbits and from donkeys to yak and buffaloes.

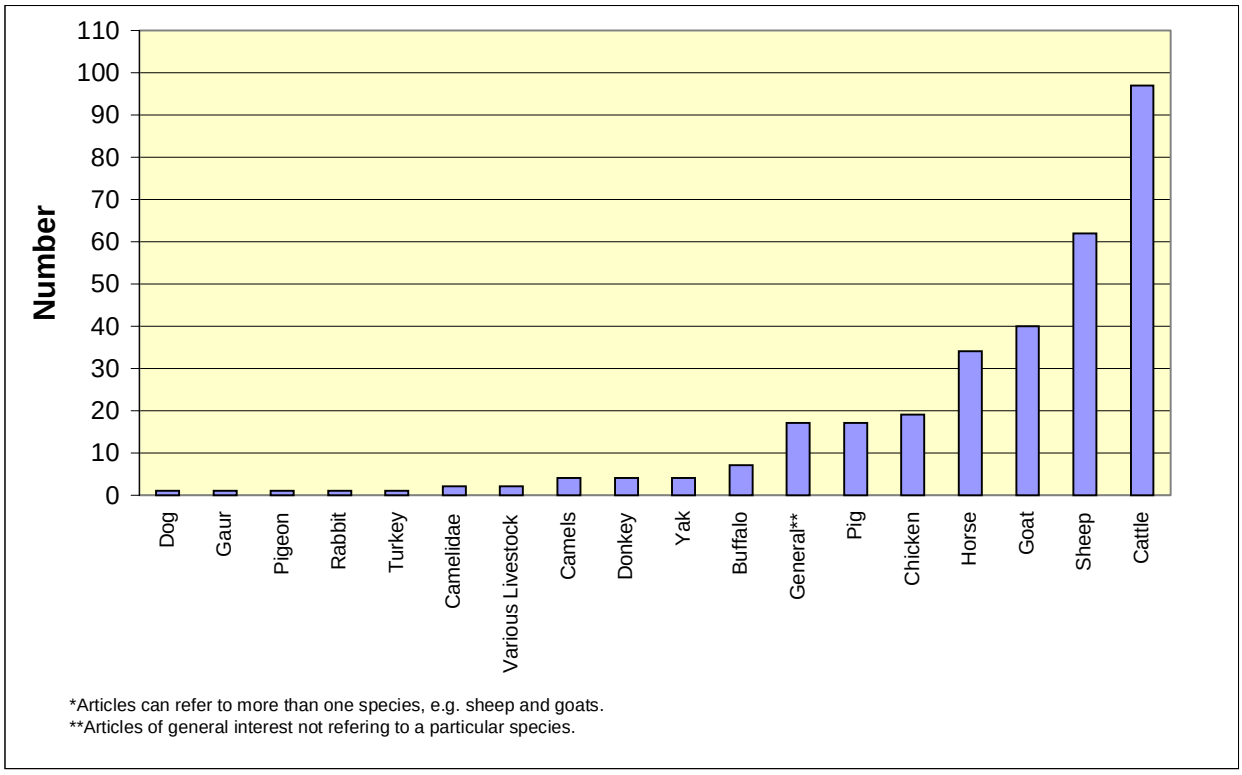
In 1997 we launched a questionnaire (see annex) to update our database and individual circulation list; this excluded libraries and

Table 1. Countries with only one paper published.

Albania	Ivory Coast	Togo	European Nordic Countries*
Algeria	Korea	Uganda	Latin America*
Benin	Latin America	Ukraine	Mediterranean basin*
Bhutan	Malawi	Uruguay	North America*
Bulgaria	Malta	USA	Sub-Saharan francophone countries*
Burundi	Mauritania	USSR (Russia Fed.)	West and Central African countries*
Canada	Peru	Vietnam	
Chad	Russia	Yugoslavia	
Cile	Saudi Arabia	Zanzibar	
Cina	Scandinavia	Central and Eastern European countries*	
Denmark	Somalia		
Estonia	South Africa		
Germany	South America	Central Asia*	
Guatemala	Tanzania	Europe*	

*Papers refering to subregions.

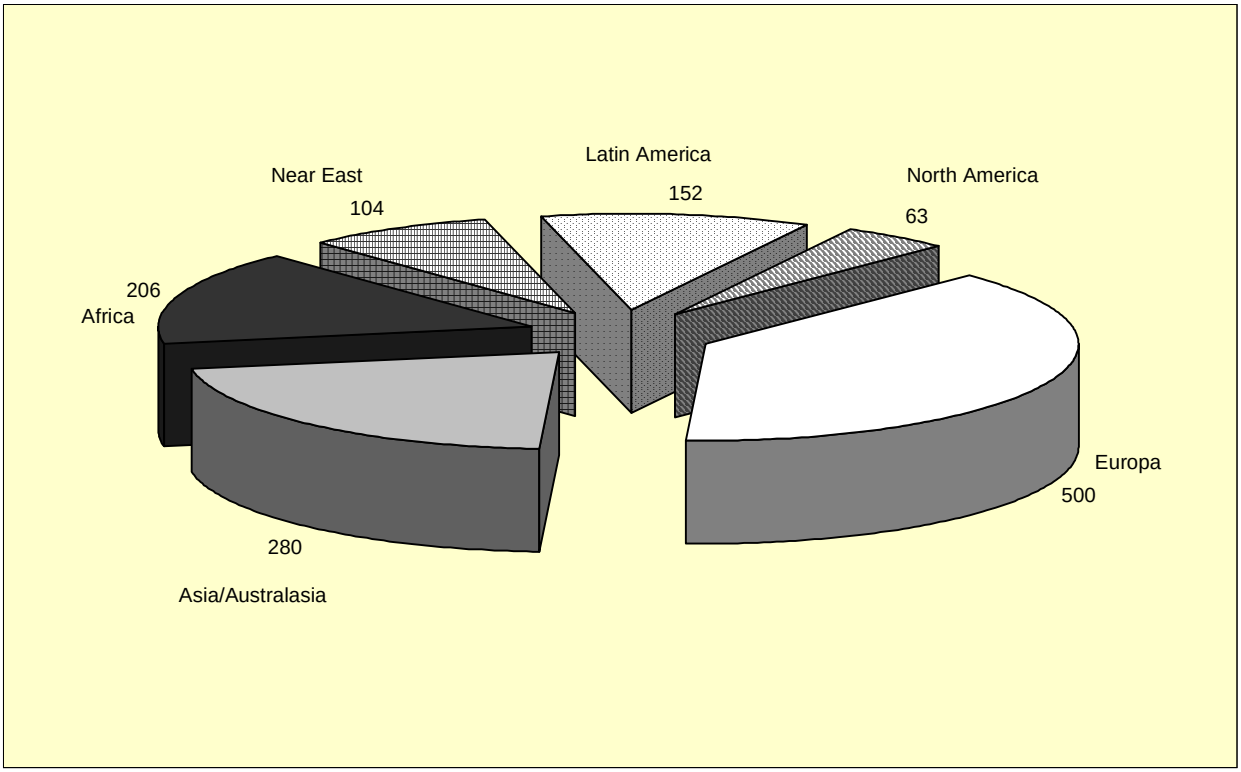
Figure 4. Number of articles published in AGRI, per species.*



institutions. We received 1 305 valid answers with an arbitrary division of 1/2 English, 1/4 French and 1/4 Spanish speaking *readers*. The geographic distribution of the readership that correctly answered the questionnaire (figure 5) was just over 38% from Europe (many from Eastern and Southern Europe), 21% from Asia/Australasia, 16% from Africa, 12% from Latin America, 8% from the Near East; less than 5% of the readership being from North America. Thus, a majority of the individual readers who personally receive AGRI are from less developed countries or countries in transition. Italy (table 2) has the largest national individual readership (136) followed by India (89) and Spain (65). The readers of AGRI are shown to be mainly involved with teaching, training and research (figure 6) while the main *fields* of interest are small ruminants (sheep and goats) and the cattle sector, followed by genetics and breeding (figure 7).

While defending the idea that this bulletin must accept all types of articles giving information on domesticated animal breeds, we realised very soon the need to standardise as much as possible the form and presentation to help the authors present better prepared articles and the readers to have more comprehensible material while giving the minimum necessary information relating to the breeds and line comparisons, within the framework of the locally prevailing production systems. Since the beginning we encouraged authors to include a maximum of photos and graphics which are more explicit than long discourse; maps, even sketchy ones, allowing a better localisation of the population described and its distribution than listing geographic names. This approach was received very favourably as shown by the growing number of interesting manuscripts received for the publication. This allowed to assure the regular publication of AGRI in the

Figure 5. Number of AGRI subscribers in the different regions of the world.*



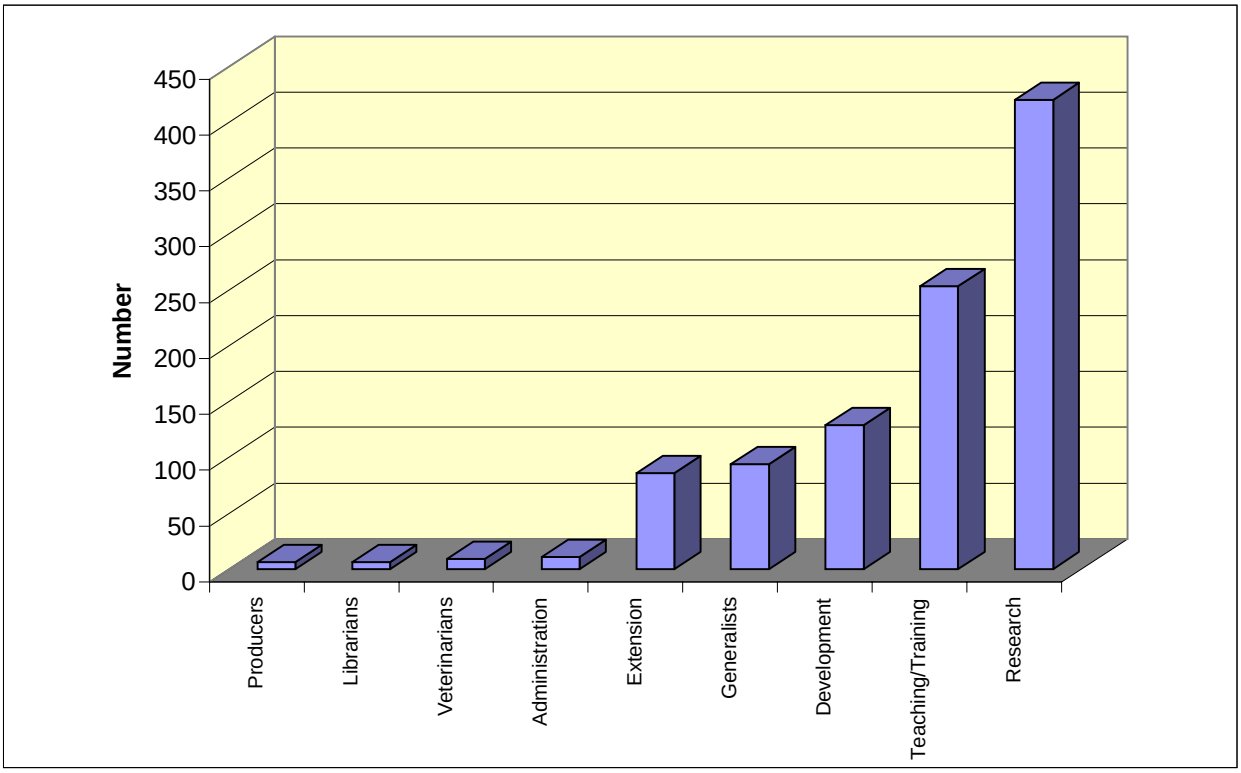
*This figure refers only to those *individual readers* who answered the 1997/1998 questionnaire.

Table 2. Individual country readership distribution of AGRI.

Class	Country
1-5 readers	Albania, Algeria, Angola, Antigua and Barb, Austria, Bahrain, Barbados, Benin, Bermuda, Bhutan, Bolivia, Bosnia and Herzegovina, Botswana, Bulgaria, Burundi, Cambodia, Cameroon, Cape Verde, Central African, Chad, Taiwan, Congo, Congo, Cook Islands, Costa Rica, Croatia, Cyprus, Czech Republic, Dominican Republic, Ecuador, El Salvador, Equatorial Guinea, Eritrea, Estonia, Falkland Islands, Fiji, Finland, French Guyana, Gambia, Guadeloupe (France), Guam (USA), Guatemala, Guinea, Guinea-Bissau, Guyana, Haiti, Honduras, Hungary, Iceland, Iran, Islamic Re, Ireland, Israel, Jamaica, Jordan, Kazakhstan, Korea, Kuwait, Kyrgyz Republic, Laos, Latvia, Lebanon, Lesotho, Liberia, Libya, Lithuania, Luxembourg, Macedonia, Madagascar, Maldives, Malta, Mauritania, Mauritius, Moldavia, Mongolia, Mozambique, Myanmar, Namibia, Netherlands Antilles, New Zealand, Nicaragua, Niger, Oman, Papua New Guinea, Puerto Rico (USA, Romania, Russian Federation, Rwanda, Samoa, Saudi Arabia Kingdom, Sierra Leone, Slovakia, Slovenia, Solomon Islands, Sri Lanka, Swaziland, Tanzania, Togo, Trinidad and Tobago, Tunisia, Uganda, Ukraine, United Arab Emirates, Vanuatu, Venezuela, Vietnam, Yemen, Yugoslavia, Zambia
6-10 readers	Argentina, Bangladesh, Burkina Faso, Ivory Coast, Cuba, Denmark, Ethiopia, Ghana, Greece, Iraq, Malawi, Malaysia, Mali, Morocco, Nepal, Norway, Poland, Portugal, South Africa, Syria, Turkey, Uruguay, Zimbabwe
11-15 readers	Colombia, Indonesia, Japan, Kenya, Peru, Senegal, Sudan, Sweden, Thailand
16-20 readers	Australia, Chile, Mexico, Nigeria, Pakistan, Switzerland
21-30 readers	Belgium, Canada, China, Netherlands, Philippines
31-42 readers	Brazil, Egypt, France, Germany, United Kingdom, United States of America
65 readers	Spain
89 readers	India
136 readers	Italy

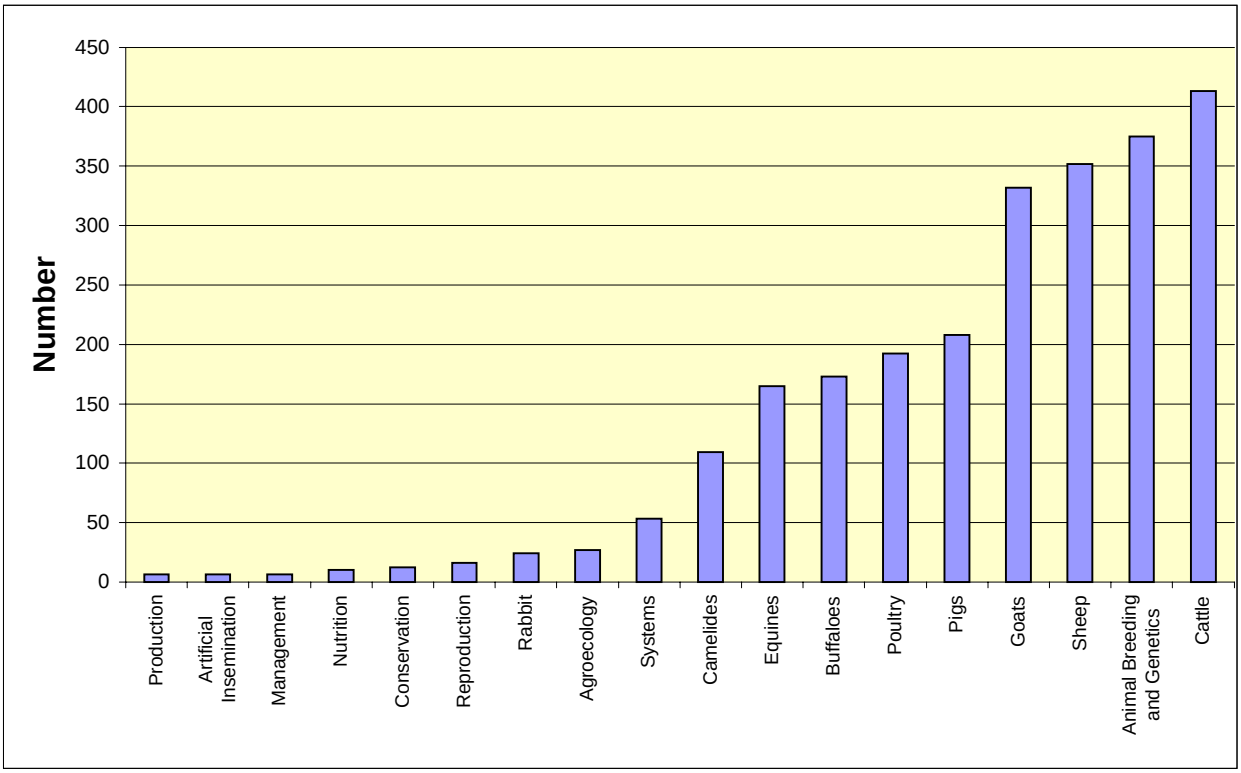
This table refers only to those *individual readers* who answered the 1997/1998 questionnaire, (1305 valid answers received).

Figure 6. Main responsabilities of AGRI readers.*



*Many readers may have two or more responsabilities, e.g. research and teaching.

Figure 7. Main interests of AGRI readers.*



*Many readers may have two or more interests, e.g. sheep and goats or reproduction and pigs.

years 1992-1996 and also considerably increased the number of pages per issue. Evidently the regular flow of AGRI depends and will depend even more in the future on the availability of the necessary funds and the collaboration and voluntary input of all persons involved with the publication.

As the one that has been the longest involved voluntarily with the journal, I should underline that, in my humble opinion, a very important feature of AGRI is that it is one of the few remaining FAO periodicals offered free of cost to all those requesting it in writing, in line with the strong recommendations made by the Country Expert Consultation in 1980. In this respect, the very meaningful financial and moral support of UNEP must be acknowledged. It is important also to refer here to the loyalty of this journal's readership, the great majority of which is in the developing world. The number of answers received (more than 1 500 of which 1 305 correctly filled in) to the 1997-98 questionnaire is an impressive showing of interest in the journal; over 75% of the questionnaires circulated to the global individual readership (some 2 000 addresses) has been duly filled-in and returned!

Jean Boyazoglu
Co-Editor of AGRI

Animal Genetic Resources Information

S. Galal and J. Boyazoglu (Editors)
FAO, Animal Production and Health Division
Via delle Terme di Caracalla, 00100 Rome, Italy
Room C-579; tel.: +39-6-57056139; fax.: +39-6-57053927; Email: <Salah.Galal@fao.org>

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Occupation: • Research • Teaching/training • Development
• Extension • Others (pls. specify) .....

Specialization: • Animal breeding and genetics • Generalist • Systems
• Others (pls. specify) .....

Species of interest: • Buffalo • Camelides • Cattle • Equines (horse, ass, etc.)
• Goat • Sheep • Pig • Poultry
Others (specify):.....

Signature.....

Date.....

The state of African cattle genetic resources I. Classification framework and identification of threatened and extinct breeds

J.E.O. Rege

*International Livestock Research Institute (ILRI), P.O. Box 5689, **Addis Ababa**, Ethiopia*

Summary

A field and literature survey was conducted to determine the status of cattle genetic resources of sub-Saharan Africa and to identify cattle breeds at risk and those which may have become extinct over the last century. This paper - in two parts - summarises preliminary results of the survey. The survey revealed that sub-Saharan Africa is home to a total of 145 cattle breeds/strains comprising two taurine Longhorns, 15 taurine Shorthorns, 75 zebu *(Bos indicus*), 30 sanga, eight zenga (zebu-sanga), nine breeds derived from interbreeding of indigenous breeds/strains located in close proximity to each other, and six systematically created composite breeds. Out of the 145 breeds identified from the survey, 47 (about 32%) were considered to be at risk of extinction. Risk categories used were: Critical (most severe), Endangered, Vulnerable, and Rare (least severe). Of the breeds identified to be at risk of extinction, six were in the "Rare" category, 10 were "Vulnerable", another 10 were "Endangered" and 15 were in the "Critical" category. A total of 22 breeds (about 13%) previously recognised in the continent have become extinct in the last century. This number excludes some populations which have lost their individual identity due to admixtures involving two or more originally distinct breeds.

Resumen

Se llevó a cabo un estudio bibliográfico y de campo para determinar cuál era el estado de los recursos genéticos ganaderos del Africa subsahariana y para identificar las razas ganaderas en peligro así como aquellas que se hayan podido extinguir durante el último siglo. Este artículo, dividido en dos partes, resume los resultados preliminares del estudio. El estudio reveló que el Africa subsahariana alberga un total de 145 razas bovinas/estirpes, comprendiendo dos razas taurinas Longhorn, 15 Shorthorn, 75 zebu (*Bos indicus*), 30 sanga, 8 zenga (zebu-sanga), 9 razas derivadas de cruzamientos entre razas autóctonas y estirpes estrechamente relacionados y 6 razas compuestas creadas de forma sistemática.
De los 145 razas identificadas en el estudio, 47 (alrededor del 32%) se consideraron en peligro de extinción, las categorías de riesgo utilizadas siendo las siguientes: crítica (más severa), en peligro, vulnerable, y rara (menos severa). De las razas identificadas como en peligro de extinción, seis se encontraban en la categoría "rara", 10 eran "vulnerables", otras 10 estaban "amenazadas" y 15 estaban en la categoría "crítica". Un total de 22 razas (alrededor del 13%) previamente reconocidas en el continente se han extinguido en el último siglo. Esta cifra excluye algunas poblaciones que han perdido su identidad individual debido a mezclas entre dos razas originalmente distintas.

Key Words: *Breed classification, Cattle, Endangered breeds, Extinct breeds, Phenotypic diversity, Sub-Saharan Africa.*

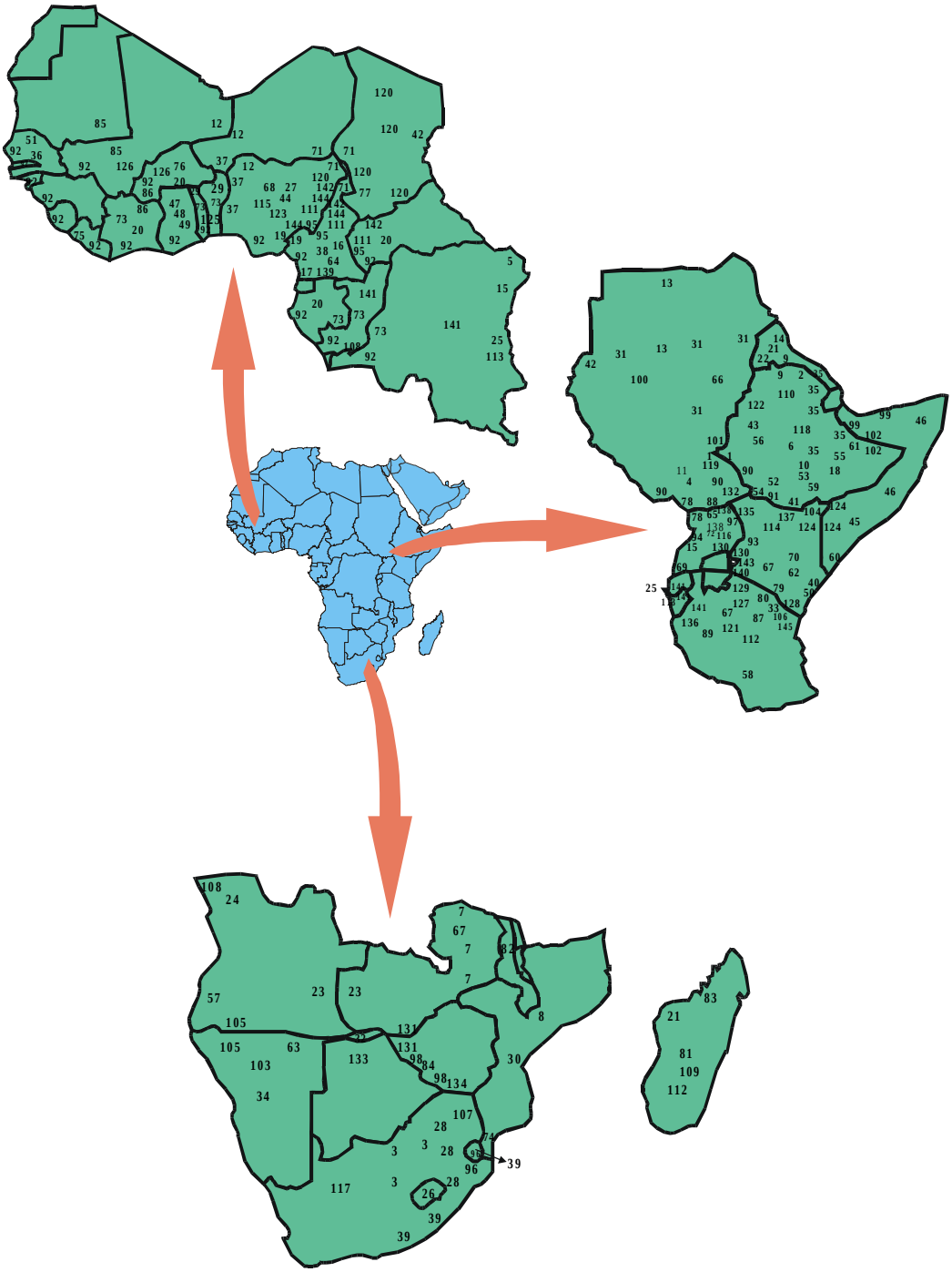

Figure 1. Distribution of cattle breeds in some African countries

Introduction

The origins of indigenous cattle of Africa still remain uncertain despite available archaeological, anthropological and historical evidence (Epstein and Mason, 1984; Blench, 1993). It is generally accepted that the African cattle populations arose from three main phases of introduction from Asia through the Nile valley in Egypt or via the Horn of Africa.

Subsequent migrations led to dense populations of cattle in the East African highlands, around the present-day Ethiopia

List of breed codes reported in figure 1

1.Abigar
2.Adwa
3.Afrikaner
4.Aliab Dinka
5.Alur (Nioka, Blukwa)
6.Ambo
7.Angoni
8.Angonia (Angone)
9.Arado
10.Arsi
11.Aweli Dinka
12.Azaouak (Tuareg)
13.Baggara
14.Baherie
15.Bahima
16.Bakosi
17.Bakweri
18.Bale
19.Banyo
20.Baoulé
21.Baria
22.Barka
23.Barotse
24.Barra do Cuanzo
25.Bashi
26.Basuto
27.Biu
28.Bonsmara
29.Borgou
30.Bovines of Tete
31.Butana
32.Caprivi
33.Chagga (Wachagga)
34.Damara (Herero)
35.Danakil
36.Djakore
37.Djelli (Diali)
38.Doayo (Namichi)
39.Drakensberger
40.Duruma
41.Ethiopian Boran (Borana)
42.Fellata (Bororo)
43.Fogera
44.Forest Muturu
45.Garre (Gherra)
46.Gasara
47.Ghana "sanga"
48.Ghana Dwarf Muturu
49.Ghana Shorthorn
50.Giriama
51.Gobra
52.Goffa
53.Guraghe
54.Hammer
55.Harar
56.Horro
57.Humbi
58.Iringa Red
59.Jem-Jem
60.Jiddu
61.Jijiga
62.Kamba
63.Kaokoveld
64.Kapsiki
65.Karamajong zebu
66.Kenana
67.Kenya (Improved) Boran
68.Keteku
69.Kigezi
70.Kikuyu
71.Kuri
72.Kyoga
73.Lagune
74.Landim
75.Liberia Dwarf Muturu
76.Lobi
77.Logone
78.Lugware
79.Maasai (Kenya)
80.Maasai (Tanzania)
81.Madagascar zebu
82.Malawi Zebu
83.Manjan'i Boina
84.Mashona
85.Maure
86.Méré
87.Mkalama Dun
88.Mongolla
89.Mpwapwa
90.Murle
91.Mursi
92.N'Dama
93.Nandi
94.Nganda
95.Ngaundere
96.Nguni
97.Nkedi
98.Nkone
99.North Somali Zebu
100.Nuba Mountain Zebu
101.Nuer
102.Ogaden
103.Okavango
104.Orma Boran
105.Ovambo
106.Pare
107.Pedi
108.Porto-Amboim
109.Rana (Omby Rana)
110.Raya-Azebo
111.Red Fulani
112.Renitelo
113.Ruzizi
114.Sabmuru
115.Savanna Muturu
116.Serere
117.Shangan
118.Sheko
119.Shilluk
120.Shuwa
121.Singida White
122.Smada
123.Sokoto
124.Somali Boran
125.Somba
126.Sudanese Fulani (Peul Zebu)
127.Sukuma (Tinde)
128.Taita
129.Tarime (Shashi)
130.Teso
131.Tonga
132.Toposa
133.Tswana
134.Tuli
135.Turkana
136.Ugogo Grey
137.Unimproved Boran (Borana)
138.Usuk
139.Wakwa
140.Watende
141.Watusi
142.White Fulani
143.Winam (Kavirondo)
144.Yola
145.Zanzibar Zebu

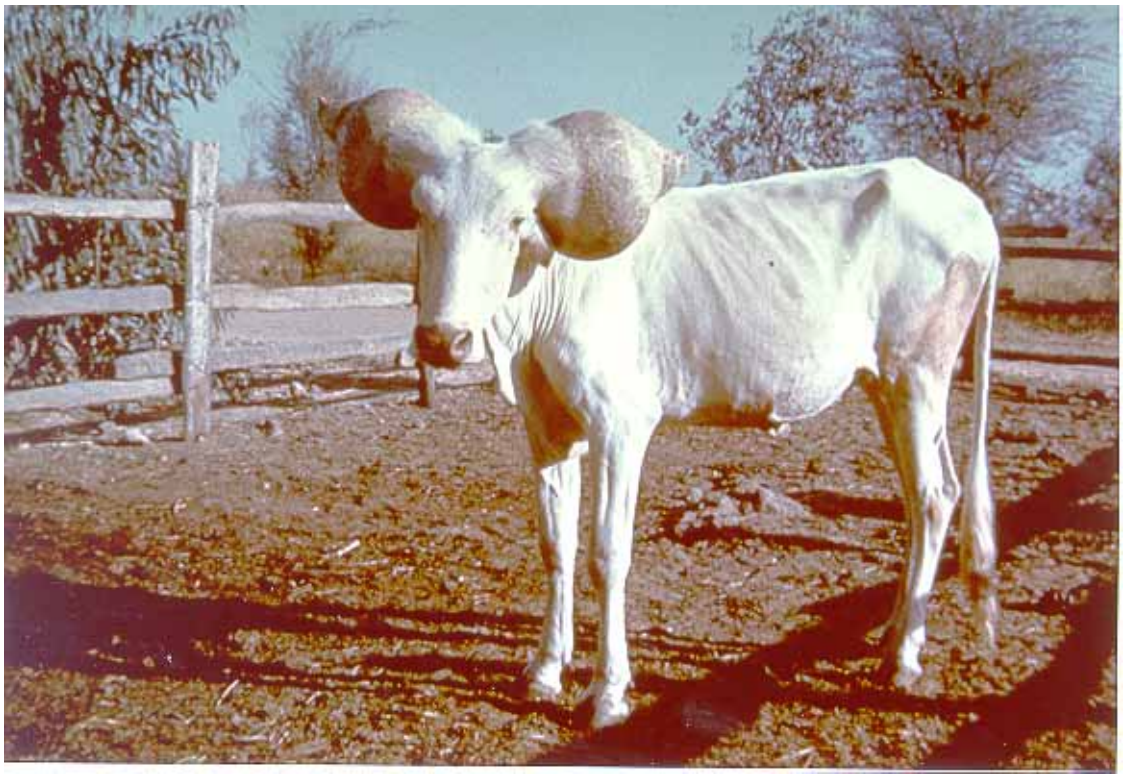

Figure 2. Kuri cattle.

and Kenya. The humpless Longhorns arrived in the continent approximately 5000 BC, followed by the humpless Shorthorns around 2500 BC. Humpless Shorthorn cattle were historically distributed in almost all ecological zones. Isolated populations were recorded in Sudan and Central Tanzania in historical times and remnant populations still exist in Ethiopia. The humped zebu first arrived about 1500 BC and later in large numbers around 670 AD (Eptsein, 1971). The first zebu cattle in Ethiopia are thought to have been brought through Somalia by Semitic people from Arabia, and their subsequent interbreeding with the taurine Longhorns are considered to have produced the present-day sanga cattle, although recent (unpublished) evidence from ILRI work questions the "crossbred origin" of the sanga. The second introduction of zebu cattle led to a major replacement of sanga cattle from most parts of eastern Africa, emergence of intermediate zebu-sanga breeds in some cases, and separate evolution into different strains in the diverse ecological zones. The zebu cattle further spread westwards and southwards to become the major group of cattle in the region bordered by latitude 20°N in northern Sudan, in the north, the western rain-forest barrier in the west and the Zambezi river, latitude 15°S, in the south.

Present-day African cattle can be classified into four broad categories: the humpless *Bos taurus,* widely distributed in West and Central Africa; the humped *Bos indicus* (zebu), distributed widely in eastern and the dry parts of West Africa; the sanga, found mainly in eastern and southern Africa; and sanga x zebu types ("zenga") found in eastern Africa. The taurine (humpless) type has two groups, Longhorns (*B. taurus longifrons*) and Shorthorns (*B. taurus brachyceros*), both of which are restricted to West and Central Africa.

In addition to the four broad groups of African cattle, there are more recent derivatives that have resulted either as a consequence of close proximity of two or more indigenous populations, sometimes accelerated by deliberate crossing (e.g. the Borgou, Méré and Ghana Sanga of West

Africa), or as a product of efforts to create composite commercial breeds (e.g. the Bonsmara of South Africa and the Mpwapwa of Tanzania).

There is very little information on the diversity in indigenous African livestock populations, both at phenotypic and genetic levels. Indeed, not even the number of breeds of the various species is known. Working estimates are: 100-150 indigenous cattle, 50-60 sheep and 45-50 goat breeds in sub Saharan Africa (Rege, 1998). Additionally, with very few exceptions, there is no data on the population sizes of the different breeds and their status, i.e. whether their numbers are decreasing, increasing or stable.

About the Survey

Starting in 1992, the International Livestock Centre for Africa (ILCA), now the International Livestock Research Institute (ILRI), initiated activities aimed at determining the status of, and compiling information on characteristics of, indigenous African domestic ruminant livestock, specifically cattle, sheep and goats. These activities consisted of:

1) sending out mail questionnaires to scientists in national programmes;
2) field visits to assess the status of individual breeds/populations identified from questionnaires;
3) requests for specific information from collaborating scientists;
4) conduct of rapid surveys in selected countries or of selected breeds/populations within a country; and
5) review of literature, especially the non-conventional (grey) publications such as annual reports, proceedings of national meetings (conferences, seminars), research project reports, etc.

In addition to these sources, a substantial amount of information was obtained from field expeditions conducted during a continent-wide exercise to collect blood samples for molecular characterisation, to quantify between- and within-population genetic diversity at the DNA level, which is part of ILRI's overall programme on animal genetic resources. Field visits included interviews with government officials, national scientists and farmers. The aim of the interviews was to obtain, for each breed/population, indications of:

1) major uses;
2) trends (decreasing, increasing or stable) as perceived by local communities, extension personnel and scientists;
3) possible reasons for the perceived trends;
4) phenotypic description of the breed; and
5) levels of performance, where available.

Whereas the information on uses, trends and determinants of trends, as well as breed description, was mainly obtained from field visits and, to a lesser extent, mail questionnaires, most of the quantitative data on performance was obtained from comprehensive reviews of literature. Data on physical measurements (e.g. withers height) were, in a few cases, obtained by measuring representative animals on-farm or on-station during the field visits or through collaboration with national scientists.

This survey represents a first attempt to assess the status of the ruminant genetic resources of sub-Saharan Africa. It does not constitute the level of assessment required to make decisions on conservation and use. However, it provides a basis for additional, targeted surveys. As this was a very broad-brush survey, the information is incomplete, and may even contradict facts unknown to us. We are aware of this but feel the publication of these results will provoke action, particularly at national levels, that will help improve the information base on domestic African breeds/strains. In the meantime, efforts are underway to conduct in-depth breed surveys in pilot countries. One such survey, in Ghana, is already completed and will be published shortly. Additionally, activities on molecular characterisation of African cattle are well underway. Similar studies have also been initiated for sheep and goats.

Figure 1 shows the geographic distribution of cattle breeds in some African countries

Breed Groups and Clusters

As has been alluded to, the survey recognised four broad categories of African cattle: the humpless Bos taurus; the humped Bos indicus or zebu; the sanga; the zenga (sanga x zebu derivatives). Fifth and sixth categories included were the "recent derivatives" created from interbreeding amongst indigenous breeds, and the composite breeds developed from systematic crossing of two or more breeds for specific purposes. The taurine category was further subdivided into two groups – the Longhorns and the Shorthorns - while the zebu and the sanga were divided into several groups and clusters. A group is defined here as a collection of breeds or strains considered to have a common ancestry but not necessarily inhabiting the same geographical area. Cluster, on the other hand, is used to refer to a collection of breeds or strains which belong to the same category and, usually, group, and occupy the same geographical area e.g. a country and/or a defined ecozone within one or more countries. Thus, the sub-category "Small East African Zebu" was divided into groups represented by the Abyssinian Shorthorned Zebu, The Somali Zebu, The Teso Zebu, etc. Examples of clusters were the Kenya cluster of zebus, the Tanzania cluster of zebus and the Ovambo and southwestern cluster of sangas. Although the motivation behind the "clustering" was purely presentational convenience, an attempt was made to lump together only those breeds and strains which, because of geographical proximity have had a high likelihood of interbreeding and hence may have more common genetic background than other populations with similar evolutionary history but which have been more isolated. The term group is also used to refer to such broad categories as the humpless Longhorn and the humpless Shorthorn, members of which are considered to be genetically closely related and have not undergone the same differentiation as seen in the zebu or, to some extent, the sanga.

This paper, the first in a two-part series, provides a framework for the classification of African cattle breeds/strains on the bases of historical evidence, phenotypic appearance and geographical location, and identifies populations that may be threatened with extinction and those which may have become extinct in the last 100 years or so. The second paper (Rege and Tawah, 1999) describes the physical characteristics and status of each of the existing breeds in terms of breed development as well as their distribution, main uses and known or speculated evolutionary relationships among breeds.

Figures from 2 to 5 show some cattle breeds.

Classification of Breeds

The taurine cattle

The humpless Shorthorns and Longhorns of West and Central Africa have lived in their present niches for several millenia. The stringency of this environment has supposedly contributed to their small size and to the "low productivity" of these breeds compared to most zebus found in the more arid areas of the tropics. Nonetheless, they have acquired a hardiness to the harsh climatic conditions and resistance to the various diseases endemic to their environments. Notable among these adaptations is their tolerance to trypanosomosis, the major disease limiting introduction of non-native livestock into the vast humid and sub-humid areas of West and Central Africa. Aboagye *et al*. (1994) and Rege *et al*. (1994a; b; c) have reviewed the distribution and important characteristics of the Shorthorn cattle while ILCA (1979) summarised the attributes of the major trypanotolerant populations of West and Central Africa.

Table 1 summarises the classification of the humpless cattle of Africa. There are two humpless Longhorn breeds, the N'Dama and the Kuri, both found in West Africa and 14 humpless Shorthorn breeds widely distributed in the humid and sub-humid zones

Table 1. Humpless cattle breeds of sub-Saharan Africa.

Group and Breed/Strain	Location/Country	Estimated[a] Population	Mature weight (kg)		Withers height (cm)		Main uses (In order of importance)
			Male	Female	Male	Female	
1. Humpless Longhorns							
1. N'Dama	All coastal countries of West and Central Africa, plus Mali, B. Faso and C.A. Republic	4 863 000	220-360	180-300	95-120	90-115	Meat; Work; Manure
2. Kuri	Chad; Niger; Nigeria; Cameroon	110 000	500-750	360-450	140-180	126-145	Meat; Milk; Work
2. Humpless Shorthorns (West and Central Africa)							
3. Ghana Shorthorn		738 000	190-395	163-280	105-117	99-110	Meat; Work; Milk
4. Baoulé	Central African Republic; Ivory Coast, Gabon, B. Faso	1 082 000	160-300	150-240	100-106	90-103	Milk; Meat
5. Lobi	Burkina Faso	490 000					Meat; Milk
6. Savanna Muturu	Nigeria	58 000		150-225			Meat
7. Liberia Dwarf Muturu	Liberia	5 500			86-95	82-94	Meat
8. Bakweri	Cameroon	1 300					Meat; Rituals
9. Somba	Benin; Togo	216 000	150-215	115-185	89-106	85-103	Meat; Milk; Rituals
10. Doayo (Namchi)	Cameroon	7 000			100-110	97-106	Meat; Rituals
11. Kapsiki	Cameroon	3 300			105-117	100-109	Meat; Rituals
12. Ghana Dwarf Muturu	Ghana	100					Meat
13. Bakosi	Cameroon	1 300					Meat; Rituals
14. Lagune	Benin; Congo; Ivory Coast, Gabon; Togo; Zaire	65 700	180-280	165-262	89-106	85-103	Meat; Manure
15. Logone	Chad	NA					Meat
16. Forest Muturu	Nigeria	40 000			85-95	83-93	Meat; Rituals
3. Humpless Shorthorns (Eastern Africa)							
17. Sheko	Ethiopia	31 000					Meat; Work

[a]Latest available estimate; if multiple in same year, highest estimate used; combines estimates from different countries, if applicable.

Table 2. Zebu cattle breeds of sub-Saharan Africa.

Group and Breed/Strain	Location/Country	Estimated[a] population	Mature weight (kg) Male	Mature weight (kg) Female	Withers height (cm) Male	Withers height (cm) Female	Main uses (in order of importance)
1. Large East African Zebu							
1. Ethiopian Boran (Borana)	Ethiopia	1 896 000	300-385	300-350			Milk; Meat
2. Kenya (Improved) Boran	Kenya, Tanzania, Zambia	580 570	550-850	400-550			Meat; Milk; Work
3. Unimproved Boran (Borana)	Kenya	1 882 000	255-395	250-355			Milk; Meat
4. Orma Boran	Kenya	547 000					Milk; Meat
5. Somali Boran	Somalia	NA	295-410	230-355			Milk; Meat
6. Karamajong zebu	Uganda	510 000	320-490	300-410			Milk; Meat
7. Toposa	Sudan	398 000	350-600	250-390	130-147	120-133	Milk; Meat; Work
8. Murle	Sudan, Ethiopia	NA	300-410	220-320	128-134	100-122	Milk; Meat; Work
9. Butana	Sudan	258 000	395-600	300-440	131-149	123-139	Milk; Meat
10. Kenana	Sudan	1 670 000	400-610	300-435	132-148	124-138	Milk; Meat
11. Baggara	Sudan	3 270 000	300-600	230-450			Meat; Milk; Work
12. Barka	Eritrea	850 000	335-490	295-415	122-138	120-133	Milk; Meat
13. Turkana	Kenya	621 750					Milk; Meat
2. Small East-African Zebu							
2.1 Abyssinian Shorthorned Zebu							
14. Arsi	Ethiopia	2 012 000					Work; Meat; Milk
15. Adwa	Ethiopia	NA					Work; Meat; Milk
16. Ambo	Ethiopia	NA					Work; Meat; Milk
17. Bale	Ethiopia	738 000					Work; Meat; Milk
18. Goffa	Ethiopia	NA					Work; Milk; Meat

Continued ....

.... *Table 2.*

Group and Breed/Strain	Location/Country	Estimated[a] population	Mature weight (kg) Male	Mature weight (kg) Female	Withers height (cm) Male	Withers height (cm) Female	Main uses (in order of importance)
19. Guraghe	Ethiopia	NA					Work; Meat; Milk
20. Harar	Ethiopia	NA					Work; Meat; Milk
21. Jem-Jem	Ethiopia	434 000					Work; Meat; Milk
22. Smada	Ethiopia	NA					Work; Meat; Milk
23. Mursi	Ethiopia	NA					Milk; Meat; Work
24. Hammer	Ethiopia	NA					Milk; Work; Meat
25. Jijiga	Ethiopia	100 000					Work; Milk; Meat
26. Ogaden	Ethiopia; Somalia	NA					Milk; Meat; Work
2.2 ***The cluster of southern Sudan and Vicinity***							
27. Lugware	Uganda, D.R. Congo	196 200	295-355	230-260	102-111	98-109	Work; Meat; Milk
28. Mongolla	Sudan	240 000		130-225	101-110	100-105	Milk; Meat
29. Nkedi	Uganda	752 000	240-450	270-325	102-121	99-107	Work; Milk; Meat
30. Nuba Mountain Zebu	Sudan	44 000	200-225	175-225			Meat (for ceremonies)
2.3 ***The «Somali» group***							
31. Garre (Ghenna)	Somalia	NA	290-340	265-305	115-133	100-120	Milk; Meat
32. Gasara	Somalia	NA	205-295	200-230	102-129	101-115	Milk; Meat
33. North Somali Zebu	Somalia	NA					Milk; Work
34. Baherie	Eritrea	10 000	190-285	170-220	109-124	98-120	Milk; Meat
2.4 ***The Kenya cluster***							
35. Kikuyu	Kenya	89 500					Meat
36. Taita	Kenya	NA	194-405	125-360	90-130	94-122	Meat; Milk; Work
37. Giriama	Kenya	NA					Meat; Milk; Work
38. Duruma	Kenya	NA					Meat; Milk; Work

Continued ....

.... *Table 2.*

Group and Breed/Strain	Location/Country	Estimated[a] population	Mature weight (kg) Male	Mature weight (kg) Female	Withers height (cm) Male	Withers height (cm) Female	Main uses (in order of importance)
39. Kamba	Kenya	897 000					Meat; Milk; Work
40. Maasai	Kenya	1 398 000	300-445	275-385	118-140	110-135	Milk; Meat
41. Winam (Kavirondo)	Kenya	2 110 000	215-410	195-365	95-132	94-125	Milk; Work; Meat
42. Nandi	Kenya	389 000	215-420	200-320	118-122	110-119	Milk; Work; Meat
43. Samburu	Kenya	19 000					Milk; Meat
44. Watende	Kenya	NA					Milk; Meat; Work
2.5 The Teso group							
45. Teso	Kenya, Uganda	NA					Milk; Meat; Work
46. Usuk	Uganda	NA					Milk; Meat; Work
47. Kyoga	Uganda	NA					Milk; Meat; Work
48. Serere	Uganda	NA					Milk; Meat; Work
2.6 The Tanzania cluster							
2.6.1 Tanganyika Shorthorned group							
49. Iringa Red	Tanzania (Mainland)	NA					Milk; Meat
50. Maasai	Tanzania (Mainland)	100 000					Milk; Meat
51. Ugogo Grey	Tanzania (Mainland)	100 000					Milk; Meat
52. Mkalama Dun	Tanzania (Mainland)	1 000					Milk; Meat; Work
53. Singida White	Tanzania (Mainland)	5 000					Milk; Meat; Work
54. Pare	Tanzania (Mainland)	1 000					Milk; Meat; Work

Continued ....

.... *Table 2.*

Group and Breed/Strain	Location/Country	Estimated[a] population	Mature weight (kg) Male	Mature weight (kg) Female	Withers height (cm) Male	Withers height (cm) Female	Main uses (in order of importance)
55. Tarime (Shashi)	Tanzania (Mainland)	100 000	160-210	150-190			Milk; Meat; Work
56. Chagga (Wachagga)	Tanzania (Mainland)	1 000	170-240	155-190			Milk; Meat; Work
2.6.2 Zanzibar group							
57. Zanzibar Zebu	Tanzania (Zanzibar & Pemba)		250-350	190-300			Milk; Work; Meat
2.7 The Angoni group							
58. Angoni	Zambia	300 000	270-730	180-480	122-127	119-122	Meat; Work; Milk
59. Malawi Zebu	Malawi	796 700		265-280			Meat; Work; Milk
60. Angonia (Angone)	Mozambique	64 400	265-730	175-470	121-125	110-120	Meat; Work; Milk
2.8 The Madagascar group							
61. Madagascar zebu	Madagascar	7 000 000	350-450	250-350	117-140	110-135	Meat; Milk; Work
62. Baria	Madagascar	500					Not used (wild)
3. West African Zebu							
3.1 Gudali Group							
3.1.1 The Sokoto sub-group							
63. Sokoto	Nigeria	4 352 000	495-660	240-355	130-138	116-132	Milk; Meat; Work
3.1.2 The Adamawa sub-group							
64. Ngaundere	Cameroon; Nigeria; C. Africa Republic	999 000	400-565	330-410	132-136		Milk; Meat; Work
65. Banyo	Cameroon; Nigeria	NA	300-410	350-365			Milk; Meat; Work

Continued ....

.... *Tablew 2.*

Group and Breed/Strain	Location/Country	Estimated[a] Population	Mature weight (kg) Male	Mature weight (kg) Female	Withers height (cm) Male	Withers height (cm) Female	Main uses (in order of importance)
66. Yola	Cameroon; Nigeria	NA	350-355	315-340			Milk; Meat; Work
3.2 Fulani Group							
67. Gobra	Senegal	1 300 000	300-350	250-300	130-144	124-140	Milk; Meat; Work
68. Sudanese Fulani (Peul *Zebu*)	Mali, B. Faso	5 616 000	280-345	248-300	120-138	115-126	Milk; Work; Meat
69. White Fulani	Nigeria; Cameroon; C. Africa Republic	9 645 000	425-665	250-380	130-152	1180138	Milk; Meat; Work; Manure
70. Red Fulani	Nigeria, Cameroon; C.. Africa. Rep.	4 924 000					Milk; Meat; Work; Manure
71. Fellata (Bororo)	Chad; Sudan	50 000 in Sudan	400-450	255-410			Milk; Meat; Work
72. Djelli (Diali)	Niger; Nigeria	NA					Milk; Meat; Work
3.3 ***Other West African Zebu***							
73. Azaouak (Tuareg)	Mali; Nigeria; Niger	506 000	350-500	300-410	128-135	122-130	Meat; Work; Milk
74. Shuwa	Chad; Nigeria; Cameroon	4 554 000	350-475	250-300	135-140	125-128	Work; Milk; Meat;
75. Maure	Mauritania; Mali	673 000	250-700	250-350	125-140	110-128	Milk; Meat; Work

NA = Not available.

[a]Latest available estimate; if multiple in same year, highest estimate used; combines estimates from different countries, if applicable.

Figure 3. Raya Azebo cattle.

of West and Central Africa. In addition there is one humpless Shorthorn breed in eastern Africa: The Sheko of Ethiopia.

The zebu cattle

Although zebu cattle are trypano-susceptible, in the absence of tsetse fly the large size and high production levels of many zebu breeds give them a competitive advantage over the trypanotolerant N'Dama Longhorn and Shorthorns (Rege *et al*., 1994a;b). The zebu breeds or strains are abundant in the continent and exhibit a high level of resistance to harsh environmental conditions, making them the only type of cattle that can survive over a large part of Africa.

The zebu is the largest single cattle type in Africa. It is represented by some 75 breeds (Table 2). The highest concentration of the zebu is in eastern Africa and neighbouring countries in south-central Africa which, together, have 61 breeds. West Africa has only 13 zebu breeds, principally inhabiting the dry savanna and sahelian belts. The East African Zebu can be divided into two major sub-groups - the "Large" and the "Small" East African Zebu. The former has some 13 breeds, all restricted to the relatively drier parts of Sudan, Eritrea, Ethiopia, Somalia, Kenya, Tanzania and Uganda. The 49 Small East African zebu breeds are also principally found in the same countries as their "Large" counterparts. However, a small number inhabit south-central Africa (Zambia, Malawi, Mozambique) and Madagascar. Other than Zaire, the eastern border of which is inhabited by "spill-over" zebu from eastern Africa, the humid zone of Central Africa is devoid of zebu.

The Small East African zebu is further sub-divided into several *groups* or *clusters*: The Abyssinian Shorthorned Zebu (represented by 13 breeds/strains); the Cluster of southern Sudan and vicinity (4); the Somali group (4); the Kenya cluster (10); the Teso group (4); the Tanzania cluster consisting of the Tanganyika

Table 3. The sanga cattle breeds of sub-Saharan Africa.

Group and Breed/Strain	Location/Country	Estimated[a] Population	Mature weight (kg) Male	Mature weight (kg) Female	Withers height (cm) Male	Withers height (cm) Female	Main uses (in order of importance)
1. The sanga of eastern Africa							
1.1 The Nilotic group							
1. Abigar	Ethiopia	548 600					Milk; Meat; Work
2. Aliab Dinka	Sudan	NA					Milk; Meat
3. Aweil Dinka	Sudan	NA					Milk; Meat
4. Nuer	Sudan	NA					Milk; Meat
5. Shilluk	Sudan	NA					Milk; Meat
1.2 The Abyssinian sanga							
6. Danakil	Ethiopia, Eritrea	680 500	250-380	200-305	130-145	120-125	Milk; Meat; Work
7. Raya-Azebo	Ethiopia	521 000					Work; Milk; Meat
1.3 The Ankole group							
8.Watusi	Uganda; Rwanda; Burundi; Tanzania; D.R.C	1 600 000	350-425	290-350	132-135	110-127	Milk; Meat; Work
9. Bahima	Uganda; D.R.C.	*					Milk; Meat; Work
10. Kigezi	Uganda	*	220-380	200-330	112-132	108-120	Milk; Meat; Work
11. Bashi	D.R.C.	*	235-400	220-340	115-135	110-124	Milk; Meat; Work
12. Ruzizi	DRC; Rwanda; Burundi	*					Milk; Meat; Work
2. The sanga of southern Africa							
2.1 The Shona group							
13. Mashona	Zimbabwe	500 000	350-635	260-410			Meat; Work
2.2 The Nguni group							
14. Nguni	S. Africa; Swaziland	2 156 000	400-680	225-450			Meat; Work; Milk

.... *Continued...*

.... *Table 3.*

Group and Breed/Strain	Location/Country	Estimated[a] Population	Mature weight (kg) Male	Mature weight (kg) Female	Withers height (cm) Male	Withers height (cm) Female	Main uses (in order of importance)
15. Nkone	Zimbabwe	400		300-450			Meat; Milk
16. Pedi	S. Africa	400					Meat; Work; Milk
17. Shangan	S. Africa	600					Meat; Work; Milk
18. Landim	Mozambique	536 400					Meat; Work; Milk
2.3 The Zambia/Angola cluster							
19. Tonga	Zambia	993 000	485-530	310-495	118-130		Milk; Meat; Work
20. Porto–Amboim	Angola	NA	400-530	350-425	120-140	118-129	Meat
2.4 Ovambo and south-western cluster		NA					
21. Ovambo	Namibia	NA					Meat; Work; Milk
22. Kaokoveld	Namibia	NA					Meat; Work; Milk
23. Okavango	Namibia	NA					Meat; Work; Milk
24. Caprivi	Namibia	NA					Meat; Work; Milk
25. Humbi	Angola	NA					Meat; Work; Milk
2.5 The Setswana group							
26. Barotse	Zambia; Angola	793 000	255-700	240-455	120-137	114-129	Milk; Meat; Work
27. Damara (Herero)	Namibia	NA					Milk; Work; Meat
28. Tswana	Botswana	1 395 000	310-520	290-420	140	131	Meat; Work; Milk
29. Tuli	Zimbabwe	3 300	450-820	360-570			Meat
2.6 The Afrikaner group							
30. Afrikaner	South Africa	302 000	450-950	360-555	130-150	128-140	Meat; Work

NA = Not available.

[1]Possibly included in Watusi population figure.

[a]Latest available estimate; if multiple in same year, highest estimate used; combines estimates from different countries, if applicable.

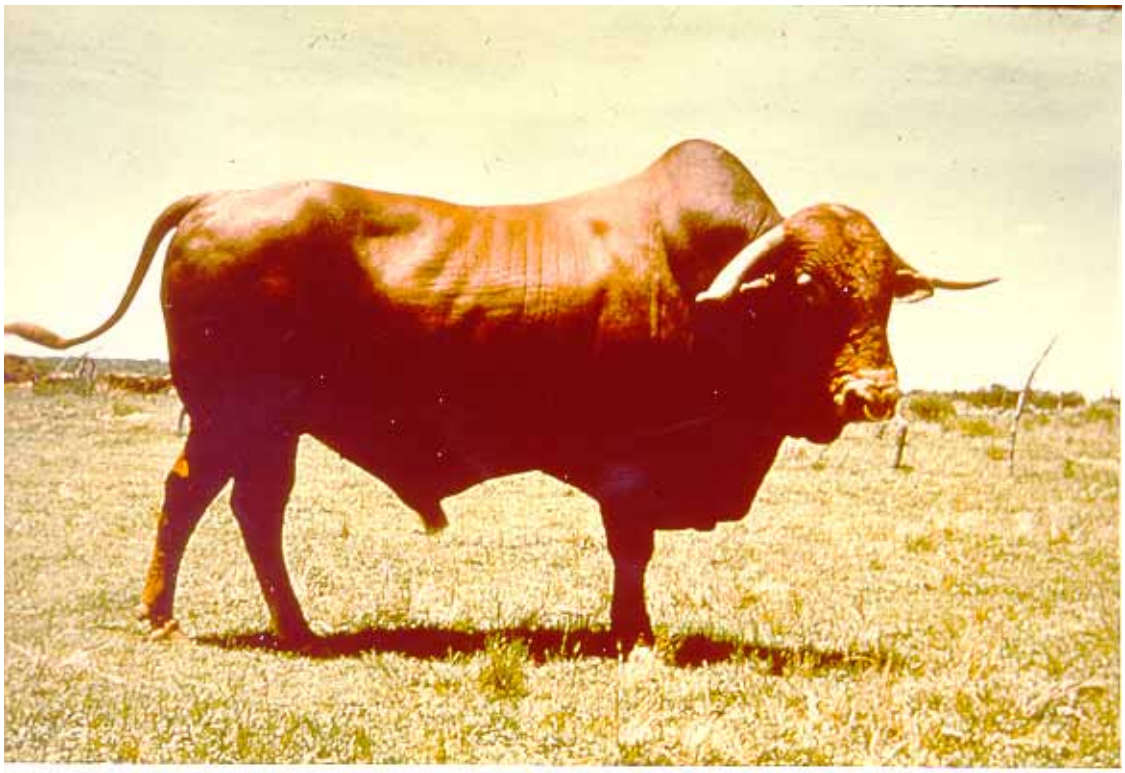

Figure 4. Afrikaner cattle.

group (8) and the Zanzibar Zebu (1); the Angoni group (3); and the Madagascar group (2).

The West African zebu consists of two main groups: The Gudali group represented by two sub-groups (Sokoto with only one breed, and Adamawa with 3 breeds/strains); and the Fulani group (with 6 breeds/strains). In addition, there are three other zebu breeds in West Africa, the Azoauak, Shuwa and Maure, which do not belong to either the Gudali or the Fulani groups.

The sanga cattle

Table 3 summarises the sanga cattle breeds/strains of Africa. There are 30 sanga breeds/strains sub-divided on the basis of location into the sanga of eastern (12 breeds/strains) and sanga of southern (18) Africa. The sanga of eastern Africa consist of three groups: Nilotic sanga of southern Sudan and south-western Ethiopia; the Abyssinian sanga of Ethiopia and Eritrea; and the Ankole group with representatives in Uganda, Rwanda, Burundi, Tanzania and Democratic Republic of Congo (former Zaire).

The sanga of southern Africa are represented by six groups or clusters: the Shona represented by the *Mashona* of Zimbabwe; the Nguni group (5 breeds/strains); the Zambia/Angola cluster (2); the Ovambo and south-western cluster (5); the Setswana group (4); and the Afrikaner group represented only by the *Afrikaner* breed.

The zenga cattle

Several breeds have supposedly resulted from crossbreeding between the zebu and sanga populations in the East African highlands where large concentrations of zebu (arriving from Asia) initially occurred, providing opportunity for admixture with sanga cattle, then already resident there. The resulting breeds have been classified into a separate category. The name "*zenga*" is suggested for this category. Exclusively located in eastern

Africa, some members are found in predominantly zebu habitat, others in sanga habitat. Indeed, the location of the zenga forms a natural division between the "zebu country" in the north and the predominantly "sanga country" in the south. Members of the zenga - a total of eight - are: the *Arado*, *Fogera*, and *Horro* (of Ethiopia); *Jiddu* (southern Somalia); *Alur,* also called *Nioka* (*Nyoka*) or *Blukwa* cattle (Democratic Republic of Congo); *Nganda* (Uganda); *Sukuma* (Tanzania); and *Bovines of Tete* (Mozambique). The zenga cattle are summarised in Table 4.

Recent derivatives

There are several cattle breeds which have been formed as a result of the coexistence of two or more breeds in close proximity to each other. In most cases this has been facilitated by increased interaction among tribal groups and, sometimes, deliberate but non-systematic attempts to improve specific attributes. A good example of the process, but one which has not produced a recognised, distinct breed or strain, is the crossbreeding between the Kuri and zebu of the Lake Chad Basin (see Tawah *et al*, 1997) to produce a draught animal. Table 4 summarises breeds/strains in this category.

Commercial composites

Sub-Saharan Africa is home to, at least, six commercial composite breeds with varying proportions of exotic blood. Unfortunately, only two of them - the *Drakensberger* and the *Bonsmara,* both of South Africa - are secure in terms of numbers and existence of

Figure 5. Ankole cattle.

Table 4. Zenga (zebu-sanga) cattle, recent derivatives and synthetic breeds.

Group and Breed/Strain	Location/Country	Estimated[a] Population	Mature weight (kg) Male	Mature weight (kg) Female	Withers height (cm) Male	Withers height (cm) Female	Main uses (in order of importance)
1. Zenga (zebu x sanga) cattle							
1. Arado	Eritrea; Ethiopia	510 000	205-430	192-350	117-144	93-126	Work; Milk; Meat
2. Fogera	Ethiopia	86 800			110-145	100-121	Work; Milk; Meat
3. Horro	Ethiopia	3 286 000	320-480	210-400			Work; Milk; Meat
4. Jiddu	Somalia	NA	340-590	325-430	109-133	108-124	Milk; Meat
5. Alur (Nioka, Blukwa)	D.R.C.	NA	290-550	225-380	110-131	108-122	Milk; Meat; Work
6. Nganda	Uganda	1 365 000	280-420	200-340	115-124	115-122	Milk; Meat; Work
7. Sukuma (Tinde)	Tanzania	100 000	230-410	210-370	94-132	93-127	Milk; Meat
8. Bovines of Tete	Mozambique	NA					Meat; Milk; Work
2. Recent derivatives							
1. Borgou	Benin; Togo	428 000	190-330	180-295			Meat; Work; Manure
2. Méré	B. Faso; Cote d'Ivoire	693 000					Meat; Work; Manure
3. Ghana «sanga»	Ghana	124 000					Milk; Meat; Work; Manure
4. Keteku	Nigeria	293 000					Meat; Work; Manure
5. Djakore	Senegal	350 000					Milk; Meat; Work; Manure
6. Bin	Nigeria	NA					Meat; Work; Manure
7. Basuto	Lesotho	NA					Work; Meat; Milk
8. Barra do Cuanzo	Angola	NA	370-620	360-500			Meat; Work; Milk
9. Rana (Omby Rana)	Madagascar	40 000-85 000					Milk; Meat

.... Continued

programmes for genetic improvement. The other four are the *Mangan'i Boina* of Madagascar (a synthetic dairy breed), the *Renitelo*, also of Madagascar (beef), the *Mpwapwa* of Tanzania (dairy) and the *Wakwa* of Cameroon (beef). Details of these breeds are discussed in the second paper (Rege and Tawah, 1999).

Breeds at Risk

As has been alluded to, one of the objectives of the survey was to establish the status of sub-Saharan African cattle breeds and to identify those which are at risk as well as those which may have become extinct in the recent past. In the absence of time-trend census data, it was not possible to provide quantitative information on trends. However, the study results, mainly qualitative, together with an assessment of pressures currently affecting breeds, were used to draw conclusions regarding possible threat categories of different breeds considered to be at risk. A total of 47 (32%) breeds/strains were identified to be at risk (Table 5). Four risk categories were defined according to FAO (1992): Critical (most threatened), Endangered, Vulnerable, and Rare (least threatened). Out of the 47 breeds at risk, 15 (Pare, Mkalama Dun and Chagga of Tanzania; Bakweri, Kapsiki, Bakosi and Wakwa of Cameroon; Ghana Dwarf Muturu or Shorthorn; Nkone of Zimbabwe; Pedi and Shangan of South Africa; Renitelo and Baria of Madagascar; and Sengologa and Seshaga of Botswana) were classified in the "Critical" category, 10 were "Endangered", another 10 were "Vulnerable" and six were "Rare" (Table 5). The remaining six could not be definitively classified: Five were classified as lying somewhere between "Rare" and "Vulnerable" and one between "Endangered" and "Vulnerable".

Extinct Breeds

Starting with the 145 breeds identified in this survey and working backwards, a review of old literature dating as far back as 1902 was

.... Table 4.

Group and Breed/Strain	Location/Country	Estimated[a] Population	Mature weight (kg) Male	Mature weight (kg) Female	Withers height (cm) Male	Withers height (cm) Female	Main uses (in order of importance)
3. Systematic synthetics/composites							
1. Drakensberger	South Africa; Swaziland	149 000					Meat; Work; Milk
2. Bonsmara	South Africa	143 000					Meat
3. Renitelo	Madagascar	2 000-3 000	420-655	305-450			Meat; Work
4. Manjan'i Boina	Madagascar	200					Milk
5. Mpwapwa	Tanzania	1 500	360-620	290-455			Milk
6. Wakwa	Cameroon	NA					Meat

NA = Not available.

[a]Latest available estimate; if multiple in same year, highest estimate used; combines estimates from different countries, if applicable.

Table 5. Breeds of sub-Saharan African cattle considered at risk.

Risk status	Breed/strain	Principal location	Main causes of threat*
Rare	Sekgatla	Botswana	Interbreeding with "Tswana"; Crossbreeding with Afrikaner
	Basuto	Lesotho	Crossbreeding
	Jiddu	Somalia	Neglect; Conflict
	Bovines of Tete	Mozambique	Conflict; Crossbreeding
	Biu	Nigeria	Interbreeding
	6. Manjan'i Boina	Madagascar	Early stage of breed development
Rare/Vulnerable	Dongola	Northern Sudan	Interbreeding with Red Butana
	Shendi	Northern Sudan	Interbreeding with Red Butana
	Bambawa	Sudan (near Eritrea border)	Interbreeding with Red Butana
	Ingessana	Sudan-Ethiopia border	Conflict; interbreeding
	Kuri	Lake Chad Basin	Reduction in habitat; Crossbreeding; Conflict
Vulnerable	Kyoga	Uganda	Conflict; interbreeding
	Usuk	Uganda	Conflict; interbreeding
	Singida White	Tanzania	Interbreeding with neighbouring breeds
	Tarime (Shashi)	Tanzania	Interbreeding with neighbouring breeds
	Watusi	Rwanda, Burundi	Conflict, crossbreeding/interbreeding
	Bahima	Uganda	Conflict, crossbreeding/interbreeding
	Bashi	D.R. Congo	Conflict, crossbreeding/interbreeding
	Ruzizi	Burundi	Conflict, crossbreeding/interbreeding
	Landim	Mozambique	Conflict, Crossbreeding, Replacement
	Rana	Madagascar	Continued, unsystematic crossbreeding
Vulnerable/Endangered	Nigerian Forest Muturu	Nigeria	Neglect; Replacement

.... Continued

.... *Table 5.*

Risk status	Breed/strain	Principal location	Main causes of threat*
Endangered	Serere	Uganda	Conflict; interbreeding
	Watende	Kenya	Interbreeding with neighbouring breeds/strains
	Iringa Red	Tanzania	Interbreeding with Ugogo Grey
	Sheko	Ethiopia	Interbreeding with zebus
	Kikuyu Zebu	Kenya	Neglect; Crossbreeding
	Liberian Dwarf Muturu	Liberia	Neglect; Replacement; Conflict
	Logone	Chad	Neglect
	Doayo (Namchi)	Cameroon	Neglect
	Damara (Herero)	Namibia	Neglect; Crossbreeding, Replacement
	Mpwapwa	Tanzania	Absence of sustained dev. Programme
Critical	Pare	Tanzania	Interbreeding
	Mklama Dun	Tanzania	Interbreeding
	Chagga (Wachagga)	Tanzania	Crossbreeding and interbreeding
	Bakweri	Cameroon	Neglect
	Kapsiki	Cameroon	Neglect
	Bakosi	Cameroon	Neglect
	Ghana Dwarf Muturu/Shorthorn	Ghana	Neglect
	Nkone	Zimbabwe	Neglect
	Pedi	S. Africa	Interbreeding; Replacement
	Shangan	S. Africa	Interbreeding; Replacement
	Sengologa	Botswana	Interbreeding with "Tswana"; Neglect
	Seshaga	Botswana	Interbreeding with "Tswana"; Neglect
	Renitelo	Madagascar	Interbreeding; Dermatophilosis
	Baria	Madagascar	Neglect; Lives in the wild
	Wakwa	Cameroon	Absence of sustained dev. programme

*Crossbreeding as used here involves exotics; interbreeding involves other (neighbouring) indigenous breeds.

Table 6. Breeds of sub-Saharan African cattle considered to be extinct.

Breed/strain	Class	Location	Last Report	Reference
1. Nuba (Delami or Koalib) Shorthorn	Humpless shorthorn	Sudan	1900s	Epstein (1971)
2. Cimira («Kuri»)	Humpless Longhorn	Ethiopia	1929	Encyclopadeia Brittanica (1929)
3. Karagwe Shorthorn	Humpless Shorthorn	Uganda?	1927	Stuhlmann (1927)
4. Sesse Shorthorn	Humpless Shorthorn	Sesse Islands, L. Victoria	1909	Epstein (1971)
5. Kigezi Shorthorn	Humpless Shorthorn	Uganda	1920s	Ford and Hall (1947)
6. Socotra Shorthorn	Humpless Shorthorn	Socotra Islands, Off Horn of Africa	1960s	Payne (1964)
7. Unguja (Pemba or Mafia) Shorthorn	Humpless Shorthorn	Pemba, Mafia Islands	1920s	Payne (1964)
8. Manjaca	Humpless Shorthorn	Guinea Bissau	1980s	ILCA (1992)
9. Bimal	Zebu	Somalia	1955	Rosetti and Congiu (1955)
10. Singhi	Zebu	Somalia	1953	Bozzi and Triulzi (1953)
11. Baria (not Madagascar Baria)	Zebu (zenga?)	Eritrea	1929	Marchi (1929)
12. Ugogo	Zebu	Tanzania	1920s	McCall (1928)
13. Senegambia Shorthorn	Humpless Shorthorn	The Gambia; Southern Senegal (Casamance)	1950s	Mason (1951); Epstein (1971)
14. Arussi-Galla	Sanga	Ethiopia	1900s	Lydekker (1912)
15. Ugoi	Sanga	Tanzania	1850s	Burton (1961)
16. Ngami (Botawana)	Sanga	Botswana	1900s	Lydekker (1912), Curson (1934)
17. Nama	Sanga	Botswana	1906	Groenewald and Curson (1933)
18. Bolowana	Sanga (?)	South Africa	Late 1890s	Thompson (1932)
19. Sakalava	Sanga (?)	Madagascar	Late 1890s	Keller (1898); Lydekker (1912); Murdock (1959)
20. Hottentot	Sanga (?)	S. Africa	Late 1800s/Early 1900s	Kolb (1719); Smith (1827); Jones (1953); Martinho (1955)
21. Wadai Dinka	Sanga	D.R. Congo	1936	Curson and Thornton (1936)
22. Mbulu	Zebu	Tanzania	1953	Jeffreys (1953)

done. Each breed or population appearing in the old literature was followed progressively in subsequent publications. Of the breeds that could not be found in more recent literature, a large number was due to change in breed names over the years. However, some breeds which existed previously could not be found in recent literature under any name. To determine what may have happened to these "missing" breeds or strains, clarification was sought from the locations at which they were last reported. This process resolved some of the anomalies and helped to identify those populations which, on the basis of information available, had ceased to exist. Some of these were on record in the countries concerned as officially extinct while the rest could only be considered to be extinct because local officials and communities could not recall their previous existence or were certain that they had, through the years, disappeared as a result of one reason or another. A total of 22 breeds which existed at some point during this (20th) century could not be located and were considered extinct (Table 6). Of the extinct breeds, only one (*Gimira* of Ethiopia) was a humpless Longhorn, eight were humpless Shorthorns, four were zebu (one of them – the Baria of Eritrea – may have been a zenga), while the remaining seven were sanga, although the classification of three of these, Bolowana, Sakalava and Hottentot, as sanga was not certain.

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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 queu 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±0.97 µ, 64.37±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. Arboles 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
	Recorded	With population size data	At risk*	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-stablished 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 under-estimate 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}
Protein Coding			
Swamp	-.004(.062)	.182(.041)	.181(.083)
River	-.068(.048)	.108(.036)	.048(.059)
Microsatellites			
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.

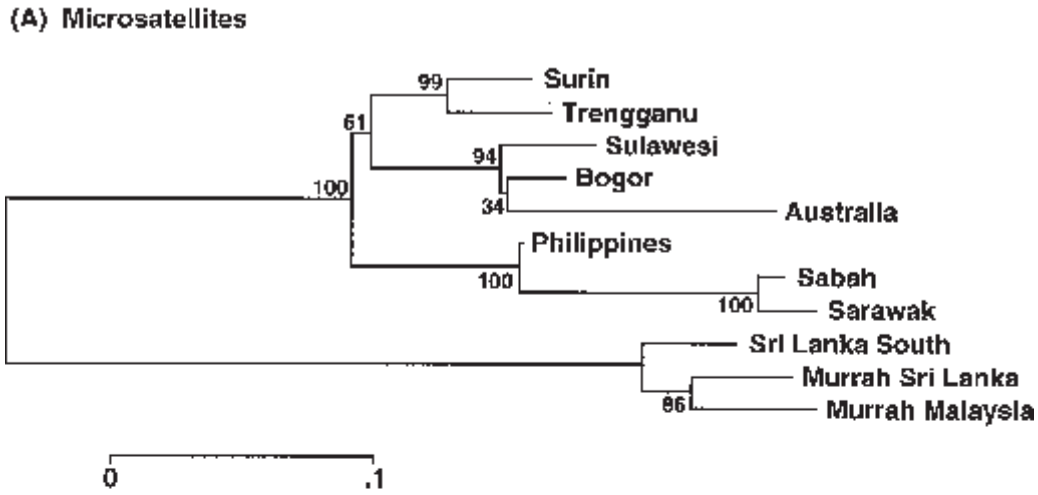
Setting Priorities for Conservation

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



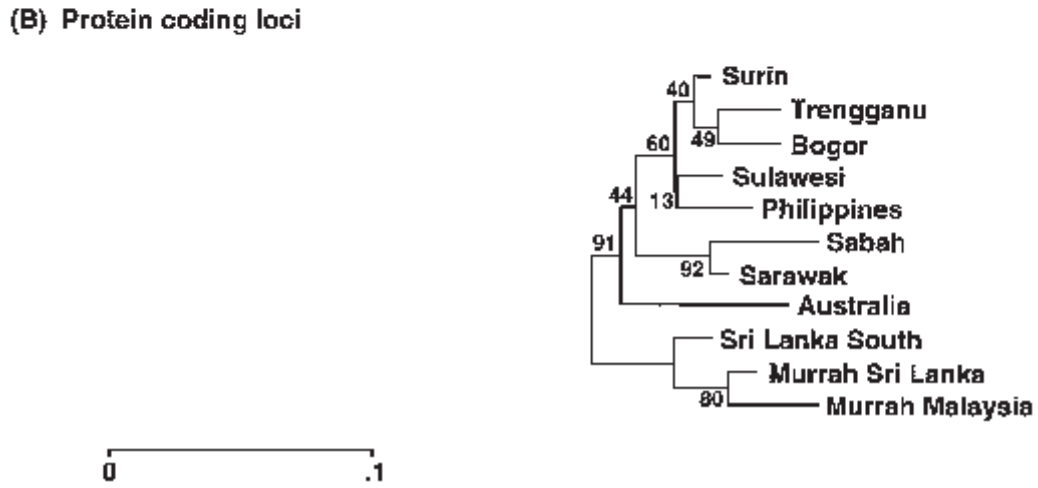


Figure 1. Neighbour-joining trees constructed using the DA distance measure for (a) microsatellite loci and (b) protein coding loci.

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 coefficent 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.

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

	Index				
Herd	Ht slope	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.

		% change						
Cow	Age (m)	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.

		Index					
Herd	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. Bolet[1], M. Monnerot[2] , C. Arnal[3], J. Arnold[4], D. Bell[5], G. Bergoglio[14], U. Besenfelder[6], S. Bosze[7], S. Boucher[4], J.M. Brun[1], N. Chanteloup[8], M.C. Ducourouble[9], M. Durand-Tardif[10], P.J. Esteves[11], N. Ferrand[11], G. Hewitt[5], T. Joly[12], P.F. Koehl[13], M. Laube[9], S. Lechevestrier[9], M. Lopez[3], G. Masoero[14], R. Piccinin[15], G. Queney[2], G. Saleil[1], A. Surridge[5], W. van der Loo[16], J. Vanhommerig[15], J.S. Vicente[17], G. Virag[18] & J.M. Zimmermann[4]

[1]Institut National de la Recherche Agronomique, S.A.G.A., P.O. Box 27, F31326 ***Castanet-Tolosan*** *Cedex, France*
[2]Centre National de la Recherche Scientifique, C.G.M., Avenue de la Terrasse, F91198 ***Gif sur Yvette*** *Cedex, France*
[3]Universidad de Zaragoza, Facultad de Veterinaria, Miguel Servet, 177. 50013 ***Zaragoza****, Spain*
[4]Fédération Française de Cuniculture, 28 rue du Rocher. F75008 ***Paris****, France*
[5]University of East Anglia, School of Biological Sciences, NR4 7TJ. ***Norwich****, Great Britain*
[6]Interuniversitäres Forschungsinstitut Für Agrarbiotechnologie, Konrad Lorenz Strasse 20, A3430 ***Tulln****, Austria*
[7]Agricultural Biotechnology Center, Institute for Animal Science, PO Box 411, ***Gödöllö*** *H2101, Hungary*
[8]Institut National de la Recherche Agronomique, P.A.P., F37380 ***Nouzilly****, France*
[9]Centre d'Enseignement Zootechnique, Ecole d'Aviculturte, Parc du Chateau, F78120 ***Rambouillet****, France*
[10]Bureau des Ressources Génétiques, 16 rue Claude Bernard, F75231 ***Paris*** *Cedex 05, France*
[11]Faculdade de Ciências do Porto, Departamento de Zoologia-Antropologia, Praça Gomes Teixeira, P4050 ***Porto****, Portugal*
[12]Institut Supérieur d'Agriculture Rhône Alpes, 31 Place Bellecour, F69288 ***Lyon*** *Cedex 02, France*
[13]Institut Technique de l'Aviculture, 28 rue du Rocher. F75008 ***Paris****,* France
[14]Istituto Sperimentale per la Zootecnia, Via Pianezza, 115. 10151 ***Torino****, Italy*
[15]Entente 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.

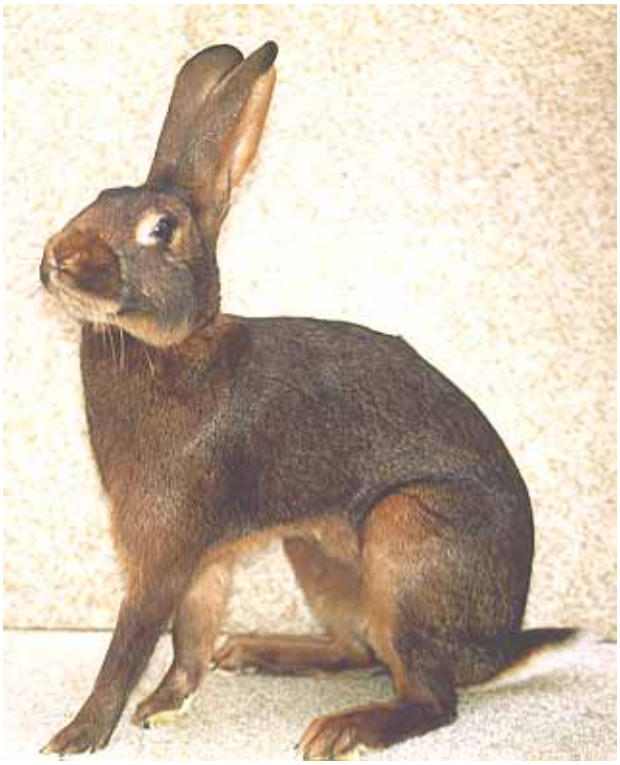

Figure 3. Belgian Hare rabbit.

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

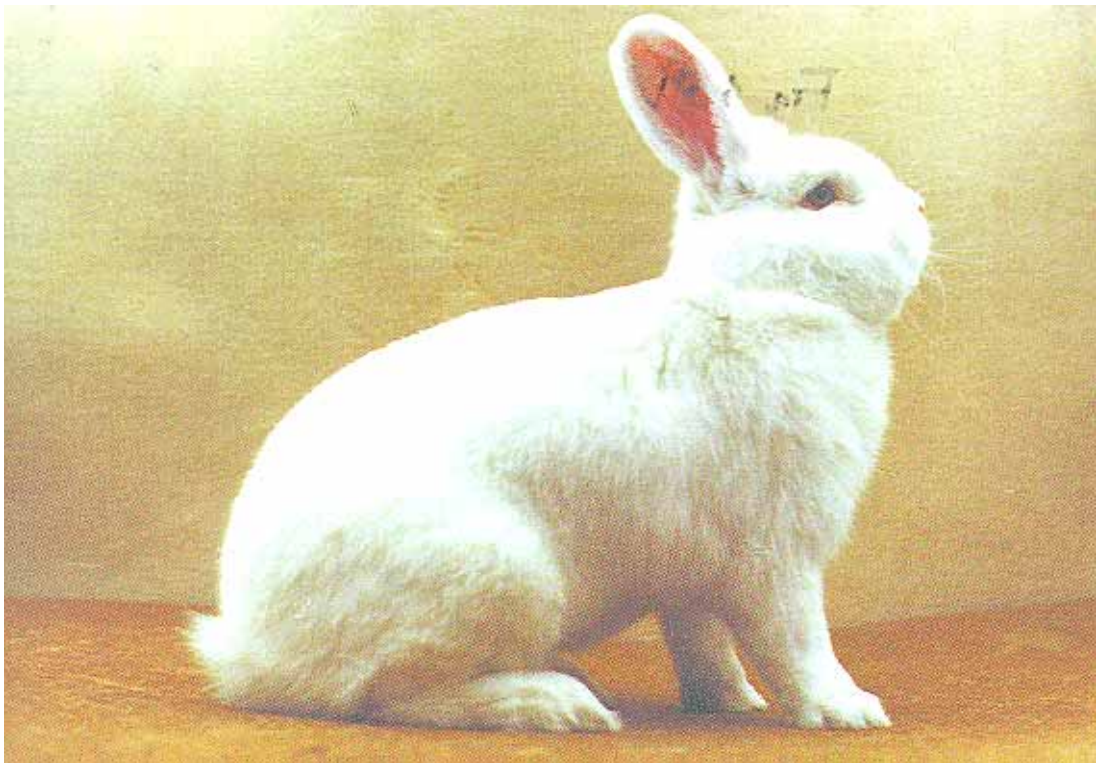

Figure 4. Vienna White rabbit.

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.

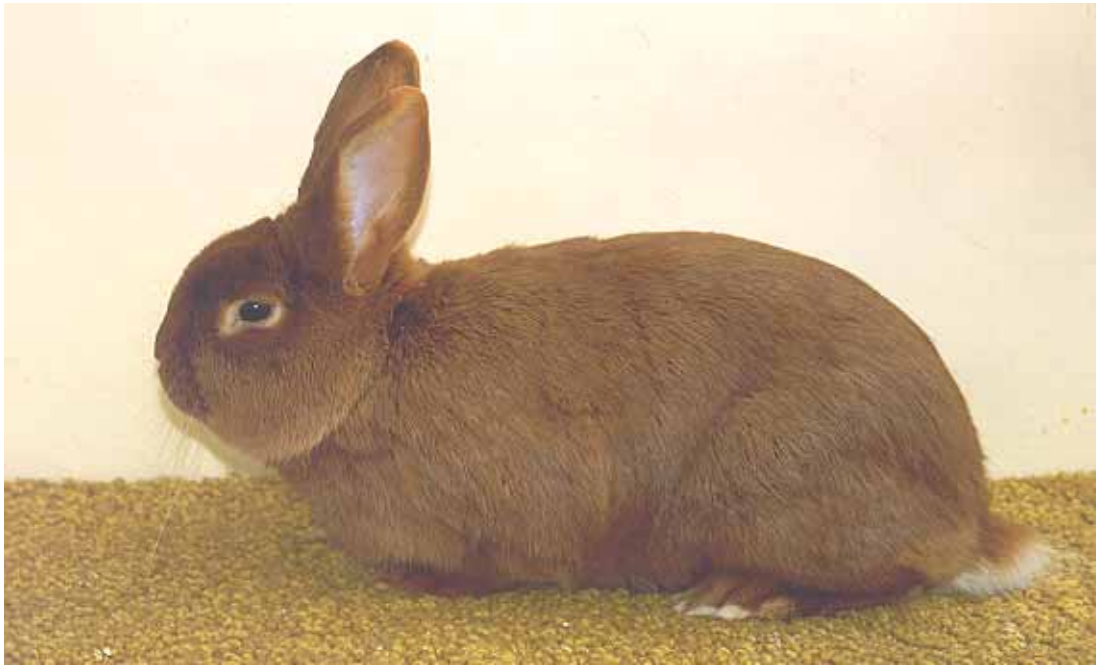

Figure 7. Fauve de Bourgogne rabbit.

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.

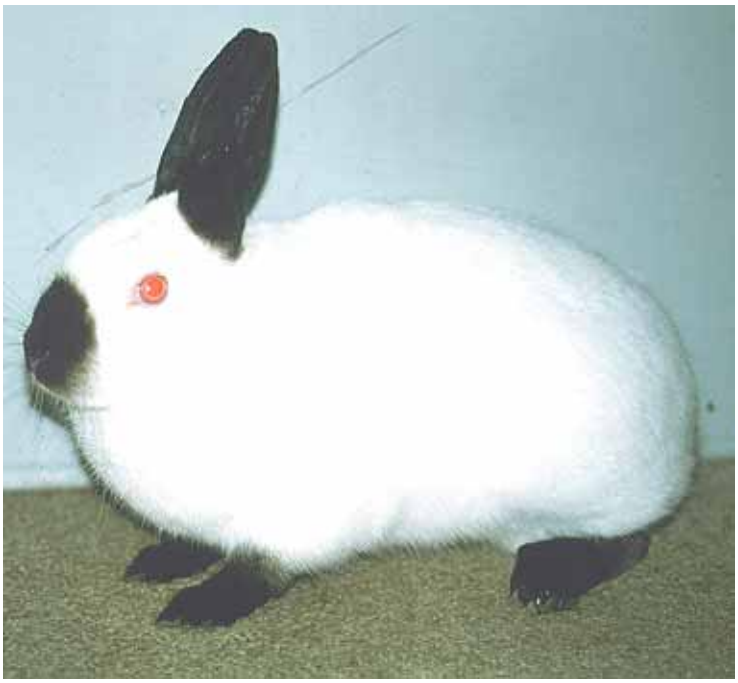

Figure 9. Himalayan rabbit.

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-, αs1- αs2- 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 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 αs2 casein will be examined with isoelectric focusing of milk samples (Virág *et al.*. 1996).

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; Mougel *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; Mougel, 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 Guatémala. C'est une race à viande et à production d'oeufs teintés brun clair. Les poules sont couveuses, protègeant leurs poussins jusqu'à leur indépendence. Elles sont aussi d'excéllentes 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 spécimènes. 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).

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 ?

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 45º (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 then 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 scavening 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 (> 30ºC); 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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European approaches to conservation of farm animal genetic resources

D.L. Simon

Institute of Animal Breeding and Genetics, School of Veterinary Medicine, Buenteweg 17p, 30559 ***Hanover****, Germany*

Summary

Based on several sources of information an overview has been given on the development, present situation and problems of conservation of animal genetic resources in Europe.

Presently, 1 029 breeds of cattle, sheep, goats, pigs, horses and asses are registered by the EAAP-Animal Genetic Data Bank, Hanover. 42.8 % of the breeds are classified as being 'at risk'. More than 360 conservation programmes are underway, which, however, in many cases seem to be operated independently of the status of endangerment and of similar breeds in other countries.

The primary objectives of conservation in Europe, i.e. 'conservation for potential use, later' and 'conservation for cultural reasons', are different from the objective 'conservation for sustainable use, now', which is primarily expressed for developing countries. Different objectives call for different answers to questions, such as: are breeds appropriate units of genetic diversity, how should endangerment be defined, what should be conserved and is incrossing and selection compatible with conservation?

In view of the large number of breeds 'at risk' and of similar breeds existing in different countries as well as the high costs of conservation it is concluded that characterisation of breeds for genetic uniqueness is presently the most urgent task in conservation. This requires effective co-operation across national borders in Europe.

Résumé

Sur la base de différentes sources d'information on présente une révision sur le développement, la situation actuelle et les problèmes de la conservation des ressources génétiques animales en Europe.

Actuellement 1 029 races de bovins, ovins, caprins, porcins et équins sont enregistrés dans la Base de Données sur les Ressources Génétiques Animales de la FEZ à Hannover. Parmi ces races, 42,8% sont classées dans la catégorie "à risque". En ce moment plus de 360 programmes de conservation sont en oeuvre, cependant, dans plusieurs des cas, ils semblent opérer indépendemment du niveau de danger de disparition et de la présence des mêmes races dans d'autres pays.

Les objectifs principaux de la conservation en Europe, tels que "la conservation pour l'utilisation potentielle future" et "la conservation pour des raisons culturelles", sont bien différents des objectifs de "conservation pour l'utilisation durable actuellement" présentés comme prioritaires par les pays en voie de développement. Les différents objectifs mènent à différentes réponses aux questions telles que: Est-ce que les races sont des unités appropriées pour la diversité génétique? Comment pourrait-on définir le niveau de danger? Que devrait-on conserver et est-ce que le croisement et la sélection sont compatible avec la conservation?

Etant donné le nombre de races "à risque" et la présence de ces mêmes races dans d'autres pays, ainsi que le coût élevé de la conservation, on conclu que la caractérisation des races dans le seul but génétique est

actuellement le thème plus urgent de la conservation. Ceci nécessite d'une coopération effective entre tous les pays européens.

***Key words**: Genetic diversity, Farm animals, Endangerment, Conservation programmes, Objectives, Europe*

Introduction

Europe is a heterogeneous region of the world with 46 or so countries, several supra-national institutions and many Non-Governmental Organisations (NGOs). As a result approaches to conservation of farm animal genetic resources (FAGR) differ not only in the observed objectives and species but also in length of involvement and, possibly, in the effectiveness of actions in this field.

According to FAO's World Watch List for domestic animal diversity (1995), about 34 per cent of the so far listed breeds of the major farm animal species; cattle, goats, horses, pigs and sheep are bred in Europe and about 69 per cent of the active conservation programmes of breeds at risk of the mentioned species are underway in this region. Obviously, Europe can play an important part in the maintenance of the world's farm animal genetic resources.

The activities in Europe started some time before the UNCED Rio Conference in 1992 formulated the Convention on Biological Diversity. One significant milestone in the process of growing awareness of conservation was the informal and later formal foundation of the Rare Breeds Survival Trust (RBST) in 1968 and 1973, respectively, and the foundation of the Rare Breeds Farm Park, 1969, at Warwickshire in the United Kingdom. Subsequent milestones were:

1969 Discussion of 'Needs and methods of gene conservation in animal breeding' in the Genetics Commission of the European Association for Animal Production (EAAP), in Helsinki (Maijala, 1970).

1970 Use of markers to estimate genetic distances among breeds (Kidd and Pirchner,1971).

1979 Animal breeding scientists propose a definition of the status of endangerment of breeds and criteria for conservation of endangered breeds (Deutsche Gesellschaft für Züchtungskunde,1979).

1979 Foundation of the Nordic Working Party on Animal Gene Banks for the Scandinavian countries (Maijala *et al*.,1992).

1980 Set-up of the Working Group on Animal Genetic Resources (EAAP-WGAGR) by the Commission on Animal Genetics of the European Association for Animal Production.

1983 Survey by the EAAP-WGAGR on breeds and country populations in Europe (Maijala et al.,1984).

1987 Set-up of the EAAP Animal Genetic Data Bank (EAAP-AGDB) at the Institute of Animal Breeding and Genetics, Hanover (Simon, 1990).

1992 Commission of European Communities 'Workshop and Training Course on data collection, conservation and use of animal genetic resources' in Hanover.

1993 EAAP-publication No. 66 'Genetic diversity of European livestock breeds', with status of endangerment and formation of groups of similar breeds.

1994 Nomination of National Focal Points in FAO Member-Countries of Europe as national co-ordinators for conservation of FAGR.

1996 INTERNET presentation of information of European breeds by the EAAP-Animal Genetic Data Bank, Hanover, and INTERNET-presentation of information of the FAO Domestic Animal Information System DAD-IS, Rome.

Conservation of farm animal genetic resources is a continuous process, which in Europe is taking place on several levels and with different kinds of actions. Earlier reports

on the situation in Europe were given by Maijala et al.(1984), as a report of the EAAP-Working Group on Animal Genetic Resources, Simon and Buchenauer (1993), as a report of the EAAP Animal Genetic Data Bank, and by Ollivier et al. (1994), with concluding remarks on the situation in different regions of Europe and on urgent tasks. Since then the nomination of National Co-ordinators for conservation in European countries and the forthcoming of the EC-Regulations 2078/92 and 1467/94 have given additional strength to the idea of conservation of FAGR in this region.

For the preparation of this paper, information of the following sources could be used: From the EAAP-AGDB, Hanover, information on breeds of the major farm animal species; cattle, sheep, goats, pigs, horses and asses, as registered until February 1997; in addition information from the National Organisations of EAAP, the National Focal Points for Animal Genetic Resources of European countries, the European Commission in Brussels, from many NGOs and from individual experts who are active in this field.

The intention of this paper is to collect present information of various sources and form one integrated picture of approaches to conservation of farm animal genetic resources in Europe and to come to conclusions on priorities of actions in this field.

Quantity of Farm Animal Genetic Resources, Number of Breeds

Following the practice of the EAAP-WGAGR, the quantity of farm animal genetic resources is measured in terms of breeds. This term is used for a group of similar interbreeding animals within a country, which, according to the people who work with them, should be regarded as a breed. The term 'breed' includes groups of animals, which by other people may be called strain, variety or line. A synonymous term could be 'country population' as explained by Maijala et al. (1984).

The number of breeds of the major farm animal species; cattle, sheep, goats, pigs, horses and asses which have been recorded by the EAAP-AGDB until 1997 is presented in table 1.

In 36 countries a total of 1 029 breeds is recorded. Only breeds are listed for which a reasonable amount of information could be obtained. The number of breeds of the individual species; cattle, sheep, goats, pigs, horses and asses is 311, 338, 101, 134, 139 and 6, respectively. These numbers are quite impressive; however, due to the recording systems within countries they may include several breeds with the same or similar genetic background. This can be a problem if decisions have to be made, such as which one out of several endangered breeds should be conserved and which not. It will be of interest to know how many of these breeds are considered to be endangered.

Status of Endangerment of Breeds

The question which criteria should be used to define the status of endangerment of a breed is not settled. Several systems have been proposed (Deutsche Gesellschaft für Züchtungskunde DGfZ, 1979; Maijala *et al.*,1984; European Commission 1992,1994; Bodo, 1995; FAO,1995; Simon,1995; and others). The procedure applied here is basically the same as that proposed by Simon and Buchenauer (1993). It considers four conditions which represent danger for the continuance of the present genetic makeup of a breed:

- Low number of breeding herds and decreasing population size, each as an indicator of imminent danger of the loss of the breed in the near future,
- 'immigration' or use of animals of other breed(s) for reproduction, as a factor in the genetic change of the breed,

Table 1. Number of breeds in six farm animal species in European countries (EAAP-Animal Genetic Data Bank, 2/1997).

Country	Species						Total
	Cattle	Sheep	Goats	Pigs	Horses	Asses	
Albania	5	8	8	4	4	0	29
Austria	8	2	0	0	2	0	12
Belgium	10	6	3	3	4	0	26
Bulgaria	2	0	0	0	0	0	2
Croatia	5	4	1	1	4	0	15
Cyprus	2	2	2	3	0	0	9
Czech Republic	1	1	0	1	1	0	4
Denmark	5	4	1	2	2	0	14
Estonia	3	0	0	1	1	0	5
Finland	4	2	1	2	11	0	20
France	44	55	6	17	31	0	153
Germany	27	26	5	16	11	0	85
Greece	3	12	2	0	2	0	19
Georgia	3	0	0	1	0	0	4
Hungary	1	3	0	1	6	0	11
Iceland	2	2	1	0	1	0	6
Ireland	12	5	1	2	5	0	25
Italy	31	54	29	9	20	5	148
Latvia	1	0	0	1	0	0	2
Lithuania	2	0	0	1	0	0	3
Luxembourg	4	1	0	1	3	0	9
Netherlands	4	11	2	3	3	0	23
Norway	3	6	1	2	4	0	16
Poland	4	8	0	8	2	0	22
Portugal	8	9	3	1	3	0	24
Romania	5	5	1	7	0	0	18
Slovakia	2	3	0	1	0	0	6
Slovenia	3	2	0	3	1	0	9
Spain	34	37	18	3	1	1	94
Sweden	2	3	1	0	2	0	8
Switzerland	8	9	9	3	3	0	32
Ukraine	6	0	0	3	0	0	9
United Kingdom	36	56	4	14	10	0	120
Other*	21	2	2	20	2	0	47
Total	311	338	101	134	139	6	1029

*former CSFR, USSR, Yugoslavia

Table 2. Assumed maximum values of inbreeding in 50 years of conservation, F-50% (), and resulting range of effective population size Ne per class of endangerment.

Species	Class of endangerment 1) Not endang. (≤10%)	2) Potentially endang. (11-20%)	3) Minimally endang. (21-30%)	4) Endang. (31-40%)	5) Critically endang. (>40%)
Pigs	≥ 157	156- 74	73- 47	46- 33	< 33
Sheep+goats	≥ 95	94- 45	44- 28	27- 20	< 20
Cattle	≥ 67	66- 32	31- 20	19- 14	< 14
Horses/asses	≥ 52	51- 25	24- 16	15- 11	< 11

- low 'effective population' Ne size as a condition which affects the increase of inbreeding as well as random drift of the population's gene frequencies.

A three-step procedure is applied.

Firstly, definition of species' specific minimum values of effective population size Ne for five classes of endangerment, depending on the maximum values of acceptable inbreeding, F-50, after 50 years of conservation. For the five classes of endangerment the following maximum values of F-50 were assumed:

1) not endangered ≤10%,
2) potentially endangered 10-20%,
3) minimally endangered 21-30%,
4) endangered 31-40%,
5) 5 critically endangered >40%.

The corresponding maximum increase of inbreeding per generation ΔF is deduced from F-50 by solving formula (1)

$$Fg = 1 - (1- \Delta F)^g \quad \text{(Falconer, 1989)} \quad (1)$$

$$\text{for } \Delta F = 1 - (1- Fg)^{1/g} \quad (2) \quad , \quad \text{where Fg= F-50.}$$

The generation interval y (in years) with the resulting number of generations g in 50 years are assumed for the six species as follows (y/g): pigs 1.5/33, sheep and goats 2.5/20, cattle 3.5/14, horses and asses 4.5/11.

The required minimum effective population size per species and class of endangerment is deduced from ΔF per generation by formula (3)

$$Ne = 1/(2\Delta F) \quad \text{(Falconer, 1989)} \quad (3)$$

The resulting values of effective population size Ne per species and class of endangerment are listed in table 2.

Secondly, for the individual breed computation of the effective population size Ne' by means of the formula (4)

$$Ne' = 4mf/(m + f) \quad \text{(Falconer, 1989)} \quad (4)$$

with m and f the number of male and female breeding animals, respectively, which are used for the reproduction of the breed. We defined f as the number of females which are registered in a herdbook (since these allow pedigree-information in planning of matings for reproduction to be observed), and which are used in the order of 100 per cent for purebreeding. In case these requirements are not met f is estimated as ¼ of the number of unregistered females U (or of the total population size T), times the percentage of purebreeding p:

$$f = pU/4 \quad \text{or} \quad f = pT/4.$$

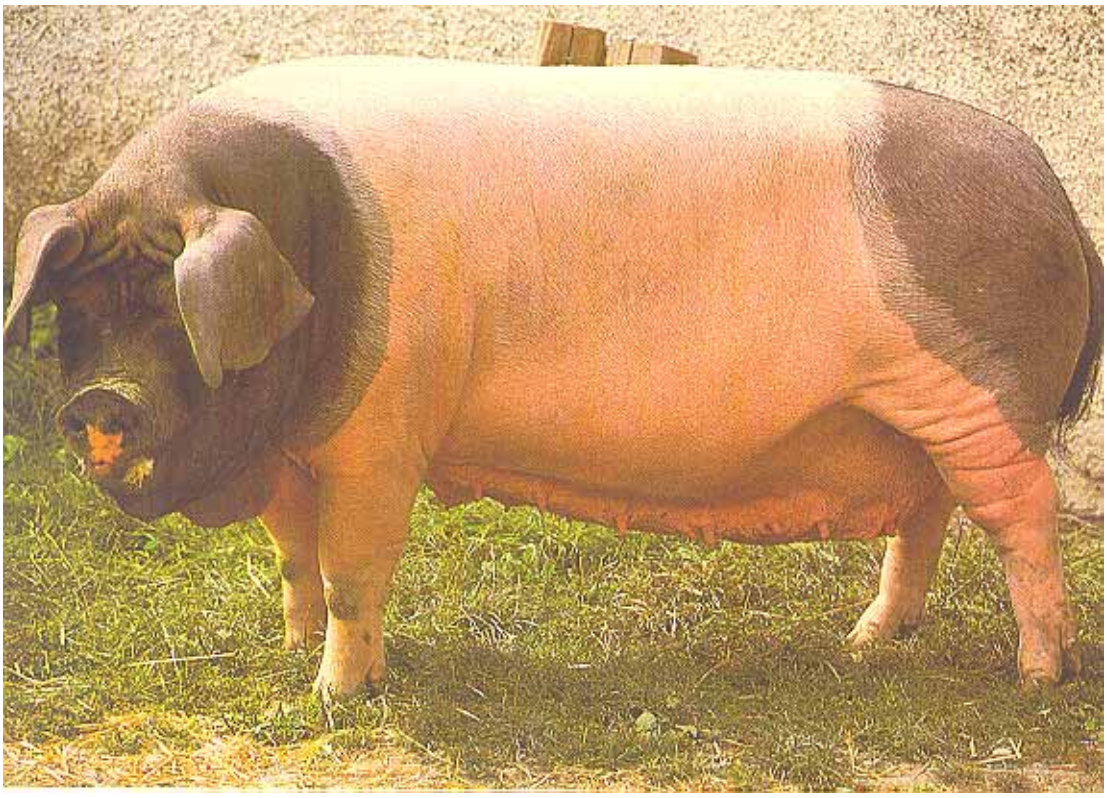

Figure 1. Sow of breed German Saddel Back. For seven similar breeds conservation programmes are under way in six European countries. (Photo: Anonymous)

Table 3. Number of breeds classified for endangerment.

Species	Total	Class of endangerment					
		Not endang.	Poten-tially endang.	Mini-mally endang.	Endang.	Criti-cally endang.	"At risk"
		(1)	(2)	(3)	(4)	(5)	(2-5)
Cattle	305	165	87	24	9	20	140
Sheep	322	210	58	21	7	26	112
Goats	88	64	8	7	4	5	24
Pigs	126	61	23	10	3	29	65
Horses	135	59	51	12	5	8	76
Asses	6	3	1	0	0	2	3
Total	982*	562	228	74	28	90	420

*47 additional breeds - due to missing information - could not be classified.

For a known number of registered female breeding animals that are used for purebreeding only with a percentage of p f is reduced accordingly by multiplication with p.

If m, the number of male breeding animals used for reproduction of the breed is not known m is estimated from f as m = f/30, i.e. by assuming a mating ratio of m:f = 1:30.

If m is less than 40 and the number of males MC is known of which cryoconserved semen is available, the number of males m is increased by addition of the value of MC/3, i.e. it is assumed that 1/3 of the number of males with cryoconserved semen can be regarded as additional males which are available for reproduction of the breed.

By comparing Ne' of the breed with the minimum values of Ne for the relevant species in table 2 the breed is allocated to one of the five classes of endangerment.

Thirdly, downgrading the breed into one class of higher endangerment for each one of the following additional conditions:

- The number of breeding herds is less than 10 and the number of female breeding animals is below 500,
- the number of female breeding animals is decreasing and already below 1000,
- the percentage of matings for reproduction of the breed with animals of other breed(s) is equal or higher than 20 percent.

Compared with the system of Simon and Buchenauer (1993) the starting points for acceptable F-50 values of the classes 1 to 4 were raised and the maximum value of incrossing was increased from 10 to 20 percent. This resulted in fewer downgradings and a higher percentage of breeds classified as being not endangered.

Following this system 420 or 42.8 % of a total of 982 breeds with sufficient information were allocated to classes 2 to 5 and as such were classified as breeds 'at risk' (table 3).

The species with the highest percentage of breeds classified as being 'at risk' was horses (56.3%), followed by pigs (51.6), asses (50.0%) and cattle (45.9%). Sheep and goat breeds appear to be least endangered with 34.8% and 27.3% 'at risk', respectively. It is interesting to note that in all species the number of breeds classified as being 'critically endangered' is remarkably higher than the number of breeds classified as being 'endangered'.

Conservation Activities

Apart from breeding companies for poultry and pigs, nothing is known about activities of commercial breed - societies on conservation of rare breeds. However, in Germany some breed - societies are committed to the herdbook operation for a rare breed of their region. Actual conservation is mainly performed by farmers, hobby-farmers, research institutions and state-farms.

Live-animal conservation programmes

Live-animal conservation in reproducing herds is the most frequently adopted conservation method. It is an attractive method, allowing adaptation of the breed to changing production and environmental conditions and an immediate use of animals for evaluation, research and commercial breeding. Information on the number of live-animal conservation programmes was obtained from three sources: The EAAP-Animal Genetic Data Bank (EA), the newly nominated National Focal Points in Europe (NFP) and from the European Commission (D. Dessylas, Brussels, 1997, personal communication) (EU).

The information from the EU is related to endangered breeds that are supported according to EEC Regulation 2078/92. So far this support has been restricted to local breeds in danger of extinction of the cattle, sheep, goat and *equidae* species in the 15 EU-Member States.

A total of 365 programmes is registered by EA for the major farm animal species, 285 of these or nearly 78 per cent are underway in EU-Member States (table 4). The total sum reported by NFP is in the same order (334); however, within countries and within species the numbers of the reported conservation programmes can be quite different (e.g. in France, Italy and Portugal). The NFP also

Table 4. Live animal conservation programmes in countries of Europe, as registered by EAAP Animal Genetic Data Bank EA, National Focal Points NF and European Union EU, respectively; NR = No response to request

Country	Cattle			Sheep			Goats			Horses			Pigs		Total per country		
	EA	NF	EU	EA	NF	EU	EA	NF	EU	EA	NF	EU	EA	NF	EA	NF	EU
a) 15 EU-member countries																	
Austria	6	NR	10	1	NR	4		NR	4	2	NR	6		NR	9	NR	26
Belgium	2	3	2		8						2	2			2	13	8
Denmark		4		1	1		1	1		1	3		2	2	5	11	0
Finland	3	3	3	1	2	1			1	1	1	1			5	6	6
France	40	18	14	43	22	9	1	5	2	2		15	5	6	91	51	40
Germany	14	11	9	12	14	12	2	3	3	7	12	12	6	4	41	44	36
Greece		2			8			2		1	2				1	14	0
Ireland		3	3	1	2	7			1			1		2	1	7	5
Italy	25	10	16	1	7	19		11	7	7	3	18	4	4	37	35	60
Luxembourg	2	2								1	1	1			3	3	1
Netherlands	3	5		4	4		2	1		1	2				10	12	0
Portugal	6	2	4	6	1	3	1		2	3					16	3	9
Spain	12	NR	25	4	NR	13	2	NR	4		NR	12	2	NR	20	NR	54
Sweden	2	3	3	2	3	3		2	2		2			1	4	11	8
United Kingdom	12	9		16	23		2	7		4	6		6	2	40	47	0
EU-Countries	127	75	89	92	95	70	11	32	26	30	34	68	25	21	285	257	253
b) 18 Non EU-Member countries	16	21		22	21		12	3		19	24		11	8	80	77	
Total	143	96	89	114	116	70	23	35	26	49	58	68	36	29	365	334	253

Table 5. Ex-situ *keeping of farm animal breeds in zoos and farm parks on 124 locations in Germany. Raw data from Falge (1996); Ne = effective population size.*

Species	Number of			Average number of		
	Breeds	"Herds"	Animals per "herd"	Animals per breed (in different herds)	Males per breed	Ne
Cattle	28	136	4.9	20.3	6.3	20.7
Sheep	30	253	10.3	86.9	15.9	54.1
Goats	24	172	8.6	61.3	15.1	48.2
Pigs	12	131	5.4	59.3	19.5	59.7
Horses	23	120	5.0	26.1	7.0	22.1
Asses	6	80	3.7	48.8	14.8	45.9
Chickens	42	112	7.7	20.6	5.6	18.7
Geese	10	48	3.3	16.0	6.3	19.5
Ducks	12	39	5.3	17.3	7.5	21.8
Total	187	1091	6.0	39.6	10.9	31.1

reported live-animal conservation programmes for additional species, i.e. for asses, dogs, rabbits, chickens, ducks, geese and even for bees, fishes and silkworms. It can be noted that the EU-Member States Denmark, Greece, Netherlands and the United Kingdom have not participated in the EEC-project 2078/92 so far.

Contributions of zoos and farm parks

As already mentioned, conservation of endangered breeds of farm animal species is generally performed on farms. However, such animals are also kept 'ex situ' in zoos, farm parks and in so-called Ark-farm projects (Seibold, 1996). Falge (1996) reported animal numbers in 124 institutions of this kind in Germany (table 5):

Animals of 187 breeds of 9 farm animal species are kept in these institutions. The average number of males and of total animals per breed, spread over several locations, is quite low (10.9 and 39.6, respectively). Computation of the effective population size Ne according to formula (4), chapter 3, resulted in values from Ne = 19 for geese and ducks to Ne = 60 for pigs. These values appear rather low if long-term conservation should be achieved.

Thirty-five farm-parks with *ex-situ* conservation of several rare breeds are reported from seven European countries, with 25 farm-parks alone in the United Kingdom (J. Guenterschulze, Warder, 1997, personal communication). In the UK, farm-parks are visited on average approximately by 100 000 people per year (L. Alderson, Warwickshire, 1997, personal communication). The Rare Breeds Survival Trust in the UK and the Gesellschaft zur Erhaltung alter und gefährdeter Haustierrassen, GEH, in Germany developed approval schemes for farm-parks in order to ensure given standards (Chiperzak *et al.*,1995). No information is available on the number of animals and on the farm animal breeds and species which are kept in zoos and farm-parks in the whole region of Europe. The specific value of zoos and farm-parks is that they offer visible

Table 6. Programmes for cryconservation of semen and embryos. T=total, IS=programmes with information on number of sires involved. Data from EAAP-AGDB.

Species	Semen		Embryos	
	T	IS	T	IS
Cattle	194	173	74	49
Sheep	46	39	6	3
Goats	18	15	1	1
Pigs	30	29	0	0
Horses	26	25	4	3
Asses	0	0	0	0
Total	314	281	85	56

evidence of endangered breeds to the public, hence contributing to an increased awareness of the need of conservation.

Cryoconservation of semen and embryos

Cryoconservation of gametes and embryos is a quick and rather inexpensive way to prevent the loss of the genetic potential of a breed (Brem *et al.*, 1984). Properly structured stores of frozen semen and embryos can also be used to support live animal conservation programmes with a minimum increase of inbreeding (Simon, 1993). Table 6 summarises the information on cryoconservation as reported by the EAAP-AGDB.

The largest number of projects of semen and embryo storage is reported for breeds of cattle. Here the number of programmes for semen (194) is even higher than the number of live-animal conservation programmes (139, table 4). Possibly, these numbers include projects of cryostored semen for commercial use. Information on the number of males or sires represented in stored semen and embryos is important to judge their usefulness for the re-activation of an extinct breed. As can be seen in table 6 this information is available in most cases, though completion appears necessary.

Activities on a supra-national level in Europe

Several organisations and institutions are active in projects of conservation which involve more than one country in Europe. In chronological order – according to the start of their activities – the following have to be mentioned:

1. EAAP, the European Association for Animal Production, regularly offers a platform for the presentation of papers on topics of conservation of FAGR at its annual meetings (see 'milestone' 1969, chapter 1). Its Commission on Animal Genetics established the EAAP Working Group on Animal Genetic Resources in 1980, whose main objectives are the study, documentation and cataloguing of conservation and development of animal genetic resources in Europe. In 1987 the working group suggested setting up a data bank, which, with the support of the Deutsche Forschungsgemeinschaft DFG, was founded as the EAAP- Animal Genetic Data Bank at the School of Veterinary Medicine, Hanover, in the same year. Since then the volume and quantity of European breed resources could steadily be increased. During the years 1989-1992 the Hanover data bank accepted responsibilities as 'EAAP-FAO-Global Animal Genetic Data Bank'; since then the responsibility of a Global Animal Genetic Data Bank has been transferred to the newly established FAO Domestic Animal Information System DAD-IS in Rome. Since 1997 EAAP has been acting as co-ordinator for the EU-concerted action 'A Permanent Inventory of European farm animal genetic resources'. This project is

Figure 2. Heifers of breed Tyrol Grey. For five similar breeds conservation programmes are under way in five European countries. (Photo: Averdunk).

supported by EC-Regulation 1467/94 and delegates additional responsibilities to EAAP.

2. NAGB, the Nordic Working Party on Animal Gene Banks, was established in 1979 by the five Scandinavian countries Denmark, Finland, Iceland, Norway and Sweden. It has mapped out conservation needs and activities and built a Nordic Information Centre with a data bank. The Nordic Council of Ministers, NCM, is funding the secretary of the working party, the operation of the Nordic Data Bank and specific research (Maijala *et al.*,1984). Breed information of Scandinavian countries is transferred via the Nordic Data Bank to the EAAP-AGDB Hanover.
3. DAGENE, the Danubian Countries Alliance for Conservation of Genes in Animal Species, was founded in 1989 as a group of individual experts, NGOs and governmental institutions of 10 countries of the Danubian region which are interested in conservation of FAGR in this area. Main objectives are the exchange of information and co-operation in similar projects and the organisation of meetings on regional aspects (I. Bodo, Budapest, 1997, personal communication).
4. Commission of the European Communities. The European Union has become an important factor in improving co-ordination and actual support for conservation of FAGR in the 15 Member-States: Council Regulation No. 2078/92 'On agricultural production methods compatible with the requirements of the protection of the environment and the maintenance of the country side'. The scheme allows support of farmers who 'rear animals of local breeds in danger of extinction'. An EU-specific system for the classification of endangerment is used, which presently allows the promotion of 253 breeds with up to 100 ECU per livestock unit. - Council Regulation 1467/94 'On the

conservation, characterisation, collection and utilisation of genetic resources in agriculture'. The main objective is to co-ordinate and promote existing work on plant and animal genetic resources in the Member States. Until now 12 plant and 3 animal projects have been supported, the animal side having been severely underrepresented so far. One of the projects deals with the initiation of a 'Permanent Inventory of European farm animal genetic resources and of current work on conservation, characterisation, collection and utilisation of those resources'; it is hoped that this can be developed into an efficient instrument. - AIRE 2066, the concerted action project 'Analysis of genetic diversity to preserve future breeding option'. The main objective is to co-ordinate the work of 27 participating laboratories in 14 countries, in particular to use the same set of DNA-markers for assessing genetic diversity within and between cattle breeds. In addition, a Cattle Diversity Data Base, CaDBase, was set up in Edinburgh with a link to the EAAP-AGDB, Hanover.

5. SAVE, Safeguard for Agricultural Varieties in Europe, was founded in 1995 as an umbrella-organisation for NGOs in Europe. Main objectives are: co-ordination of similar activities in different countries, development of awareness of conservation, exchange of know-how and actual support for specific conservation projects. SAVE became particularly active in countries of Eastern Europe (Gruenenfelder, 1995; W. Kugler, St.Gallen, 1997, personal communication).

Number of Registered Conservation Programmes and Its Relation to the Degree of Endangerment

Table 4 shows that the number of registered live-animal conservation programmes is quite high. The differences in numbers reported by the three sources, EAAP, National Focal Points and European Union, can be explained in part by different countries involved in the respective survey, different ways of assessing endangerment, different requirements for support, (e.g. number of female breeding animals, accepted herdbook) and possibly by different interpretation of what is meant by conservation.

It is of special interest to look at the relation between the percentage of conservation programmes and the class of endangerment of breeds. The figures are presented in table 7, including the coefficient of Spearman's rank correlation r_s. The average of the five species shows no tendency of an increased proportion of conservation programmes in classes of higher endangerment. Spearman's rank correlation r_s=0.12 is low and not significant. None of the five species has the highest proportion of conservation programmes in class five of the breeds with the highest risk status. For sheep, goat and horse breeds the rank correlation even turns out to be negative (-0.44, -0.62 and –0.32, respectively). In class 1, with breeds classified as 'not endangered', conservation programmes are reported for 32% of the breeds. This is remarkable since the system of assessment of endangerment applied here appears to be rather severe, compared with the system used by FAO (1995) (see chapter "Assessment of breeds for endangerment").

It is difficult to explain these results. However, it seems to be meaningful in countries of Europe to examine more closely the objective of conservation, the system of assessing the status of endangerment of breeds and the question whether all breeds which have been classified as being endangered equally deserve to be conserved.

Table 7. Percentage of breeds with live animal conservation programmes by class of endangerment. Rank correlation r_s between class of endangerment and percentage of conservation programmes.

Species	Class of endangerment 1 Not end.	2 Pot. end.	3 Min. end.	4 Endan-gered	5 Crit. end.	R_S
Cattle	38.8	59.8	41.7	66.7	50.0	0.60 n.s.*
Sheep	30.0	48.3	66.7	28.6	19.2	-0.44 n.s.
Goats	29.7	12.5	14.3	25.0	0	-0.62 n.s
Pigs	13.1	34.8	60.0	33.3	37.9	0.62 n.s.
Horses	42.4	25.5	41.7	40.0	37.5	-0.32 n.s.
Total	32.0	44.9	48.6	42.9	33.3	0.12 n.s.

* $p < 0,05$

Table 8. Live animal conservation programmes LAC for 'similar' breeds SB, total and in classes of endangerment

Subgroup of similar breeds, formed by EAAP-AGDB	Total number of			Number of SB and LAC			
	Coun-tries involv.	SB	LAC	In class 1 (not endang.) SB	LAC	In class 2-5 ('at risk') SB	LAC
Cattle							
1.2 Origin Black Pied	6	8	6	6	4	2	2
3.7 White Lineback	4	5	5	4	4	1	1
5.2 Alpine Brown	4	6	4	3	2	3	2
5.4 Iberian Brown	2	11	9	7	6	4	3
6.2 Grey Mountain	5	7	5	4	3	3	2
Sheep							
5.2 S.Europ.Milk Sheep	6	15	7	11	4	4	3
8.4 Churra Type	2	8	4	7	3	1	1
Pigs							
3.1 Saddle Backs	6	8	7	1	0	7	7
Horses							
5.10 South Europ. Ponies	4	6	5	3	3	3	2
Total		74	52	46	29	28	23

Figure 3. An example of original Black Pied cattle.

Conservation Programmes within Groups of Similar Breeds

For breeds registered in the EAAP-AGDB, an attempt was made to form groups of similar breeds by use of information of breed history, geographic origin, phenotypic appearance, type of use, known genetic background, etc. (Simon and Buchenauer, 1993). For this report an additional analysis was run in order to find out to what extent conservation programmes are underway for similar breeds in different countries. An extract of the results is presented in table 8.

In nine subgroups of similar breeds a total number of 74 breeds is listed; 28 of them were classified as being 'at risk'. The breeds within subgroups are located in 2 to 6 countries, the number of conservation programmes for breeds at risk is n = 23. Obviously the decisions to conserve endangered breeds are made without taking into account the existence of conservation programmes for similar breeds in other countries. The situation appears even worse if we realise that for 46 breeds of the same subgroups, which were classified as being not endangered, 29 additional conservation programmes are reported. This draws attention to the need of clarifying the genetic relationship among breeds and to the need of co-operation across national borders.

Discussion

In the previous chapters it could be shown for Europe that:

- the quantity of farm animal genetic diversity – if expressed in the number of breeds – is still quite large,
- on average some 43 per cent of these breeds have to be regarded as more or less endangered,
- and that an impressive number of conservation programmes (~ 360) is underway.

However, it has become also apparent that in many cases decisions to conserve breeds seem to be not only independent of their status of endangerment but also of the existence of conservation programmes for similar breeds in other countries. This calls for

a closer look at the essential elements of present approaches to conservation in Europe.

Breeds as appropriate units of genetic diversity and of conservation

All groups of interbreeding animals which according to the practice in the reporting countries should be regarded as breeds are registered as such by the EAAP-AGDB. This number probably includes several breeds with the same or similar background. The total number of registered breeds of a species therefore has to be regarded as an overestimate of the available genetic diversity.

From genetic theory we know that genetic diversity of populations is a function of the frequencies of genes and of gene combinations. As a consequence, the objective of conservation in principle should be genes and gene combinations. It is interesting to note that the UN-Agenda 21 (1992), in chapter 15 'Conservation of biological diversity', calls 'to conserve and maintain genes, species and ecosystems', not of breeds.

However, our ability to identify genes of farm animal species and their interaction has been very limited, so far. In addition, for several reasons, farm animal species are subdivided into breeds as operating units within which the decisions and actions for breeding are performed. Therefore, for the time being, it is realistic to use breeds as indicators of available genetic diversity of a species. However, if it comes to conservation of genetic diversity, preference should be given to those breeds which can be assumed to be 'containers' of a unique genetic potential, i.e. of genes or gene combinations which are not available in other breeds.

Assessment of breeds for endangerment

By use of the system explained in chapter 3 a higher percentage of breeds was classified as being 'at risk' in Europe (42.8 %) than by the FAO-system of WWL-2 (1995) (32.8 %). The two systems differ essentially in three criteria:

- The way of considering a minimum population size, below which a breed should be regarded as being 'at risk',
- the way of dealing with incrossing or migration, i.e. the use of animals of other breed(s) for reproduction,
- and taking account of the number of breeding herds in which the breed is kept .

For the minimum population size the FAO-system asks for absolute numbers of breeding animals, i.e. that the total number of breeding females and males are greater than 1000 and 20, respectively; same numbers for breeds of all species.

In contrast, the system we used for our analysis asks for a minimum effective population size Ne – a term from population genetics – of the breed in question, where the minimum value of Ne is deduced from the maximum increase of inbreeding, which appears acceptable in a time period of 50 years of conservation (F-50). Taking account of different generation intervals of different species, species-specific values of Ne are obtained (see table 2).

If the minimum numbers of the FAO-system are transformed into the corresponding effective population size the resulting value of Ne = 82 is - compared with the respective values of table 2 - above the value for breeds of horses and asses (52), but below the values for sheep and goats (95) and for pigs (157). In other words breeds of the latter three species will be declared earlier to be more or less endangered by the system used here than by the FAO-system. In addition, in our system only females that are registered in a herdbook – or an estimate of these - are used in estimation Ne of a particular breed. This again increases the probability that the breed will be classified as

being 'at risk', compared with considering the total number of female breeding animals or the overall population size.

The factor migration, i.e. incrossing or the use of animals of other breed(s), is not considered in the FAO-system. In our system a breed is transferred into one class of higher endangerment, if more than 20 per cent of the matings for reproduction are performed with animals of other breed(s). Taking account of migration appears meaningful since migration results in a deviation from the Hardy-Weinberg-equilibrium of gene frequencies, which in essence is not compatible with preservation of the present known and unknown genetic potential of a breed.

The number of breeding herds or breeding locations in which the breed is kept: If this number is less than 10 and the number of female breeding animals is below 500 then the breed is downgraded into a class of higher endangerment. A low number of breeding herds can increase the risk of rapid disappearance of the breed due to disease hazards, natural disasters or loss of interest of people.

Considering the three mentioned criteria (time based population size, incrossing and the number of herds) in the risk assessment, results in a higher proportion of breeds at risk than by the FAO-system. However, we feel that it allows a better coverage of breed dynamics, which is relevant to conservation.

Two other systems are of practical importance in Europe: The European Union defines the maximum number of female breeding animals for an endangered breed by EC-regulation 2078/92 (STAR-reports 1992, 1994) with 5 000 for cattle and horses and with 7 500 for sheep and goats, respectively (stable population size assumed). These numbers are 5 to 7 times larger than the limit set by the FAO-system with the result that many more breeds can be declared to be at risk and can apply for support. A justification for these high numbers cannot be seen.

The acceptance procedure of the Rare Breeds Survival Trust (RBST) (Alderson, 1995) on the other hand is quite demanding: Continuous existence of the breed for 75 years and at least 2 of the 3 following requirements:

Table 9. Relative importance of risk factors for downgrading a breed from 'not endangered' into classes of endangerment (in percent)

Risk factor	Species					All
	Cattle	Sheep	Goats	Pigs	Horses	Species
Effective Pop. Size Ne	44.8	62.4	57.6	71.8	46.5	57.9
Incrossing/Migration	29.8	13.1	11.9	6.2	29.9	18.7
Decreasing No of females	13.6	15.2	25.4	12.3	16.5	15.1
Low number of herds	7.5	9.3	5.1	9.7	7.1	8.3
Total	100.0	100.0	100.0	100.0	100.0	100.0

Accepted herdbook for six generations, less than 20 per cent contribution by other breeds and thirdly parent breeds used in the formation of the breed are no longer available. In addition: fewer than the following number of breeding females: pigs 500, goats 500, cattle 750, horses 1 000 and sheep 1 500. Last but not least, the factors minimum number of distinct male lines, decreasing population size and low number of breeding units are considered.

This acceptance procedure appears to be a well-founded system with many valuable criteria (although the critical animal numbers seem to be defined independently of the generation intervals of species). However, it will probably be difficult, in general, to supply both the quantity and quality of the required information on those breeds which are approaching endangerment.

Compared with the various systems of risk assessment mentioned above we feel that the system we used for the breeds of the EAAP-AGDB is an acceptable compromise between considering population genetic theory, short term risk factors and obtainable information. Table 9 presents information on the relative importance of the four factors used in our system for the downgrading of a breed from the status of 'not endangered' into classes of endangerment. Summarising all species, 57.9 per cent of the downgradings are due to a low effective population size, 18.7 % are caused by incrossing and 15.1 % by a decreasing number of female breeding animals. A low number of herds affects endangerment only in the order of 8.3 %. However, this may be caused in part by missing information of the number of herds. For breeds of cattle and horses the use of breeding animals of other breeds for reproduction is obviously not uncommon, because 29.8% and 29.9% of the downgradings, respectively, are due to these factors. In pigs incrossing (6.2%) is of least significance to endangerment, whereas the effective population size Ne is of relatively highest importance (71.8%).

Of course, the results of the applied classification system depend on the observed criteria and on the way of combining these into a system of risk assessment. For example it may be questioned whether the assumed values of maximum coefficients of inbreeding, length of generation intervals of species, maximum percentage of incrossing, etc., are the best possible ones and whether formula (4) for estimation of the effective population size is adequate for small populations with decreasing numbers of breeding animals and with generally increased variance of family size. Nevertheless, for a rational approach to conservation it appears necessary to take a position on these criteria.

Different objectives of conservation call for different approaches

One of the main differences among the various systems of risk assessment can be seen in the fact, whether migration, i.e. use of breeding animals of other breeds, is considered as a risk factor or not. The question whether this is meaningful depends on the primary objective of conservation (Simon,1999). From the many statements on conservation objectives of FAGR, e.g. by Bowman (1974), DGfZ (1979), Maijala *et al*. (1984), Simon (1984), UNEP (1992), Blair (1995), Hammond (1995), Cunningham (1996), British Society of Animal Science (1997), three main objectives have become apparent:

1. Subunits of species, such as populations, breeds, lines or strains, which under predominantly favourable production conditions are no longer competitive, may possess – unknown so far – a genetic potential which may become useful for future breeding options. The resulting argument, which we may call 'Conservation for potential use, later'(Simon,1999), is mainly expressed in developed countries of Europe and North America.
2. In regions with predominantly unfavourable production conditions, indigenous populations or breeds – in spite of their usually limited production

potential – generally form the basis of food security for an increasing human population because of their generally good adaptation to harsh production conditions. The argument, which we may call 'Conservation for sustainable use, now', is expressed mainly in and for developing countries of the world.

3. Rare breeds can be regarded as part of our living heritage and as such deserve to be preserved for historical, ethical or local reasons. This argument, which we may call 'Conservation for cultural reasons', seems to be expressed mainly in developed countries of Europe and North America.

Since objective number 1, 'conservation for potential use, later', aims to preserve an unknown genetic potential for requirements that are as yet unknown in far distant unknown future, it is essential to avoid all influences that can change the genetic makeup of the population, or – in terms of population genetics – that can change the Hardy-Weinberg-equilibrium of the population (Simon, 1995; 1999).

This requires avoidance of migration or the use of animals of other populations for reproduction, avoidance of artificial selection of mates in pursuit of defined breeding goals 'for improvement' and it requires the minimisation of random drift of gene frequencies and inbreeding by providing a sufficient effective population size Ne (Falconer, 1989). Therefore, it appears necessary to observe migration or incrossing already in the risk assessment, if conservation for potential later use is the primary objective of conservation, which at least in Europe is of high relevance (Simon, 1995).

Objective number 2, 'conservation for sustainable use, now', asks for a completely other strategy of conservation. Here, immediate use of endangered breeds is required in order to serve the immediate needs of the human population for food security. Genetic changes of breeds for improvements both by artificial selection within the breeds and by planned incrossing of animals of other, highly-productive breeds is an essential tool of sustainable use and conservation (see, for example, Rege and Bester, 1998; Mariante and Fernandez-Baca,1998). For this reason the situation of incrossing need not be considered in risk assessment, if 'conservation for sustainable use, now' is the main objective.

Finally, if objective number 3, 'conservation for cultural reasons' is the main objective of conservation, the situation of incrossing or use of animals of other breeds can be dealt with in either way. Purists may demand strict purebreeding and may reject any minor 'contamination' by 'foreign blood'. Others may tolerate the introduction of animals of similar breeds as long as the outside appearance of the breed is not severely changed. In other words, the consideration of incrossing is not a major issue in risk assessment, if conservation is pursued mainly for cultural reasons. A similar position may be taken on the question of selection of mates for 'genetic improvement' or for adaptation during conservation.

Summing up this section, we can see that the primary objectives of conservation in Europe are different from the ones in developing countries, say in Africa, South America or in Asia. It also follows that different procedures of risk assessment and of practical conservation should be applied (Simon, 1999).

The problem of choice of endangered breeds for conservation

An adequate approach to dealing with this problem is again affected by the primary objective of conservation. Within the context of conservation for cultural reasons, preference for specific breeds is usually expressed by the people or institutions which actually work with the breed. In this situation it is probably not adequate to impose criteria from outside as long as support from outside is not requested. Nevertheless, for example the NGO Rare Breeds Survival Trust requires in its acceptance procedure 'a distinct

characteristic not found elsewhere', if other requirements are not met completely (Alderson,1995).

For the primary objective 'conservation for sustainable use, now' candidate breeds for the combined goal conservation and improvement should be the most promising adapted local breeds, preferably evaluated on the basis of reliable data of their adaptive value and on their combining ability with highly productive exotic breeds, as explained by Rege and Bester (1998).

For the primary objective 'conservation for potential use, later' priority should be given to those endangered breeds which – unknown so far - could possess a genetic potential which could become valuable in the future and which cannot be expected in other breeds. The main criterion for selection of a breed, therefore, should be the degree of genetic uniqueness or the degree of genetic distance in comparison to other breeds, i.e. both to the more popular breeds and to other endangered breeds, as explained for example by DGfZ (1979), Camussi *et al*.(1985), Weitzman (1993), Barker (1994) and Ollivier,1996).

Bearing in mind the relatively high number of breeds 'at risk' in Europe (Table 3), the availability of similar breeds in different countries and the generally high costs of conservation (Brem *et al*., 1984; Smith, 1984; Lömker and Simon, 1994), clarification of genetic uniqueness of breeds appears to be one of the most urgent tasks in conservation of FAGR in Europe. This can only be achieved in a satisfying way on a supra-national level, for which effective co-operation among all acting institutions across national borders is required.

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Inbreeding and loss of founder alleles in four variations of a conservation programme using circular mating, for Danish Shorthorn Cattle

M. Trinderup[1], J.N. Jørgensen[1] & M. Hansen[2]

[1]Department of Animal Science and Animal Health, the Royal Veterinary and Agricultural University, 13 Bülowsvej, 1870 ***Frederiksberg C****, Denmark*
[2]The Danish Agricultural Advisory Centre, The National Committee of Danish Cattle Husbandry, 15 Udkjærsvej, Skejby, 8200 ***Århus N****, Denmark*

Summary

The beef cattle breed Danish Shorthorn is used as a model for simulation of four variations of the circular mating scheme running for 50 years. Schemes 1 and 2 used a fixed exchange of bulls between female groups while schemes 3 and 4 used a random exchange of bulls between female groups. The number of bulls used in schemes 1 and 4 was 16 while the number of bulls used in schemes 2 and 3 was 8. Inbreeding levels were computed and gene dropping was applied to estimate the risk of founder allele loss. In the population of year 50 the inbreeding levels for the four mating schemes are not statistically different. The male founder alleles contribute strongly to the population of year 50. The female founder alleles are in greater risk of being lost than the male founder alleles.

Résumé

La race bovine à viande Danish Shorthorn est utilisée comme modèle pour la simulation de quattre variations du schéma circulaire d'accouplement au long de 50 ans. Les schémas 1 et 2 utilisent un échange fixe de taureaux dans des groupes de femmelles. Le nombre de taureaux utilisés dans les schémas 1 et 4 a été de 16, tandis que le nombre de taureaux utilisés dans les schémas 2 et 3 était de 8. On a établi les niveaux de consanguinité et appliqué le comptage des gènes pour estimer le risque de perte d'allèles de base. Dans la population de la 50ème année les niveaux de consanguinité pour les quattre schémas d'accouplement ne sont pas statistiquement différents. Les allèles mâles de base contribuent fortement à la population de la 50ème année. Les allèles femmelles de base se trouvent en plus grand péril de perte que ceux des mâles.

Key words*: Gene dropping, Diversity, Beef cattle.*

Introduction

Several methods for the conservation of animal genetic diversity have been developed. Cryogenic storage is a conservation method free from human interference which might bring about genetic change (Bodó, 1990). Though storage of frozen semen and embryos has been known and used for years, the most important and practical method of conserving genetic diversity now and in near future is to manage genetic variability in some small living populations (Smith, 1984; Wang *et al.*, 1994). For most livestock breeds the conservation of a living population involves private breeders. Therefore it is necessary to have the support of the breeders if a conservation programme is to be a success (Rognoni & Finzi, 1984). This calls for breeding plans that are fairly easy for the breeders to implement in the population, e.g. breeding plans that fit the demographic structure of the population.

Many studies have been carried out on the topic of conserving small populations with a minimum of inbreeding (Kimura & Crow, 1963; Smith, 1984; Chevalet & Rochambeau, 1985; Bodó, 1990; Wang *et al.*, 1994). The majority of the authors suggested dividing the population into breeding groups of females and a rotation of males among the groups in a circular mating scheme. Chevalet & Rochambeau (1985) compared three turnover rates of the males in a circular mating scheme implemented in a small dairy cattle breed by simulations. In the first and second systems the males were used for two years in each group of females; totally the males were used for 16 years. In the first system the bulls were replaced by a son. In the second system the programme was initiated by selection of eight bulls and one male offspring of each bull as a replacement male. When a bull was culled the replacement male became the new bull and one of the culled bulls sons was selected as a new replacement male. Thus, the second system prolonged the generation interval of the males as compared to the first. In the third system the males were only used for two years and only in one group of females. Chevalet & Rochambeau (1985) found that prolonging the generation interval of the males delayed the inbreeding, but the rapid turnover (system three) gave the lowest inbreeding level.

Not only is the inbreeding of concern in conservation genetics, attention has also been given to the founder representation in the population under study and to preventing loss of founder alleles in the future (Chevalet & Rochambeau, 1985; MacCluer *et al.*, 1986; Lacy, 1989; Boichard *et al.*, 1997). With less breeding males than females, as is the case in cattle populations, there is a tendency of loss of female founder alleles, but a rapid turnover of the males enables the population to keep alleles from the female founders (Chevalet & Rochambeau, 1985).

In the circular mating schemes outlined by other authors (Kimura & Crow, 1963; Chevalet & Rochambeau, 1985) a fixed scheme is used for the exchange of males between the groups of females. In practice breeders might find it difficult to follow such a strict plan for the use of the males.

In this paper the objectives are:

1. to test the hypothesis that a random exchange of males between the groups of females increases the inbreeding level compared to an exchange of males that follows a fixed scheme;
2. to test the hypothesis that increasing the number of males will result in a decrease in female founder alleles.

Materials and Methods

Data of the beef cattle breed Danish Shorthorn (figure 3), provided by The National Committee of Danish Cattle Husbandry, is used as a model for simulations of four variations of the circular mating scheme. The first generation in the simulation of the mating schemes is founded by the Danish Shorthorn population of 1997 which consisted of 96 females and 8 males (Trinderup *et al.*, 1998). This year is referred to as year zero in the simulations.

Initially the females are divided into eight breeding groups, each of 12, referring to the original herds found in the data material. The number of females is fixed through the time period simulated to exclude the effect of fluctuations in population size.

Based on the age distribution of the females found in the data the replacement rates over age classes were computed (table 1). These replacement rates were used as culling probabilities for the cows in the simulations. As can be seen in table 1, the maximum age of females was set to 12 years in the simulations. The females were at least two years before they were mated for the first time. Once a cow was mated it was assumed that she gave birth to one calf of random sex each year until she was culled. To prevent loss of female founder alleles and to reduce variation in female family size the first choice of a replacement heifer was a daughter of the culled cow. A cow's offspring were kept in the population until she was replaced in order to maximize the possibility of having a daughter for

replacement. Otherwise a heifer from the same breeding group or herd was randomly selected.

The difference between the four mating schemes was the way the breeding bulls were used in the population as illustrated in figure 1 and outlined in the following.

Scheme 1

Each of the eight bulls were assigned to one of the eight herds in year 0. Each bull was mated to all the females of his herd in year 0 and one son was randomly selected. Each of the eight selected young bulls were sent from the *j*'th herd to the *j+1*'th herd, except for the 8'th herd where the young bull was sent to the first herd. After year 0 the 'old' bulls were mated to the cows and the 'young' bulls were mated to the heifers. The following year, after a new rotation of young bulls, the 'old' bulls were culled and replaced by the 'young' bulls, who now were mated to the cows, and the new 'young' bulls were mated to the heifers. Thus, each breeding bull was used in two years. The rotation of bulls follows a fixed system which ensures that the male descendant of a certain bull returns to the herd with the female descendants after eight rotations. This scheme doubles the number of males from the original eight to sixteen.

Scheme 2

This scheme was similar to scheme one, except that here was only one bull per herd. This bull was mated to both heifers and cows. The bulls were only used for one year before they were replaced by one of their sons and the number of bulls was kept at the original eight.

Scheme 3

As scheme 2, but here the bulls were randomly assigned to a herd. This means that a bull was allowed to breed in the herd that he was born in.

Scheme 4

As scheme 1, except that the 'young' bulls were randomly selected among all the bull calves born and all living, non-breeding bulls up to 10 years of age. As in scheme 1 the breeding bulls were culled after two years. The selected bulls were not assigned to any herd, but could be mated to all cows and heifers in the population just like bulls from artificial insemination centres (A.I.-bulls).

PASCAL programmes were written to simulate the circular mating schemes. Each simulation of a mating scheme had a time span of 50 years or approximately 12 generations and were repeated 200 times.

The inbreeding coefficient for each animal was computed as proposed by Quaas (1976). The base animals for the inbreeding coefficient computation were the animals with unknown parents found in the data of Danish Shorthorn (Trinderup *et al*., 1998). The founders of the circular mating schemes, the Danish Shorthorn population of 1997, were therefore not unrelated animals as defined by other authors (e.g. Lacy, 1989), but the animals entering the circular mating schemes (Foose, 1986; Falconer & Mackay, 1996). The founders of the circular mating schemes were the reference generation of a gene dropping (MacCluer *et al*., 1986) which was conducted in order to estimate the founder representation after 50 years of breeding.

Results

Figure 2 shows the change in mean inbreeding coefficient over time in the four circular mating schemes. The inbreeding coefficients were highest in the schemes with random exchange of bulls in the first seven years of the simulations. But for animals born after year eight the inbreeding coefficients were almost the same in all four mating schemes.

Table 2 shows the inbreeding levels and trends with the standard deviation for the animals in the population of year 50. To reduce the confounding of the year of birth and the number of ancestral generations the

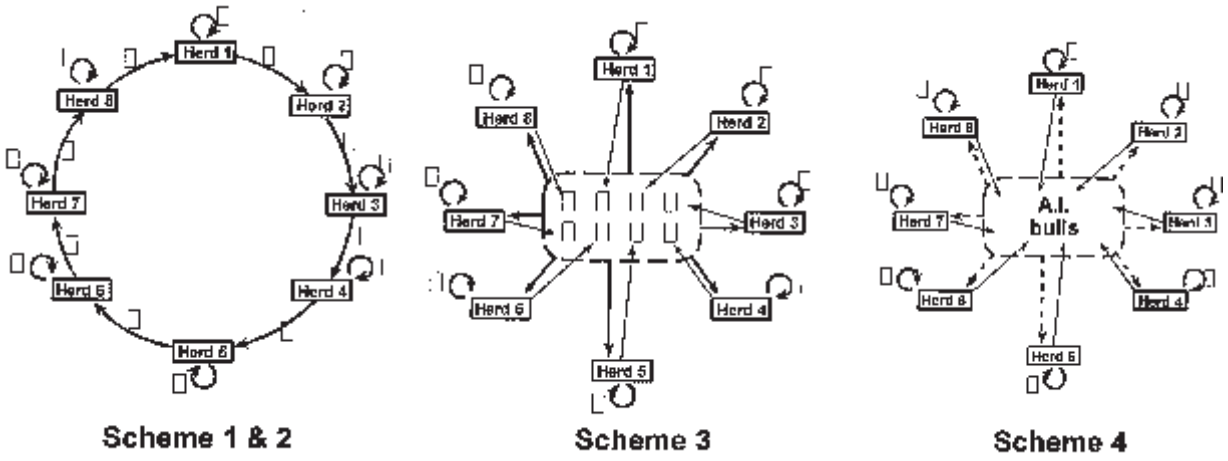

Figure 1. Illustration of the differences between the four mating schemes.

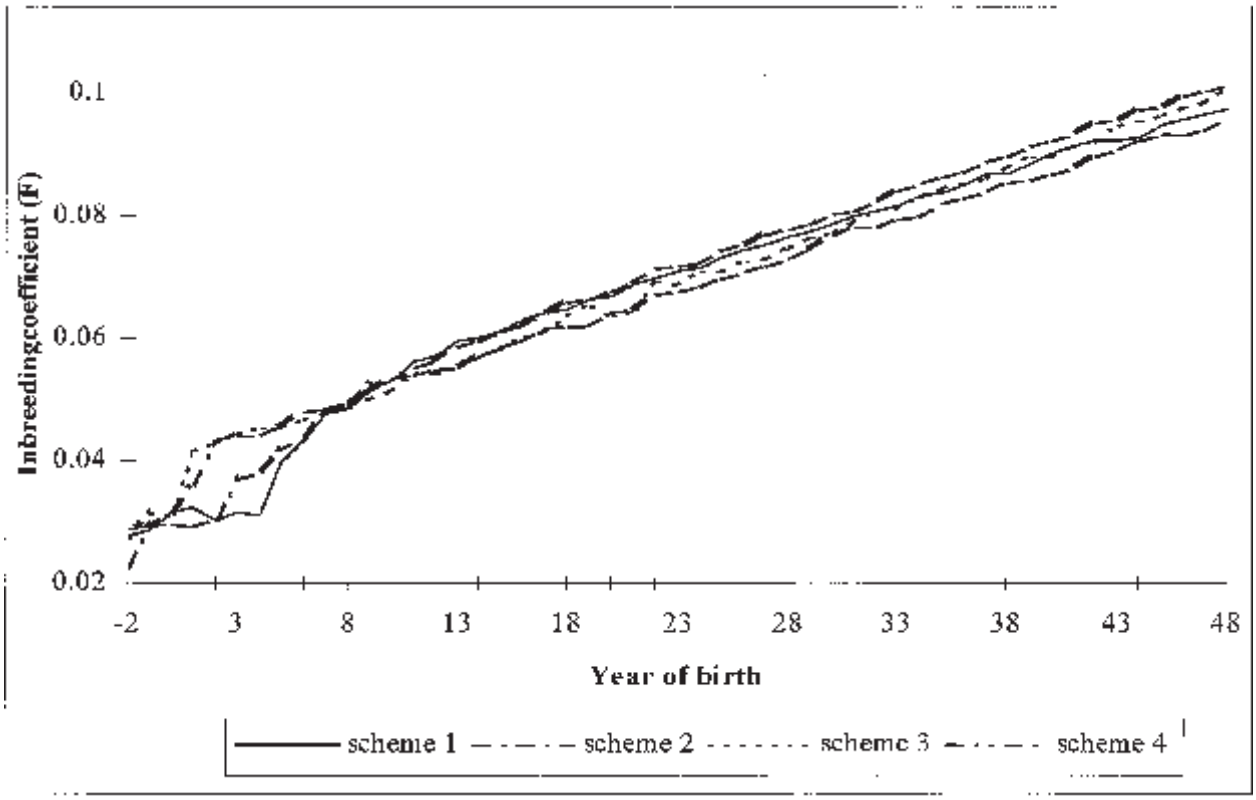

Figure 2. Average inbreeding levels per year of birth.

inbreeding trends should be tabulated for animals with more than seven ancestral generations (Te Braake *et al*., 1994). Thus, the inbreeding trends were tabulated from the two last generations in the simulations. The schemes with random exchange of bulls had the largest inbreeding trend and thus the smallest effective population size. Though scheme 4 (16 bulls) had the second highest inbreeding trend, this scheme resulted in the lowest mean inbreeding trend in the population of year 50. Scheme 1 (16 bulls) had the lowest inbreeding trend and the second lowest mean inbreeding levels at the end of the simulations. However, the standard deviations indicate that there is no statistical difference between the four mating schemes in rate of inbreeding and mean inbreeding level in the population of year 50.

Table 3 shows the result of the gene dropping. The criteria used here were the average contribution of alleles from each male and female founder, the total male and female founder allele contribution and the minimum and maximum percentage of the 200 replicates in which the alleles of a male or female founder was lost. The mating schemes using 16 bulls (i.e. schemes 1 and 2) resulted in the largest individual and total contribution of male founder alleles and the smallest minimum values of percent replicates with male founder allele loss. In all four mating schemes the maximum and minimum percent replicates with male founder allele loss were lower than the percent replicates with female allele loss. The percentages of replicates where the alleles of a female founder were lost were very much the same for all four mating schemes, due to the fact that the replacement strategy was identical in all four mating schemes.

Discussion

It was expected that if there were any differences in inbreeding trends among the four mating schemes they would be small, because the same replacement strategy for the females were used in all the mating schemes, the difference in population size was very small and there were only small variations in the generation length for the males. In the simulations there was no significant difference in inbreeding trend or in inbreeding level after 50 years. In the first few years there seems to be a difference between the schemes using random exchange of males and the schemes using a fixed plan for exchange of males. This confirms the hypothesis that random use of males results in an instantly higher inbreeding level, but the difference is not permanent. When the first rotation of males is completed, the inbreeding increases in the schemes with fixed exchange of males to the level of the schemes with random exchange of males after which the rate of inbreeding is fairly similar in all four mating schemes.

Concerning the inbreeding level and trend it can be concluded that it is not important that the breeders follow a strict plan for the exchange of males as long as they follow the guidelines used in these simulations: minimising the variation of family size within sires and dams and avoid fluctuations of population size. The size of inbreeding trend found in these simulations of about 0.5% is acceptable in any breeding plan, because with such a low increase in inbreeding it is possible to select the animals showing the least inbreeding depression (Adalsteinsson *et al*., 1994).

The distribution of male and female alleles in the founder population (year 0) is 7.7% male founder (8 bulls among 104 animals) alleles versus 92.3% female founder alleles (96 cows among 104 animals). The total contribution to the population of year 50 found in schemes 2 and 3, using eight bulls, was 20% male founder alleles and 80% female founder alleles (table 3), as found by Chevalet & Rochambeau (1985) in a simulation study running over 40 years. The change in the contribution of male and female founder alleles over years is due to the more intense use of bulls. Hence the male founder alleles are over-contributing to the population of year 50, whereas the schemes fail to some extent to keep the female founder alleles segregating.

Table 1. Replacement probabilities for female age classes.

Age, years	3	4	5	6	7	8	9	10	11	12
Probability	0.178	0.159	0.209	0.137	0.267	0.189	0.267	0.318	0.333	1.0

Table 2. Mean inbreeding and inbreeding trend with standard deviation in the population of year 50.

Mating scheme	Inbreeding trend [a] %	S.D.	N_e [b]	Mean inbreeding [c] %	S.D.
1	0.47	0.22	106	9.48	0.29
2	0.52	0.19	97	9.82	0.37
3	0.62	0.37	81	9.71	0.53
4	0.55	0.32	91	9.28	0.46

a) Computed from the last two generations and averaged over the 200 replicates.
b) Calculated by the equation: $N_e = 1/(2*\Delta F)$.
c) Mean inbreeding coefficient of the last generation averaged over the 200 replicates.

Table 3. Founder contribution to the population of year 50 and risk of allele loss.

Mating scheme	Individual contribution of the two sexes, %		Total contribution of the two sexes, %		Replicates with founder allele loss, % males		females	
	males	females	males	females	min.	max.	min.	max.
1	3.07	0.79	24.52	75.48	4.5	12.0	30.5	48.0
2	2.44	0.84	19.54	80.46	10.5	16.5	30.0	48.0
3	2.54	0.83	20.31	79.69	11.5	20.0	33.0	48.0
4	3.04	0.79	24.34	75.66	4.0	22.0	32.0	47.5

Our simulations indicate that in a conservation programme using a circular mating scheme it can be up to the individual breeders to manage the exchange of bulls among the groups of females. The over contribution of founder sire alleles found in this investigation indicates that the initiating sires of a conservation programme should be selected carefully. A method to ensure that the founder sires of a conservation programme are of the type of interest is the gene dropping method as shown by Trinderup *et al*. (1998). The observed small differences between the four mating schemes indicate that other factors, such as economy, should be considered in the choice of conservation programme.

Figure 3. Danish Shorthorn cattle.

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Advances in the Brazilian animal genetic resources conservation programme

A. da S. Mariante[1], M. do S. M. Albuquerque[1], A. A. do Egito[1] & C. McManus[2]

[1]National Centre for Genetic Resources, EMBRAPA-CENARGEN, Sain Parque Rural, P.O.Box 02372, 70849-970 ***Brasilia****, Brazil*
[2]Universidade de Brasília, ***Brasília****, DF, Brazil*

Summary

Brazil has various species of domestic animals which developed from breeds brought by the Portuguese settlers soon after the discovery. Over the last five centuries, these breeds have been submitted to natural selection in particular environments and therefore today, they present characteristics adapted to the specific environmental conditions. From the beginning of this century, some exotic breeds, selected in temperate regions, have begun to be imported. Although more productive, these breeds lack adaptation traits, such as resistance to disease and parasites found in breeds considered to be "native", but even so, little by little, they have substituted the native breeds to such an extent that the latter are, today, in danger of extinction. To avoid the loss of this important genetic material, Brazil created an Animal Genetics Resource Conservation Programme, coordinated by the National Research Centre for Genetic Resources and Biotechnology (Cenargen) of the Brazilian Agricultural Research Corporation (EMPRAPA). The conservation has been carried out by various Research Centres of EMPRAPA, Universities, State Research Corporations, as well as by private farmers, with a single coordinator at national level, Cenargen. The conservation is being carried out through Conservation Nuclei, situated in the habitats where the animals have been subjected to natural selection (*in situ*), and by the storage of semen and embryos (*ex situ*). The recently created Animal Genetics Laboratory of Cenargen allowed genetic characterisation studies on cattle and horse breeds to begin, and, in the near future, work with asses, buffalo and sheep will be conducted.. From the results of this research it will be possible to compare the native breeds and estimate genetic distances between them. The harmonisation of chosen micro-satellites with those which have been used in other Latin America and Iberian Peninsula countries will be extremely useful for comparative studies and will allow future exchange of germplasm between countries.

Resumen

Los colonizadores portugueses, cuando vinieron al Brasil, trajeron consigo, animales domésticos. Estos se multiplicaron, y han sido sometidos a un amplio proceso de selección natural, adquiriendo características adaptativas y/o de producción para las diversas situaciones ecológicas del país y se han transformado en lo que conocemos como razas "locales" o "criollas". Cerca de tres siglos después del descubrimiento, muchos criadores comenzaron a importar animales de razas nuevas, buscando mayor productividad. El establecimiento de políticas que promovieron la dilución de germoplasma autóctono a través de programas extensivos de cruzamiento con esas razas importadas resultó en rápida substitución de las razas locales. Aunque éstas presenten productividad más baja que las exóticas, están extremamente bien adaptadas a las condiciones ambientales, a los que estuvieron sometidos bajo selección natural. En este trabajo discutimos la situación actual de la

conservación de las razas todavía existentes en Brasil. La investigación sobre evaluación, conservación y utilización de reservas genéticas de razas con características únicas, debe proveer la fundación para la utilización efectiva del germoplasma a nivel global. Complementariamente al uso tradicional de recursos genéticos animales, están los avances significativos en genética animal alcanzados en las dos últimas décadas, usando técnicas de biología molecular, tales como el mapeamento y la identificación de genes. Toda esta preocupación con la diversidad de los animales domésticos ha llamado la atención de los investigadores a la rápida desaparición de las razas locales, y, consecuentemente con la dilución del germoplasma autóctono a través del uso extensivo de programas de hibridación. La conservación de recursos genéticos animales en Brasil viene realizada en diversos Centros de Investigación de EMPRAPA (Empresa Brasileira de Pesquisa Agropecuária), Universidades, Empresas de Investigación de distintos Estados, bien como por productores privados, involucrando todo el país, bajo la coordinación del Cenargen (Centro Nacional de Investigación de Recursos Genéticos y Biotecnologia). La conservación se realiza por medio de núcleos de conservación, mantenidos en el habitat donde los animales están adaptados (*in situ*) y por el almacenamiento de semen y embriones (*ex situ*), incluyendo 7 especies animales: bovinos, bubalinos, cerdos, ovejas, cabras, caballos y asnos. Una importante tarea del Programa es aumentar la conscientización sobre la importancia de la conservación de recursos genéticos animales.

Introduction

Brazil has various species of domestic animals (Figure 1 to 4), which developed from breeds brought by the Portuguese settlers soon after the discovery. For almost five centuries, these breeds have been submitted to natural selection in determined environments so that, today, they present characteristics adapted to the specific environmental conditions.

From the beginning of this century, some exotic breeds, selected in temperate regions, have begun to be imported. Although more productive, these breeds lack adaptation traits, such as resistance to disease and parasites found in breeds considered to be "native", but even so, little by little, they have substituted the native breeds, to such an extent that the latter are, today, in danger of extinction. To avoid the loss of this important genetic material, Brazil created an Animal Genetic Resources Conservation Programme, coordinated by the National Research Centre for Genetic Resources and Biotechnology (Cenargen) of the Brazilian Agricultural Research Corporation (EMPRAPA).
The conservation has been carried out by various Research Centres of EMPRAPA, Universities, State Research Companies, as well as by private farmers, with a single coordinator at national level, Cenargen. This programme includes the following stages:

1. identification of populations in an advanced stage of genetic dilution;
2. phenotypic and genetic characterisation of germplasm; and
3. evaluation of productive potential. The conservation is being carried out by Conservation Nuclei, situated in the habitats where the animals have been subjected to natural selection (*in situ*), and by the storage of semen and embryos (*ex situ*). An important challenge for this programme is to increase awareness among the different segments of society for the importance of the conservation of animal genetic resources.

Objectives of The Brazilian Conservation Programme

The objectives of the Brazilian Animal Genetic Resource Conservation Programme are:

1. Identifying and characterising phenotypically conservation nuclei, establishing centres of originand assessing genetic diversity and variability for the groups of animals in danger of extinction;

Figure 1. Lavradeiro horse (Northern region).

2. Monitoring existing animal conservation nuclei;
3. Starting new conservation nuclei of breeds, which are identified as being in danger of extinction;
4. Conserving *ex situ* genetic material by cryopreservation of semen and embryos;
5. Genetically characterising the breeds involved in the Programme; and
6. Increasing the awareness of the diverse segments of society about the importance of the conservation of animal genetic resources.

Brazilian Animal Genetic Resources

Native breeds

The first cattle arrived in the American continent with the settlers in 1493, when some animals were left on the *Hispaniola* Island, which today is the Dominican Republic and Haiti. Cattle arrived in Brazil for the first time in 1532, introduced by the Portuguese. New introductions were made from the Archipelago of Cape Verde, where the Portuguese had been since 1460.

With its continental dimensions, Brazil has a huge variety of ecosystems where the different species of domestic animals brought by the first settlers began to establish themselves. Through centuries of natural selection, these animals attained special adaptation features specific to the ecological niche where they developed. Little by little, these animals dispersed over the whole Brazilian territory, and adapted to the very diverse environmental conditions with special characteristics such as in the Mato Grosso Pantanal, the North Eastern Agreste, the southern Brazilian Plateau and the Pampas of Rio Grande do Sul.

Due to the increasing demand for food of animal origin, farmers from many developing countries followed a course which, inevitably, led to the dilution of the "local" germplasm

by the use of intensive crossbreeding with animals of exotic breeds. Many of these programmes failed, since the introduced animals had lower productive indices than the "local" breeds. This meant that a considerable number of farmers, in establishing their production systems, started to give a deserved importance to the "local" breeds, because of their adaptation to the environment which is usually hostile especially in the tropical region.

Zebu breeds

At the end of the last century, the introduction of animals, which until then had been considered extremely exotic – the zebu, began. Today these breeds are responsible for almost the total meat production in the country, as purebred or crossbred animals, from the latitude of São Paulo State northwards.

The zebu was first introduced into Brazil at the end of the 19th century. These animals, which originated in India, were originally crossed with the local breeds. Little by little the local breeds were absorbed. As a result, Brazil has today the largest zebu population in the world, while in their country of origin, where they are considered sacred, they are raised freely and protected by the community until they die a natural death.

Before the first importation of zebu cattle to the Southeast region of Brazil, the Southern region, of temperate climate, had already imported British cattle breeds which were highly productive. The latter did not have the same adaptation problems as animals of the same breeds in the tropical regions of the country. As in central Brazil, the British breeds introduced in the south of the country were used in crossbreeding schemes, leading again to a drastic reduction in the effective population size of the local breeds.

The expansion of the zebu breeds in Brazil is an undisputed reality. Today about 80% of the Brazilian cattle population is made up of zebu cattle or their crosses with Creole and European cattle. Although, up to this time, the conservation Programme is only involved with the native breeds, as they are threatened with extinction, there is already a demand from the zebu breeders that these breeds also be included. This is due to the almost total domination of the Nellore breed in Central Brazil. Of the six principal zebu breeds that exist in Brazil, approximately 85% of the total number of animals registered are Nellore.

Another aspect, which should be highlighted, is the fact that the use of new technologies and more efficient methods in genetic improvement programmes have led to profound changes in the procedures used by the breeders in the selection and reproductive management of their herds. Since 1984, when the first Bull Summary was published (Mariante *et al*., 1984), the breeders began to have more precise information about the genetic merit of each individual selection candidate. This, together with techniques which allowed the increase in reproductive capacity of the genotypes of interest (artificial insemination, embryo transfer and in vitro fertilization), have made the decision taking process more objective, especially when referring to the choice of animals for reproduction and mating schemes.

From the beginning of the publication of the Bull Summaries a large number of breeders started to put greater emphasis on the productive traits (taken from the Classification Table of the Summary), leaving behind the qualitative traits, such as breed characteristics and type. Bulls which up to then may have been left aside because of one or another external trait, which did not please the more conservative breeders, sired offspring with exceptional weight gains, proving that they imprinted production traits which were more important at slaughter. These bulls then became highly demanded by the Artificial Insemination Centres and their semen was sold at very high prices.

This situation resulted in the use of a small number of bulls, especially those classified as Elite, which, certainly led to the reduction in genetic variability. Ironically, this bull classification due to merit, together with more modern practices in animal reproduction

Figure 2. Pantaneiro horse (Northern region).

already mentioned, are partially responsible for the reduction in genetic variation (Mariante, 1990).

These preocupations of breeders led to the demand for the creation of a Germplasm Bank where semen and oocytes of zebu breeds would be stored, and would be monitored by EMPRAPA-Cenargen, although it would be situated at the headquarters of the Brazilian Association of Zebu Breeders in Uberaba, Minas Gerais State. The choice of animals which would be selected to donate semen and oocytes could be based on the Family Catalogue, which to date has been published for the Nellore breed (Magnabosco *et al*., 1997). The catalogues for the other zebu breeds should be published in the near future.

Information is presented about the zebu breeds originally introduced and selected in Brazil (Gir, Guzerat, Nellore and Sindi), and those formed there (Indubrasil and Tabapuã). Some animals of the Kangaian breed were also imported, but today their effective population size is greatly reduced.

Gir

The first animals of the Gir breed were probably imported around 1906. The greater portion of the importation, which resulted in creation of nuclei which exist today, dates from 1920.

Guzerat

The main importations of the Guzerat breed were to the Curvelo region, Minas Gerais State. Later, farmers in the Uberaba district, of the same state, became interested in raising this breed. The breed continued to expand to the north of São Paulo State and from there to other regions of the country. In the region known as the Minas Triangle, Minas Gerais State, it was used in crossing programmes with the Gir and Nellore breeds, creating the Indubrasil breed.

Nellore

The Nellore breed belongs to the second Indian group (cattle with white or grey hair and short horns), by the classification of Joshi and Phillips, referred to by SANTIAGO (1987). The Brazilian Nellore population is originated from importations made in 1930 and notably those in 1960 and 1962. At the present time the Brazilian Nellore is tending to the type of the Indian Ongole. Of all the zebu cattle found in Brazil the Nellore stands out because of its production qualities and it is becoming more prized by the breeders. Although for some time it had been left aside because of its short ears, similar to those of European cattle, today it is in first place in terms of Genealogical Registration, as well as its overwhelming use as bulls in herds of other breeds. The animals are highly fertile, resistant to parasites and to tropical disorders, precocious and have extraordinary maternal ability. In Brazil, the Nellore is essentially a meat producer, which has been subjected to highly intensive selection to obtain males for slaughter.

Sindi

The Sindi breed is very similar to the Gir from the west of India,to Sahiwal, from Punjab and the red cattle of Afghanistan. Due to the movement of nomad tribes in its home track, it had been crossed with Gir in some regions. The Sindi, which arrived in Brazil in about 1906 and 1930, had the Baixada Fluminense region, in the state of Rio de Janeiro, as their destination as well as the Novo Horizonte and Jardinópolis townships, in the São Paulo State. In general, these animals were small, good looking and useful in areas where there was a lack of forage, where it would be more difficult to maintain larger animals.

Table 1. Species and breeds included in research projects in the Brazilian Programme of Animal Genetic Resources Conservation - 1999.

Species	Breed	Region of the country
Cattle	Mocho Nacional (National Polled)	Southeast
	Pantaneiro	Centrewest (Pantanal)
	Curraleiro or Pé-duro	North east
	Criollo Lageano	South
Buffaloes	Baio	North
	Carabao	North
Asses	Jumento Nordestino (North-eastern Ass) or Jegue	Northeast
	Jumento Brasileiro (Brazilian Ass)	Southeast
Horses	Pantaneiro	Centrewest (Pantanal)
	Lavradeiro	North
Goats	Canindé, Gurguéia, Moxotó, Marota, Repartida	Northeast
Sheep	Criollo Lanado	Northeast
Diverse species	Animal Gene Bank (AGB)	Centrewest

Table 2. Number of semen doses and embryos stored in the Animal Germplasm Bank (AGB) of Cenargen, in 1999.

Species/Breed	No. of semen doses	No. of embryos
Cattle		
Criollo Lageano	6 159	9
Mocho Nacional	6 533	54
Caracu	3 950	47
Curraleiro	5 300	17
Criollo Argentino	288	-
Pantaneiro	4 277	20
Junqueira	2 143	4
Patuá	250	-
Goats		
Moxotó	546	-
Canindé	109	-
Sheep		
Criolo Lanado	500	56
Horses		
Pantaneiro	-	1
Asses		
J. Nordestino	150	-
Total	30 205	208

Indubrasil

The Indubrasil, according to Santiago (1984), was the first zebu breed formed by Brazilian breeders, based on cattle imported from India. Initially, its pioneers in the Minas Triangle gave it the name of Induberaba, but only in 1936 was it officially recognised as the Indubrasil, a name that it keeps today. Its origin, although basically founded from the Gir, Nellore and Guzerat breeds, is obscure as to the exact genetic contribution of each of the breeds or zebu types used.

Tabapuã

According to Santiago (1984), the first polled zebu, object of selection in Brazil, was the Tabapuã, named after the township where it was formed in São Paulo State. Phenotypically, these cattle resemble the American Zebu (Brahman), which means that several Brahman cows, when dehorned, are confused with Tabapuã animals. Despite this, its racial composition is mainly Nellore with some Guzerat and Gir.

Formation of Conservation Nuclei

The Conservation Nuclei, organised in the form of research projects, can be found all over the country. The elaboration of research projects, usually based in research centres near the habitats where the animals were naturally selected over the last few centuries, was the solution adopted to try and rescue the small effective populations of the breeds in danger of extinction.

The articulation of Cenargen with these Conservation Nuclei (Germplasm Banks) is made by Germplasm Curator (based in Cenargen), in collaboration with the Curators of the Germplasm Banks (normally the research project leaders). In the present collaborative programme, there are 3 Germplasm Curators for animals at Cenargen: one for large species (cattle, buffaloes, horses and asses), one for small species (sheep, goats and pigs) and one for wildlife.

The Animal Germplasm Curators are researchers of Cenargen, attributed with giving advice to the Technical Head in relation to germplasm considered relevant to national agriculture and animal production. They work at national and international level, with subjects related to the enrichment of knowledge and conservation of product germplasm, being supported by technical areas for these activities. Among other functions, the animal Germplasm Curator has to promote, start and follow activities related to conservation, multiplication and/or regeneration of germplasm of products under their responsibility. The Curators of the Germplasm Banks have the responsibility to

Table 3. Recent Scientific Events which included Conservation of Animal Genetic Resources in their programmes.

	Date	Event
Tampico, Mexico	November, 1998	4th Ibero American Congress for Criollo Breeds
Kathmandu, Nepal	August 1998	4th World Conference on Conservation – RBI
Colina, SP, Brazil	July 1998	National Equine Forum
Soeul, Korea	July 1998	8th World Congress of Animal Production
Valdivia, Chile	May 1998	X Chilean Veterinary Medicine Congress
Armidale, Australia	January 1998	5th World Congress on Genetics Applied An. Production
Niterói, RJ, Brazil	December 1997	Workshop of the Rio de Janeiro Research Corporation
Amsterdam, Holland	November, 1997	CEDLA Workshop
Brasilia, DF, Brazil	July 1997	Workshop on Conservation of Animal Genetic Recourses
B.Horizonte, MG, Brazil	May 1997	Brazilian Animal Production Congress – Zootec'97
Ottawa, Canada	February 1997	Symposium organised by Ag-Canada
Guadeloupe, F.W.I.	December 1996	Caribbean Meeting, INRA
Bogota, Colombia	November 1996	3rd Ibero American Congress for Creole Breeds
C.Grande, MS, Brazil	October 1996	XV Pan American Veterinary Congress (PANVET)
R. Preto, SP, Brazil	May 1996	33rd Brazilian Animal Breeding Society Congress
Brasília, DF, Brazil	November 1995	Workshop for curators of Conservation Nuclei
Orlando, USA	July 1995	87th Annual Meeting American Society of An. Science
San José, Costa Rica	July 1995	Towards an Inter American System for An. Genet. Res.
Circello, Italy	June 1995	Expert Consultation of FAO
Guelph, Canada	August 1994	4th World Congress on Genetics Applied An. Production
Kingston, Canada	August 1994	3rd World Conference on Conservation – RBI
Buenos Aires, Argentina	July 1994	Argentinean Association of Animal Production Congress
Rio de Janeiro, RJ, Brazil	July 1993	Annual Meeting of the Brazilian Na. Production Society
Santiago, Chile	July 1993	Conservation Symposium (ALPA Meeting)
Zafra, Spain	September 1992	1st Ibero American Congress for Creole Breeds
Córdoba, Spain	September 1992	World Meeting on Domestic Animal Breeds
Turrialba, Costa Rica	July 1992	Conservation & Development of An. Genet. Res. in L.A.
Rio de Janeiro, RJ, Brazil	June 1992	Science Forum (Earth Summit)
Nanjing, China	January 1992	FAO International Course on Regional Gene Banks

maintain the Conservation Nuclei as well as to multiply, regenerate and distribute the germplasm.

At the present time the Programme of Conservation of Animal Genetic Resources has 13 ongoing research projects (Table 1).

As already mentioned, the Conservation Nuclei are being kept where the animals were naturally selected over centuries. In a huge country such as Brazil, with several different climates, there is no reason to conserve animals in environments different from those to which they are adapted. Trips for the identification of new nuclei, in order to maintain endangered breeds considered to be native, means that new populations are continually being identified. Some are very similar to breeds officially included in the *in situ* conservation programme and others have totally distinct characters. In general, these populations, which have been identified in the last few years, have extremely reduced effective population sizes. The strategy used has been to include them initially in the cryopreservation programme, so as to assure the storage of genetic material in the BGA in Cenargen. At the same time, their blood is collected to be used for genetic characterisation.

The results of genetic characterisation could reduce existing doubts about breed groupings. As an example, we can cite the case of the Criollo Lageano, Franqueiro and Junqueira cattle. All have huge horns and some breeders insist that they are the same breed, while others treat them as separate breeds. With genetic characterisation, strategies could be developed based on facts and not on suppositions.

Cryopreservation

To avoid the disappearance of local breeds, FAO began contacts in 1987 to install regional Animal Gene Banks (RAGBs) for developing

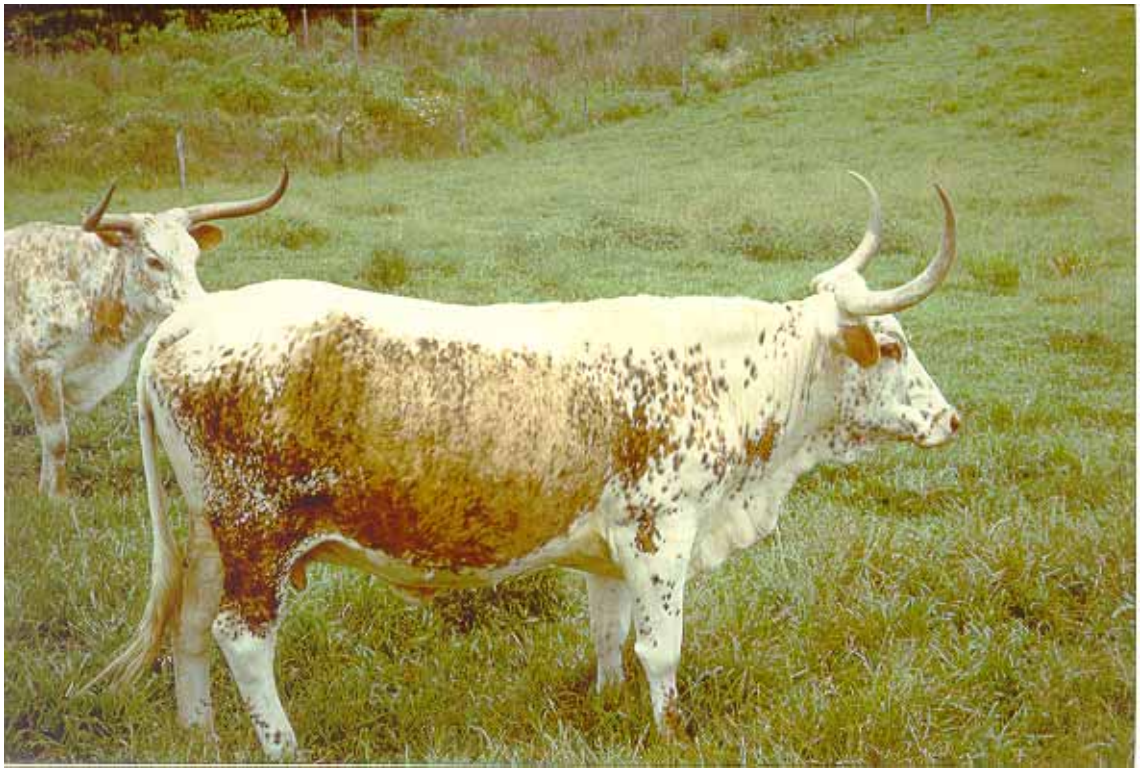

Figure 3. Criollo Lageano cow (Southern region).

Table 4. Number of animals of various breeds threatened with extinction on Cenargen's Experimental Farm in 1999.

Species/Breed	Number of males	Number of females
Cattle		
Caracu	1	1
Criollo Lageano	1	5
Curraleiro	7	10
Junqueira	2	3
Mocho Nacional	1	1
Pantaneiro	6	18
Patuá	1	2
Puganu	1	1
Goats		
Azul	1	4
Canindé	2	`3
Marota	3	6
Moxotó	3	8
Nambi	2	2
Repartida	1	4
Horses		
Campeiro	2	6
Pantaneiro	4	5
Asses		
Casco de Mula	1	1
Inhata	1	2
Monteiro	1	2
Moura	1	1
Nilo	1	2
Piau	1	1
Rabo de Peixe	1	2
Total	51	104

countries. At that time Cenargen/EMPRAPA had been chosen to host the Bank that would be responsible for the storage of semen and embryos of the breeds of domestic animals in danger of extinction in South America. A copy of the material would be stored in the Instituto Nacional de Tecnologia Agropecuaria, Argentina, for security reasons. Because of health legislation differences, regulating the entry and exit of genetic material between countries, none of these RAGBs was established. There is a need to reach a common denominator, so that the future exchange of germplasm is facilitated, as the RAGBs have no commercial purpose, just storage for future use. RAGBs were also proposed for Asia and Africa. Seeing that, at that time, this goal would be difficult to achieve, FAO decided to stimulate these countries to create their own Animal Germplam Banks or to strengthen those that already existed. At the same time it gave priority to the Domestic Animal Diversity – Information System - DAD-IS (FAO, 1998a). The erosion of domestic animal diversity is very clear as is evident from the number of breeds threatened with extinction world-wide (Hammond, 1993). With the help of many countries and organisations, particularly the European Association for Animal Production (EAAP), in 1991 FAO started a world-wide programme, with the collection of population data for seven main species of domestic animals. To date, two editions of the *World Watch List for Domestic Animal Diversity* have been published (FAO, 1993 and FAO, 1995).

In Brazil, the conservation of animal genetic resources was not jeopardised, since when FAO proposed the creation of the RAGBs, Brazil had already created its own Animal Germplasm Bank (AGB). The Brazilian AGB is kept at Cenargen, which is responsible for the storage of semen and embryos of various breeds of domestic animals threatened with extinction in Brazil. It has existed since 1983 and it is because of its existence that Cenargen was chosen to host the South American RAGB, as mentioned above. Table 2, shows the present state of the Brazilian AGB.

Conservation Nuclei must exist for semen, embryos and oocytes of the species/breeds in danger of extinction to be collected. For some breeds included in the Brazilian programme, there are less donor bulls than the number recommended by Smith (1984), which are 25 donors per breed with 100 doses/bull. Unfortunately, when the *ex situ* conservation began, some of the breeds did not have this number of males. Therefore, although more than the recommended 100 doses/bull has been collected, the number of bulls was reduced. In other cases, as the Argentine

Creole, as it is not a Brazilian Breed and its use in Brazil is not common (although some bulls were used on the Criollo Lageano of the Fazenda Canoas, Santa Catarina State) it was decided to stop the collection, and the semen already collected was kept by the AGB.

As the Conservation Nuclei are increased in size and number, or new herds are identified, the intention is to collect genetic material from the greatest possible number of animals, thereby increasing the genetic representation in the AGB.

Another National research programme of EMPRAPA, is that of Biotechnology Applied to Agriculture and Animal Production. This contemplates a project which intends to develop animal reproduction techniques that may be used in Conservation work. Among the techniques being studied are embryo bisection, *in vitro* fertilisation, cloning and the formation of transgenic animals.

Genetic Characterisation

For a long time the characterisation of different breeds of domestic animals in Brazil was based, almost exclusively, on phenotypic data (morphology and production), which sometimes is insufficient to distinguish between pure breeds and those heavily influenced by environmental factors (Panepucci, 1986). With reference to genetic characterisation, the few papers published on Brazilian native breeds include only cytogenetic studies, blood groups and protein polymorphisms.

In the bovine species, structural differences of the Y chromosome observed in different karyotypes of animals of European origin (*Bos taurus*) show that this chromosome is submetacentric, while Afro-Asian breeds (*B. indicus*) are acrocentric. While studying the Curraleiro breed, Brito (1995) verified the occurrence of polymorphism of this chromosome at a cytogenetic level. About 68% of the animals had an acrocentric Y chromosome, which indicates that, at some time during the formation of this breed, zebu type animals were introduced. This dimorphism of the Y chromosome had been observed by Tambasco (1985) in four native bovine breeds (Caracu, Mocho Nacional, Curraleiro and Criollo Lageano), which indicates that both bovine subspecies were involved in the formation of native breeds. Although the Criollo Lageano has a lower acrocentric Y chromosome frequency, this could be due to the geographical location of this breed (found in the South of the country where the zebu influence is much smaller). Crossing the two species may have been favourable for these breeds, because it associated certain qualities of the taurines, such as precocity and productivity, with hardiness and disease resistance of the zebus.

Another study with native cattle breeds was carried out by Dr. Mário Poli (personal communication), of INTA, Argentina, consultant to Cenargen, in 1985. Poli cites that from phylogenetic trees, based on data obtained from the study of thirty blood factors and genetic frequencies, only three systems were determined (F, J and L), since the lack of genealogical registers made it impossible to estimate the frequency of more complete phenogroups.

In the Caracu breed, Bicalho (1985) carried out a population study of different breeding nuclei based on blood groups and protein polymorphisms. It was concluded that this breed originated from the Portuguese breeds Alentejana and Mertolenga, although there are no registers of the latter breed entering Brazil. The author concluded that the Caracu has low genetic variability and was subdivided into four genetically distinct subpopulations. From the analyses, it was suggested that animals should be exchanged between nuclei to prevent greater loss of genetic variability.

The genetic characterisation of several cattle breeds was the subject of a doctorate thesis using protein polymorphisms. The study included three native Brazilian breeds (Caracu, Pantaneiro and Mantiqueira), one native Argentinean (Argentine Creole) and two zebu breeds (Nellore and Gir). The genetic distances between pairs of populations were calculated using NEI method (1972 and 1978), from gene

frequencies of eight protein systems, using the DISPAN programme. The highest values were obtained between pairs where one of the breeds was of *Bos taurus* origin and the other of *Bos indicus.* The average distance between the native Brazilian and the Nellore and Gir breeds was 0.1083 and 0.0964, respectively (LARA, 1998). The small values obtained for genetic distances between the Caracu, Mantiqueira and Pantaneiro with the Argentine Creole, suggest a great similarity between them and support the hypothesis that these breeds were founded by Iberian cattle, probably sharing the same ancestry.

The small number of projects in this area, up to the present time, helped establish the Animal Genetics Laboratory of Cenargen as a priority. The laboratory started to function in February 1998 and will work primarily with DNA polymorphisms for the genetic characterisation of the populations of animals of the conservation programme. At the same time, a DNA Bank is being set up, which already has samples from several species of animals (60 heads of cattle, 18 horses, 113 asses, 154 goats and 89 buffaloes). The intention is that, in the short term, cells and tissues of several species, including wild animals, should be stored.

For the first stage, the intention is to verify the degree of diversity within the breeds/native populations, to gain a global idea of genetic distances using similarity indices. Following an FAO recommendation, 50 animals of each breed will be used. Since the sampling process is vital for the success of the proposed plan, an investigation will be made into the Conservation Nuclei and/or Breed Societies, when they exist, of the geographical distribution of each breed, so that the samples are representative of the whole population known to exist. The DNA may be collected from blood or semen.

For comparative studies, two methods for the evaluation of DNA polymorphisms will be used. Since there is not sufficient data in the literature to evaluate, from molecular information, what constitutes a distinct breed, it is necessary to compare different markers (Grattapaglia, personal communication).

A priori, the RAPD will be used as it is relatively cheap and fast, as well as relevant to the study (Egito, 1995). Micro-satellites will also be used, as they are well developed in cattle studies. This technique differentiates the heterozygotes which are co-dominant thus generating more information to discriminate the variability within populations, helping in the choice of individuals for conservation. In the Animal Genetic Laboratory, work has already begun on cattle and horses and will soon include asses, buffaloes, goats and sheep species.

The primers for the micro-satellites on cattle were selected from thirty identified by the International Society of Animal Genetics (ISAG), after a meeting in 1996. These primers are the same recommended by MoDAD-FAO (FAO, 1998b) and are being used for genetic characterisation of the Iberian breeds in a project being carried out by the University of Porto, Portugal, and financed by the European Community. This fact will make the comparison of the breeds studied in both projects easier and facilitate the exchange of germplasm between the countries.

Public Awareness of the Importance of Conservation of Animal Genetic Resources

Another objective of the programme is to make the various sectors of society aware of the importance of conservation of animal genetic resources. Presenting the programme on various opportunities has helped significantly. The creation of a *Farm Park,* as has occurred in several European countries will be another strategy to bring this theme to the public attention.

Presentation of the Brazilian Animal Genetic Resources Conservation Programme

The presentation of the Brazilian Programme has stimulated the creation of Conservation Nuclei in Brazil, as well as of other National

Animal Germplasm Banks in other Latin American countries. The creation of these other banks may allow, in the medium term, the collection of all the material in one place - the RAGB (with a duplicate in a second country) as proposed by FAO in 1987. In this way, the Programme has been presented in different events in Brazil and abroad. In Brazil the intention is to bring the philosophy of the work with animal conservation to society, as well as the actual state of development of the programme (often stimulating the creation of new Conservation Nuclei); abroad the intention is to

1) show the state of animal genetics resources conservation in Brazil, stimulating the creation of new National Banks and
2) present the actual conservation situation on the continent as a whole. It is hoped that the awareness level of society on the importance of conservation of animal genetic resources is being raised at both the national and international level.

Since the conservation of animal genetic resources is a relatively new topic, it has only recently been included in the programmes of congresses and symposia. Until recently, the researchers who dared to breach this topic were labelled as philosophers. It was said that the so-called "native" breeds should be conserved in Zoological Gardens. Fortunately, this point of view is changing rapidly, and the most important congresses in the animal area are including sessions or symposia on this topic. At last, traits such as adaptation, hardiness and disease and parasite resistance, which many of these local breeds have, are being recognised and valued. Table 3 presents some of the places and sessions where the Brazilian Animal Genetic

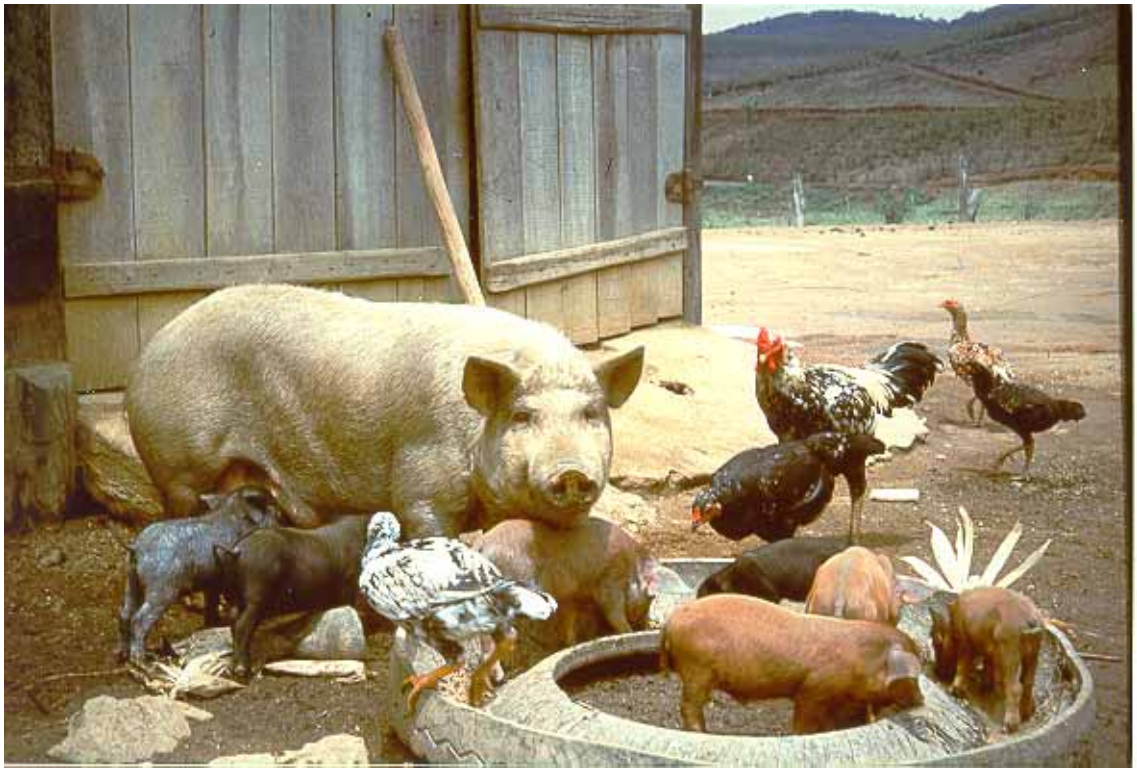

Figure 4. Tatu pig (South-Eastern region).

Resources Conservation Programme has been presented over the last seven years, so that the increasing status of conservation can be evaluated.

Brazilian farm park

In 1993, the Animal Germplasm Bank (AGB) of Cenargen was recognised by the Brazilian Ministry of Agriculture, who donated an area of 900 ha for the installation of a *Farm Park*, which will be called Farm Park for the Animal Diversity in Brazil. The main objective of this park will be to bring together, in Brasilia, living examples of domestic animal breeds of different species (cattle, buffaloes, horses, asses, sheep, goats, pigs and poultry) which are in danger of extinction. This Farm Park will be open to the public and is already being built on Cenargen's Experimental Farm. Up to the present time, a large part of the animals that will be shown on the Farm Park have already been brought to Brasilia, and are being used for semen and embryo collection stored in the AGB. Table 4 shows the number of animals of the various species/breeds that can be found in Brasilia and which will be part of the Farm Park.

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[2]Citation: **issue number**: pages

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Editorial Policies and Procedures

The mission of the Animal Genetic Resources Information Bulletin (AGRI) is the promotion of information on the better use of animal genetic resources of interest to food and agriculture production, under the Global Strategy for the Management of Farm Animal Genetic Resources. All aspects of the characterization, conservation and utilization of these resources are included, in accordance with the Convention on Biological Diversity. AGRI will highlight information on the genetic, phenotypic and economic surveying and comparative description, use, development and maintenance of animal genetic resources; and on the development of operational strategies and procedures which enable their more cost-effective management. In doing this AGRI will give special attention to contributions dealing with breeds and procedures capable of contributing to the sustainable intensification of the world's medium to low input production environments (agro-ecosystems), which account for the substantial majority of the land area involved in livestock production; the total production of food and agriculture from livestock; and of our remaining farm animal genetic resources.

Views expressed in the paper published in AGRI represent the opinions of the author(s) and do not necessarily reflect those of the institutions which the authors are affiliated, FAO or the Editors.

The suitability of manuscripts for publication in AGRI is judged by the Editors and reviewers.

Electronic publication

AGRI is available in full electronically on the Internet, in addition to being published in hard copy, at:
<< http://www.fao.org/dad-is>>

Types of Articles

The following types of articles are published in AGRI.

Research articles

Findings of work on characterization, conservation and utilization of farm animal genetic resources (AnGR) in well described production environments, will be considered for publication in AGRI. Quality photographs of these genetic resources viewed in the primary production environment to which they are adapted, accompanying the manuscripts are encouraged.

Review articles

Unsolicited articles reviewing agro-ecosystems, country-level, regional or global developments on one or more aspects of the management of animal genetic resources, including state-of-the-art review articles on specific fields in AnGR, will be considered for publication in AGRI.

Position papers

Solicited papers on topical issues will also be published as deemed required.

Other published material

This includes book reviews, news and notes covering relevant meetings, training courses and major national, regional and international events and conclusions and recommendations associated with the outcomes of these major events. Readers are encouraged to send such items to the editors.

Guidelines for Authors

Manuscript submission

Manuscripts prepared in English, French or Spanish with an English summary and

another summary in either French or Spanish, should be submitted to AGRI Editor, AGAP, FAO, Viale delle Terme di Caracalla, 00100 Rome, Italy. Alternatively a manuscript may be sent as a WinWord Electronic Mail attachment to < agri@fao.org >. Photographs, coloured or black and white, and figures must be always sent by mail.

Manuscripts should be typed double-spaced and with lines numbered in the left margin. All pages, including those of references, tables etc., must be consecutively numbered. The corresponding author is notified of the receipt of a manuscript.

For manuscripts that are accepted after revision, authors are encouraged to submit a last version (3½" disc format) in Word 6.0 for Windows of their revised manuscript along with the printed copy.

Preparation of the manuscript

The first page of the manuscript must include the running head (abbreviated title), title, names of authors, institutions, full addresses including postal codes and telephone number and other communication details (fax, e-mail, etc.) of the corresponding author. The running head not exceeding 45 characters plus spaces, should appear at the top of page 1 of the manuscript entirely in capital letters. The title of the manuscript is typed in upper and lower case letters. The title should be as brief as possible not exceeding 150 characters (including spaces) with species names when applicable. Authors, institutions and addresses are in upper and lower case italics. There is one blank line between the title and the authors. Addresses are typed as footnotes to the authors after leaving one blank line. Footnotes are designated numerically. Two lines are left below the footnotes.

Headings

Headings of sections, for example Summary, Introduction, etc., are left-justified. Leave two blank lines between addresses footnotes and Summary and between the heading Summary and its text. Summary should not exceed 200 words . It should be an objective summary briefly describing the procedures and findings and not simply stating that the study was carried on such and such and results are presented, etc. Leave one line between the summary text and Keywords which is written in italics as well as the keywords themselves. All headings of sections (14 regular) and sub-sections (12 regular) are typed bold and preceded and succeeded by one blank line and their text begins with no indention. The heading of a sub-subsection is written in italics, and ends with a dot after which the text follows on the same line. Keywords come immediately after the summaries. They should be no more than six, with no "and" or "&".

Tables and figures

Tables and figures must be enclosed with the paper and attached at the end of the text according their citation in the document. Photos will not be returned

Tables

Tables, including footnotes, should be preceded and succeeded by 2 blank lines. Table number and caption are written, above the table, in italics (12) followed by a dot, then one blank line. For each column or line title or sub-title, only the 1st letter of the 1st word is capitalized. Tables should be numbered consecutively in Arabic numerals. Tables and captions should be left justified as is the text. Use horizontal or vertical lines only when necessary. Do not use tabs or space-bar to create a table but only the appropriate commands.

Figures

Figures including titles and legends should be preceded and succeeded by two blank lines. Figure number and title are written, below the figure, in italics (12) and end with a dot. The term figures includes photos, line drawings, maps, diagrams etc.

All the submitted diagrams, must be

accompanied with the original matrix of the data used to create them. It is strongly advised to submit diagrams in Word 6.0 or Excel 5.0. Figures should be numbered consecutively in Arabic numerals.

References

Every reference cited in the text should be included in the reference list and every reference in the reference list should have been mentioned in the text at least once. References should be ordered firstly alphabetically by the first author's surname and secondly by year.

Example for reference in a periodical is:

Köhler-Rollefson, I., 1992; The camel breeds of India in social and historical perspective. Animal Genetic Resources Information 10, 53-64.

When there are more than one author:

Matos, C.A.P., D.L. Thomas, D. Gianola, R.J. Tempelman & L.D. Young, 1997; Genetic analysis of discrete reproductive traits in sheep using linear and nonnlinear models: 1. Estimation of genetic parameters 75, 76-87.

For a book or an ad hoc publication, e.g., reports, theses, etc.:

Cockril, W.R., (Ed), 1994; The Husbandry and Health of the Domestic Buffalo. FAO, Rome, Italy, pp 993.

For an article in the proceedings of a meeting:

Hammond, K., 1996; FAO's programme for the management of farm animal genetic resources. In C. Devendra (Ed.) Proceedings of IGA/FAO Round Table on the Global Management of Small Ruminant Genetic Resources, Beijing, May 1996, FAO, Bangkok, Thailand, 4-13.

Where information included in the article has been obtained or derived from a World Wide Web site, then quote in the text, e.g. "derived from FAO. 1996" and in the References quote the URL standard form:

FAO, 1996; Domestic Animal Diversity Information System <http://www.fao.org/dad-is/>, FAO, Rome

Normes et règles éditoriales

L'objectif du Bulletin d'Information sur les Ressources Génétiques Animales (AGRI) est la vulgarisation de l'information disponible sur la meilleure gestion des ressources génétiques animales d'intérêt pour la production alimentaire et agricole, d'après les recommendations de la Stratégie Mondiale pour la Gestion des Ressources Génétiques des Animaux Domestiques. Tous les aspects relatifs à la caractérisation, la conservation et l'utilisation de ces ressources seront pris en considération, suivant les normes de la Convention pour la Biodiversité.

AGRI désire diffuser de l'information sur la génétique, les enquêtes phénotypiques et économiques et les desciptions comparatives, l'utilisation et la conservation des ressources génétiques animales, ainsi que toute information sur le développement de stratégies opérationnelles et de normes qui puissent permettre une meilleure gestion de la relation coût/efficacité. C'est pour cela que AGRI prendra spécialement en considération toutes les contributions référées aux races et aux normes capables de permettre une intensification durable des milieux (agroécosystèmes) à revenus moyens et bas dans le monde; qui comprennent la majeur partie des terres consacrées à l'élevage, à la production totale des aliments et l'agriculture provenants de l'élevage; et tout ce qui reste comme ressources génétiques des animaux domestiques.

Les opinions exprimées dans les articles publiés dans AGRI appartiennent seulement aux auteurs et donc ne représentent pas nécessairement l'opinion des instituts pour lesquels ils travaillent, la FAO ou les éditeurs.

L'opportunité ou non de publier un article dans AGRI sera jugée par les éditeurs et les réviseurs.

Publication électronique

En plus de sa version imprimée, la version totale de AGRI se trouve disponible sur Internet, sur le site:
<<http://www.fao.org/dad-is/>>

Types d'articles

Les articles suivants pourront être publiés sur AGRI:

Articles de recherche

Seront prises en considération pour leur publication sur AGRI les études sur la caractérisation, la conservation et l'utilisation des ressources génétiques des animaux domestiques (AnGR) accompagnées d'une bonne description du milieu. On encourage les auteurs à envoyer des photographies de bonne qualité qui montrent les races en question dans leur milieu naturel de production.

Révisions

Occasionnellement, des articles contenant une révision des agroécosystèmes, au niveau national, régional ou mondial, avec un ou plusieurs aspects se rapportant à la gestion des ressources génétiques animales, y comprises les mises à jour des différentes zones de AnGR, seront pris en considération.

Articles spécifiques

Ponctuellement, des articles sur des thèmes spécifiques pourront être demandés pour la publication d'éditions spéciales.

Autre matériel pour publication

Ceci comprend la révision de livres, nouvelles et notes de réunions importantes, cours de formation et principaux évènements nationaux, régionaux et internationaux; ainsi que les conclusions et recommendations par rapport aux objectifs des ces principaux évènements. Les auteurs sont priés d'envoyer ce genre de matériel aux éditeurs.

Guide pour les auteurs

Présentation du manuscript

Les articles se présenteront en anglais, français ou espagnol, avec un résumé en anglais et sa traduction en français ou en espagnol; et seront envoyés à l'éditeur de AGRI, AGAP, FAO, Viale delle Terme di Caracalla, 00100 Rome, Italie. L'autre possibilité est d'envoyer l'article par courrier électronique avec le document adjoint en version WinWord à <agri@fao.org>. Les photographies, en couleur ou en blanc et noir, seront toujours envoyées par courrier normal.

Les manuscripts se présenteront à double interligne et avec le numéro correspondant à chaque ligne sur la marge gauche. Toutes les pages seront numérotées, y comprises celles avec les références bibliographiques, les tableaux, etc. L'auteur recevra une lettre lui donnant bonne réception de son document.

Lorsqu'un article, après sa révision, sera accepté, on demandera à l'auteur d'envoyer la version finale révisée sur disquette (format 3$^{1}/_{2}$″) en Word 6.0 x Windows, ainsi qu'une copie sur papier.

Préparation du manuscript

Sur la première page du manuscript on indiquera le titre de l'article en abrégé, le titre et noms des auteurs, des institutions, les adresses complètes (y compris code postal et numéro de téléphone); ainsi que tout autre moyen de contact tel que fax, e-mail, etc. avec l'auteur principal. Le titre abrégé ne devra pas dépasser les 45 caractères, plus les espaces nécessaires, et s'écrira sur la partie supérieure de la page 1 du manuscript en majuscules. Le titre en entier du manuscript sera écrit en majuscules et minuscules; il devra être aussi bref que possible, sans dépasser les 150 caractères (y compris les espaces nécessaires), et avec l'indication des noms des espèces. Les noms des auteurs, des institutions et les adresses seront en italique et en lettres majuscules et minuscules. On laissera un espace en blanc entre le titre et les noms des auteurs. Les adresses seront indiquées comme des notes à pied de page pour chacun des auteurs après avoir laissé un espace en blanc après les noms. Chaque note de pied de page sera numérotée. On laissera deux espaces en blanc après les adresses.

Titres

Les titres de chaque chapitre, par example Résumé, Introduction, etc. seront alignés à gauche. Laisser deux espaces en blanc entre les notes de pied de page avec les adresses et le Résumé, et entre le titre Résumé et le texte qui suit. Le résumé ne devra pas dépasser les 200 mots. Il s'agira d'un résumé objectif qui fasse une brève description des processus utilisés et des résultats obtenus, et non pas une simple présentation du travail réalisé avec une description générale des résultats. Laisser un espace en blanc entre la fin du texte du résumé et les mots-clés, qui seront écrits en italique ainsi que le titre Mots-clés. Les mots-clés seront au maximum six et il ne devra pas y avoir de "et" ou "&". Tous les titres principaux de chapitre (14 regular) et sous-chapitre (12 regular) seront en gras avec un espace en blanc avant et après. Le texte commencera sans retrait. Un titre à l'intérieur d'un sous-chapitre s'écrira en italique, suivi d'un point, avec le texte à continuation.

Tableaux et figures

Les tableaux et les figures iront à la fin du texte en suivant l'ordre d'apparition dans le texte. Les photographies ne seront pas dévolues aux auteurs.

Tableaux

Les tableaux, y compris les notes de pied de page, devront avoir un espace en blanc avant et après. Le numéro du tableau et le titre s'écriront sur la partie supérieure en italique (12) avec un point à la fin et un espace en blanc en dessous. Sur chaque colonne, titre d'en-tête ou sous-titre, seulement la première lettre du premier mot sera en majuscule. Les tableaux et leur titre seront alignés à gauche, ainsi que le texte. Les lignes verticales et

horizontales seront utilisées seulement si nécessaires. Ne pas utiliser les tabs ou la barre de séparation pour créer un tableau.

Figures

Les figures, y compris les titres et les légendes, seront précédés et suivis de deux espaces en blanc. Le numéro de la figure et le titre s'écriront sur la partie supérieure en italique (12) avec un point à la fin. Sous la rubrique figure on trouvera les photographies, les graphiques, les cartes, les diagrammes, etc. Dans le cas des diagrammes, la matrice originale avec les données utilisées pour son élaboration devra être envoyée. On recommande l'utilisation de Word 6.0 ou Excel 5.0 pour la présentation des diagrammes.

Références

Toute référence présente dans le texte devra apparaître sur la liste des références, et chaque référence de la liste aura été citée au moins une fois dans le texte. Les références iront en ordre alphabétique du nom de l'auteur, suivi de l'année. Example dans le cas d'une référence sur une revue:

Köhler-Rollefson, I.,1992; The camel breeds of India in social and historical perspective. Animal Genetic Resources Information 10, 53-64.

Lorsqu'il s'agit de plus d'un auteur:

Matos, C.A.P., D.L. Thomas, D. Gianola, R.J. Tempelman & L.D. Young, 1997; Genetic analysis of discrete reproductive traits in sheep using linear and nonnlinear models: 1. Estimation of genetic parameters 75, 76-87.

Dans le cas d'un livre ou d'une publication ad hoc, par example un rapport, une thèse, etc.:

Cockril, W.R., (Ed), 1994; The Husbandry and Health of the Domestic Buffalo. FAO, Rome, Italy, pp 993.

S'il s'agit d'un acte d'une réunion:

Hammond, K., 1996; FAO's programme for the management of farm animal genetic resources. In C. Devendra (Ed.) Proceedings of IGA/FAO Round Table on the Global Management of Small Ruminant Genetic Resources, Beijing, May 1996, FAO, Bangkok, Thailand, 4-13.

Lorsque l'information contenue dans l'article ait été obtenue ou dérive d'un site World Wide Web, il faudra mettre le texte entre guillemets; par example "tiré de la FAO. 1996" et indiquer dans les Références la forme standard URL:

FAO, 1996; Domestic Animal Diversity Information System <http://www.fao.org/dad-is/>, FAO, Rome

Reglas y normas editoriales

El objetivo del Boletín de Información sobre Recursos Genéticos Animales (AGRI) es la divulgación de la información sobre una mejor gestión de los recursos genéticos animales de interés para la producción alimentaria y agrícola, siguiendo la Estrategia Mundial para la Gestión de los Recursos Genéticos de los Animales Domésticos. Todos los aspectos referidos a la caracterización, la conservación y el uso de estos recursos serán tomados en consideración, de acuerdo con la Convención sobre la Biodiversidad.

AGRI publicará información sobre genética, encuestas fenotípicas y económicas y descripciones comparativas, uso, desarrollo y conservación de los recursos genéticos animales, así como sobre el desarrollo de estrategias operacionales y normas que permitan una gestión más eficaz de la relación costo/eficacia. Por ello, AGRI prestará especial atención a las contribuciones referidas a razas y normas capaces de contribuir a la intensificación sostenible de los medios (agroecosistemas) con ingresos medio y bajos en el mundo, que comprenden casi la mayor parte de las tierras dedicadas a la producción ganadera; la producción total de alimentos y agricultura provenientes de la ganadería; y el resto de los recursos genéticos de animales domésticos.

Los puntos de vista expresados en los artículos publicados en AGRI son solamente las opiniones de los autores y, por tanto, no reflejan necesariamente la opinión de las instituciones para las cuales trabajan dichos autores, de la FAO o de los editores.

La oportunidad o no de publicar un artículo en AGRI será juzgada por los editores y revisores.

Publicación electrónica

Además de su publicación impresa, la versión íntegra de AGRI se encuentra disponible electrónicamente sobre Internet, en el sito: <<http://www.fao.org/dad-is/>>

Tipos de artículos

Serán publicados en AGRI los siguientes tipos de artículos:

Artículos sobre investigación

Se tomarán en consideración para su publicación en AGRI los estudios sobre la caracterización, conservación y uso de los recursos genéticos de los animales domésticos (AnGR) con una buena descripción del entorno. Se agradecerá el envío de fotografías de calidad que presenten a las razas en cuestión en su ambiente natural de producción.

Artículos de revisión

Se podrán tener en consideración ocasionalmente aquellos artículos que presenten una revisión de los agroecosistemas, a nivel nacional, regional o mundial, con el desarrollo de uno o más aspectos referidos a la gestión de los recursos genéticos animales, incluidas las revisiones sobre el estado actual de las distintas áreas de AnGR.

Artículos específicos

Se solicitarán puntualmente artículos sobre temas específicos para ediciones especiales.

Otro material para publicación

Incluye la revisión de libros, noticias y notas referidas a reuniones importantes, cursos de formación y principales eventos nacionales, regionales e internacionales, así como conclusiones y recomendaciones relacionadas con los objetivos de estos principales eventos. Se invita a los lectores a enviar este tipo de material a los editores.

Guía para los autores

Presentación del manuscrito

Los artículos se presentarán en inglés, francés o español, junto con un resumen en inglés y su traducción en francés o español, y se enviarán al editor de AGRI, AGAP, FAO, Viale delle Terme di Caracalla, 00100 Roma, Italia. Otra posibilidad es enviar el artículo por correo electrónico adjuntando el documento en versión WinWord a <agri@fao.org>. Las fotografías, a color o en blanco y negro, se enviarán siempre por correo normal.

Los manuscritos se presentarán con doble espacio y con el número correspondiente a cada línea en el margen izquierdo. Todas las páginas serán numeradas, incluidas las de las referencias bibliográficas, cuadros, etc. El autor recibirá una notificación sobre la recepción de su documento.

En el caso de aceptación de un artículo después de su revisión, se solicitará al autor una versión final de su artículo revisado en disquete (formato 3$1/2''$) en Word 6.0 x Windows, así como una copia impresa del mismo.

Preparación del manuscrito

En la primera página del manuscrito se indicará el título abreviado del artículo, títulos y nombres de los autores, instituciones, direcciones completas (incluido código postal y número de teléfono); así como otros medios de contacto tales como fax, e-mail, etc., del autor principal. El título abreviado no deberá sobrepasar los 45 caracteres más los espacios correspondientes, y aparecerá en la parte superior de la página 1 del manuscrito en mayúsculas. El título entero del manuscrito viene escrito en mayúsculas y minúsculas. Dicho título debe ser lo más breve posible y no sobrepasar los 150 caracteres (incluidos los espacios necesarios), con los nombres de las especies, si necesario. Los nombres de los autores, instituciones y direcciones se escribirán en cursiva y en letras mayúsculas y minúsculas. Se dejará una línea en blanco entre el título y los nombres de los autores. Las direcciones se escribirán como notas de pie de página de cada autor después de dejar una línea en blanco entre los nombres y éstas. Cada nota de pie de página con la dirección vendrá indicada numéricamente. Se dejarán dos líneas en blanco después de las direcciones.

Títulos

Los títulos de cada sección, por ejemplo Resumen, Introducción, etc., vienen alineados a la izquierda. Dejar dos líneas en blanco entre las notas de pie de página con las direcciones y el Resumen y entre el título Resumen y el texto que sigue. El resumen no deberá exceder de 200 palabras. Deberá ser un resumen objetivo que describa brevemente los procesos y logros obtenidos, y no una presentación de cómo se ha llevado a cabo el estudio y una descripción genérica de los resultados. Dejar una línea en blanco entre el final del texto del resumen y las palabras clave, que se escribirán en cursiva así como el titulo Palabras clave. No deberán ser más de seis y no deberán contener "y" o "&". Todos los títulos principales de capítulo (14 regular) y subcapítulo (12 regular) serán en negrita e irán precedidos y seguidos de una línea en blanco. El texto correspondiente empezará sin sangrado. Un título dentro de un subcapítulo se escribirá en cursiva e ira seguido de un punto con a continuación el texto correspondiente.

Cuadros y figuras

Los cuadros y las figuras se incluirán al final del texto siguiendo el orden de cita dentro del mismo. Las fotografías no serán devueltas a sus autores.

Cuadros

Los cuadros, incluidas las notas de pie de página, deberán ir precedidos y seguidos por dos líneas en blanco. El numero del cuadro y su título se escribirán en la parte superior en cursiva (12) con un punto al final y seguido

de una línea en blanco. En cada columna o título de encabezamiento o subtítulo, sólo la primera letra de la primera palabra irá en mayúscula. Los cuadros irán numerados de forma consecutiva con números árabes. Los cuadros y sus títulos se alinearán a la izquierda, así como el texto. Se utilizarán líneas horizontales o verticales sólo cuando sea necesario. No utilizar tabuladores o la barra espaciadora para crear un cuadro.

Figuras

Las figuras, incluidos los títulos y leyendas, irán precedidas y seguidas de dos líneas en blanco. El número de la figura y el título se escribirán en la parte superior en cursiva (12) con un punto al final. La palabra figura incluye las fotografías, los gráficos, los mapas, los diagramas, etc. En el caso del diagrama se enviará la matriz original con los datos utilizados para crearlo. Se recomienda encarecidamente la utilización de Word 6.0 o Excel 5.0 para la presentación de los diagramas.

Referencias

Toda referencia presente en el texto deberá aparecer en la lista de referencias y, de la misma manera, cada referencia de la lista deberá haber sido citada por lo menos una vez en el texto. Las referencias deben ir en orden alfabético del apellido del autor, seguido por el año.

Ejemplo en el caso de una referencia de una revista:

Köhler-Rollefson, I.,1992; The camel breeds of India in social and historical perspective. Animal Genetic Resources Information 10, 53-64.

Cuando se trata de más de un autor:

Matos, C.A.P., D.L. Thomas, D. Gianola, R.J. Tempelman & L.D. Young, 1997; Genetic analysis of discrete reproductive traits in sheep using linear and nonnlinear models: 1. Estimation of genetic parameters 75, 76-87.

En el caso de un libro o de una publicación ad hoc, por ejemplo informes, tesis, etc.:

Cockril, W.R., (Ed), 1994; The Husbandry and Health of the Domestic Buffalo. FAO, Rome, Italy, pp 993.

Cuando se trate de un artículo dentro de las actas de una reunión:

Hammond, K., 1996; FAO's programme for the management of farm animal genetic resources. In C. Devendra (Ed.) Proceedings of IGA/FAO Round Table on the Global Management of Small Ruminant Genetic Resources, Beijing, May 1996, FAO, Bangkok, Thailand, 4-13.

Cuando la información contenida en el artículo haya sido obtenida o derive de un sito World Wide Web, poner el texto entre comillas; por ejemplo "sacado de la FAO. 1996" e indicar en las Referencias la forma estándar URL:

FAO, 1996; Domestic Animal Diversity Information System <http://www.fao.org/dad-is/>, FAO, Rome