



**REPORT
OF A WORKSHOP
ON DISEASE RESISTANCE**

Animal genetic resources and their resistance/tolerance to diseases, with special focus on parasitic diseases in ruminants

**A Joint FAO/INRA Workshop
Jouy-en-Josas, France, June 2009**

(Editors: Matthias Gauly, Badi Besbes and Leyden Baker)



Table of contents

Foreword	3
Executive Summary	5
Introduction	7
SECTION 1: CURRENT RESEARCH AND LATEST FINDINGS IN THE FIELD OF BREEDING FOR DISEASE RESISTANCE IN RUMINANTS AND HOST-PATHOGEN INTERACTIONS	8
A review: Assessing Evidence for Disease Resistance in Livestock (S. Bishop)	8
A review: latest findings in the host-pathogen interactions in parasitic diseases. Can they be used for practical breeding? (S. Thévenon)	11
General discussion	17
SECTION 2: ACTUAL STANDING AND PERSPECTIVES FOR THE SUSTAINABLE USE AND DEVELOPMENT OF RESISTANT OR TOLERANT BREEDS	19
Actual standing and perspectives for the sustainable use and development of parasite resistant or tolerant breeds in developed regions: Australia and New Zealand as an example (J.C. Greeff, L.J.E. Karlsson and A.C .Schlink)	19
Actual standing and perspectives for the sustainable use and development of parasite resistant or tolerant breeds in Asia (R.L. Baker)	26
Actual standing and perspectives for the sustainable use and development of parasite resistant or tolerant breeds in the US (J. Miller)	32
Actual standing and perspectives for the sustainable use and development of parasite resistant and tolerant breeds in Africa (J. M. Mugambi)	36
Actual standing and perspectives for the sustainable use and development of parasite resistant or tolerant breeds in South America (A.F.T. Amarante)	43
Actual standing and perspectives for the sustainable use and development of trypanosoma resistant or tolerant breeds (L. Dempfle)	46
Recommendations for ways to describe local breeds for disease resistance. What are the needs? (M. Tibbo and A. Haile)	49
General discussion	53
SECTION 3: COLLABORATION BETWEEN DEVELOPED AND DEVELOPING COUNTRIES FOR SCIENTIFIC INVESTIGATIONS OF DISEASE RESISTANCE OF CANDIDATE BREEDS	57

Example of collaboration and recommendations for beneficial collaboration: Integration of tolerance to gastrointestinal (GI) nematodes into a Creole goat breeding programme in Guadeloupe - An application of developed country research in developing animal production systems. (N. Mandonnet)	57
Example of collaboration and recommendations for beneficial collaboration: Integration of tolerance to trypanosomiasis into breeding programmes (I. Sidibe)	62
General discussion	64
SECTION 4: TECHNOLOGY TRANSFER BETWEEN DEVELOPED AND DEVELOPING COUNTRIES	66
What classical technologies could be realistically applied in developing countries for breed development? How can the traits of disease resistance be incorporated into breeding programmes? (L. Dempfle)	66
What new technologies could be realistically applied in developing countries for breed development? How can the knowledge be incorporated into breeding programmes? (M. Malek)	68
General discussion	71
SECTION 5: BENEFIT SHARING (ABS) AND INTELLECTUAL PROPERTY RIGHTS (IPR)	72
Access and Benefit Sharing (ABS) and Intellectual Property Rights (IPR) issues that may arise from finding potential major genes in a local breed and transferring them to highly selected commercial populations, or vice versa. (S.J. Hiemstra)	72
General discussion	76
SECTION 6: CONCLUSIONS AND RECOMMENDATIONS OF THE WORKSHOP	77
ANNEX 1. Detailed answers to questions	79
ANNEX 2. Workshop program	87
ANNEX 3. List of participants	89

Foreword

Parasitic diseases such as gastrointestinal (GI) nematodes and trypanosomosis are an important cause of reduced production efficiency in ruminant livestock worldwide. GI nematodes are among the most important infections faced by livestock (particularly sheep and goats), especially affecting poor small-scale farmers in the tropics (Perry et al., 2002). A potential alternative measure to alleviate the problem is breeding for disease resistance. It has been well established that the ability of animals to acquire immunity and express resistance against diseases varies substantially among and within breeds and is, at least partly, under genetic control (Axford et al., 2000; Bishop, 2005; Bishop and Morris, 2007).

Besides the scientific evidence, there is much anecdotal evidence pointing to the greater disease resistance of different breeds, particularly in the tropical developing world. For example, when countries enter details of their livestock breeds in FAO's Domestic Animal Diversity Information System (DAD-IS), they have the opportunity to indicate whether the breeds have any particularly interesting traits like disease resistance. Currently four goat breeds (Carpatina, Cashgora, Jamnapari, Katjang Yei) and 13 sheep breeds (Churra Lebrijana, Criolla Mora, Criollo, Garut, Gulf Coast Native, Kumumawa, Madagascar, Malin (Malaysian Indigenous), Morada Nova, Priangan, Rahmani, Solognot, Tsigai) were reported to DAD-IS as having resistance or tolerance to a certain degree against parasitic diseases in general or against specific parasites. Surprisingly, a number of sheep and goat breeds that have been shown to be disease resistant in soundly based experiments are not identified in DAD-IS (e.g. the Red Maasai sheep and Small East African goats in East Africa which are resistant to GI nematodes). In contrast, there are 86 cattle breeds in DAD-IS identified as being disease resistant, including the trypanotolerant N'Dama breed in West Africa and a number of breeds that are resistant to ticks (e.g. Sahiwal, Nguni, Bonsmara and Tuli). Even if the claims in DAD-IS are not based on scientific investigations, they may be correct and may warrant more in depth investigation.

GI nematodes and their ancestors have been infecting sheep, goats and their ancestors ever since the divergence of the bovidae from the cervidae 20 to 40 million years ago. This long evolutionary history has produced a rich and complex series of co-adaptations by host and parasite (Stear et al., 2009). The fundamental theorem of natural selection suggests that evolution will fix genes/alleles that improve fitness (Fisher, 1930). For example, gene variants or alleles which are related to parasite resistance should mainly be found, or at least be at a higher frequency, in breeds which originate from regions with high parasite burden because of high selection pressure. In many parts of the developed world, this natural selection pressure was reduced drastically with the advent of anthelmintic drugs about 60 years ago. However, in large part of the tropical developing world, where little or no anthelmintics are used, the natural selection pressure still exists today. In this context, the importance of maintaining and utilising such native breeds, which until recently were neglected because these animals were often considered to be unproductive, is receiving increasing attention.

However, the genetic component of resistance or tolerance against diseases has not been investigated for most of these local indigenous breeds. Therefore, more information is needed which supports the need for conserving these unique animal genetic resources.

References

- Axford, R.F.E., Bishop, S.C., Nicholas, F.W. and Owen, J.B.** 2000. Breeding for Disease Resistance in Farm Animals, 2nd edition. CAB International, Wallingford, UK.
- Bishop, S.C.** 2005. Disease resistance: Genetics. In: Encyclopedia of Animal Science. Edited by Pond, W.G. & Bell, A.W. New York: Marcel Dekker, Inc., pp. 288-290.

Bishop, S.C. and Morris, C.A. 2007. Genetics of disease resistance in sheep and goats. *Small Ruminant Research* 70: 48-59.

Fisher, R.A. 1930. *The Genetical Theory of Natural Selection*. Clarendon Press, Oxford

Perry, B.D., McDermott, J.J., Randolph, T.F., Sones, K.R. and Thornton, P.K. 2002. Investing in animal health research to alleviate poverty. International Livestock Research Institute (ILRI), Nairobi, Kenya.

Stear, M.J., Boag, B., Cattadori, I and Murphy, L. 2009. Genetic variation in resistance to mixed, predominantly *Teladorsagia circumcincta* infections of sheep: from heritabilities to gene identification. *Parasite Immunology* 31: 274 – 282.

Executive Summary

At the first International Technical Conference on Animal Genetic Resources for Food and Agriculture held in September 2007 in Interlaken, Switzerland, the international community decided to make strategic choices on the future management of animal genetic resources to develop and conserve them, and to raise awareness and appreciation of the various stakeholders and policy makers vis-à-vis the importance of such genetic resources. Along with this came the need of describing local breeds on different levels. One of the most promising complex traits of local breeds is the expected genetically-based disease resistance or tolerance. This raises a series of questions:

1. Is there a need to look for genetically based disease resistance/tolerance in certain breeds in different parts of the world?
2. What are the breeds and what are the diseases we should look for?
3. How could classical and/or new technologies realistically be applied to identify the tolerant or resistant breeds?
4. What are the perspectives for the sustainable use and development of such breeds in different parts of the world?

The Joint FAO/INRA Workshop “Animal genetic resources and their resistance/tolerance to diseases, with special focus on parasitic diseases in ruminants”, held in Jouy-en-Josas, France, 22-23 June 2009, tried to answer these questions based on the latest findings in the field of host-pathogen interaction and current experiences of genetic based disease control strategies, particularly where other methods are not sustainable or affordable. A summary of the answers are presented below.

Is there a need to look for genetically based disease resistance/tolerance?

Local breeds represent the vast majority of breeds in different parts of the world. This is explained, partly, by their resistance/tolerance/adaptation attributes. Information gathered in the last 10–15 years has yielded ample evidence that many importations of exotic breeds into Africa and Asia have not worked as it was expected. We need to know the best breeds to use in different places, and have strategies for conserving and exploiting such breeds. This is of particular interest when the disease is imperfectly controlled by the current available methods: no efficient vaccine available, appearance of resistance of the pathogen agents to drugs, residues present in the environment and/or in the milk and the meat, interest in decreasing the inputs, especially important for low-input systems. This is the case for some parasitic diseases (trypanosomosis, nematodes, tick and tick-born diseases).

What are the breeds and what are the diseases we should look for?

The question, however, of which breeds we should look for, is very difficult to answer because of the lack of information on the breeds, the number of breeds involved and the logistics to access and evaluate the large number of breeds. One can start with those reported in DAD-IS (or other databases), in the various FAO survey documents, or published in literature as having resistance or tolerance against parasitic diseases. In many cases, candidate breeds are identified by the fact that they live (or survive) and produce in endemic tropical environments without any modern health interventions (e.g., drugs or vaccines). However, initially, we should be most interested in breeds that are resistant or tolerant to those diseases that are difficult or expensive to control by drugs or vaccines (or these do not exist yet) and thus will have the biggest impact on herd/flock productivity. Most important diseases to be considered will be endemic, and in a developing country context these include GI nematodes, ticks (and TBD), the various forms of theileria and trypanosomosis.

How could classical and/or new technologies realistically be applied to identify the tolerant or resistant breeds in different parts of the world?

The phenotypic characterization of local [candidate] breeds and, ideally, their comparison with other susceptible breeds present in the same region, will allow the identification of tolerant or resistant ones. Recording of phenotypes will include not only qualitative and quantitative descriptive measures but also production and reproduction traits, as well as disease incidence and other related traits. By also recording pedigree in each population, it would be possible to initiate a selection programme for disease resistance and improved performance using classical quantitative genetics. A community-based breeding approach could be one way to introduce selection for disease resistance in developing countries. Introducing molecular based information in such breeding programme requires higher capacities (expertise and infrastructure) if it is to be sustainable. This would be difficult in most developing countries.

What are the perspectives for the sustainable use and development of such breeds in different parts of the world?

In many developing countries, the prospects for the sustainable use and development of local breeds are probably quite bleak. Only where there is sustainable infrastructure and governance, can proper progress be made. The main problems are linked to the absence of breeders' organisation and institutional framework. The agricultural ministries must provide incentives for local breeds' development and marketing, and must support the establishment of suitable breeding programmes and the creation of breeders' associations. Breeds' improvement will be based on classical "quantitative genetics approach", with the need to estimate breeding values, through phenotypes assessment, selection criteria, and pedigree record. However, there is urgent need for smallholder farmers in the tropical developing world to be made more aware of the value of their local indigenous livestock even though they may not be the biggest or most good looking livestock.

In conclusion, there is an urgent need to look for genetically based disease resistance or tolerance in certain breeds in different parts of the world. This trait complex is probably one of the reasons why we still have indigenous and local breeds in different parts of the world.

Introduction

Sustainable use, development and conservation of the world's livestock genetic resources are of vital importance to agriculture, food production, rural development and the environment. In recognition of the need to develop an effective framework for the management of these resources and to address the threat of genetic erosion, 109 countries came together in September 2007 at the first International Technical Conference on Animal Genetic Resources for Food and Agriculture held in Interlaken, Switzerland. The Conference adopted the Global Plan of Action for Animal Genetic Resources – which included 23 strategic priorities for action to promote the wise management of these vital resources. Along with this came an increasing interest in describing local breeds on different levels. One of the most promising trait complexes for local breeds is the expected genetically based disease resistance or tolerance. This was the topic of the workshop on animal genetic resources and their resistance or tolerance to diseases, with special focus on parasitic diseases in ruminants. The purposes of the workshop were:

1. to present and discuss the current research and latest findings in the field of breeding for disease resistance in ruminants and host-pathogen interactions (section 1),
2. to present and discuss the actual standing and perspectives for the sustainable use and development of resistant or tolerant breeds in different regions of the world. Can we learn from the experiences gained in developed countries? (section 2),
3. to provide recommendations for mutually beneficial collaboration between developed and developing countries for scientific investigations in this field (section 3),
4. to provide recommendations about the technologies that could be realistically used and applied in developing countries (section 4), and
5. to discuss Access and Benefit Sharing (ABS) and Intellectual Property Rights (IPR) that may arise from finding potential major genes in a local breed and transferring them to highly selected commercial populations, or *vice versa* (section 5).

In particular, the participants were asked the following questions:

- Is there a need to look for genetically based disease resistance/tolerance in certain breeds in different parts of the world?
- What are the breeds and what are the diseases we should look for?
- How could classical and/or new technologies realistically be applied to identify tolerant or resistant breeds? What are the requirements and costs?
- What type of collaboration between developed and developing countries is needed for that?
- What are the perspectives for the sustainable use and development of such breeds in different parts of the world?

The participants addressed these questions and gave some recommendations. These are presented in the final section of these proceedings (section 6).

SECTION 1: CURRENT RESEARCH AND LATEST FINDINGS IN THE FIELD OF BREEDING FOR DISEASE RESISTANCE IN RUMINANTS AND HOST-PATHOGEN INTERACTIONS

A review: Assessing Evidence for Disease Resistance in Livestock (S. Bishop)

Genetic variation in disease resistance is ubiquitous, being seen across all major livestock host species and all types of pathogen or parasite, from viruses to flies and ticks (Bishop, 2005). Furthermore, disease resistance itself takes many forms, including resistance to infection *per se*, the ability to limit proliferation or transmission of the pathogen or parasite, or actual tolerance of infection (i.e. minimal disease). Examples of all of these types of resistance have been published. In the developing country context, natural selection has often produced locally adapted breeds which have the ability to withstand essentially continuous disease pressure. Well publicised examples include breeds of sheep able to withstand or tolerate gastrointestinal (GI) parasite infections and typanotolerant breeds of cattle.

Prioritisation of diseases for further study is not straightforward, as diseases can be important for a variety of reasons, including industry concern, economic impact, public concern, human health impacts (including zoonoses), animal welfare and impacts on international trade. An assessment of diseases (or health conditions) in developing countries, in which subjectively assigned scores were summed across disease categories to give rankings, is shown in Table 1 (from Perry *et al.*, 2002). When combined across host species, helminthosis (i.e. disease caused by GI parasites) was easily the top ranking disease, followed by neonatal mortality, foot and mouth disease and ectoparasites. This approach was extended by Davies *et al.* (2009) to include evidence for host genetic variation as a further assessment criterion. When applied in a European context this resulted in a revised ranking of diseases, with GI parasite infections and mastitis being the most important ruminant diseases.

Table 1: Top-ranked diseases and health conditions, according to their impact on the poor, by species (adapted from Perry *et al.*, 2002)

	Cattle	Sheep/Goat	Poultry	Pigs
1	Foot & mouth disease	Helminthosis	Newcastle disease	Ectoparasites
2	Nutritional deficiency	PPR ²	Helminthosis	Helminthosis
3	Reproductive disorders	Haemonchosis	Coccidiosis	Swine fever
4	Haemorrhagic septicaemia	Neonatal mortality	Ecto-parasites	Neonatal mortality
5	<i>Brucella abortus</i>	Respiratory complexes	Neonatal mortality	Foot & mouth disease
6	Trypanosomosis	Sheep & goat pox	Fowl cholera	African swine fever
7	Liver fluke	Ecto-parasites	Infectious coryza	Cystercosis
8	Anthrax	Anthrax	Fowl pox	Brucella suis
9	CBPP ¹	Liver fluke	DVE ³	Trypanosomosis
10	<i>Toxocara vitulorum</i>	Heartwater	Nutritional deficiency	Japanese B encephalitis

¹. Contagious bovine pleural pneumonia. ². Peste-des-petits ruminants. ³. Duck virus enteritis

Assessing evidence for host genetic variation to disease resistance usually entails the collection and interpretation of field data. The interpretation of such data requires an understanding of the disease epidemiology and the properties of the diagnostic test. Diseases for which there is a continuous disease pressure will often provide data that can be interpreted in a manner analogous to performance data. However, if the disease prevalence is low or the data arise from epidemic conditions, then factors such as the timing and extent of challenge become important. It can be shown that incomplete exposure of the population to infection, or incomplete sensitivity/specificity of the diagnostic test, add noise to the genetic signal and hence lead to underestimates of the true heritability. Therefore, if a disease is heritable despite data ascertainment issues, then it is likely there are stronger underlying genetic effects.

Relationships between performance and resistance are also of concern to researchers aiming to breed livestock for increased disease resistance or tolerance. This topic apparently leads to much confusion, perhaps arising from the paradigm that locally adapted breeds, i.e. those resistant/tolerant of specific diseases, tend to have poor productivity whereas highly producing exotic breeds tend to be susceptible to prevalent diseases in tropical areas. Most likely this phenomenon reflects previous (long-term) selection history and says little about the relationship between resistance and performance. This relationship will be a function of two counterbalancing factors: (i) the **costs** of being resistant, in terms of the resources used to protect against infection and (ii) the **benefits** of being resistant, in terms of the damage foregone. Clearly, this relationship will vary between diseases, between environments (e.g. nutritional regimen), and with the infection pressure. Examples are seen in the comparison of GI parasite resistant and susceptible breeds of sheep (e.g. Red Maasai vs. Dorper) under heavily and lightly challenged conditions (Baker *et al.*, 2004). Examples are also seen in temperate countries where under some circumstances GI parasite resistance and productivity in sheep are favourably correlated whereas under other circumstances they are adversely correlated. These considerations lead to expected genotype x environment interactions if animals are evaluated under different environmental conditions.

From many perspectives (disease importance, amenability of data collection and evidence of genetic variation), ruminant GI parasite infections come at or near the top of the pecking order for focussed genetic studies. Further, there are many potentially selectable traits for GI parasite resistance, including indicators of the level of infection (faecal egg count (FEC)), immune response (antibody levels or eosinophilia) and pathology (pepsinogen or fructosamine concentrations, packed cell volume (PCV) and even growth rate). All these traits are heritable. However, FEC and PCV are preferred traits under many conditions with FEC being particularly important as it also indicates rates of pasture contamination. These are complex time-dependent traits and likely to be controlled by many genes. Results from QTL studies do indeed suggest polygenic control, implying that simple genetic solutions are unlikely. Therefore, although there are many opportunities to breed animals for improved parasite resistance, there is much work to do at various levels. This includes characterisation of genetic resources, definition of sustainable breeding objectives and definition and development of appropriate technologies. Appropriate technologies may include targeted single nucleotide polymorphism (SNP) arrays, but in the short term the development of infrastructure for phenotype collection is a necessity.

Acknowledgements

Concepts and data arose from research funded by many sources, including EADGENE (an EU Framework VI Network of Excellence), Defra, the BBSRC and the MLC. I wish to thank

many colleagues, particularly Gail Davies, Sem Genini, Elisabetta Giuffra, John Woolliams, Mike Stear, Frank Jackson and Marie-Hélène Pinard-van der Laan.

References

Baker, R.L., Mugambi, J.M., Audho, J.O., Carles, A.B. and Thorpe, W. 2004. Genotype by environment interactions for productivity and resistance to gastrointestinal nematode parasites in Red Maasai and Dorper sheep. *Animal Science* 79: 343-353.

Bishop, S. C. 2005. Disease resistance: Genetics. In: *Encyclopedia of Animal Science*. Edited by Pond, W. G. & Bell, A. W. New York: Marcel Dekker, Inc., pp 288-290.

Davies, G., Genini, S., Bishop S.C. and Giuffra, E. 2009. An assessment of the opportunities to dissect host genetic variation in resistance to infectious diseases in livestock. *Animal* 3: 415-436.

Perry, B.D., McDermott, J.J., Randolph, T.F., Sones, K.R. and Thornton, P.K. 2002. Investing in animal health research to alleviate poverty. International Livestock Research Institute (ILRI), Nairobi, Kenya.

A review: Latest findings in the host-pathogen interactions in parasitic diseases. Can they be used for practical breeding? (S. Thévenon)

The risk of infection and the severity of a disease are determined by the interactions between the host, the parasite and the environment. In this short review, environmental effects will be ignored and the author will focus on host - parasite interactions with particular interest in factors that impact disease evolution. The severity of the disease is function of the physiological status of the host, its behaviour and its genetic make up, and, on the other side, of the species and the strain of the parasite.

For the host species, it is well known that some breeds or populations are more or less susceptible to disease. For the parasite, the virulence and the pathogenicity vary within and between strains. The host will develop different mechanisms to limit the multiplication and the deleterious effects of the parasite through physical barriers, non specific clearance mechanisms, the innate and the acquired immune systems. The parasite tries to evade the host defence mechanisms by hiding in the host cells, modulating the immune response, blocking, inhibiting host molecules or changing its surface antigens.

Molecular biology and cellular biology tools, and especially high through-put techniques associated with large bioinformatic databases and efficient algorithms allow new insights into host-parasite interactions and the effects of the host and parasite genetic variability. QTL studies, association analyses and the search for selection signatures allow identification of genomic regions that show polymorphisms associated with tolerance or susceptibility. Depending on the experiment, genomic regions ranging from several tens cM to few Kb are identified. Transcriptomic tools (real-time Reverse-Transcript PCR, microarray, Digital Gene Expression, RNA-seq) are used to highlight genes differentially expressed in a host tissue (or in the parasite), between susceptible and tolerant animals during the disease challenge or infection. Proteomics allows us to look for differentially expressed proteins in the host and the parasite and, in association with transcriptomic tools, may lead to information on post-transcriptional modifications. Finally, cellular experiments look at the cellular mechanisms of the interactions and potentially validate the activities of some molecules.

The information brought by the experiment can sometimes be directly linked to DNA, RNA and protein databases. *Cis*-acting candidate genes may be highlighted if some genes are present within a QTL and are differentially expressed between tolerant and susceptible animals. *Trans*-acting genes may be discovered by linking genomic, transcriptomic and proteomic data by pathway analyses. Without being exhaustive, this review will focus on two host species, cattle and sheep, and three main parasite families, trypanosomes, ticks and gastrointestinal (GI) nematodes.

Latest findings in cattle tolerance/susceptibility towards *Trypanosoma congolense*

Trypanosomes are blood and extra-cellular protozoan parasites transmitted by tsetse flies. They cause anaemia and cachexia leading to death in trypanosusceptible animals. The first genomic study was conducted in a F2 cross between tolerant *Bos Taurus* N'Dama and susceptible *B. indicus* Boran cattle and identified 18 QTL linked to parasitemia, body weight and/or anaemia control (Hanotte *et al.*, 2003). The confidence intervals of the QTL were large (40 cM on average). Association analysis conducted on candidate QTL identified by Hanotte *et al.* (2003), showed a microsatellite marker associated with PCV (Packed Cell Volume) control in a West African crossbred population (Dayo *et al.*, 2008). A selection signature study revealed signs of selection in trypanotolerant West African breeds on BTA02 and BTA13 (Dayo *et al.*, 2009). Finally, a recent study on selection signatures using a 50K SNP

chip showed 53 genomic regions harbouring selection signals and 42 strong candidate genes associated with three main physiological functions (i.e. immune response, the nervous system and hair and skin properties) (Gautier *et al.*, 2009). O’Gorman *et al.* (2006) studied cytokines’ genes expression in N’Dama and Boran, and highlighted some genes that were differentially expressed (INF γ , IL1 α , TNF and IL12 up-regulated in N’Dama, IL6 and IL10 up-regulated in Boran, indicating an earlier response with pro-inflammatory cytokines in the N’Dama). Berthier *et al.* (2003, 2006, 2008), using Serial analyses Gene Expression, also found some differentially regulated genes in the N’Dama versus Fulani Zebu (β 2microglobulin, platelet factor, lysozyme, cytochrome B245, class II CMH).

Recently, O’Gorman *et al.* (2009) published the results of a microarray experiment, showing numerous genes differentially expressed during the disease course between N’Dama and Boran. The Gene Ontology process showed differential regulation of the defence mechanisms, arginine metabolic process, erythrocyte differentiation. The next steps in the comprehension of host breeds and parasite interactions will rely on linking genomic and transcriptomic data using bioinformatic process and pathways study. Accordingly, Rennie *et al.* (2008) provided a list of candidate genes. To discover causal mutations, study of candidate genes polymorphism and *in vitro* cellular experiment - used to validate the effect of genes polymorphism and expression on the interaction between host cells and parasites - will have to be undertaken.

Latest findings in resistance to ticks in cattle

Generally, *Bos indicus* breeds are considered more resistant to tick attachment than European *Bos taurus* breeds. Two studies showed an association between DRB3 alleles (in the BoLA – Bovine Leucocytes Antigens – region) and either the total tick engorgement weight or the tick count. The first study used the *Amblyomma americanum* tick and a cross between Red Poll/Simmental/Simbrah (Untalan *et al.*, 2007). The second study used the *Rhipicephalus microplus* tick and a cross between Gir and Holstein (Martinez *et al.*, 2006). A QTL experiment was conducted in a F2 population (Gir X Holstein) infected by *R. microplus*, and had focused on three candidate chromosomes (Gasparin *et al.*, 2007). One QTL was identified on BTA05 in the rainy season and another QTL on BTA14 in the dry season. Interestingly, this study highlighted an interaction between the genotype and the environment. Moreover, only a small proportion of the phenotypic variance was explained by the QTL (1.7% for BTA05 and 3.2% for BTA14) and it was suggested that polygenic effects or epistatic interactions could be important.

There are a number of articles related to gene expression studies. Piper *et al.* (2008) and Piper *et al.* (2009) could show a strong innate inflammatory immune response in susceptible Holstein infected by *R. microplus*, whereas Piper *et al.* (2009) and Kongsuwan *et al.* (2008) found a strong development of the cell-mediated immune response in the *B. indicus*. The immune response in the susceptible Holstein and tolerant *B. indicus* seems very different during tick attachment.

Latest findings in resistance to gastrointestinal (GI) nematodes in cattle and sheep

Latest findings in cattle

Only one QTL study was reported and it was based on a daughter design in Holstein cattle, under natural infection (Coppieters *et al.*, 2009). Four QTL were found to be associated to EPG (Eggs per Gram) on BTA7, BTA9, BTA 14 and BTA19. Fine mapping using SNP (Single Nucleotide Polymorphism) was done on the two most significant chromosomes

(BTA9, BTA19), allowing fine mapping for BTA19. The size of the QTL region was around 3.3cM on BTA19, of which the orthologous genome segment in Human identified 95 annotated genes. One of the most interesting genes is ITAGE, coding integrin alpha chain that is preferentially expressed on the surface of intestinal intraepithelial T lymphocytes, and that is thought to be important for immune response to mucosal pathogens.

A microarray experiment conducted on Angus cattle under natural infestations showed 100 genes differentially expressed that may be associated with ten functions (immunoglobulins, antigen presentation, cell activation and motility, tissue factors, cytokines, chemokines, cell communication and cell cycle, complements, adhesion molecules and unknown functions) (Araujo *et al.*, 2009). The results supported the idea that an effective immune response is based on a balance between TH1- (associated with macrophage activation) and TH2 (associated with B-cell activation) types. This contrasts with results in rodent models supporting a resistance to intestinal nematodes associated with a TH2 type immune response. Another interesting study focussed on the main cytokine genes analysed by qRT-PCR in Nerole cattle naturally infected by *Cooperia* (Bricarello *et al.*, 2008). In this case, the authors found a clear up-regulation of IL4, IL13, associated with TH-2 immune response type in resistant animals, versus an up-regulation of IL2, IL12p35, MCP1 and INF γ linked to a TH-1 immune response type in susceptible animals.

Latest findings in sheep

Bishop & Morris (2007) and Stear *et al.* (2009) published reviews on resistance to nematodes in sheep, providing a list of the main QTL identified to date. The most interesting QTL lie in OAR3, in INF γ region, in OAR20 and in the CMH region. Several studies on gene expression have been performed. For instance, Ingham *et al.* (2008) studied the cytokines gene expression level by qRT-PCR in several flocks: one selected for resistance against *Haemonchus contortus*, one selected for susceptibility towards *H. contortus*, one selected for resistance against *Trichostrongylus colubriformis* and one selected for susceptibility towards *T. colubriformis*. Groups from the 4 flocks were infected either with *H. contortus* or with *T. colubriformis* and tissues were harvested during a primo-challenge or further challenge to analyse potential differences in innate and acquired immunity development. Based on their results, the authors proposed the hypothesis that the innate period would be critical to the development of *H. contortus* resistance, whereas the acquired period would be critical to the development of *T. colubriformis* resistance. Moreover, TLR (Toll Like Receptor) are up-regulated in resistant animals in general. No TH1 versus TH2 polarization was detected.

Disparate and numerous data make it difficult to perform a synthesis. However, one can notice that there are numerous QTL identified in sheep that depend on the breed, the parasite species, the type of infection and the environment. The most interesting QTL seem to lie in OAR3 and OAR20. In cattle, the QTL discovered on BTA9 (Coppieters *et al.*, 2009) corresponds to the orthologous region in sheep lying on OAR8, with a QTL identified by Crawford *et al.* (2006). Moreover, the QTL on BTA19 corresponds to the orthologous region in sheep lying on OAR11, with a QTL identified by Crawford *et al.* (2006) and Beh *et al.* (2002), but with a moderate significance. Important genes related to nematodes resistance are likely to lie in these regions.

Concerning the transcriptome studies, differences depending on the parasites species can be highlighted. It seems that expression of TLR, genes conducting to O₂ and NO production, MHC, IgA and IgE production are important for resistance. But there are some discrepancies concerning a possible polarisation of the TH1 / TH2 immune response type that remains to be elucidated. Some studies show a resistance associated with a TH2 immune response, others show association with a more balanced response between TH1 and TH2. May be some

candidate genes can be highlighted: the ITAGE gene is within the BTA19 QTL (Coppieters *et al.*, 2009) and is also up-regulated in resistant cattle (Araujo *et al.*, 2009). MIP-1 α is over-expressed in resistant cattle (Li *et al.*, 2007) and GRO gene, coding for MIP-2 α , is within the sheep OAR6 QTL (Beh *et al.*, 2002).

Synthesis and practical uses in animal breeding

While there are several QTL studies in sheep resistance against GI nematodes that usually identified different QTL, there are far less QTL experiments in cattle for parasitic diseases; only one in trypanotolerance, one for resistance to nematodes and one for resistance to ticks. The poor number of QTL studies may have several explanations. Firstly, it is difficult to record reliable phenotypes for disease resistance; there are numerous parasites species, especially for nematodes; there are co-infections among parasites; there are numerous covariates; there may be interactions with the environment; there are differences in the immune response between the primary infection and later infections; and it is very difficult to record data in the field since it requires farmers to let their animals be withheld from treatments, which is almost impossible. Moreover, some diseases may be difficult to diagnose with high levels of specificity and sensitivity. Secondly, for tropical diseases, pedigrees are missing to perform linkage studies. Lastly, until now, there are minor interests in Europe for disease resistance compared to the numerous QTL studies for milk, meat production or fertility. Therefore, the genomic regions identified are still too large to allow a positional candidate gene approach. There are more studies aiming at identifying differences in gene expression levels. They provide numerous data that are usually difficult to analyse and interpret: is a differential expression a cause or a consequence of the resistance? Does the statistical significance reflect the biological significance? Pathway analyses and gene Ontology are currently not accurate enough (e.g. immuno-globulins, antigen presentation) and often provide expected information like a global activation of the immune response.

Finally, current data are not directly usable for genetic improvement programs, or for elaboration of new drugs. What we need is more accurate phenotypes, knowing that with fine mapping using several thousands of SNP markers genotyping is no longer a problem, at least for cattle and sheep. Combining linkage analyses, linkage disequilibrium analyses and the search for selection signatures should give enough resolution to provide a shorter list of candidate genes to be associated with transcriptome data via pathways. However, we will have to pay attention to host breed by pathogen strain by environment interactions and to the potential trade-offs between diseases or between resistance to some diseases and production (Doeschl-Wilson *et al.*, 2008; Coppieters *et al.*, 2009).

References

- Araujo, R. N., Padilha, T., Zarlenga, D., Sonstegard, T., Connor, E.E., Van Tassell, C., Lima, W.S., Nascimento, E. and Gasbarre, L.C.** 2009. Use of a candidate gene array to delineate gene expression patterns in cattle selected for resistance or susceptibility to intestinal nematodes. *Veterinary Parasitology* 162: 106-115.
- Beh, K., Hulme, D., Callaghan, M.J., Zeish, Z., Lenane, I., Windon, R.G. and Maddox, J.F.** 2002. Aggenome scan for quantitative trait loci affecting resistance to *Trichostrongylus colubriformis* in sheep. *Animal Genetics* 33: 97-106.
- Berthier, D., Chantal, I., Thevenon, S., Marti, J., Piquemal, D. and Maillard, J.-C.** 2006. Bovine transcriptome analysis by SAGE technology during an experimental *Trypanosoma congolense* infection. *Annals of the New York Academy of Sciences* 1081: 286-299.

- Berthier, D., Chantal, I., Thevenon, S., Sakande, H., Maillard, J.-C., Bamngaly, Z., Piquemal, D., Marti, J. and Cuny, G.** 2008. Study of bovine trypanotolerance by whole transcriptome analysis. *Annals of the New York Academy of Sciences* 1149: 71-76.
- Berthier, D., Quere, R., Thevenon, S., Belemsaga, D., Piquemal, D., Bamngaly, Z., Marti, J. and Maillard, J.-C.** 2003. Serial analysis of gene expression (SAGE) in bovine trypanotolerance: preliminary results. *Genetics Selection Evolution* 35 Suppl 1: S35-47.
- Bishop, S. C. and Morris, C. A.** 2007. Genetics of disease resistance in sheep and goats. *Small Ruminant Research* 70: 48-59.
- Bricarello, P. A., Zaros, L.G., Coutinho, L.L., Rocha, R.A., Silva, M.B., Kooyman, F.N.J., De Vries, E., Yatsuda, A.P. and Amarante, A.F.T.** 2008. Immunological responses and cytokine gene expression analysis to *Cooperia punctata* infections in resistant and susceptible Nelore cattle. *Veterinary Parasitology* 155: 95-103.
- Coppieters, W., Mes, T.H.M., Druet, T., Fanir, F., Tamma, N., Schrooten, C. Cornelissen, A.W.C.A., Georges, M. and Ploeger, H.W.** 2009. Mapping QTL influencing gastrointestinal nematode burden in Dutch Holstein-Friesian dairy cattle. *BMC Genomics* 10: 96.
- Crawford, A.M., Paterson, K.A., Dodds, K.G., Diez Tascon, C., Williamson, P.A., Roberts Thompson, M., Bisset, S.A., Beattie, A.E., Greer, G.J., Green, R.S., Wheeler, R., Shaw, R.J., Knowler, K., McEwan, J.C.** 2006. Discovery of quantitative trait loci for resistance to parasitic nematode infection in sheep: 1. Analysis of outcross pedigrees. *BMC Genomics* 7:178.
- Dayo, G.K., Thevenon, S., Poivey, J.P., Sidibe, I., Bengaly, Z., Eggen, A., Boichard, D., Gautier, M.** 2008. Etude de QTL lies à la trypanotolérance bovine dans une population métisse ouest-africaine par analyse d'association. *Les Actes du BRG 7* : 95-115.
- Dayo, G. K., Thevenon, S., Berthier, D., Moazami-Goudarzi, K., Denis, C., Cuny, G., Eggen, A. and Gautier, M.** 2009. Detection of selection signatures within candidate regions underlying trypanotolerance in outbred cattle populations. *Molecular Ecology* 18: 1801-1813.
- Doeschl-Wilson, A. B., Vagenas, D., Kyriazakis, I. And Bishop, S.C.** 2008. Exploring the assumptions underlying genetic variation in host nematode resistance (Open Access publication). *Genetics Selection Evolution* 40: 241-264.
- Gasparin, G., Miyata, M., Coutinho, L.L., Martinez, M.L., Teodoro, R.L., Furlong, J., Machado, M.A., Silva, M.V.G.B., Sonstegard, T.S. and Regitano, L.C.A.** 2007. Mapping of quantitative trait loci controlling tick [*Rhipicephalus (Boophilus) microplus*] resistance on bovine chromosomes 5, 7 and 14. *Animal Genetics* 38: 453-459.
- Gautier M., Flori L., Riebler A., Jaffrézic F., Laloé D., Gut I., Moazami-Goudarzi K and Foulley J.L.** 2009. A whole genome Bayesian scan for adaptive genetic divergence in West African cattle. *BMC Genomics* 10:550.
- Hanotte, O., Ronin, Y., Agaba, M., Nilsson, P., Gelhaus, A., Horstmann, R., Sugimoto, Y., Kemp, S., Gibson, J., Korol, A., Soller, M. and Teale, A.** 2003. Mapping of quantitative trait loci controlling trypanotolerance in a cross of tolerant West African N'Dama and susceptible East African Boran cattle. *Proceedings of the National Academy of Sciences of the United States of America* 100: 7443-7448.
- Ingham, A., Reverter, A., Windon, R., Hunt, P. And Menzies, M.** 2008. Gastrointestinal nematode challenge induces some conserved gene expression changes in the gut mucosa of genetically resistant sheep. *International Journal of Parasitology* 38: 431-442.

- Kongsuwan, K., Piper, E.K., Bagnall, N.H., Ryan, K., Moolhuijzen, P., Bellgard, M., Lew, A., Jackson, L., Jonsson, N.N., Pinard, M.H., Gay, C. and Pastoret, P.P.** 2008. Identification of genes involved with tick infestation in *Bos taurus* and *Bos indicus*. In: *Animal Genomics for Animal Health*. (Eds -Pinard M-H, Gay C, Pastoret P-P, Dodet B). *Developments in Biologicals* (Basel) 132: 77-88.
- Li, R. W., Sonstegard, T. S. Van Tassell, C.P. and Gasbarre, L.C.** 2007. Local inflammation as a possible mechanism of resistance to gastrointestinal nematodes in Angus heifers. *Veterinary Parasitology* 145: 100-107.
- Martinez M.L., Machado M.A., Nascimento C.S., Silva M.V.G.B., Teodoro R.L., Furlong J., Prata M.C.A., Campos A.L., Azevedo A.L.S., Pires M.F.A. and Verneque R.S.** 2006. Association of BoLA-DRB3.2 alleles with tick (*Boophilus microplus*) resistance in cattle. *Genetics and Molecular Research* 5: 513-24.
- O'Gorman G.M., Park S.D., Hill E.W., Meade K.G., Coussens P.M., Agaba M., Naessens J., Kemp S.J. and MacHugh D. E.** 2009. Transcriptional profiling of cattle infected with *Trypanosoma congolense* highlights gene expression signatures underlying trypanotolerance and trypanosusceptibility. *BMC Genomics* 10: 207.
- O'Gorman G.M., Park S.D., Hill E.W., Meade K.G., Mitchell L.C., Agaba M., Gibson J.P., Hanotte O., Naessens J., Kemp S.J. and MacHugh D. E.** 2006. Cytokine mRNA profiling of peripheral blood mononuclear cells from trypanotolerant and trypanosusceptible cattle infected with *Trypanosoma congolense*. *Physiol Genomics* 28: 53-61.
- Piper, E.K., Jackson, L.A., Bagnall, N.H., Kongsuwan, K.K., Lew, A.E. and Jonsson, N.N.** 2008. Gene expression in the skin of *Bos taurus* and *Bos indicus* cattle infested with the cattle tick, *Rhipicephalus* (*Boophilus*) *microplus*. *Veterinary Immunology and Immunopathology* 126: 110-119.
- Piper E.K., Jonsson N.N., Gondro C., Lew-Tabor A.E., Moolhuijzen P., Vance M.E., and Jackson L.A.** 2009. Immunological profiles of *Bos taurus* and *Bos indicus* cattle infested with the cattle tick, *Rhipicephalus* (*Boophilus*) *microplus*. *Clinical and Vaccine Immunology* 16: 1074-1086.
- Rennie C., Hulme H., Fisher P., Hall L., Agaba M., Noyes H.A., Kemp S.J., Brass A.** 2008. A systematic, data-driven approach to the combined analysis of microarray and QTL data. In: *Animal Genomics for Animal Health* (Eds - Pinard M-H, Gay C, Pastoret P-P, Dodet B). *Development in Biologicals* (Basel) 132: 293–299.
- Stear, M.J., Boag, B., Cattadori, I and Murphy, L.** 2009. Genetic variation in resistance to mixed, predominantly *Teladorsagia circumcincta* infections of sheep: from heritabilities to gene identification. *Parasite Immunology* 31: 274 – 282.
- Untalan, P.M., Pruett, J.H. and Steelman, C.D.** 2007. Association of the bovine leukocyte antigen major histocompatibility complex class II DRB3*4401 allele with host resistance to the Lone Star tick, *Amblyomma americanum*. *Veterinary Parasitology* 145: 190-195.

General discussion of the current research and latest findings in the field of breeding for disease resistance in ruminants and host-pathogen interactions

Question:

What are the requirements before incorporating disease resistance in breeding programs?

Answer:

First, we need information on the importance and impact of diseases in the geographical region to make a disease priority list. However, it is often difficult to get such information. Quite often, one cannot rely on farmers' information as they may confuse certain disease symptoms.

Second, we have to consider the alternatives (e.g. vaccines, drugs, etc.) to control the disease. Experience shows that where sustainable alternatives are available breeding is of low interest for breeders. Therefore, for many pathogens, breeding for disease resistance is difficult to implement at this point in time, and this will probably remain the case at least in the short term.

If we decide to breed for resistance to a disease, we need indicator traits and sensitive and specific diagnostic tools to describe the level of resistance in animals. Then, field studies need to be carried out to collect epidemiological data. Good indicator traits are the basis for accurately describing phenotypes, which in their turn are the basis for breeding activity. There are good indicators for a number of important diseases, as it is well documented later in these proceedings.

Question:

How useful are molecular markers at the moment?

Answer:

Once we have accurate phenotypes, markers could be developed and become useful tools. However, currently, they are used mainly for research purposes and not for practical breeding. Experimental designs for molecular studies were often weak, and consequently, QTL that were described to be related to specific disease resistance could not be confirmed in other studies. Furthermore, QTL usually describe only a small part of the genetic variation.

Question:

How can breeding programmes work in developing countries?

Answer:

We need to offer something interesting and promising with short term success. Breeding should be combined with other programs: management, health, feeding, etc. Positive effects are then quickly seen, which may motivate livestock keepers to support breeding programmes for the longer term.

Question:

When is the right time for phenotyping animals for disease resistance?

Answer:

The answer to the question should be based on good knowledge of the disease epidemiology. The best time for phenotyping depends very much on the pathogen. In most cases, it is when the challenge is highest as it leads to higher heritability values.

Question:

Is an artificial or experimental challenge better to describe genetic differences? Does working under very standardized environments not raise the question of whether the results can be extrapolated to practical farming situations?

Answer:

Field analyses are often difficult to arrange. For example, it is important that farmers do not treat their animals during a challenge period. On the other hand, experimental challenges are relatively easy to conduct. However, they may be of limited value for several reasons as, for example, the use of only one strain of the pathogen under experimental conditions. In the case of trypanosomosis this may lead to confusion or even wrong results.

SECTION 2: ACTUAL STANDING AND PERSPECTIVES FOR THE SUSTAINABLE USE AND DEVELOPMENT OF RESISTANT OR TOLERANT BREEDS

Actual standing and perspectives for the sustainable use and development of parasite resistant or tolerant breeds in developed regions: Australia and New Zealand as an example (J.C. Greeff, L.J.E. Karlsson and A.C. Schlink)

Introduction

Lack of disease resistance is an important constraint to animal production. The major endemic diseases that pose a threat and cost to sheep production in Australia and New Zealand are intestinal nematodes, ovine cutaneous myiasis (blowfly strike), lice and footrot. It is estimated that these four diseases cost the Australian sheep industry in excess of A\$772 million annually (Sackett *et al.*, 2006). The first three parasitic diseases are generally treated and controlled with drugs and chemicals. However, these methods are not sustainable as the parasites are becoming increasingly resistant to the available chemicals. The following is a short summary of the situation regarding genetic research into controlling blowflies, intestinal nematodes, lice and footrot in Australia and New Zealand.

Blowfly strike

Cutaneous myiasis or blowfly strike is caused primarily by *Lucilia cuprina* (Raadsma, 2000a) and is a serious sheep production issue in Australia and New Zealand. The first attempt to identify the underlying causal factors was carried out by Seddon and Belschner (1937) who showed that wrinkles in Merino sheep is a key indicator trait for breech and flystrike. Since then, prevention of blowfly strikes focused mainly on management practices such as mulesing, crutching, shearing and jetting animals with insecticides at critical times. However, increased consumer expectations of ethically acceptable sheep production systems, shortage of labour and the fact that the parasite is becoming increasingly resistant to the available chemicals, make these practices unsustainable. Genetic options to breed resistant sheep offer a permanent solution. In this respect, Australia (Raadsma, 2000a; James, 2006; Greeff and Karlsson, 2009; Smith *et al.*, 2009) and New Zealand (Morris, 2009; Scobie *et al.*, 2007; Scobie *et al.*, 2008) have made huge investments over the last 50 years to identify the key indicator traits that makes sheep susceptible or resistant and their genetic and phenotypic relationships with blowfly strike. Two experimental Merino flocks have recently been established in Australia to examine and demonstrate the effectiveness of breeding for breech strike resistance by using the key indicator traits (Greeff and Karlsson, 2009; Smith *et al.*, 2009).

Intestinal nematodes

Most sheep farms in Australia and New Zealand rely on anthelmintics to control intestinal nematodes. This has resulted in nearly all farms experiencing some form of resistance to the available anthelmintics.

Extensive research on the genetics and breeding for worm resistance has been carried out in Australia (Woolaston and Piper, 1996; Karlsson and Greeff, 2006), New Zealand (Morris, 2009) and recently also in South Africa (Cloete, 2007). It has been shown that faecal worm egg count (FEC) is a very effective indicator trait that can be used in breeding for worm resistance (Gasbarre and Miller, 2000; Pollott *et al.*, 2004). Numerous experiments have

shown it to be heritable (average estimate about 0.30 and ranging from about 0.20 to 0.40). Good response to selection has been demonstrated (Woolaston and Piper, 1996; Karlsson and Greeff, 2006; Morris, 2009). The resulting resistant animals were more profitable than non selected animals (Greeff and Karlsson, 2006). Breeding values for FEC are now generally available to ram breeders to allow them to breed for increased worm resistance in Australia (Sheep Genetics - www.sheepgenetics.org.au/) and in New Zealand (Sheep Improvement Limited (SIL) - www.sil.co.nz). Prediction and publication of such breeding values have resulted in significant genetic changes in industry flocks both in Australia (Gill, 2009) and New Zealand (Amer, 2009).

The above mentioned experimental breeding programmes have lead to the establishment of unique genetic resources in Australia and New Zealand. The Rylington Merino is the most worm resistant Merino flock in Australia (www.sheepgenetics.org.au/) and it has become the major resource for genetic studies into the physiological mechanisms of worm resistance (Liu *et al.*, 2005 a, b; Williams *et al.*, 2008). In New Zealand, three different sheep resource flocks for nematode studies are available; two flocks have been selected for resistance and one flock has been selected for resilience (Morris, personal communication).

Marker assisted selection offers opportunities to make faster genetic gains for traits such as disease resistance that is difficult to measure (McEwan, 2009). The first commercial genetic marker (Wormstar TM) for worm resistance was released recently in New Zealand (www.catapultsystems.co.nz). This genetic marker accounts for about 2-3% of the variation in FEC. This company also provides services to determine pedigrees and to test sheep for a range of other single genes using DNA markers.

There are also other research programmes underway by the International Sheep Genomics Consortium (www.Sheephapmap.org/) focusing on the development of SNP (single nucleotide polymorphisms) markers. An Ovine SNP50 chip was released recently by Illumina (www.illumina.com/) and is currently being evaluated in different research flocks in the participating groups. This DNA information will be used to predict a genomic breeding value for a wide range of traits in the future.

Diarrhoea (scouring) is a major problem in wool sheep and is generally caused by intestinal parasites (Williams *et al.*, 2008). We now recognize two sub-types. Type one is due to low immune competence and is associated with high FEC whereas type two is due to a hyper-immune response and associated with low FEC. Scouring is a major predisposing factor for breech strike and it has been extensively studied in Australia (Karlsson *et al.*, 2004) and New Zealand (Scobie *et al.*, 2008). It is a heritable trait (with a heritability of about 0.20) and offers the opportunity to breed for reduced diarrhoea (Greeff and Karlsson, 1998).

Lice

Little information is available on the actual prevalence of lice but anecdotal information indicates that lice have become a significant problem. It is a serious issue for the specialized Merino wool producers since infected animals rub themselves which results in coting of the wool. Lice are managed through chemical treatments which in some cases can cause serious contamination of lanolin byproducts and effluent from the wool scouring process. There is evidence for both within and between breed variations in resistance to lice (James, personal communication). However, no genetic research on resistance to lice is currently being carried out in Australia. New Zealand investigated whether Romney sheep that have been bred for worm resistance would also be resistant to lice but no evidence was found to support this idea (Pfeffer *et al.*, 2007).

Footrot

Footrot is a serious disease in the higher rainfall regions and is caused by a bacteria *Dichelobacter nodosus* (Raadsma, 2000b). Although studies have shown that resistance to footrot is a heritable trait (Nieuwhof *et al.*, 2008) and that breeding could be effective, the availability of effective vaccines has reduced the need for genetic studies. These vaccines are now routinely used in Australian and New Zealand sheep flocks and no other quantitative genetic research is currently being carried out on footrot in Australia.

Conclusion

Blowflies and intestinal worms are the two most important parasites facing the Australian and New Zealand sheep industry. Relying on chemicals to control parasites is not a sustainable option as parasites have become increasingly resistant to the available chemicals. A new anthelmintic is currently being evaluated (Besier personal communication) but as with previous chemicals the development of resistance is to be expected. Hence the only long term solution is to breed animals resistant to parasites. Australia and New Zealand have developed genetic technologies and have established an infrastructure that makes it possible for breeders to breed for resistance to worms. Similar technologies are being developed to breed for increased resistance to blowfly strike.

Recommendations

Demographic information

There are indigenous sheep breeds that are well adapted to environments where nematodes are endemic such as the Red Maasai in Kenya (Baker *et al.*, 1999, 2003) and the Nguni in South Africa (Kunene and Fossey, 2006) which is on the brink of becoming extinct. Hence there is an urgent need to preserve these breeds and to identify other breeds across the world that are also resistant/tolerant to diseases. All diseases are important but some diseases will be more important in certain areas than others. However, as nematodes are the major threat to sheep production, there is a serious need to identify breeds that are resistant to intestinal worms. This can be done by firstly identifying environments that are favourable to nematode development, and secondly by identifying indigenous breeds within these environments that may be potentially resistant/tolerant.

Measurements

It is expected that many of the resistant/tolerant breeds would be found in subsistence farmer systems where it would be difficult to generate reliable data. However, basic measurements such as growth rate, body condition, faecal worm egg counts at critical times and scoring sheep for signs of anaemia by using the FAMACHA scoring system (Van Wyk and Bath, 2002), can be used effectively to determine animals susceptibility or resistance to disease. With this information, plus information on the feeding conditions and the controlled use of anthelmintics in flocks, a preliminary assessment can be made as to whether a breed may be tolerant or resistant to a parasite species.

Benchmarking

Basic benchmarking of animals/breeds is still the cornerstone to identifying genetic differences. Where breeds have been identified as potentially tolerant/resistant, it would be necessary to evaluate a sample of animals from different flocks within each breed. Animals should be sourced and evaluated under the same environmental conditions where the animals are challenged with the parasite, to determine their level of tolerance/resistance to the parasites.

Benchmarking of different breeds should preferably occur at a central site under the same experimental conditions. The available funds, facilities, technical staff and transport infrastructure will determine the number of animals that can be tested. Alternatively, animals can be tested at different sites on private properties that are genetically linked with a reference team of animals from a well characterized source. The availability of a suitable reference population could be a limiting factor, but where this is not the case many different breeds and groups can be evaluated effectively. A key factor in determining the success of such an approach is the availability of easily accessible contact person who can advise the host of such a trial on a continuous basis. This contact person should primarily be responsible for overseeing the trial and for the timely collection of all the relevant data.

Sustainable use of breeds

Once a resistant/tolerant breed has been identified, it is recommended to establish a nucleus flock in the regions where the breed might have the highest impact. Production statistics of the nucleus flock should be collected and used for extension purposes to demonstrate the superior productivity of the breed. Such a flock could become an important source of genetic material for the farming community to improve the existing populations and to prevent indiscriminate crossbreeding with exotic types.

Genomic selection for resistant breeds/animals

Genetic markers and marker assisted selection provide opportunities for genetic improvement. However, practical limitations currently suggest that classical genetic methodologies provide better short term options. Establishing a nucleus flock based on proven genetic resistance that can act as a reference flock should be a priority. Pedigree, production and disease data should be recorded in this reference flock, in an environment where the disease is endemic. This information will make it possible to identify single nucleotide polymorphisms (SNP) in the breed possibly explaining performance differences between animals/breeds (van der Werf 2006). SNP markers are currently being used in the dairy industry to predict a genomic breeding value for young bulls (Hayes, 2007). A reference population with complete records will allow the same opportunities in indigenous populations. The ability to demonstrate the resistance/tolerance level of the population without the need to challenge the animals and the ability to predict a breeding value for individual animals based on their SNP information will have strong implications for future breeding programmes and the sustainable use and development of such breeds.

Collaboration between countries

The above recommendations require technical expertise on a number of levels. It appears that there is keen support from all sectors for a programme where developed and developing countries can collaborate in scientific investigations to identify disease resistant breeds and to participate in programmes to multiply and disseminate genetic material to areas where resistant breeds can make a contribution to animal production.

References

- Amer, P.R.** 2009. Rates of genetic progress being achieved throughout the New Zealand ram breeding industry. *Proceedings of the New Zealand Society of Animal Production* 69: 155-157.
- Baker, R.L., Mwamachi, D.M., Audho, E.O. and Thorpe, W.** 1999. Genetic resistance to gastro-intestinal nematode in Red Maasai, Dorper and Red Maasai x Dorper ewes in the sub-humid tropics. *Animal Science* 69: 335–344.
- Baker, R.L., Rodriguez-Zas, S.L., Southey, B.R., Audho, J.O., Aduda, E.O. and Thorpe, W.** 2003. Resistance and resilience to gastrointestinal nematode parasites and relationships with productivity of Red Maasai, Dorper and Red Maasai x Dorper crossbred lambs in the sub-humid tropics. *Animal Science* 76: 119-136.
- Cloete, S.W.P., Olivier, J.J., Du Toit, E. and Dreyer, F.H.** 2007 Genetic analysis of faecal worm egg counts in South African Merinos under natural challenge. *South African Journal Animal Science* 37:237-247.
- Gasbarre, L.C. and Miller, J.E.** 2000. Genetics of Helminth Resistance. In *Breeding for Disease Resistance in Farm Animals*. CAB International. Edited R.F.E. Axford, S.C. Bishop, F.W. Nicholas and J.B. Owen.
- Gill, S.** 2009. Unpublished Sheep Genetics report. Meat and Livestock Australia
- Greeff, J.C. and Karlsson, L.J.E.** 1998. Genetic relationships between faecal worm egg count, faecal scouring. 6th World Congress on Genetics Applied to Livestock Production. Vol. 24. page 63-66.. Held in Armidale, 11-16 January 1998, Australia.
- Greeff, J.C. and Karlsson, L.J.E.** 2006. Economic benefit of breeding for worm resistance. 8th World Congress on Genetics Applied to Livestock Production. Held in Belo Horizonte, Brazil from 14-18 August 2006.
- Greeff, J.C. and Karlsson, L.J.E.** 2009. Opportunities to breed for breech strike resistance in Merino sheep in a Mediterranean environment. *Proceedings Association Advancement Animal Breeding Genetics* 18: 272-278. Held in Adelaide, Australia.
- Hayes, B.J., De Roos, A.P.W. and Goddard, M.E.** 2007. Predicting genomic breeding values within and between populations. *Proceedings Association for the Advancement of Animal Breeding and Genetics* 17: 296-303.
- James, P.J.** 2006. Genetic alternatives to mulesing and tail docking in sheep- a review. *Australian Journal of Experimental Agriculture* 46:1-18.
- Karlsson, L.J.E. and Greeff, J.C.** 2006. Selection response to fecal worm egg counts in the Rylington Merino parasite resistant flock. *Australian Journal Experimental Agriculture* 46:725-979.
- Karlsson, L.J.E., Pollott, G.E., Eady, S.J., Bell, A. and Greeff, J.C.** 2004. Relationship between faecal worm egg counts and scouring in Australian Merino sheep. *Animal Production in Australia* 25:100-103.
- Kunene, N. and Fossey, A.** 2006. A survey on livestock production in some traditional areas of Northern Kwazulu Natal in South Africa. *Livestock Research and Rural Development* Vol 18, Article 113. Retrieved from <http://www.lrrd.org/lrrd18/8/kune18113.htm>
- Liu, S.M., Smith, T.L., Briegel, J., Murray, A., Masters, D.G., Karlsson, L.J.E., Palmer, D.G., Greeff, J.C., Besier, R.B. and Gao, S.B.** 2005a. Comparing productive performance of

nematode resistant Merino sheep with non-resistant control. *Livestock Production Science* 97:117-129.

Liu, S.M., Smith, T.L., Karlsson, L.J.E., Palmer, D.G. and Besier, R.B. 2005b. The cost for protein and energy requirements by nematode infection and resistance in Merino sheep. *Livestock Production Science* 97:131-139.

McEwan, J.C. 2009. Current and future impact of DNA technologies on the New Zealand sheep industry. *Proceedings of the New Zealand Society Animal Production* 69:157- 160.

Morris, C.A. 2009. Review of genetic parameters for disease resistance in sheep in New Zealand and Australia. *Proceedings of the Association for the Advancement for Animal Breeding and Genetics* 18 (In press).

Nieuwhof, G.J., Conington, J., Bunger L., Haresign, W. and Bishop, S.C.2008. Genetic and phenotypic aspects of foot lesion scores in sheep of different breeds and ages. *Animal* 2:1289-1296.

Pfeffer, A., Morris, C.A., Green, R.S., Wheeler, M., Shu, D., Bisset, S.A. and Vlassoff, A. 2007. Heritability of resistance to infestation with the body louse, *Bovicola ovis*, in Romney sheep bred for differences in resistance or resilience to gastrointestinal nematode parasites. *International Journal of Parasitology* 37: 1589-1597.

Pollott, G.E., Karlsson, L.J.E., Eady, S.J. and Greeff, J.C. 2004. Genetic parameters for indicators of host resistance to parasites from weaning to hogget age in Merino sheep. *Journal Animal Science* 82:2852-2864.

Raadsma, H.W. 2000a. Genetic aspects of resistance to Ovine Cutaneous Myiases. In *Breeding for Disease Resistance in Farm Animals*. CAB International. Edited R.F.E. Axford, S.C. Bishop, F.W. Nicholas and J.B. Owen.

Raadsma, H.W. 2000b. Genetic aspects of resistance to Ovine Footrot. In *Breeding for Disease Resistance in Farm Animals*. CAB International. Edited R.F.E. Axford, S.C. Bishop, F.W. Nicholas and J.B. Owen.

Raadsma, H.W. 2000c. Genetic aspects of resistance to Ovine footrot. In *Breeding for Disease Resistance in Farm Animals*. CAB International. Edited R.F.E. Axford, S.C. Bishop, F.W. Nicholas and J.B. Owen.

Sackett, D., Holmes, P., Abott, K., Jephcott, S. and Barber, M. 2006. Assessing the economic cost of endemic disease on the profitability of Australian beef cattle and sheep producers. *Animal health and welfare report to Meat and Livestock Australia*. Published April 2006. Meat and Livestock Australia Ltd, Sydney.

Scobie, D.R., O'Connell, D.O., Morris, C.A. and Hickey, S.M. 2007. A preliminary genetic analysis of breech and tail traits with the aim of improving the welfare of sheep. *Australian Journal Agricultural Research* 58: 161-167.

Scobie, D.R., O'Connell, D., Morris, C.A., Hickey, S.M. 2008. Dag score is negatively correlated with breech bareness of sheep. *Australian Journal Experimental Agriculture* 48: 999-1003.

Seddon, H.R. and Belschner, H.G. 1937. The classification according to susceptibility to breech strike. *New South Wales Department of Agriculture Science Bulletin* No 54 pp 111-122

Smith, J.L., Brewer, H.G. and Dyall, T. 2009. Heritability and phenotypic correlations for breech strike and breech strike resistance indicators in Merinos. *Proceedings of the*

Australian Association for the Advancement for Animal Breeding and Genetics 18: 334-337. Held in Adelaide, Australia.

Van der Werf, J.H.J. 2006. Marker Assisted Selection in Sheep and Goats. FAO Invited Book Chapter 13.

Van Wyk, J.A. and Bath, G.F. 2002. The FAMACHA system for managing the haemonchosis in sheep by clinically identifying individual animals for treatment. *Veterinary Research* 33: 509–529.

Williams, A.R., Karlsson, L.J.E., Palmer, D.G., Williams, I.H., Vercoe, P.E., Greeff, J.C. and Emery, D.I. 2008. Increased levels of cysteinyl leukotrienes and prostaglandin E2 in gastrointestinal tract mucus are associated with decreased faecal dry matter in Merino rams during nematode infection. *Australian Journal Experimental Agriculture* 48:873-878.

Woolaston, R.R. and Piper, L.P. 1996. Selection of Merino sheep for resistance to *Haemonchus contortus* - genetic variation. *Animal Science* 62: 55-67.

Young M.J. and Newman S.A.N. 2009. SIL-ACE - Increasing access to genetic information for sheep farmers. *Proceedings of the New Zealand Society for Animal Production* 69:145-146.

Actual standing and perspectives for the sustainable use and development of parasite resistant or tolerant breeds in Asia (R.L. Baker)

Breed differences

The first indication of genetic variation for disease resistance often comes from the observation that some breeds or populations have the ability to tolerate better endemic diseases or to survive an epidemic disease that more susceptible breeds cannot. In the case of small ruminants in Asia this is well illustrated in Table 1 (extracted from Baker and Gray, 2004) by the resistance and/or tolerance of a number of sheep and goat breeds to gastrointestinal (GI) nematodes (worms) and liver fluke infections. The Indonesian Thin Tail sheep have been shown to be resistant to both worms and liver fluke while the Garole sheep in India are resistant to worms. The indigenous native goats in Thailand and the Philippines are also somewhat resistant to worms.

Many of the studies upon which this evidence is based are characterized by poor experimental design, both in terms of the small numbers of animals of each breed tested (amply demonstrated in Table 1), and lack of information on how the breeds were sampled. In addition, very few of the studies took account of variation among sires within breeds. For diseases for which the heritability of resistance or tolerance is of moderate size (e.g. 0.2 - 0.4), an adequate experimental design for breed comparison would be to sample 20 unrelated sires of each breed and produce about 3-5 progeny per sire.

Not much research on resistant to disease of cattle, buffalo or yak is carried out in Asia. However, research done by CSIRO at Rockhampton, in tropical northern Australia, is probably of direct relevance to the situation in hot and humid climates in Asia. Research since 1970 has clearly identified the advantages of the Brahman (*Bos indicus*) and Africander (Sanga – tropically adapted *B. taurus*) in crossbreeding and backcrossing programmes with the *B. taurus* Hereford and Shorthorn breeds originally farmed in this environment. These breeds have been shown to be resistant to ticks and worms, as well as being heat tolerant and having the ability to utilize poor quality feeds (Pragaya *et al.*, 2006; Corbett *et al.*, 2007). It is probable that the tropically adapted Zebu breeds in Asia have all or some of the same attributes but sound studies to verify this are lacking to date.

Within-breed genetic variation

There is reasonable evidence (Bishop *et al.*, 2002) that heritability tends to increase as we progress from relatively poorly defined traits (e.g. dead or alive after a viral epidemic) where estimates are commonly 0.10 or less, to moderate estimates (0.2 to 0.4) for resistance to well defined endemic diseases (e.g. worms), to highly heritable (0.4 to 0.6) when specific immune responses (e.g. antibody responses) can be measured. In sheep and goats, almost all of the heritability estimates for disease resistance are from studies undertaken in the temperate developed world (Bishop and Morris, 2007). A review of disease resistance studies in sheep in Australia and New Zealand (Morris, 1998) found an average heritability of 0.28 for the six diseases studied (i.e. resistance to GI nematodes, facial eczema, ryegrass staggers, fly strike, dermatophilosis and footrot) which is very similar to the heritability estimates for the production traits such as milk yield or body weight.

There are very few reliable estimates of heritabilities of disease resistance derived from indigenous breeds in Asia, although some studies report variation among sire progeny groups (usually very few sires) for resistance to different diseases (Gray *et al.*, 1995). Adequate experimental design is as important for estimating heritabilities as it is for estimating breed differences, but larger experiments are required to estimate heritabilities reasonably precisely. For example, if the true heritability in a population is 0.3 then the optimum family size is

about 10 (i.e. about 10 ewes mated to each ram), and to reduce the standard error of this estimate to about 0.10 or less, about 80 sires are required.

Mandel and Sharma (2008) in a study with 69 bucks and records on 891 Barbari goats reported a heritability estimate for resistance to GI nematodes (predominantly *Haemonchus contortus*) of 0.13 (s.e.0.04). In the Rockhampton cattle studies, average heritabilities for resistance to ticks and worms from a number of different experiments were 0.36 and 0.37, respectively (Prayaga *et al.*, 2003)

Genotype by Environment interaction

Another important issue when assessing breed differences is to recognise the potential importance of genotype by environment interactions. Prayaga *et al.* (2003) used data from cattle crossbreeding studies in northern Australia to derive optimal breed proportions in composites for tropical environments at high, medium and low parasite challenge. A decrease in European *Bos taurus* and an increase in Zebu breed proportion was observed in optimal composites with increased parasite challenge indicating an important breed by environment interaction.

Sustainable breeding for parasite resistance

Some of the reasons for lack of implementation of breeding for disease resistance in both the temperate and tropical regions of the world include:

- A belief in the adequacy of existing control strategies, even when there is evidence that these are failing.
- A lack of appreciation of the opportunities offered by breeding for disease resistance. This is often hampered by the lack of appropriate interdisciplinary skills required. For example, geneticists often have a poor understanding of diseases and their epidemiology while veterinarians or parasitologists often have a poor appreciation of genetic opportunities.
- Lack of the infrastructure required to exploit the genetic opportunities, especially in the tropical developing world. This includes not only the multidisciplinary scientific teams required to establish breeding programmes but also the extension personnel to deliver the animals or technology to farmers. It is also very important that farmers are included in this process from the outset so that they are convinced of the need for the new technologies being developed.

Some of the requirements that need to be met to address the constraints above and to ensure that the opportunities offered by breeding for genetic resistance to disease are realised include:

- For each production system and each livestock species there is a need to document and prioritise the economic impact of different diseases (Perry and Randolph, 1999). There are relatively few examples of attempts to do this in the developed world (McLeod, 1995; Davies *et al.*, 2009) and the task is more difficult in the tropical developing world (Perry *et al.*, 2002). The shortfalls of the studies which have attempted to estimate the total cost of a disease has been discussed (Perry and Randolph, 1999) and shown to be a realistic assessment only in a very limited set of circumstances where disease eradication is a feasible option.
- Once diseases have been adequately prioritised, an assessment of the adequacy and sustainability of currently advocated or implemented disease control strategies is required. If such strategies are found to be sustainable and cost-effective, investing in the genetic improvement for disease resistance might not be a viable option.

- When current disease control strategies are found to be inadequate and non-sustainable, breeding for disease resistance can be considered. Where there is already evidence of differences among breeds in resistance or tolerance to a particular disease, then exploitation of this resource is a relatively quick and straight-forward strategy to pursue. The resistant breed can either be utilised as a purebred or in a crossbreeding system with more susceptible but possibly more productive breeds.
- In some situations, utilisation of a resistant breed is not a viable option. For example, while the resistance and tolerance to GI nematodes is well established for the Red Maasai sheep in East Africa, it is a hair breed and it could not be used in a crossbreeding programme with a wool breed because it would severely damage the income from wool production, and particularly fine wool production in Merino sheep. In this situation, there is no choice but to embark upon selection for resistance within the susceptible breed (s) as has been successfully accomplished in Australia and New Zealand (Woolaston and Baker, 1996; Morris, 1998). However, there are still some issues that need to be resolved in this situation, including in particular how to assign economic weights to disease resistance and production traits in a multi-trait selection index, and the need for more precise estimates of genetic correlations among the disease resistance traits and the production traits (Woolaston and Baker, 1996). For some diseases, such as GI nematodes, there is also the need to establish the consequences of selection for resistance or tolerance on the epidemiology of the disease (Bishop et al., 2002).
- It is highly unlikely, in most cases, that breeding for disease resistance will result in breeds or selected lines within breeds that are absolutely resistant and do not need any other method of control. For example, the resistant Red Maasai sheep under strong challenge with GI nematodes in a sub-humid environment in Kenya still require 1-2 anthelmintic treatments in young lambs between 2 and about 12 months of age, compared to the susceptible Dorper lambs which require at least 4-6 treatments in this period to avoid high mortality rates. ILRI and partners carried out research in South East Asia to develop and test integrated disease control strategies for GI nematode infections (Sani et al., 2004), which included combining resistant hosts with minimal drenching at the most critical times of the year, based on epidemiological studies or the use of the FAMACHA (Van Wyk and Bath, 2002) scoring system (which should reduce the rate of development of resistance to the drugs by the parasites), nutritional supplementation (particularly high protein diets), grazing management (e.g. rotational grazing where this is feasible) and improved management (e.g. housing animals in simple slatted floor sheds in the wet season).

References

- Baker, R.L. and Gray, G.D.** 2004. Appropriate breeds and breeding schemes for sheep and goats in the tropics: the importance of characterizing and utilizing disease resistance and adaptation to tropical stresses. In – “Worm Control for Small Ruminants in Tropical Asia”. (Sani, R, Gray, G.D., Baker, R.L., Eds.), Australian Centre for International Agricultural Research (ACIAR) Monograph No. 113 p 63-95
- Bishop, S. C. and Morris, C. A.** 2007. Genetics of disease resistance in sheep and goats. *Small Ruminant Research* 70: 48-59.
- Bishop, S.C. Chesnais, J. and Stear, M.J.** 2002. Breeding for disease resistance: Issues and opportunities. *Proceedings of the 7th World Congress on Genetics Applied to Livestock Production, Montpellier, France* 31: 597-604.

- Corbet, N.J., Prayaga, K.C., Johnston, D.J. and Burrow, H.M.** 2007. Genetic variation in adaptive traits of cattle in north Australia Proceedings of the Association for the Advancement of Animal Breeding and Genetics, 17: 348-351.
- Davies, G., Genini, S., Bishop S.C. and Giuffra, E.** 2009. An assessment of the opportunities to dissect host genetic variation in resistance to infectious diseases in livestock. *Animal* 3: 415-436.
- Gray, G.D., Woolaston, R. and Eaton, B.T.** 1995. Breeding for Resistance to Infectious Diseases of Small Ruminants. Australian Centre for International Agricultural Research (ACIAR) Monograph No. 34, Canberra, Australia.
- Mandel, A and Sharma, D.K.** 2008. Inheritance of faecal nematode egg counts in Barbari goats following natural *Haemonchus contortus* infection *Veterinary Parasitology* 155:89-94.
- McLeod, R.S.** 1995. Costs of the major parasites to the Australian livestock industries. *International Journal for Parasitology* 25:1363-1367.
- Morris, C.A.** 1998. Responses to selection for disease resistance in sheep and cattle in New Zealand and Australia. Proceedings of the 6th World Congress on Genetics Applied to Livestock Production, Armidale, Australia 27: 295-302.
- Perry, P.D. and Randolph, T.F.** 1999. Improving the assessment of the economic impact of parasitic diseases and their control in production animals. *Veterinary Parasitology* 84:145-168.
- Perry, B.D., Randolph, T.F., McDermott, J.J., Sones, K.R. and Thornton, P. K.** 2002. Investing in Animal Health Research to Alleviate Poverty. International Livestock Research Institute, Nairobi, Kenya.
- Prayaga, K.C., Barendse, W. and Burrow, H.M.** 2006. Genetics of tropical adaptation in northern Australian cattle. Proceedings of the 8th World Congress on Genetics Applied to Livestock Production CD Rom Communication No. 16-01, ISBN 85-60088-01-6 (invited paper, 8 pages).
- Prayaga, K.C., Henshall J.M. and Burrow, H.M.** 2003. Optimisation of breed proportions in tropically adapted beef composites based on growth and resistance traits. Proceedings of the Association for the Advancement of Animal Breeding and Genetics, 15, 302-305.
- Sani, R, Gray, G.D. and Baker, R.L.** 2004 Worm Control for Small Ruminants in Tropical Asia. Australian Centre for International Agricultural Research (ACIAR) Monograph No. 113.
- Van Wyk, J.A. and Bath, G.F.** 2002 The FAMACHA system for managing the haemonchosis in sheep by clinically identifying individual animals for treatment. *Veterinary Research* 33: 509–529.
- Woolaston, R.R. and Baker, R.L.** 1996. Prospects of breeding small ruminants for resistance to internal parasites. *International Journal for Parasitology* 26: 845-855.

Table 1 Sheep and goat breed comparisons for resistance to internal parasites in Asia (Baker and Gray, 2004).

Resistant Breed(s)¹ (No.)	Other Breed(s)¹ (No.)	Traits²	Type of Infect.³	Sp.⁴	Age-mo (Sex)⁵	Reference
SHEEP						
Sumatra(S) (90)	1/2S-1/2St. Croix(106)	E	N	Hc	3 (M & F)	Subandriyo et al. (1996)
St. Croix (22)	1/2S-1/2JFT(117)					Romjali (1995)
1/2S-1/2BB (65)	Sumatra(S) (10) 1/2S-1/2St. Croix(10) 1/2S-1/2BB (10) 1/2S-1/2JFT(10)	E, P	A	Hc	18-24 (Rams)	Romjali et al. (1996) Romjali (1995)
1/2S-1/2BB (10)	Sumatra(S) (9) 1/2S-1/2St. Croix(9) 1/2S-1/2JFT(7)	PPR	N	Hc	24 (Ewes)	Romjali et al. (1997)
1/2Djallonke – ½ Malin wool sheep	Malin wool sheep	E	N	Hc	3-12 (M & F)	Pandey (1995)
	¼ Djallonke- 3/4Malin ½ Dorset- 1/2Malin	E	N	Hc	0-14 (M & F)	Sani (1994)
St. Croix (39)	Katahdin (27) Rambouillet (10) Philippine Native (30)	E, P	N	Hc	3-8 (M & F)	Suba et al (2002)
Indonesian Thin Tail - ITT (24)	St. Croix (12)	FC	A	Fg	6-12 (M & F)	Roberts et al. (1997a)
	ITT (20) Merino (12)	FC	A	Fh	6-12 (M & F)	Roberts et al. (1997a)
ITT (20)	ITTxSt. Croix (20) St. Croix (10)	FC	A	Fg	9-12 (M & F)	Roberts et al. (1997b)
½ Garole (G) – ½ Deccani (D) or ½ Bannur (B) (75)	B, D, ½ B – ½ D (192)	E	N	Hc	3-7 (M & F)	Nimbkar et al. (2003)
½ Garole (G) – ½ Deccani (D) or ½ Bannur (B) (65)	B, D, ½ B – ½ D (171)	E, P	A	Hc	6-11 (M & F)	Nimbkar et al. (2003)
GOATS						

Thai Native(12)	1/2TN-1/2AN(8) 3/4TN-1/4AN(8)	E, P, A W		Hc	3-6 (M & F)	Pralomkarn et al. (1997)
Philippine Native (25)	Anglo -Nubian (25) Boer (25) Saanen (25)	E, P	N	Hc	20+ (Does)	Suba et al. (2000)
PN (41) Boer (50)	Anglo-Nubian (47) Saanen (14)	E, P	N	Hc	8 (M & F)	Suba et al. (2002)

¹ No. = number of records; BB = Barbados Blackbelly; JFT = Javanese Fat Tail; ITT = Indonesian Thin Tail (thin tail sheep from both Sumatra and Java); TN = Thai Native; AN = Anglo-Nubian; PN = Philippine Native

² E = eggs per gram; P = packed red cell volume; W = worm count; FC = fluke count; PPR = peri-parturient rise in worm egg counts

³ N = natural infection from pasture; A = artificial infection

⁴ Sp = parasite species; Hc = *Haemonchus contortus*; Fg = *Fasciola gigantica*; Fh = *Fasciola hepatica*

⁵ M = males; F= females

Actual standing and perspectives for the sustainable use and development of parasite resistant or tolerant breeds in the USA (J. Miller)

With the advent of anthelmintic resistance becoming an issue for sustainability of ruminant (especially small ruminants) production in the USA, genetics of resistance has attracted some limited interest that may provide a means of maintaining production and reducing reliance on anthelmintics. There is also a growing market for natural/organic products which restrict the use of drugs/chemicals. The impetus for pursuing the genetic approach for disease control is to eventually provide a means to identify resistant animals through genetic marker assisted selection (MAS). Unfortunately, that goal is still a ways off as resistance is most certainly controlled by a number of genes which makes finding the right combination difficult. Therefore, traditional breeding to select for resistant animals or identifying and maintaining resistant breeds are the only means currently available.

The MAS approach for cattle has been investigated using an Angus population that was managed to select, within breed, for low, high and intermediate infection lines (Gasbarre *et al.*, 1995; Sonstegard and Gasbarre, 2001; Araujo *et al.*, 2009). The nematodes of primary concern were *Ostertagia ostertagi* and *Cooperia* spp. To date, using various approaches (microsatellites, SNPs and microarrays), results have not been rewarding, but the search continues. Resistance between breeds was investigated in one study, where Brangus (*Bos indicus*) cows, calves and heifers were more resistant than Angus (*Bos taurus*) cows, calves and heifers to infection, where the predominant nematodes were *Haemonchus* and *Cooperia* (Pena *et al.*, 2000).

Small ruminant investigations have received more attention. Early work was directed at identifying resistant breeds and defining the host mechanism for resistance with the primary aim of building on the academic knowledge of nematode biology and host interaction. When it became apparent that anthelmintic resistance was an ongoing issue that threatened productivity, the potential role of these resistant breeds in providing an alternative that would reduce reliance on chemical intervention became important. The predominant nematode involved was *Haemonchus contortus*. The Florida Native (now considered part of the Gulf Coast Native complex) was the first breed to be characterized as being more resistant in comparison with the Rambouillet breed (Radhakrishnan *et al.*, 1972; Bradley *et al.*, 1973). Subsequently, Courtney *et al.* (1985) showed that Florida Native ewes were more resistant than exotic (St. Croix and Barbados Blackbelly), domestic (Finn-Dorset x Rambouillet) and exotic x domestic ewes. Two other comparisons showed that the St. Croix was more resistant than Dorset/Rambouillet (Zajac *et al.*, 1988) and the Louisiana Native (another part of the Gulf Coast Native complex) was more resistant than Suffolk (Bahirathan *et al.*, 1996; Miller *et al.*, 1998). A multi breed comparison showed that St. Croix, Gulf Coast Native, Katahdin and Suffolk were most resistant to most susceptible, respectively (Miller and Fernandez, 2005). Some consider the Katahdin sheep to be the most resistant breed, but as lambs they are relatively susceptible, and only after they mature they become more resistant. Hair breeds have also been considered more resistant than wool breeds. Most recently, relative resistance of mature Dorper crossbred ewes was similar to that of Katahdin and St. Croix ewes but superior to that of Hampshire ewes (Burke and Miller, 2002). Parasite resistance among Dorper, St. Croix and Katahdin lambs was similar when the nematode infection was relatively low, and as the nematode challenge escalated, resistance was greatest in St. Croix lambs, followed by Katahdin and Dorper lambs (Burke and Miller, 2004). The Navajo Churro breed has a similar history of introduction to the US as the Gulf Coast Native and is considered to be relatively resistant to diseases (<http://www.navajo-churrosheep.com/sheep-character.html>), but no documentation is available. There have been no reports of goat breeds in the US that are resistant to infection, but anecdotic evidence suggests that the Kiko and Saanan breeds

may be relatively resistant to some diseases.

Of the resistant breeds mentioned above, the American Livestock Breeds Conservancy lists the Navajo Churro and St. Croix as threatened (estimated global population less than 5000) and the Gulf Coast Native as critical (estimated global population less than 2000). In addition, the National Center for Genetic Resources Preservation maintains in their animal collection genetic material from 38 and 12 sheep and goat breeds, respectively, including all those that are resistant. The mission of these two organizations is to provide information and resources in the effort to promote preservation and conservation of valuable animal genetic material.

Host response to infection is an integral part of the genetic basis for resistance. A better understanding of how the host is able to either prevent or eliminate infection is important to direct investigations into how genetics can be used to manipulate the host/parasite interaction and/or assist in the search for genetic markers. Evidence that resistance has a major immunological component has been demonstrated by numerous laboratories, and in the USA it was shown by dexamethasone suppression (Pena *et al.*, 2004) and CD4 T lymphocyte depletion (Pena *et al.*, 2006) in Gulf Coast Native sheep. Almost all within and between breed resistant/susceptible investigations have shown that resistance has consistently been associated with increased blood and gut mucosal tissue, eosinophils and gut tissue, globule leukocytes and mast cells. In the USA, this was found to be the case for St. Croix compared to Dorset (Gamble and Zajac, 1992) and Gulf Coast Native compared to Suffolk (Shakya *et al.*, 2009). Following this line, the immunological response has been described as a Th2 type response with increased IL-5 cytokine expression and IgE specific antibody production (Shakya *et al.*, 2009).

In pursuit of the MAS approach to improve the genetics of sheep for resistance, the only programme actively producing reference families is at Louisiana State University. Since 1998 five F2 reference families (Gulf Coast Native x Suffolk) have been produced which include 450 lambs that have been phenotyped (FEC and PCV) after weaning and summer pasture challenge. Each year, resistance / susceptibility has segregated nicely (Miller *et al.*, 2006). A whole genome scan has been ongoing at Utah State University, using microsatellites and SNPs for genotyping. QTL have been found on a number of chromosome regions (unpublished observations). Also, in support of the HapMap project of International Sheep Genome Consortium, DNA from 96 Gulf Coast Native sheep were provided from several sources (gene pools) across the Gulf Coast of the south east USA.

With MAS a ways off yet, some progressive producers in the USA have started selecting more resistance individuals within their flock/herd. Some have been using FECs and PCVs, but many have found the FAMACHA system to be useful. FAMACHA is an indirect method to estimate the level of anaemia which has been a great tool for monitoring *H. contortus* infection (Kaplan *et al.*, 2004). By retaining animals that maintain low FAMACHA scores and culling those with high scores (Burke and Miller, 2008), use of anthelmintics has decreased and producers have reported fewer issues with parasites (specifically *H. contortus*). Because FEC is highly heritable, an ongoing investigation (Virginia Tech University) is developing a fecal egg count measure of expected progeny differences (FEC - EPD) in Katahdin sheep which is supported by the National Sheep Improvement Programme (NSIP).

There has been little interest in using resistant breeds in production systems, except for the Katahdin breed. Katahdin is an improved breed of hair sheep, the first hair breed to meet North American industry standards for carcass quality. Katahdin sheep are hardy, adaptable, low maintenance sheep that have demonstrated some resistance to nematodes, especially mature animals.

References

- Araujo, R.N., Padilha, T., Zarlenga, D., Sonstegard, T., Connor, E.E., Van Tassel, C., Lima, W.S., Nascimento, E. and Gasbarre, L.C.** 2009. Use of a candidate gene array to delineate gene expression patterns in cattle selected for resistance or susceptibility to intestinal nematodes. *Veterinary Parasitology* 162: 106-15.
- Bahirathan, M., Miller, J.E., Barras, S.R. and Kearney, M.T.** 1996. Susceptibility of Suffolk and Gulf Coast Native suckling lambs to naturally acquired strongylate nematode infection. *Veterinary Parasitology* 65: 259–268.
- Bradley, R.E., Radhakrishnan, C.V., Patil-Kulkarni, V.G. and Loggins, P.E.** 1973. Responses in Florida Native and Rambouillet lambs exposed to one and two oral doses of *Haemonchus contortus*. *American Journal of Veterinary Research* 34: 729–735.
- Burke J.M. and Miller, J.E.** 2002. Relative resistance of Dorper crossbred ewes to gastrointestinal nematode infection compared with St. Croix and Katahdin ewes in the southeastern United States. *Veterinary Parasitology* 109: 265-275.
- Burke, J.M. and Miller, J.E.** 2004. Resistance to gastrointestinal parasites in Dorper, Katahdin, and St. Croix lambs in the southeastern United States. *Small Ruminant Research* 54: 43-51.
- Burke, J.M. and Miller, J.E.** 2008. Use of the FAMACHA system to evaluate gastrointestinal nematode resistance in offspring of stud rams. *Veterinary Parasitology* 153: 185-192.
- Courtney, C.H., Parker, C.F., McClure, K.E. and Herd, R.P.** 1985. Resistance of non lambing exotic and domestic ewes to naturally acquired gastrointestinal nematodes. *International Journal of Parasitology* 15: 239–243.
- Gamble, H.R. and Zajac, A.M.** 1992. Resistance of St. Croix lambs to *Haemonchus contortus* in experimentally and naturally acquired infections. *Veterinary Parasitology* 41: 211-225.
- Gasbarre, L.C., Leighton, E.A. and Bryant, D.** 1995. Genetically controlled resistance to gastrointestinal nematode infections of cattle. In: *Proceedings of Beef Improvement Federation*, pp. 212–217.
- Kaplan, R.M., Burke, J.M., Terrill, T.H., Miller, J.E., Getz, W.R., Mobini, S, Valencia, E, Williams, M, Williamson, L.H., Larsen, M. and Vatta, A.F.** 2004. Validation of the FAMACHA8 eye color chart for detecting clinical anaemia on sheep and goat farms in the southern United States. *Veterinary Parasitology* 123: 105-120.
- Miller, J.E., Bahirathan, M., Lemarie, S.L., Hembry, F.G., Kearney, M.T. and Barras, S.R.** 1998. Epidemiology of gastrointestinal nematode parasitism in Suffolk and Gulf Coast Native susceptibility to *Haemonchus contortus* infection. *Veterinary Parasitology* 74: 55–74.
- Miller, J.E. and Fernandez, J.M.** 2005. Relative susceptibility of Suffolk, Gulf Coast Native, Katahdin and St. Croix lambs to naturally acquired gastrointestinal nematode infection. *Proc Hair Sheep Workshop, Virginia State University*, 24.
- Miller, J.E., Bishop, S.C., Cockett, N.E. and McGraw, R.A.** 2006. Segregation of natural and experimental gastrointestinal nematode infection in F2 progeny from susceptible Suffolk and resistant Gulf Coast Native sheep and its usefulness in assessing genetic variation. *Veterinary Parasitology* 140: 83-89.
- Pena, M.T., Miller, J.E., Wyatt, W. and Kearney, M.T.** 2000. Differences in susceptibility to gastrointestinal nematode infection between Angus and Brangus cattle in south Louisiana.

Veterinary Parasitology 89: 51-61.

Peña, M.T., Miller, J.E. and Horohov, D.W. 2006. Effect of CD4+ T lymphocytes depletion on resistance of Gulf Coast Native lambs to *Haemonchus contortus* infection. *Veterinary Parasitology* 138: 240-246.

Pena, M.T., Miller, J.E. and Horohov, D.W. 2004. Effect of dexamethasone treatment on the immune response of Gulf Coast Native lambs to *Haemonchus contortus* infection. *Veterinary Parasitology* 119: 223-235.

Radhakrishnan, C.V., Bradley, R.E. and Loggins, P.E. 1972. Host responses of worm free Florida Native and Rambouillet experimentally infected with *Haemonchus contortus*. *American Journal of Veterinary Research* 33: 817-823.

Shakya, K.P., Miller, J.E. and Horohov, D.W. 2009. A Th2 type of immune response is associated with increased resistance to *Haemonchus contortus* in naturally infected Gulf Coast Native lambs. *Veterinary Parasitology* 163: 57-66.

Sonstegard, T.S. and Gasbarre, L.C. 2001. Genomic tools to improve parasite resistance. *Veterinary Parasitology* 101: 387-403.

Zajac, A.M., Herd, R.P. and McClure, K.E. 1988. Trichostrongylid parasite populations in pregnant or lactating and unmated Florida Native and Dorset/Rambouillet ewes. *International Journal of Parasitology* 18: 981-985.

Actual standing and perspectives for the sustainable use and development of parasite resistant and tolerant breeds in Africa (J. M. Mugambi)

Introduction

Diseases of domestic animals cost farmers millions of dollars each year. The costs arise from the price of drugs, time taken to treat animals, professional fees, reduced productivity and sometimes mortality. A major problem is the emergence of resistant strains of pathogens. Parasite resistance is a consequence of the intensive use of antiparasitic drugs (trypanocidals, anthelmintics, acaricides, insecticides), and there is substantial evidence that when a parasite has developed resistance to one drug, it will usually also be resistant to other products from the same chemical group (Sangster, 2001). Where strains of parasites resistant to more than one drug exist, the options for treatment are seriously restricted. In Africa, resistance to trypanocidal drugs, acaricides and anthelmintics pose a formidable challenge to livestock production.

Options for controlling parasites where drug resistance has set in and also forestall environmental pollution from the chemical anti-parasiticides are being explored by researchers in many parts of the world. One such option is the use of resistant breeds. This paper highlights the evidence for resistance/resilience of some parasitic diseases in Africa, the prospects for exploiting that resistance and the anticipated challenges.

Important Parasitic diseases in Africa

The most important parasitic diseases of livestock in Africa include Bovine theileriosis, heartwater, anaplasmosis, babesiosis, trypanosomosis and helminthosis. Ticks transmit diseases to domestic animals but they are themselves parasites. Apart from transmitting diseases, the ticks cause irritation, lesions and lower the quality of hides and skins.

Natural immunity/resistance

Theileriosis

Indigenous cattle that have lived in endemic areas for a long time are more resistant than exotic animals. There is anecdotal evidence that the Ankole longhorn and Tarime cattle breeds suffer a less severe disease and have lower mortality than European Taurine (*Bos taurus*) cattle breeds.

Trypanosomosis

Using animals that had never been previously exposed to trypanosomes, it was confirmed that N'Dama were significantly more resistant than Zebu to experimental challenge with wild-caught infected tsetse (Stephen, 1966; Roberts and Gray, 1973), natural field exposure (Toure *et al.*, 1978; Murray *et al.*, 1981), and to trypanosomes inoculated by syringe (Murray *et al.*, 1979; Saror *et al.*, 1987). The resistance of the West African Shorthorn appeared to be intermediate between N'Dama and Zebu (Roberts and Gray, 1973). Several other breeds were reported by ILCA (International Livestock Centre for Africa) to have some degree of trypanotolerance (Table 1), a trait that allows breeds of domestic animals to survive and produce in tsetse-infested areas without the aid of trypanocidal drugs (Trail J.C.M and d'Ieteren G.D.M., <http://www.fao.org/documents>).

Further evidence that trypanotolerance has a genetic basis and is not due only to resistance acquired to local trypanosome populations was adduced from the successful establishment of cattle from West Africa in distant tsetse-infested areas of West and Central Africa: for

example, the introduction of Lagune in 1904 and N'Dama in 1920 into Zaire and of N'Dama into the Central African Republic, Gabon, and Congo (ILCA, 1979). Resistance to trypanosomosis has also been reported in other local cattle. A few reports exist which describe differences in resistance to trypanosomosis in certain *B. indicus* types: for example, in Zebu in Upper Volta following needle challenge (CRTA, 1981); in Zebu from Western Kenya following both field and experimental challenge (Cunningham, 1966) and Orma Boran in South-eastern Kenya exposed to continuous tsetse challenge (Njogu et al., 1985). However, as the animals in these studies had all been previously exposed to trypanosomiasis, it was not possible to assess the relative contribution of innate and acquired resistance to their susceptibility status. More recently, molecular techniques using mice and cattle have identified genomic regions that control trypanotolerance in animals. The findings give hope of producing 'synthetic' breeds of animals with high trypanotolerance (Hanotte et al., 2003; Abenga and Vuza, 2005).

There is also evidence that trypanotolerant breeds of cattle may be resistant to several other important infectious diseases. Thus, N'Dama and West African Shorthorn are very resistant to streptothricosis (Stewart, 1937; Coleman, 1937). The N'Dama has also been reported to be more resistant to tick-borne diseases, including heartwater, anaplasmosis, and babesiosis compared to other cattle breeds (Epstein, 1971).

Table 1. Classification of trypanotolerant cattle (ILCA, 1979).

Group	Breed
N'Dama	N'Dama
West African Shorthorn (Muturu)	
Dwarf West African Shorthorn	Lagune/Dahomey, Forest Muturu, Liberian Dwarf
Savanna West African Shorthorn	Baoule, Ghana Shorthorn, Somba, Savanna Muturu, Doayo, Bakozi, Kapsiki
Zebu × Trypanotolerant	

Evidence in sheep and goats for genetic resistance to trypanosomosis

In West Africa, it is generally accepted that the indigenous Djallonke sheep and the Dwarf West African goats are trypanotolerant, and experimental evidence attests to this in sheep (Toure et al., 1981). However, there are reports demonstrating that Dwarf goats can be highly susceptible to experimental infection (Murray *et al.*, 1982). Trypanotolerance in small ruminants is less pronounced than in cattle and should be considered as resilience rather than resistance (Geerts *et al.*, 2009). West African Dwarf (WAD) goats seem to be less trypanotolerant than Djallonke sheep. Recent studies have shown that there is an important introgression of genes of trypanosusceptible breeds into WAD goat populations, which possibly explains the loss of trypanotolerance in these animals. Similarly, there is evidence that indigenous breeds of sheep and goats in East Africa are more resistant to trypanosomosis than exotic breeds (Murray *et al.*, 1982). This has been confirmed experimentally in the case of Red Maasai sheep and the small east African goats in Kenya (Griffin and Allonby, 1979).

Evidence in sheep and goats for genetic resistance to helminthosis

Gastrointestinal (GI) nematodes constitute a formidable disease constraint especially in sheep and goats. Most of the economic losses caused by internal parasites are not due to mortality but insidious production loss (Waller, 2004). Other losses arise from anthelmintic drug costs and the time taken to administer them.

Genetic variation in resistance or tolerance to GI nematodes in goats (Preston and Allonby, 1978; Shavulimo *et al.*, 1988; Baker *et al.*, 2001) and sheep (Preston and Allonby, 1979;

Baker *et al.*, 1999; Mugambi *et al.*, 1997; 2005a) in Africa has been documented. Under natural pasture challenge, there was no difference in resistance to endoparasites between the indigenous Menz and Horro sheep evaluated in the highlands of Ethiopia (Tembely *et al.*, 1998; Rege *et al.*, 2002). However, under artificial challenge, there was some evidence that the Menz may be somewhat more resistant than Horro lambs (Haile *et al.*, 2002). The reverse was found with Red Maasai *versus* the Dorper, where the Red Maasai was superior under natural but not under artificial challenge (Mugambi *et al.*, 2005a,b).

A genome-wide scan for QTL affecting gastrointestinal parasite resistance (predominantly *Haemonchus contortus*) has been undertaken in Kenya using a double backcross resource family derived from Red Maasai and Dorper sheep (Mugambi *et al.*, 2005a, Silva *et al.*, 2010). Highly significant QTL were identified on four chromosomes (3, 6, 14, and 22) for FEC, PCV at the end of the pasture challenge period and for decline in PCV during challenge. The most significant QTL for parasite resistance and immune response were co-located at the same position on chromosome 22, suggesting a single causative mutation may be associated with these three traits.

In many areas of the tropics and temperate regions of the world, liver fluke infections (*Fasciola hepatica* and *Fasciola gigantica*) are also an important constraint to sheep and goat production. While it is well documented that sheep can mount an effective immune response (self-cure) to nematodes, it has been demonstrated that sheep are unable to acquire resistance to liver flukes (e.g. Haroun and Hillyer, 1986; Boyce *et al.*, 1987). It is perhaps for this reason that little research has been undertaken on genetic resistance to liver fluke infections.

Ticks

The relative resistance to tick infestation of zebu (*Bos indicus*) was compared to zebu-taurine crossbreeds. Pure zebu cattle were less infested than the crosses under identical field conditions in Tanzania (Wambura *et al.*, 1998). In Ethiopia, the local Arssi breed showed the highest tick resistance, followed by the Boran, whereas the Boran-Friesian cross was the least resistant. The Arssi was resistant to several tick species (Solomon and Kaaya, 1996).

Productivity of resistant animals

Trypanotolerant livestock

It was widely believed that because of their smaller size (no more than 250 kg mature weight for the N'Dama - ILCA, 1979), trypanotolerant breeds were less productive than more susceptible ones. However, productivity indices of trypanotolerant breeds maintained under low levels of nutrition in endemic areas were often compared with data collected from a variety of breeds of cattle kept under good conditions.

In a major survey of the status of trypanotolerant livestock in 18 countries in West and Central Africa, indices of productivity were examined using all the basic production data that could be found for each region, each management system, and for different levels of tsetse challenge (ILCA, 1979). Cattle herds were evaluated for reproductive performance, cow and calf viability, milk production, growth, and cow body weight. These parameters were used to compute the index of the total weight of calf and live weight equivalent of milk produced per 100 kg of cow maintained per year. This final index related these production traits back to the actual weight of breeding cow that had to be supported, this being closely connected with maintenance costs. The traits and production indices were derived for two basic management systems, village and ranch or station, and for four levels of tsetse challenge, arbitrarily designated zero, low, medium, and high. Estimates of productivity for Zebu herds under

ranch/station conditions in low or tsetse-free areas averaged 38.6 kg per 100 kg of cow maintained per year. This compared with 37.1 kg for trypanotolerant herds in ranch/station conditions in low tsetse challenge areas. Thus the productivity of Zebu was only four per cent higher than that of the N'Dama and West African Shorthorn, strongly indicating that the productivity of trypanotolerant cattle relative to other indigenous types was much higher than previously assumed. Directly comparable data between breeds were not available in many areas because the level of tsetse-trypanosomosis risk was such that breeds other than trypanotolerant ones could not survive.

Helminth resistant livestock

Some studies on productive indices have shown that indigenous animals can actually be more productive than the bigger, faster growing but more susceptible breeds (Baker et al., 2003 and 2004). Another important finding is the breed by environment interaction that can influence productivity. This implies that productivity of breeds may also differ from place to place in the presence of challenge. The larger breeds are often exotic imported breeds that are poorly adapted to tropical conditions. The productivity and efficiency of Red Maasai and Dorper sheep, evaluated in experiments at the Kenyan coast (humid environment) and the Kenya highlands (semi-arid environment), were compared by Baker *et al.* (2004). There were important breed by location interactions for growth, mortality and reproduction rates. When all these parameters were combined, it was found that the indigenous Red Maasai sheep were three to five folds more productive and efficient than Dorper sheep in the humid coastal environment. In the semi-arid environment, Dorper sheep were slightly more productive than the Red Maasai, but there was no significant difference in flock efficiency between the breeds. In this study, efficiency was measured as kg of total meat offtake per megajoule of metabolisable energy per day, which ignores any differences between the breeds in input costs (e.g. health care costs will be lower in a Red Maasai flock than a Dorper flock) or socio-economic benefits. The reason for this interaction was that the Dorper sheep were very poorly adapted to hot humid conditions, which was reflected in their low growth, low reproductive and high mortality rates. From this study, the breed of choice in a hot humid environment is the Red Maasai, while in an arid or semi-arid environment there is little to choose between the two breeds.

The future

In many production systems, the indigenous local breeds have more to offer than is often appreciated, and there is an urgent need for more comprehensive evaluation of the net benefits that these breeds offer. Development of genetic improvement programmes in the tropics will only be successful when accompanied with a good understanding of the different farming systems and simultaneously addressing several constraints – e.g. quantity and quality of feeds, health control, management, cost and availability of credit, marketing infrastructure, tolerance to other stresses like heat and drought in an integrated improvement package.

Crossbreeding programmes with non-adapted imported breeds should be discouraged for low input smallholder systems, but crossbreeding among the local indigenous tropically adapted breeds or with imported tropically adapted breeds may be an option in some farming systems (Baker and Gray, 2004). The Dorper breed was introduced into Kenya in the 1960s and has increased in popularity in the semi-arid Kenyan highlands because of its size, growth potential and good fat marbling. It is very common with the Maasai herdsmen to cross Dorper with their Red Maasai sheep. This is a situation where some judicious crossbreeding may be justified, as long as the crosses include at least 50% Red Maasai to maintain some degree of endoparasite resistance (Baker *et al.*, 2003; Nguti *et al.*, 2003).

There are particular issues that require special consideration in breeding for disease resistance/resilience:

1. Genetic diversity within the breeds.
2. Purity of the indigenous breeds. A lot of small-scale farmers carry out cross-breeding without any order. In fact, introgression of genes from trypanosusceptible breeds into WAD goat populations are thought to be the reason why these animals are losing trypanotolerance. Measures to safeguard and upgrade the genetic purity of trypanotolerant goat and sheep breeds in Africa are necessary (Geerts *et al.*, 2009).
3. Whether breeding is for resilience or for resistance. Breeding for resilience applies less selective pressure on the parasite than breeding for resistance; with resilience the host co-exists with the parasite (Woolaston and Baker, 1996).
4. Severity of pathogen challenge.
5. Concurrent infections, inadequate nutrition and other stresses that may affect the trait. For instance, while Djallonke sheep were able to withstand a single infection with *Trypanosoma congolense*, concurrent infection with *Haemonchus contortus* resulted in some animals losing capacity to control both infections (Goossens *et al.*, 1997).

A detailed account on how to go about breeding for resistance/tolerance has been given by Baker and Gray (2004). Structured breeding programmes run by Government, research institutions or commercial enterprises are necessary. Regional programmes for breeding of resistant/resilient livestock should be initiated alongside the establishment of animal gene banks.

In the case of worms, a minority of animals in a flock usually harbour the majority of the worms. By identifying such animals and removing them from the rest of the flock, less contamination of pastures will occur and the remaining animals will be healthier. For haemonchosis, which is the most important nematode of sheep and goats in the tropics, the FAMACHA® can be conveniently used to pick out such animals.

Although expensive at the moment and out of the reach of many farmers, embryo transfer offers a good opportunity to multiply rapidly animals that have favorable traits, and also to preserve embryos with such desirable traits.

References

- Abenga, J.N. and Vunza, D.** 2005. About factors that determine trypanotolerance and prospects for increasing resistance against trypanosomosis. *African Journal of Biotechnology* 4: 1563-1567.
- Baker, R.L. and Gray, G.D.** 2004. Appropriate breeds and breeding schemes for sheep and goats in the tropics: the importance of characterizing and utilizing disease resistance and adaptation to tropical stresses. In – “Worm Control for Small Ruminants in Tropical Asia”. (Sani, R, Gray, G.D., Baker, R.L., Eds.), Australian Centre for International Agricultural Research (ACIAR) Monograph No. 113 p 63-95.
- Baker, R.L., Audho, J.O., Aduda, E.O. and Thorpe, W.** 2001. Genetic resistance to gastrointestinal nematode parasites in Galla and Small East African goats in the sub-humid tropics. *Animal. Science* 73: 61-70.
- Baker, R.L., Mugambi, J.M., Audho, J.O., Carles, A.B. and Thorpe, W.** 2004. Genotype by environment interactions for productivity and resistance to gastrointestinal nematode parasites in Red Maasai and Dorper sheep *Animal Science* 79: 343-353.
- Baker, R.L., Mwamachi, D.M., Audho, J.O., Aduda, E.O. and Thorpe, W.** 1999. Genetic resistance to gastrointestinal nematode parasites in Red Maasai, Dorper and Maasai x Dorper ewes in the sub-humid tropics. *Animal Science* 69: 335-344.

- Baker, R.L., Rodriguez-Zas, S.L., Southey, B.R., Audho, J.O., Aduda, E.O. and Thorpe, W.** 2003. Resistance and resilience to gastrointestinal nematode parasites and relationships with productivity of Red Maasai, Dorper and Red Maasai x Dorper crossbred lambs in the sub-humid tropics. *Animal Science* 76: 119-136.
- Centre de Recherches sur les Trypanosomes Animales.** 1981. In 'Immunology of Trypanosomiasis'. Annual Report, 1981. Bobo Dioulasso, Upper Volta. 1981.
- Cunningham, M. P. E.** 1966. Immunity in bovine trypanosomiasis. *African. Medical. Journal* 43: 394-397
- Dolan, R.B.** 1998. The Orma Boran: A trypanotolerant East African breed. Fifteen years of research on Galana Ranch in Kenya. Kenya Trypanosomiasis Research Institute, Kikuyu. 88p
- Epstein, H. (1971) 'The origin of the domestic animals of Africa'. Volumes 1 and 2. *Africana*, New York. 1292p
- FAO/WHO/OIE animal Health Year book.** 1981. FAO Animal Production and Health Series No. 18, FAO Rome, 1982
- Geerts, S., Osaer, S., Goossens, B. and Faye, D.** 2009. Trypanotolerance in small ruminants of sub-Saharan Africa. *Trends in Parasitology* 25: 132-138.
- Goossens, B.** 1997. The interaction of trypanosoma congolense and Haemonchus contortus in Djallonke sheep. *International Journal of Parasitology* 27: 1579-1584.
- Griffin, L. and Allonby, E.W.** 1979. Trypanotolerance in breeds of sheep and goats with an experimental infection of Trypanosoma congolense. *Veterinary Parasitology* 5: 97-105.
- Hanotte, O., Ronin, Y., Agaba, M., Nilsson, P., Gelhaus, A., Horstmann, R., Sugimoto, Y., Kemp, S., Gibson, J., Korol, A., Soller, M. and Teale, A.** 2003. Mapping of quantitative trait loci controlling trypanotolerance in a cross of tolerant West African N'Dama and susceptible East African Boran cattle. *Proceedings of the National Academy of Sciences of the United States of America* 100: 7443-7448.
- Haile, A., Tembely, S., Anindo, D.O., Mukasa-Mugerwa, E., Rege, J.E.O., Yami, A. and Baker, R.L.** 2002. Effects of breed and dietary protein supplementation on the responses to gastrointestinal nematode infections in Ethiopian sheep. *Small Ruminant Research* 44: 247-261.
- International Livestock Centre for Africa – ILCA.** 1979. 'Trypanotolerant Livestock in West and Central Africa'. Monograph 2. ILCA, Addis Ababa, Ethiopia.
- Katunguka-Rwakishaya, E.** 1997. Susceptibility of three breeds of Ugandan goats to experimental infection with trypanosoma congolense. *Tropical Animal Health and Production* 29: 7-14.
- Mugambi, J.M., Audho, J.O. and Baker, R.L.** 2005a. Evaluation of the phenotypic performance of a Red Maasai and Dorper double backcross resource population: Natural pasture challenge with gastrointestinal nematode parasites. *Small Ruminant Research* 56: 239-251.
- Mugambi, J.M., Audho, J.O., Njomo, S. and Baker, R.L.** 2005b. Evaluation of the phenotypic performance of a Red Maasai and Dorper double backcross resource population: indoor trickle challenge with Haemonchus contortus. *Veterinary Parasitology* 127: 263-275.
- Mugambi, J.M., Bain, R.K., Wanyangu, S.W., Ihiga, M.A., Duncan, J.L., Murray, M. and Stear, M.J.** 1997. Resistance of four sheep breeds to natural and subsequent artificial Haemonchus contortus infection. *Veterinary Parasitology* 69: 265-273.

- Murray, M., Morrison, W.I., and Whitelaw, D.D.** 1982. Host susceptibility to African trypanosomiasis: trypanotolerance. *Advances in Parasitology* 21: 1-68.
- Murray, M., Trail, J.C.M., and J. G. Grootenhuys, J.G.** 1984. Trypanotolerant livestock: Potential and future exploitation. *Outlook on Agriculture* 13: (1)
- Nguti, R., Janssen, P., Rowlands, G. J., Audho, J.O., and Baker, R.L.** 2003. Survival of Red Maasai, Dorper and crossbred lambs in the sub-humid tropics. *Animal Science* 76: 3-17.
- Njogu, A. R., Dolan, R.B., Wilson, A.J. and Sayer, P.D.** 1985. Trypanotolerance in east African Orma Boran cattle. *Veterinary Record* 117: 632-636.
- Preston, J.M. and Allonby, E.W.** 1978. The influence of breed on the susceptibility of sheep and goats to a single experimental infection with *Haemonchus contortus*. *Veterinary Record* 103: 509-512.
- Preston, J.M. and Allonby, E.W.** 1979. The influence of breed on the susceptibility of sheep to *Haemonchus contortus* infection in Kenya. *Research in Veterinary Science* 26: 134-139.
- Rege, J.E.O, Tembely, S., Mukasa-Mugerwa, E., Sovani, S., Anindo, D., Lahlou-Kassi, A., Nagda, S. and Baker R.L.** 2002. Effect of breed and season on production and response to infections with gastrointestinal nematode parasites in sheep in the highlands of Ethiopia. *Livestock Production Science* 78: 159-174.
- Roberts, C. J. and Gray, A. R.** 1973. Studies on trypanosome-resistant cattle. 2. The effect of trypanosomiasis on N'Dama, Muturu and Zebu cattle. *Tropical Animal Health and Production* 5: 220-223.
- Sangster, N. G.** 2001. Managing parasiticide resistance. *Veterinary Parasitology* 98: 89-109. Shavulimo, R.S., Rurangirwa, F., Ruvuna, F., James, A.D., Ellis, P.R. and McGuire, T. (1988). Genetic resistance to gastrointestinal nematodes, with special reference to *Haemonchus contortus*, in three breeds of goats in Kenya. *Bulletin of Animal Health and Production in Africa* 36: 233-241.
- Silva, M.V.B, Sonstegard, T.S., Hanotte, O., Mugambi, J.M., Iraqi, F., Garcia, J.F., Boettcher, P., S. Nagda, S., Gibson, J., McClintock, S., Kemp, S., M. Malek, M., C.P. Van Tassell, C.P. and Baker, R.L.** 2010. Detection of gastrointestinal parasite tolerance QTL derived from Red Masai sheep. *Mammalian Genome* (submitted).
- Solomon, G. and Kaaya, G.P.** 1986. Comparison of resistance in three breeds of cattle against African ixodid ticks. *Experimental and Applied Acarology* 20: 223-230.
- Stephen, L. F.** 1966. Observations on the resistance of West African N'Dama and Zebu cattle to trypanosomiasis following challenge by wild *Glossina morsitans* from an early age. *Annals of Tropical Medicine and Parasitology* 60: 230-246.
- Stewart, J. L.** 1937. The cattle of the Gold Coast. *Veterinary Record* 49: 1289-1297.
- Tembely, S., Lahlou-Kassi, A., Rege, J.E.O., Mukasa-Mugerwa, E., Anindo, A., Sovani, S. and Baker, R.L.** 1998. Breed and season effects on the peri-parturient rise in nematode egg output in indigenous ewes in a cool tropical environment. *Veterinary Parasitology* 77: 23-32.
- Toure, S. M., Seye, M., Diege, T. and Mbengue, M.** 1981. International Scientific Council for Trypanosomiasis Research and Control (ISCTRC) 17th meeting, Arusha, Tanzania. (cited by Murray, M., Trail, J.C.M. and Grootenhuys, J.G. 1984. Trypanotolerant Livestock: potential and future exploitation. *Outlook on Agriculture* 13: 43-51.)
- Waller, P.J.** 2004. Management and control of nematode parasites of small ruminants in the face of total anthelmintic failure. *Tropical Biomedicine* 21: 7-13.

Wambura, P.N., Gwakisa, P.S., Silayo, R.S. and Rugaimukamu, E.A. 1998. Breed associated resistance to tick infestation in *Bos indicus* and their crosses with *Bos Taurus*. *Veterinary Parasitology* 77: 63-70

Waweru, J.G., Kanyari, P.W.N., Mwangi, D.M., Ngatia, T.A. and Nansen, P. 1999. Comparative parasitological and haematological changes in two breeds of sheep infected with *Fasciola gigantica*. *Tropical Animal Health and Production* 31: 363-372.

Woolaston, R.R and Baker, R.L. 1996. Prospects of breeding small ruminants for resistance to internal parasites. *International Journal for Parasitology* 26: 845-855.

Actual standing and perspectives for the sustainable use and development of parasite resistant or tolerant breeds in Brazil (A.F.T. Amarante)

Introduction

Different environments are found in South America, which range from the Tropical Rain Forest in the North of the Continent, covering large areas of Brazil, Venezuela, Colombia and Peru to grasslands in the South; desert areas, like Patagonia in South Argentina; and semi-desert areas in Northeast Brazil. Savanna covers large areas of Central Brazil and Grassland is typical of Argentina, Uruguay and South Brazil.

Portuguese and Spanish settlers started to arrive in South America a little more than 500 years ago. The livestock introduced by them were submitted to a long process of natural selection in those different environmental conditions, giving origin to several breeds that are known as “crioulo”, “native” or naturalized breeds. The environment had a huge impact on the process of natural selection. For instance, in the South where low temperatures are common in the winter, sheep produce wool, e.g. the Crioula Lanada sheep, while in the Northeast Region of Brazil where the minimum temperatures are usually higher than 20 °C, the Morada Nova hair sheep is found.

Commercial breeds have begun to be imported in the last two centuries and they gradually replaced the native breeds to such an extent that the latter are in danger of extinction. To avoid further loss of this important genetic material, in 1983, the National Research Center for Genetic Resources and Biotechnology (Cenargen) of the Brazilian Agricultural Research Corporation (Embrapa) decided to include conservation of animal genetic resources among its priorities. The conservation activities have been conducted under the Brazilian Genetic Resources Network (Renargen), and are carried out by various research centres of Embrapa, Universities and State Research Institutions, as well as by private farmers. The *in situ* conservation of cattle, horses, buffaloes, donkeys, goats, sheep and pigs is being carried out by conservation nuclei, located in the animal's original habitat. *Ex situ* conservation is centred at the Brazilian Animal GermplasmBank (AGB), kept at Cenargen. AGB is responsible for the storage of semen and embryos of various breeds of domestic animals threatened with extinction. Presently, the AGB has almost 60,000 doses of semen and more than 250 embryos as well as over 7000 DNA samples. An important challenge for this programme is to increase awareness within the different segments of society in terms of the importance of the conservation of animal genetic resources (reviewed by Mariante *et al.*, 2009).

Sheep

Studies on parasite resistance of naturalized breeds are relatively scarce. Two sheep breeds have been subject to evaluation: Crioulo Lanada sheep and Santa Inês hair sheep. Crioula lanada sheep (“lanada” means wool) are found in South Brazil. They have horns and produce coarse wool. With the high commercial value of the fine wool in the last Century, these animals almost became extinct, being replaced by breeds specialized in fine wool production, such as Corriedale and Merino. Studies carried out in Rio Grande do Sul State showed that the Crioula lambs are much more resistant to *H. contortus* natural infection than Corriedale animals (Bricarello *et al.*, 2004).

Morada Nova hair sheep are small animals that have been raised for a long period of time in the Northeast Region of Brazil. The crossbreeding of Morada Nova with Bergamacia sheep gave origin to Santa Inês breed. A mature Santa Inês ewe has an average live weight of 55 kg. Its reproduction is not seasonal, allowing lamb production at any time of the year. At present, the Santa Inês sheep is predominant in most of the Brazilian territory due to its higher level of resistance to gastrointestinal (GI) nematodes, when compared with some sheep breeds of

European origin (Amarante *et al.*, 2004; Rocha *et al.*, 2004; Bricarello *et al.*, 2005; Costa *et al.*, 2007). However, Santa Inês sheep have inferior productivity, when compared with other breeds selected for higher weight gain and carcass quality. Recent studies showed that the crossbreeding of Santa Inês ewes with Ile de France, Suffolk, Texel and Dorper sires, all breeds with a high potential for growth and meat production, results in crossbred animals with high productivity and a satisfactory degree of resistance to GI nematode infection (Amarante *et al.*, 2009).

Several studies have indicated that improvement in nutrition, especially in the metabolizable protein content of the diet, can influence the host response against nematode infections and reduce the pathophysiological changes associated with GI nematodes. The effect of protein supplementation in the diet on the development of resistance to worms was evident in Santa Inês lambs naturally or artificially infected with nematodes (Louvandini *et al.*, 2006; Bricarello *et al.*, 2005).

Cattle

Several naturalized breeds of cattle are found in the different regions of South America. However, they almost became extinct with the introduction of more productive breeds of cattle. In the Central and Northern areas of the continent, where the temperatures are high, Zebu cattle (*Bos taurus indicus*) imported from Asia flourished, while in regions with lower temperature, the European breeds (*Bos taurus taurus*) predominate. There are areas of overlap or crossbreeding between these two genetic groups.

Beef cattle of the Nelore breed were brought to Brazil from Asia in the 18th Century, and today they constitute the largest proportion of the 190 million cattle raised in Brazil. Part of the success of this breed can be accredited to its high resistance to ticks (*Rhipicephalus microplus*) and also to tick-borne blood parasites, *Babesia* spp. and *Anaplasma marginale*.

Despite the high degree of resistance to ectoparasites, significant economic losses are caused by GI nematodes in young Zebu cattle. The major species are *Haemonchus placei*, *Cooperia punctata* and *Oesophagostomum radiatum*. In a study with 100 young bulls, Bricarello *et al.* (2008) observed the typical negative binomial distribution of fecal egg counts (FEC): most animals showed low mean FEC, while a few bulls presented high mean FEC. In this study, the 10 most resistant animals and the 10 most susceptible animals were selected for worm burden determination and tissue samples of the small intestine were collected for gene expression analysis. Cytokine gene expression in the small-intestine tissue samples was different between groups. A classical T_H2-type response occurred in the small intestine of animals resistant to *Cooperia* spp. and a T_H1-type response in that of susceptible animals. Therefore, the acquired immunity, which is regulated genetically, is important in the resistance to GI nematodes and can be exploited in animal selection.

Even breeds that are well-adapted to the tropics include individuals that are susceptible to nematode infections, with high worm burdens resulting in increased pasture contamination and a higher degree of herd exposure to the parasites. Selecting GI parasite-resistant animals may be an efficacious alternative for the prophylaxis of GI nematode infections, minimizing the need for anthelmintic treatments and thus reducing the rate of development of anthelmintic resistance in the parasites.

The major problem about zebu cattle is the poor quality of their carcass, in comparison with commercial breeds of European origin. For this reason, efforts have been made in order to select more productive Zebu animals. Another option is the development of a composite breed by crossbreeding susceptible and resistant animals, such as the case of Canchim cattle formed by crossbreeding Zebu with Charolais cattle.

A similar situation occurs with dairy cattle. In the South, Holstein is the predominant breed, whereas in Central and Northern Regions Gir cattle, imported from Asia, is commonly found. These animals are also resistant to tick infestation and blood parasites. As their milk production does not match that of Holstein cattle, a composite breed - Girolando - produced by crossbreeding Gir x Holstein is commonly used for milk production.

Studies are being carried out to search for Quantitative trait loci (QTL) for resistance to parasites in a population of 300 F2 animals produced by crossing Gir and Holstein cattle. Suggestive QTL for resistance to the *Rhipicephalus microplus* tick were found on chromosomes 5, 7 and 14 (Gasparin *et al.*, 2007).

The frequent use of drugs for the prophylaxis of parasitic diseases has led to the dissemination of populations of resistant parasites in South America. For this reason, farmers have successfully been using ruminant breeds that show genetic resistance to parasites in order to avoid economic losses. This is the case of Zebu cattle which are resistant to tick infestation and Santa Inês sheep which are resistant to GI nematodes.

References

Amarante, A.F.T., Bricarello, P.A., Rocha, R.A. and Gennari, S.M. 2004. Resistance of Santa Ines, Suffolk and Ile de France lambs to naturally acquired gastrointestinal nematode infections. *Veterinary Parasitology* 120: 91-106.

Amarante, A.F.T., Susin, I., Rocha, R.A., Silva, M.B., Mendes, C.Q. and Pires, A.V. 2009. Resistance of Santa Ines and crossbred ewes to naturally-acquired gastrointestinal nematode infections. *Veterinary Parasitology* 165:273-280.

Bricarello, P.A., Amarante, A.F.T., Rocha, R.A., Cabral Filho, S.L., Huntley, J.F., Houdijk, J.G.M., Abdalla, A.L. and Gennari, S.M. 2005. Influence of dietary protein supply on resistance to experimental infections with *Haemonchus contortus* in Ile de France and Santa Ines lambs. *Veterinary Parasitology* 134: 99-109.

Bricarello, P.A., Gennari, S.M., Oliveira-Sequeira, T.C.G., Vaz, C.M.S.L., Gonçalves de Gonçalves, I. and Echevarria, F.A.M. 2004. Worm burden and immunological responses in Corriedale and Crioula Lanada sheep following natural infection with *Haemonchus contortus*. *Small Ruminant Research* 51: 75-83.

Costa, R.L.D., Bueno, M.S., Veríssimo, C.J., Cunha, E.A., Santos, L.E., Oliveira, S.M., Spósito Filha, E. and Otsuk, I.P. 2007. Performance and nematode infection of ewe lambs on intensive rotational grazing with two different cultivars of *Panicum maximum*. *Tropical Animal Health and Production* 39: 255-263.

Gasparin, G., Miyata, M., Coutinho, L.L., Martinez, M.L., Teodoro, R.L., Furlong, J., Machado, M.A., Silva, M.V.G.B., Sonstegard, T.S. and Regitano, L.C.A. 2007. Mapping of quantitative trait loci controlling tick [*Rhipicephalus (Boophilus) microplus*] resistance on bovine chromosomes 5, 7 and 14. *Animal Genetics* 38: 453-459.

Louvandini, H.; Veloso, C.F.M.; Paludo, G.R., Dell'Porto, A., Gennari, S.M. and McManus, C.M. 2006. Influence of protein supplementation on the resistance and resilience on young hair sheep naturally infected with gastrointestinal nematodes during rainy and dry seasons. *Veterinary Parasitology* 137: 103-111.

Rocha, R.A., Amarante, A.F.T. and Bricarello, P.A. 2004. Influence of reproduction status on susceptibility of Santa Inês and Ile de France ewes to nematode parasitism. *Small Ruminant Research* 55: 65-75.

Actual standing and perspectives for the sustainable use and development of trypanosoma resistant or tolerant breeds (L. Dempfle)

Many people regard trypanosomosis as the biggest constraint to livestock production in sub-Saharan Africa. For a number of reasons, the disease is very difficult to cope with. However, in some situations, the importance of trypanosomosis might be over-rated. Trypanosomosis is a typical vector-borne disease, where the pathogen and the vector have some special characteristics which make the disease rather special (Table 1).

Table 1. Trypanosomosis - pathogens and vectors.

Pathogens	Vectors	Hosts
Trypanosoma congolense	Glossina species (Tsetse flies)	cattle, sheep, goats
Trypanosoma vivax	Tabanids, Stomoxys	wild life (many species)
Trypanosoma brucei brucei		Lab animals

The systematics of the pathogen is the following:

Protozoa - Flagellatae - Kinetoplastidae – Trypanosomatidae – Trypanosoma.

The pathogens for human sleeping sickness (*T. brucei gambiense*, *T. brucei rhodesiense*), for swine (*T. simiae*), camel (*T. evansi*) and horse (*T. equiperdum*) trypanosomosis are related pathogens. Trypanosomes are extra-cellular pathogens with the ability to change their surface coat. After infection, the host mounts a (mainly) humoral immune defence. Most trypanosomes die, but some are able to change their surface antigens and thus are immune to the mounted antibody response. New kinds of antibody of the host are produced and new antigens are expressed. It is estimated that the trypanosomes have more than a thousand different alleles for the surface antigens and, at any time, just one of them is expressed (cassette model). This property of the pathogens has, up to now, prevented the development of a vaccine. The trypanosomes cause anaemia in the host; they have an immune suppressive effect making the host more prone to tick-borne and other diseases. In non-tolerant hosts, the animals eventually die of extreme anaemia if not treated.

Vectors of the pathogens are haematophagous insects like Tabanids, Stomoxys and especially Glossina species. Whereas Tabanids and Stomoxys transmit the trypanosomes only mechanically by having blood meals at short intervals on two hosts, the relationship of Glossina species and trypanosomes are much more intimate. The amount of mechanical transmission of trypanosomes (mainly of *T. vivax*) in Africa is much debated, but it occurs and is a problem in South America (where there are no tsetse flies).

There are 22 different Glossina species (with about 30 subspecies) and they are classified into three groups depending on their ecological niche:

- Savannah species - Morsitans group (*G. morsitans morsitans*, *G. morsitans submorsitans*, etc.)
- Riverine species - Palpalis group (*G. palpalis palpalis*, *G. palpalis gambiensis*, etc.)
- Forest species - Fusca group (*G. fusca fusca*, *G. fusca congolensis*, etc.).

Whereas for human sleeping sickness the most important vectors are from the Palpalis group, for animal trypanosomosis the most important vectors are from the Morsitans group.

Tsetse flies live exclusively on blood and both sexes take blood meals. When the tsetse fly hatches it is free of trypanosomes. The reproduction of the tsetse fly is quite remarkable and it is sometimes said to be the mammal among the insects. The females mate only once in their lives. The development of the three larval stages takes place in the uterus of the female. At the

end of the third larval stage, the female looks for an appropriate place to drop the third instar larva which works out and immediately goes into the soil and turns into the pupal stage. After four to five weeks, the adults hatch, take their first blood meal within the first few days and the females mate. About 18 to 20 days after hatching, the first larva is 'born', and then, under good circumstances, every nine to ten days one larva is 'born'. That means that the reproductive potential of tsetse fly is quite low (no comparison with ticks or mosquitoes). The preferred host of the morsitans group is the warthog. When the tsetse fly gets infected by trypanosomes, they make a development cycle within the fly and after some time (10 to 20 days depending on the species) the fly is infectious and remains infective for her whole life.

The two main species *T. congolense* and *T. vivax* have many species as host, but there are also some differences. Whereas *T. congolense* can infect laboratory animals, *T. vivax* cannot. Among the livestock species cattle, sheep, goats, horses, camels, water buffalo and others can be infected.

There does not seem to be much difference between cattle breeds in the susceptibility to acquire trypanosome infections. Once an animal has been infected with trypanosomes, there is first a local chancre and after about nine days the trypanosomes can be found in the blood. Rapid multiplication by fission takes place and anaemia sets in so that the blood Packed Cell Volume (PCV) starts decreasing. If not treated, the PCV keeps decreasing until the animal dies. In trypanotolerant animals there is also anaemia but in most cases, after some weeks, the PCV downturn stops and the animal recovers.

To treat trypanosomosis there are a few drugs available; they are all several decades old. It is not very likely that new drugs will be developed and come on the market. In some areas, the resistance of the trypanosomes against the few drugs available is a serious problem.

The trypanotolerant breeds mostly originate in West Africa; they all belong to the *Bos taurus taurus* subspecies. However, the Orma Boran (*Bos taurus indicus*) cattle in Kenya appear to have some degree of trypanotolerance as mentioned by J. Mugambi in this proceedings. The most numerous and probably the most well characterised breed in West Africa is the N'Dama (longhorn), but there are also the shorthorn breeds; Baoule, Ghana Shorthorn, Somba, Muturu, Doayo, Kapsiki, Bakosi, Lagune and others. In addition, several breeds have originated from crosses between these breeds and zebu type breeds like Djakore, Mere, Borgou, Keteku and others. Little is known about the differences in the degree of trypanotolerance among the trypanotolerant breeds.

Trypanotolerance is, contrary to what some text books are still indicating, not specific to the trypanosomes of the origin of the cattle, but it is also effective against trypanosomes of completely different localities. However, it must be realised that also N'Dama can suffer from trypanosomosis, as was shown by Mattioli *et al.* (1998). In this study one year old naïve N'Dama, Gobra zebu and the cross of Gobra male x N'Dama female were involved (136 animals altogether) and were kept in a very high challenge area (Table 2).

Table 2. Survival rate of animals in regards to surveillance and genotype (modified from Mattioli *et al.*, 1998).

Survival rate (of more than one year):	N'Dama	F1	Gobra
High surveillance ¹⁾ :	1.00	0.92	0.54 (0.33-0.75)
Low surveillance ²⁾ :	0.85	0.30	0.07 (0.00-0.14)
Overall:	0.88	0.51	0.19

¹⁾ High surveillance: animal were checked twice a week for PCV and trypanosomes and treated if nexessary.

²⁾ Low surveillance: animal were checked monthly for PCV and trypanosomes and treated if necessary.

In this high challenge area, there are hardly any cattle during the rainy season (July – September), but at the end of the rainy season five to six thousand cattle move into the area at a time, when the density of tsetse flies is at its highest. The swampy area provides fodder which seems to be more important to the herd owners than avoiding the high risk of getting trypanosomosis due to the high tsetse density.

Another cautious lesson might also be learnt from Zanzibar. There, in 1997, the IAEA eradicated, using all means (including sterile insect technology) and at very high cost, the tsetse flies which was considered as a major constraint for livestock production. A couple of years later not very much change in livestock production was noticed.

In tsetse infested areas, the trypanotolerant breeds are a real asset for the low input livestock production system. However, in the long run, they will only be kept if they are economically competitive. Therefore, it might be much more appropriate to increase the productivity of the trypanotolerant breeds rather than trying to increase the trypanotolerance of the more productive trypanosusceptible breeds. The goal would be to increase milk and meat productivity **without losing** the adaptive properties of these breeds. The use of these breeds to improve high yielding breeds with respect to trypanotolerance by crossbreeding is theoretically a possibility and might have successfully been used by breeders, creating new breeds like Djakore, Mere, etc., but this will be a long term endeavour, even with modern methods, unlikely to be taken up by any entrepreneur.

References:

Mattioli, R.C., Jaitner, J., Clifford, D.J., Pandey, V.S. and Verhulst, A. 1998. Trypanosome infections and tick infestations: susceptibility in N'Dama, Gobra zebu and Gobra x N'Dama crossbred cattle exposed to natural challenge and maintained under high and low surveillance of trypanosome infections. *Acta Tropica* 71: 57-71.

Recommendations for ways to describe local breeds for disease resistance. What are the needs? (M. Tibbo and A. Haile)

Introduction

Parasitic diseases are very important constraints to livestock production worldwide (Klostermann et al., 1992; Tembely *et al.*, 1998; Charon, 2004). Control of gastrointestinal (GI) nematodes relies mainly on pharmaceuticals (anthelmintic drugs). This control method, however, has proved unsustainable due to resistance developed against the available drugs (van Wyk *et al.*, 1997; Jackson and Coop, 2000; Schnyder *et al.*, 2005; Papadopoulos, 2008). Other methods of parasite control include improved nutrition through protein supplementation to increase the rate of acquisition of immunity and resilience against GI nematodes (Coop and Kyriazakis, 1999; Kyriazakis and Houdijk, 2006), but its economic basis has been questioned (Coles, 2005). Dosing with nematophagous fungal spores to reduce pasture contamination has shown encouraging results, but animals have to receive an adequate daily dose of these (Larsen, 2000), which makes its use difficult. Increasing the frequency of resistant animals in the flock through breeding for resistance could be a sustainable solution (Woolaston and Baker, 1996; Baker and Gray 2004; Charon, 2004) as it offers fewer requirements for use of pharmaceuticals. It is commonly believed that these breeds are less productive than the susceptible breeds, but this is not always the case.

With a few exceptions (e.g. Red Maasai sheep of East Africa, Sabi sheep of Zimbabwe, Garole sheep of India), several local breeds (e.g. West African Djallonke sheep, the Alpine goats in France, Arsi sheep in Ethiopia) are mentioned as resistant¹ to parasites compared to exotic or other local breeds but without empirical evidence on their level of resistance. Most of these “resistant” or “resilient” breeds are owned by smallholders. They are raised and bred in traditional ways. Describing these animals for disease resistance requires organised ways of measuring the traits of importance, which is not easy in field conditions. This is partly because of lack of animal identification, animal recording, controlled breeding, and facilities to measure faecal worm egg counts, level of anaemia, and infection levels in cases of trypanosomes.

Technologies available to measure resistance or tolerance to parasites are faecal worm egg counts (FEC), packed cell volume (PCV) or FAMACHA score for blood-sucking parasites (e.g. *Haemonchus contortus* and trypanosomosis). The FAMACHA score is a system that allows anaemia to be scored by examining the animal’s eye conjunctiva using a colour score chart (VanWyk and Bath, 2002; Bath, 2006; Van Wyk *et al.*, 2006). The scale goes from 1 (mucous membranes are red – not anaemic) to 5 (mucous membranes are white – very anaemic). Riley and Wyk (2009) reported that heritability of FAMACHA score ranged from 0.06 ± 0.04 (low challenge) to 0.24 ± 0.05 (high challenge). The disadvantage of FAMACHA system, however, is that it does not work for animals infected with other non-blood sucking nematodes unless it is combined with FEC. Where internal parasites are prevalent, low FEC, low FAMACHA eye score or high PCV mean that an animal is resistant or resilient to the parasites.

Molecular techniques are also being used in developed countries. Individual phenotypes using FEC and PCV, and QTL detection by genome scanning using microsatellite markers have been published (e.g. Moreno *et al.*, 2006). Davies *et al.* (2006) reported QTL on sheep

¹ Some define resistance as the number of anthelmintic treatments needed over a given period of pasture challenge with nematode parasites. Albers et al. (1987) treated both FEC and PCV as two different measures of resistance to parasites. Resistant animals mount an immune response to reduce or eliminate the population of worms in their gut. Resilient animals do not appear to mount any significant response and appear not to show reductions in productivity. By comparison, “susceptible” animals show marked decreases in productivity.

chromosomes 2, 3, 14 and 20 for resistance to parasites that could be utilised in a marker-assisted selection scheme to increase host resistance to GI parasites. These techniques, however, are far from reach for the developing countries because of lack of capacity and infrastructure.

Observations by the authors show that evaluating animals under natural parasite challenge may not be sufficient to fully capture variation in relation to resistance to parasites. Artificial infection provides opportunities to monitor animals under strict parasite challenge minimising errors due to grazing behaviour of individuals. Individual variation in grazing behaviour of animals may affect the number of infective larvae picked while grazing as infective larvae are not distributed homogeneously on natural pasture. Moreno *et al.* (2006) who evaluated animals both on natural and artificial infection regimens in an attempt to detect QTL for resistance to *Haemonchus contortus* did mention differences in the two approaches.

Host resistance to GI nematodes (assessed by FEC) and resilience (assessed by PCV levels) are shown to be heritable (e.g. Woolaston and Piper, 1996; Baker *et al.*, 2003; Young, 2006). According to the literature, resistance to internal parasites is moderately heritable (about 30 %). Resistance incurs a small cost on metabolism, so resistant sheep may be slightly less productive. Combining production and resistance traits in a selection index allows the breeding of more resistant and more productive animals.

As local breeds are adapted to their home tract environments (feed, disease, water, climatic stresses, etc), it is important to focus on their genetic improvement through selection rather than introducing less adapted “exotic” breeds. However, information on disease resistance/tolerance from local breeds is scanty. Some breeds that are believed to have resistance to parasites are under threat (e.g. Sheko cattle of Ethiopia resistant to trypanosomes).

Genetic assessment of resistance/resilience requires a specific protocol to be followed for worm challenge and data collection.

Recommendations:

1. Identify (from literature and secondary information) animal breeds claimed to have some level of resistance to parasites.
2. Comparing breeds for the sake of comparing is futile exercise unless there is practical reason for them being able to fit into the target production system. Therefore, make a careful match of resistant/resilient breeds with the production system where they will be evaluated and used.
3. Prioritise animal breeds to be compared for resistance based on criteria such as uniqueness, level of threat, potential current and future use, etc.
4. Estimate cost and returns from evaluation of these breeds for resistance to parasites: i.e. the financial, infrastructural and human resources to do the evaluations.
5. Explore and document livestock keepers’ ways of identifying and describing disease resistance/tolerance.
6. Do not attempt to compare breeds or individuals within breed in areas (agro-ecology) where there is no parasite challenge.
7. In areas where trypanosomes are prevalent, ensure that facilities are available so that FEC, PCV or FAMACHA scores can be measured to estimate the level of parasitic load and anaemia.
8. Make use of facilities such as government or private ranches where good pedigree information is available to do genetic evaluations for resistance to parasites.

References

- Baker, R.L. and Gray, G.D.** 2004. Appropriate breeds and breeding schemes for sheep and goats in the tropics: the importance of characterizing and utilizing disease resistance and adaptation to tropical stresses. In: *Worm Control for Small Ruminants in Tropical Asia*. (Sani, R, Gray, G.D., Baker, R.L., Eds.), Australian Centre for International Agricultural Research (ACIAR) Monograph No. 113 p 63-95.
- Baker, R.L., Rodriguez-Zas, S.L., Southey, B.R., Audho, J.O., Aduda, E.O. and Thorpe, W.** 2003. Resistance and resilience to gastrointestinal nematode parasites and relationships with productivity of Red Maasai, Dorper and Red Maasai x Dorper crossbred lambs in the sub-humid tropics. *Animal Science* 76: 119-136.
- Bath, G.F.** 2006. Practical implementation of holistic internal parasite management in sheep. *Small Ruminant Research* 62: 13–18.
- Burke, J.M. and Miller, J.E.** 2008. Use of FAMACHA system to evaluate gastrointestinal nematode resistance/resilience in offspring of stud rams. *Veterinary Parasitology* 153: 85–92
- Charon, K.M.** 2004. Genes controlling resistance to gastrointestinal nematode in ruminants. Presented at the Conference “Gene polymorphisms affecting health and production traits in farm animals” held at the “ANIMBIOGEN” Centre of Excellence in Genomics and Biotechnology Improving Functional Traits in Farm Animals and Quality of their Products, 2-3 October 2003, Jastrzêbiec, Poland. *Animal Science Papers and Reports* 22(1), 135–139.
- Coles, G.C.** 2005. Anthelmintic resistance – looking to the future: a UK perspective. *Research in Veterinary Science* 78: 99-108.
- Coop, R.L. and Kyriazakis, I.** 1999. Nutrition–parasite interaction. *Veterinary Parasitology* 84: 187–204.
- Davies, G, Stear, M.J., Benothman, M., Abuagob, O., Kerr, A., Mitchell, S. and Bishop, S.C.** 2006. Quantitative trait loci associated with parasitic infection in Scottish blackface sheep. *Heredity* 96, 252–258.
- Haile A, Tibbo M., Duguma G., Mirkena T., Iñiguez, L., Mwai O., Wurzinger M and Sölkner J.** 2008. Community-based sheep breeding: a new approach to genetic improvement. Proceedings of the 16th annual meeting of the Ethiopian Society of Animal Production (ESAP), Addis Ababa, Ethiopia.
- Jackson, F. and Coop, R.L.** 2000. The development of anthelmintic resistance in sheep nematodes. *Parasitology* 120: 95–107.
- Kloosterman, A., Parmentier, H.K. and Ploeger, H.W.** 1992. Breeding cattle and sheep for resistance to gastrointestinal nematodes. *Parasitology Today* 8: 330–335.
- Kyriazakis, I. and Houdijk, J.** 2006. Immunonutrition: Nutritional control of parasites. *Small Ruminant Research* 62: 79-82.
- Larsen, M.** 2000. Prospects for controlling animal parasitic nematodes by predacious micro fungi. *Parasitology* 120: S121–S131.
- Moreno, C.R., Gruner, L., Scala, A., Mura, L., Schibler L., Amigues, Y., Sechi, T., Jacquiet, P., François, D., Sechi, S, Roig, A., Casu, Sara, Barillet, F., Brunel, J.C., Bouix, J., Carta, A. and Rupp, R.** 2006. QTL for resistance to internal parasites in two designs based on natural and experimental conditions of infection. 8th World congress on Genetics Applied to Livestock Production, August 13-18, 2006, Belo Horizonte, MG, Brazil.
- Papadopoulos, E.** 2008. Anthelmintic resistance in sheep nematodes. *Small Ruminant Research* 76: 99–103.

- Riley, D.G. and Van Wyk, J.A.** 2009. Genetic parameters for FAMACHA© score and related traits for host resistance/resilience and production at differing severities of worm challenge in a Merino flock in South Africa. *Veterinary Parasitology* 164:44-52.
- Schnyder, M., Torgerson, P.R., Schönmann, M., Kohler, L. and Hertzberg, H.** 2005. Multiple anthelmintic resistance in *Haemonchus contortus* isolated from South African Boer goats in Switzerland. *Veterinary Parasitology* 128: 285–290.
- Sölkner, J., Wurzinger, M. and Iñiguez, L.** 2008. The preliminary basis for community-based breeding plans. Small Ruminant Production Diversification and Genetic Diversity Workshop on Research Results. March 1-2, 2008, ICARDA, Aleppo, Syria
- Tembely, S., Lahlou-Kassi, A., Rege, J.E.O., Mukasa-Mugerwa, E., Anindo, D., Sovani, S. and Baker, R.L.** 1998. Breed and season effects on the peri-parturient rise in nematode egg output in indigenous ewes in a cool tropical environment. *Veterinary Parasitology* 77: 123–132.
- Van Wyk, J.A. and Bath, G.F.** 2002. The FAMACHA system for managing haemonchosis in sheep by clinically identifying individual animals for treatment. *Veterinary Research* 33: 509–529.
- Van Wyk, J.A., Hoste, H., Kaplan, R.M. and Besier, R.B.** 2006. Targeted selective treatment for worm management—how do we sell rational programmes to farmers? *Veterinary Parasitology* 139: 336–346.
- Van Wyk, J.A., Malan, F.S. and Randles, J.L.** 1997. How long before resistance makes it impossible to control some field strains of *Haemonchus contortus* with any of the anthelmintics? *Veterinary Parasitology* 70: 111–112.
- Woolaston, R.R. and Baker, R.L.** 1996. Prospects of breeding small ruminants for resistance to internal parasites. *International Journal for Parasitology* 26: 845-855
- Woolaston, R.R. and Piper, L.R.** 1996. Selection of merino sheep for resistance to *Haemonchus contortus*: genetic variation. *Animal Science* 62: 451–460.
- Yapi-Gnaore´ C.V., Oya A., Rege J.E.O. and Dagnogo B.** 1997. Analysis of an open nucleus breeding programme for Djallonke sheep in the Ivory Coast. 1. Examination of non-genetics factors. *Animal Science* 64: 291–300.
- Young, M.** 2006. Selection to increase resistance of sheep to internal parasites. SIL Technical Note. <http://www.sil.co.nz>

General discussion on the actual standing and perspectives for the sustainable use and development of resistant or tolerant breeds

Question:

Did natural selection play a role in the development of helminth resistance?

Answer:

Yes - all tropical indigenous breeds manifesting helminth resistance have evolved over hundreds if not thousands of years under high parasite challenge and natural selection is the primary reason for their resistance. However, in the temperate developed world, the degree of breed variation for helminth resistance is much less marked due to the fact that management (e.g. pasture rotation, anthelmintic treatment, etc.) over the last 50 to 60 years has acted against natural selection.

Question:

Are the sheep selected in Western Australia for helminth resistance, where *Trichostrongylus colubriformis* and *Teladorsagia circumcincta* are the dominant species, also resistant against other helminths like *Haemonchus contortus* and vice versa?

Answer:

Not completely, but at least no negative correlations were found when such animals were brought to Eastern Australia, where *H. contortus* is the predominant species. On average they showed better resistance than unselected controls.

Question:

Do helminth parasites react to selection for resistance in the host by changing their genetics (e.g. become resistant to their resistant host as they became resistant to anthelmintics)?

Answer:

Rob Woolaston and his colleagues (CSIRO) did a comparison where they used genetically resistant sheep from the worm resistant selection line at Chiswick, Armidale, and challenged the sheep artificially with worms continuously for the equivalent of 30 worm generations. They concluded that the worms did not become more resistant to the resistant sheep over this time. Selecting Merino sheep for parasite resistance started at the beginning of the 1980s, first in Eastern Australia (Armidale 1982/1984) and followed closely in Western Australia (1988). If there is a change, it must happen very slowly.

Question:

It seems that breeding for parasite resistance in sheep in Australia and New Zealand is, so far, mainly based on classical breeding technologies, and phenotypic descriptions are mainly done with very simple methods. What traits were used to describe resistance in breeds? How expensive is it to measure such traits? Are you using the new molecular technologies? Do you see any advantage for this in the near future?

Answer:

We need simple traits which can be measured in the field otherwise farmers will not use them. These traits have to be repeatable, heritable and correlated with the breeding goals. The most common phenotypic trait being used in both Australia and New Zealand is faecal egg count (FEC) which costs about 3 AUD per sample (cir. 2.6 USD or 1.8 €). The FAMACHA scoring system costs almost nothing and would be useful in those areas where *Haemonchus contortus* is the most prevalent parasite. While packed cell volume (PCV) has been measured in experimental studies, neither PCV nor FAMACHA score are currently used in industry breeding programmes in Australia or New Zealand. Classical selection strategies based on FEC have been shown to work very well. Molecular techniques are not used so far. Anyway, without having phenotypes we can not think about molecular strategies. Molecular tools are

very useful to help us understand the resistance mechanisms, but they are not developed to a stage that they can be used for practical breeding. However New Zealand is offering a gene test (Pfizer Animal Genetics WormSTAR™), but this explains less than 10 % of the variation. It was recently tested in Australian sheep and found not to be useful.

Question:

Was it difficult to convince farmers to join the breeding programme?

Answer:

At the beginning it was; farmers feared loss of genetic progress in the production traits (e.g. fleece weight, growth rate, etc.). It was easier in regions where the degree of anthelmintic resistance was high. We started with two ram breeders that were willing to include breeding for worm resistant in their breeding programmes. We had to lead them through the basic procedures of how to collect the samples, how to prepare and send the samples to the laboratory, how to use the data and interpret the breeding values over two seasons. Only then were they comfortable to do it by themselves. Afterwards, we used them to advise other ram breeders of their procedures and what they had achieved. When their success became apparent, other farmers joined the programme.

Keys for success: 1) build up the infrastructure (recording, laboratory, etc.) which is needed before starting, 2) assign a responsible person to oversee the programme, 3) promote it and give advice to the farmers from the very beginning, 4) indicators to measure the degree of resistance have to be as simple as possible.

About 30 % of rams sold in New Zealand have breeding values for FEC, and about 20 % of flocks in Western Australia measure FEC.

Question:

What selection pressure did you put on resistance traits in Australia?

Answer:

Between 20 % and 100 %. This is up to farmers. Our recommendation was around 50 % where worms are a problem but less so in regions where worms are not such a problem.

Question:

From the Australian experience, should breeding for helminth resistance be based on natural or experimental (artificial) challenge?

Answer:

Experimental (artificial) challenges can help to solve many scientific questions (see also discussion of section 1). However, for various practical reasons (like costs) breeding programmes should be based on natural challenge at pasture. In most cases, it is the best. Natural challenge automatically includes other traits which may affect disease resistance like feeding behaviour which are excluded when experimental infections are used. This depends of course on the route of infection. However, we also have to keep in mind that genetic resistance is only expressed under a certain level of challenge and results of natural challenge may be mixed with other helminth parasites. On the other hand, when the natural challenge is too low to discriminate among animals (e.g. all the FEC measurements are zero or close to zero), an experimental challenge may be required. However, if a disease is identified as an important one, the necessary level of natural challenge under normal farming conditions is normally reached.

It is also reassuring to note that when the genetic correlation between natural pasture challenge and indoor artificial has been investigated in sheep, the estimates have been high (0.87 reported by Lucas Gruner and colleagues in France and 0.75 reported by Rob Woolaston and colleagues in Australia). A recent estimate in goats was moderately positive (0.52 reported by Nathalie Mandonnet and colleagues in Guadeloupe).

Question:

How can we ensure the sustainability of breeding programs? How can genetic progress be distributed? How have the Australians done it?

Answer:

A dedicated advisor is needed to assist breeders with implementing the programme and how to interpret and use the breeding values. The results have to be visible for farmers who must feel that they are and will continuously benefit from breeding for disease resistance. To encourage Western Australian ram breeders to adopt breeding for worm resistance, the local state government through the Department of Agriculture assisted them financially to collect faecal worm egg (FEC) counts. Breeding values for FEC were provided to them for free, but these costs are now met by the sheep industry.

More and more ram breeders have adopted breeding for worm resistance mainly because they have been experiencing resistance to the available drenches. The irony is that those ram breeders that have managed their sheep well and have followed the recommended drenching protocols, experienced more worm problems due to the worms becoming resistant to the available drenches. It was not a sustainable solution and breeding offered a long term solution.

Breeding programmes can either include all breeders or can be done in nucleus flocks, which sell rams to other flocks (or multipliers). Currently, both Australia and New Zealand have sheep performance testing schemes that provide across flock breeding values for a large number of traits, including worm resistance. As more breeders started to include breeding for worm resistance in their flocks, more animals are being identified as worm resistant and that are unrelated. These animals are easily identified as trait leaders and their semen is disseminated very quickly throughout the industry, provided they also perform well on the other production traits.

One of the most important factors to maintain interest in breeding for disease resistance is to visually demonstrate the benefits of disease resistant animals and to inform the industry of these benefits on a continuous basis. This is important as breeders are not in a position to make unbiased comparisons on their own farms. They may have genetic trends but it will be difficult to show any visual phenotypic benefits on a commercial property. This information will provide support to encourage breeders to continue to breed for disease resistance.

Question:

Are there differences in breeding for disease resistance in small and large ruminants?

Answer:

The most significant difference between small and large ruminants is the generation interval. For example, in West Africa age at first calving is nearly 5 years and generation interval 7 years. Most of research/development programmes last for much shorter periods (e.g. 3 to 5 years). Therefore, even if selection programmes were not so expensive (30,000 € per year) it is difficult to convince cattle breeders to join because it takes too long until success is visible. It seems to be easier in sheep and goat because genetic progress is quicker.

Question:

Is there any difference in breeding goats or sheep for disease resistance?

Answer:

Heritability estimates for helminth resistance as assessed by FEC are lower in goats than sheep. However, selection of experimental flocks that are both resistant and susceptible to helminth parasites has been successfully demonstrated in both sheep and goats.

Question:

Is breeding for parasite resistance implemented in any breeding programme in the USA?

Answer:

No, and the future is very unclear as a new anthelmintic drug has just come on to the market (Novartis). This may reduce the pressure to look for alternatives in those regions where anthelmintic resistance is important as in the southern part of the USA. Research in this field is decreasing to almost zero. For the Gulf Coast Native (sheep or goat), fewer research flocks are now being maintained in the USA.

Question:

Well documented parasite resistant breeds (e.g. Red Maasai sheep and NDama cattle) are at risk of extinction in some regions. Why is that? Are they not competitive? Are there sufficient economic data available which can be handed out to farmers? Do we know differences in treatment frequencies, mortalities, etc.?

Answer:

Livestock keepers may consider that the traits with highest economic value (e.g. growth rate, slaughter weight, carcass composition, etc.) are better in other breeds (e.g. Dorper vs. Red Maasai) or crossbreeds. They may not know the exact numbers of losses occurring in their flock or herd. However, when reproductive rate and mortality rate are measured and total productivity calculated, the indigenous resistant breeds are actually the most productive or at least equally productive. Extension services are needed to demonstrate the advantages of indigenous breeds to livestock keepers. Advantages are related to level of challenge and range of diseases and parasites in the area. The production differences, as a result of disease resistance, are not always obvious to livestock keepers who do not always make decisions based on economics. However, if the market demand is not being met by local indigenous breeds, they often switch to other breeds or crossbreeds, which are sometimes kept in more intensive systems.

There is definitely a need for more comparative studies for disease resistance not only between breeds but also between species (e.g. sheep vs goat). It is important that these studies are large enough so that statistically significant differences between breeds can be established, and that the full array of both disease resistant traits and production traits are recorded in these studies.

Question:

What impact will the possible climate change have on the topic?

Answer:

We do not know yet but it is believed that it will increase the interest for genetic disease resistance in animals. For a number of diseases, the situation will become worse in some regions because pathogens will be in more favourable environments.

Question:

Can we quantify the value of resistance/tolerance for diseases like trypanomosis?

Answer:

We have a nice example from Zanzibar where IAEA eradicated Tsetse flies and trypanosomosis. It appears that this has had no significant impact on livestock production at all. In this case, maybe the importance of the disease was over-rated. Furthermore, a disease (pathogen) can not be seen in isolation because it may interact with many other diseases. There is evidence that East Coast fever (ECF), caused by *Theileria parva*, is an important fatal disease in cattle in Zanzibar and that exotic cattle are more susceptible to it than the indigenous zebu.

Question:

Girolondo cattle were imported from South America to West Africa. They seem to be more resistant against ticks in their natural environment. Will this also be the case for tick species found in West Africa?

Answer:

Probably not because the tick species are very different. Ticks in South America were originally introduced with animals from Europe.

SECTION 3. COLLABORATION BETWEEN DEVELOPED AND DEVELOPING COUNTRIES FOR SCIENTIFIC INVESTIGATIONS OF DISEASE RESISTANCE OF CANDIDATE BREEDS

Example of collaboration and recommendations for beneficial collaboration: Integration of tolerance to gastrointestinal (GI) nematodes into a Creole goat breeding programme in Guadeloupe - An application of developed country research in developing animal production systems. (N. Mandonnet)

The French West Indies and Guiana's INRA center is unique center of INRA located in the tropics. More than 200 people are working in the center in Guadeloupe among which 54 people are working in Animal Production. This research unit owns an experimental unit, a laboratory for chemical and parasitological analyses and a biological resources center for logistic tools. Its scientific objectives are to develop research in Animal Production for French Overseas Departments and for the Caribbean region, and to promote sustainable and reliable animal production schemes with low inputs but good production levels. To reach these objectives, the current scientific projects are:

- Characterization of tropical climate effects and genetic heat tolerance in pigs
- Nutrition of stall-fed and grazing animals
- Multi-criteria evaluation of grazing systems and mixed farming systems
- Integrated control of parasitism
- Genotype x Environment interactions in ruminants
- Genetic improvement of local Creole breeds (cattle, sheep, goat)
- Genetic resistance to gastrointestinal parasitism in small ruminants

In Guadeloupe, INRA is involved in improvement of goat meat production through selection. The programme relies on the local goat breed, the INRA research results and the dynamism of the farmers organized in a cooperative.

Caribbean genetic resources

The present domestic ruminant species were shipped to the Caribbean after the 15th century (Naves *et al.*, 2001). After the introduction of the first Iberical stocks, the stocks proceeded from African, European and sometimes Asian origins, according to the colonization process. Therefore, historical events are responsible for the livestock presently reared on the islands. Then, the combination of natural selection in a constrained environment and the multiple purpose use of Creole flocks (meat, dairy, draught) during four centuries have resulted in genetically unique resources. These local breeds make a fair contribution to animal production in the region, mainly in traditional or family-size breeding systems, in which their adaptation qualities are appreciated. In spite of their lack of specialisation, they also exhibit interesting production potential. The Creole goat appears to be an interesting population for this purpose. It is well adapted to its tropical environment and very productive (Alexandre *et al.*, 1997). On-going studies on meat qualities of the Creole goat indicate that there is scope for improvement of carcass weight and conformation (Limeas *et al.*, 2009). This breed has a place for meat production, maybe in a niche market based on specific qualities of the product.

INRA Research on resistance to Gastrointestinal (GI) Nematodes in Creole goats

Research on goats is complementary to the one conducted on Martinik sheep (Aumont *et al.*, 1997), a Black Belly phenotype bred in Martinique and known to be resistant to GI nematode infection. Parasitism with GI nematodes generates heavy zootechnical loss in the French West Indies as estimated in the experimental goat flock of INRA. The periparturient rise in faecal egg count (FEC) has a great impact on productivity (Mandonnet *et al.*, 2005). Kids from dams

with higher FEC had 17 % lower average daily weight gain between 30 and 70 days post partum. They were approximately 1 kg lighter at weaning than kids from dams with lower FEC. The risk of death due to gastrointestinal strongyles during fattening at pasture decreased by about 25 % for each additional kilogram of body weight at weaning (Mandonnet *et al.*, 2003). Comparing growth rate of infected and non infected Creole kids reared at pasture and taking mortality due to GI nematodes into account, weight loss were estimated to be 30 % of the production at yearling.

Breeding for improved GI nematodes resistance in weaned Creole kids was demonstrated to be feasible (Mandonnet *et al.*, 2001). The research programme highlighted that favorable conditions for selection are met:

- resistance traits are highly correlated between production periods (Mandonnet *et al.*, 2006);
- no maternal effects control resistance after weaning (Mandonnet *et al.*, 2006);
- no genetic correlations with growth traits were found; an antagonism was observed with prolificacy but this could be manageable as prolificacy is already high in Creole does (Mandonnet *et al.*, 2001);
- finally, the genetic link with heartwater, the other main pathology of goats in Caribbean, is verified in collaboration with CIRAD.

Faecal excretion was chosen as the synthetic selection criterion because it results from different regulation mechanisms in the host that should avoid coevolution of resistant lines of nematodes. Eosinophilia is considered as a marker of infection intensity and anaemia as a resilience criterion.

Thanks to these results, experimental tools were developed in Guadeloupe. Kids are systematically indexed in the INRA flock. Divergent lines for resistance to GI nematodes have been bred since 2007 in order to study mechanisms involved in resistance and susceptibility. Divergence is already observed (Bambou *et al.*, 2009). The genetic evaluation design is getting standardized before diffusion to professional organizations.

Development programme for meat goat production in Guadeloupe

This programme was initiated in January 2008, by the cooperative Cabricoop, the extension services and INRA. The aim was to produce high quality meat at lower cost from Creole goats by utilizing the genetic and cultural richness of the island, and increasing the technical skills of farmers. This is not an easy task. Threats to local genetic resources exist, firstly, because mistakes in previous development policies have been made due to poor knowledge of the attributes of Creole goats. Secondly, well developed breeding organizations promoting other imported breeds are still commercially aggressive in the tropics. Creole goats have been recently crossed with imported meat breeds like the Boer or Anglo-Nubian and also milk breeds like the Saanen and Alpines. This uncontrolled crossbreeding with “improved” breeds make the conservation of purebred Creole animals difficult as also observed in Martinique (Alexandre *et al.*, 2009).

To implement this program, two actions were initiated concomitantly. Financial support was applied for from the local and European authorities thanks to professional demand and the support of the extension service. It covers funds to improve the infrastructure on farms and purchase Creole bucks and does. It also assists farmers to join the program. The second action dealt with the precise definition of the demand. In 1997, a survey demonstrated that GI nematodes were the main pathology affecting small ruminants in Guadeloupe (Aumont *et al.*, 1997) with increasing problems of anthelmintic resistance. Goat production farming systems in Guadeloupe and the wishes of breeders concerning selection objectives were described

through a second survey in 2008. The survey identified a great diversity of production systems, from zero-grazing to extensive systems (Gunia *et al.*, 2010). Goat farming was a complementary activity for most of the farmers and was not the main source of income. Farmers reared goats more for pleasure than for money, contrary to other tropical countries where insurance and income were highly ranked as reason for keeping goats (Kosgey *et al.*, 2008). The production units were quite small with 60 heads on average and 1.4 people working on the farm. 90 % of the farmers had either off-farm activities or other crop or animal production enterprises. A small number of farmers kept only Creole goats (4 %). The majority (62 %) had mixed herds of Creole and crossbred animals. Most of the farmers appreciated the hardiness of the Creole goat (75 %). Creole goats were also preferred for the quality of their meat (10 %), maternal qualities (7 %) and low input level (6 %). However farmers practiced crossbreeding to improve conformation (48 %), growth rate (24 %) and thus the market price received when animals were sold (10 %). Conformation and growth were the most important traits for buck selection (77 % of the answers). They were also important for females (answer frequency 30 %). Nevertheless, maternal qualities (maternal behaviour, reproduction, milk production) were frequently cited and represented 60 % of the desired traits for females. Health and disease resistance were poorly ranked (about 10 %).

The programme went on in 3 steps.

First, a population base had to be defined. The survey enabled us to identify the breeders that were interested and technically prepared to join a selection programme. A 300 doe nucleus selection flock was required. A standard for Creole goats was built up with a notation grid, in collaboration with farmers. Teams were trained to use this grid in order to distinguish purebred local goats from crossbred ones in the nucleus selection flocks. In 2010, the extension service will install on-farm performance recording and initiate the management improvements (identification, grouping of mating and separation of young males from the herd) necessary for an easy and efficient recording, in each nucleus selection flock. Finally, a breeding organisation constituted of breeders, users and institutions will oversee and orchestrate the scheme: definition of selection objectives, conditions of spread of genetic progress, promotion of the Creole breed. A nucleus of Creole goat breeders (figure 1) will conserve and improve the breed, whereas commercial farmers will use these goats for pure or crossbreeding. This will solve problems of uncontrolled mating and loss of Creole maternal lineage.

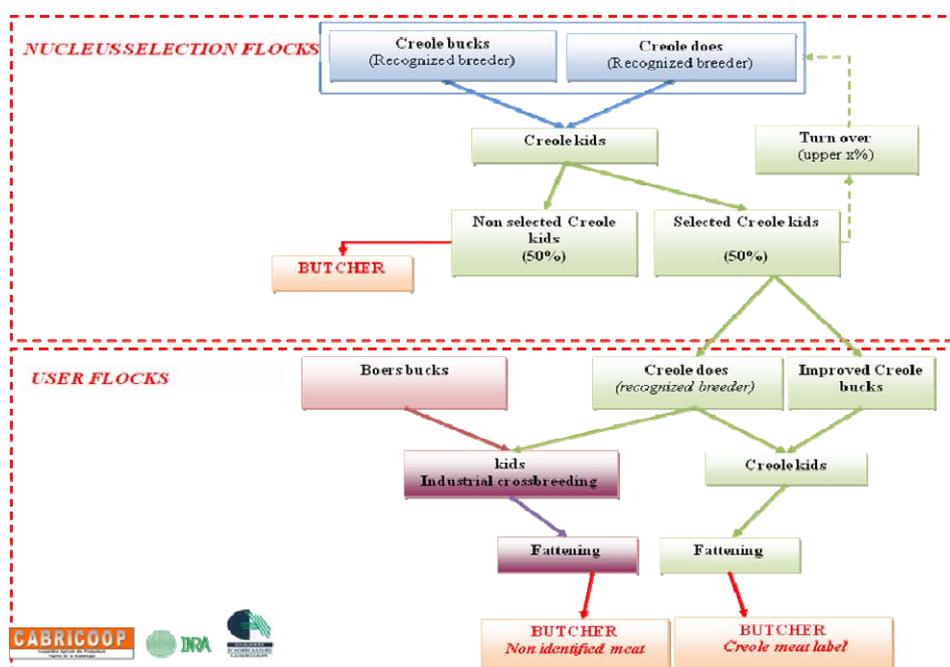


Figure 1. Future organisation of the Creole goat breeding scheme in Guadeloupe

Male kids will be primarily selected on maternal quality and pre weaning growth performance and will be reared in a breeding center until they are yearlings. It will be proposed to farmers to introduce selection for increased resistance to GI nematodes at this step using the genetic evaluation design proposed by INRA. This second sorting will eliminate the more susceptible bucks (i.e those with high faecal egg counts) in order to put some selection pressure on this trait. The weighting of the different traits in the breeding objective will rely on an economic study and the breeding scheme will be of sufficient size to optimise genetic progress.

Conclusion

Sustainability of such a development programme in the tropics is the main unknown factor. Success relies on four elements:

1. **Social sustainability:** Farmers in the breeding scheme must be included in each step of the programme to take into account their wishes in terms of how a local breed should look like in the future. At the same time, their knowledge will increase and their skills in goat production as well.
2. **Biological sustainability:** Very important to maintain the adaptation and maternal qualities of the local breed.
3. **Technical sustainability:** The reliability of pedigree and performance recording must be guaranteed by an institutional follow-up coming with financial support to breeders to improve their facilities. Simple technical innovations are essential.
4. **Economic sustainability:** A niche market based on specific qualities of the product must be developed and promoted so farmers could make a living from their livestock farming activity.

Breeding Creole goats in Guadeloupe is a beneficial collaboration between the farmers and the research institute. For the breeders it brings important technical assistance (results on genetic variability of production and resistance traits, characterisation of local breed) and for INRA it is the opportunity to validate research results and to identify new research issues.

References

- Alexandre, G., Aumont, G., Fleury, J., Coppry, O., Mulciba, P. and Nepos, A. 1997. Semi-intensive production of meat goats in a tropical area. *Productions Animales* 10: 43-53.
- Alexandre, G., Leimbacher, F., Maurice, O., Domarin, D., Naves, M. and Mandonnet, N. 2009. Goat farming systems in Martinique: management and breeding strategies. *Tropical Animal Health and Production* 41: 635-644.
- Aumont, G., Pouillot, R., Simon, R., Hostache, G., Varo, H. and Barre, N. 1997. Intestinal parasitism of small ruminants in the French West Indies. [French]. *Productions Animales* 10: 79-89.
- Bambou, J.C., Gonzalez-Garcia, E., Chevrotiere, C., Arquet, R., Vachier, N. and Mandonnet, N. 2009. Peripheral immune response in resistant and susceptible Creole kids experimentally infected with *Haemonchus contortus*. *Small Ruminant Research* 82: 34-39.
- Gunia M., Mandonnet N., Arquet R., de la Chevrotière C., Naves M., Mahieu M. and Alexandre G. 2010. Production systems of Creole goat and their implications for a breeding programme. *Animal* (in press)

- Kosgey I. S., Rowlands, G.J., van Arendonk, J. A. M. and Baker R. L.** 2008. Small ruminant production in smallholder and pastoral/extensive farming systems in Kenya. *Small Ruminant Research* 77: 11-24.
- Limea, L., Gobardham, J., Gravillon, G., Nepos, A. and Alexandre, G.** 2009. Growth and carcass traits of Creole goats under different pre-weaning, fattening and slaughter conditions. *Tropical Animal Health and Production* 41: 61-70.
- Mandonnet, N., Alexandre, G., Arquet, R., Naves, M. and Menendez Buxadera, A.** 2005. Relevance of the variability of kidding day in Creole goats in Guadeloupe. *Livestock Production Science* 92: 241-247.
- Mandonnet, N., Ducrocq, V., Arquet, R. and Aumont, G.** 2003. Mortality of creole kids during infection with gastrointestinal strongyles: a survival analysis. *Journal of Animal Science* 81: 2401-2408.
- Mandonnet, N., Aumont, G., Fleury, J., Arquet, R., Varo, H., Gruner, L., Bouix, J. and Khang, J. V.** 2001. Assessment of genetic variability of resistance to gastrointestinal nematode parasites in Creole goats in the humid tropics. *Journal of Animal Science* 79: 1706-1712.
- Mandonnet, N., Menendez-Buxadera, A., Arquet, R., Mahieu, M., Bachand, M. and Aumont, G.** 2006. Genetic variability in resistance to gastrointestinal strongyles during early lactation in Creole goats. *Animal Science* 82: 283-287.
- Naves, M., Alexandre, G., Leimbacher, F., Mandonnet, N. and Menendez-Buxadera, A.** 2001. Focus on genetic resources and their management in ruminant species in the Caribbean. *Productions Animales* 14: 181-192.

Example of collaboration and recommendations for beneficial collaboration: Integration of tolerance to trypanosomiasis into breeding programmes (I. Sidibe)

Introduction

CIRDES is a French Research-Development Centre based in West Africa. Its regional mandate is to conduct research and development activities to improve animal health and animal productivity to meet the increasing protein needs of West African populations, to alleviate poverty and maintain an ecological balance. The current research projects are investigating:

- developing non polluting techniques to control animal diseases,
- contributing to intensification of animal production systems,
- assessing the impact of production systems on the environment,
- determining ways to preserve natural resources and the environment,
- managing animal genetics resources and preservation of biodiversity,
- strengthening the partnerships with NARs, international research centers and universities and research institutes in the North,
- contributing to training of scientists in the region in animal health and production, and
- strengthening communication between stakeholders of animal health and production.

The intervention area covers 4 agro-ecological zones: arid, semi-arid, sub humid and humid zones in 7 countries (Benin, Burkina Faso, Côte d'Ivoire, Ghana, Mali, Niger and Togo). In this context, animal breeding systems are strongly influenced by several factors: ethnics groups of farmers, herd management systems (pastoralist, mixed farming, sedentary system, peri-urban breeding), animal breeds, availability of land or grass and/or water.

Over the last 10 years, three main research projects have been developed to improve the management of the disease control, integrating tolerance to trypanosomiasis. The activities have been conducted by multidisciplinary teams from different research institutes from the North and South, including NARS. The projects are:

- La race bovine SOMBA : Sa caractérisation et Recherches en vue de son amélioration - Contrat ERBIC18CT960031
- Recherche de marqueurs génétiques associés à la tolérance/sensibilité aux trypanosomoses chez les bovins d'Afrique de l'Ouest - Projet CORUS 02 313 030
- Improving the management of trypanocide resistance in the cotton zone of West Africa: a coordinated regional study- GTZ Project Number: 2001.7860.8 – 001.00

The main research findings are summarized in the following pages. In most countries covered by this research, there is no structured national breeding programme. Integration of the results into breeding programmes was discussed during the presentation. The main recommendation for beneficial collaboration should be focused on mutual interest regarding social and economic expectations, technology and sustainability.

Main Research Findings

Characterization of the Somba cattle breed using molecular markers

The polymorphism of four categories of genomic markers – 11 blood group systems, 5 lactoproteins, 2 blood protein loci and 33 microsatellites, that is to say a total of 51 loci – has been analysed in four cattle populations or "breeds" from West Africa: Somba and Lagune taurine breeds, the Sudanese Zebu Peul population and the Borgou population, a crossbred

between taurine and zebu. This study was conducted to characterize the polymorphism of the Somba breed and to evaluate its genetic distance from the other three populations, especially the Lagune breed which has a high phenotypic resemblance. Whatever the category of markers or method used, the four populations are clearly separated from each other.

Evaluation of the linkage disequilibrium in a bovine crossed population Baoule (Bos taurus) X Zebu peul (Bos indicus) and its application in the studies of association linked to the trypanotolerance

This study aims at identifying genetic markers associated with tolerance and/or susceptibility of cattle to trypanosomoses by linkage disequilibrium analysis. Analyses concerned 363 individuals in a *Bos taurus* (Baoule) X *Bos indicus* (Zebu Peul) population raised in the Southwest of Burkina Faso. Animals were genotyped with 64 microsatellite markers located on bovine chromosomes 2, 4, 7 and 13, in regions where QTL (Quantitative Trait Loci) associated with the control of anaemia or parasitemia were identified in N'Dama/zebu Boran population (Hanotte and al., 2003). Results showed a high level of expected heterozygosity (0.71) and a mean number of alleles per locus of 9.75. Linkage disequilibrium (LD) was low and extended over shorter distances than has been observed in cattle from developed countries. The effective population size (N_e) estimated from LD is large but decreases during the last generations.

The identification of causal mutation or gene(s) associated with phenotypic variation would support genetic improvement programmes of the local African cattle breeds.

Trypanotolerant cattle-keeping is less attractive but should be promoted in areas where these cattle are still maintained, as in southwest Mali and Guinea.

There are two major trypanotolerant breeds in the study areas: Baoulé kept in the East and N'Dama in the West. Although the project results indicate that farmers regard the productivity (and disease resistance) of trypanotolerant cattle quite highly, the breeds' undesirable features are also recognized: temperament, slowness while working; short legs which make them liable to damage the crop while weeding; slow growth and slow weight gain; smaller mature size; low sale price and slower sales. Promoting trypanotolerant cattle-keeping requires improving the productivity of these breeds through selection and finding export markets where trypanotolerance is the main driver and prices correspondingly high.

There are substantial, possibly insurmountable, constraints to widespread use of trypanotolerant cattle as a strategy for management of trypanosomosis and drug resistance. However, farmers are as of yet unaware of the phenomenon of drug resistance and it is possible that better knowledge of this would result in greater preference for trypanotolerant breeds. This is especially the case if drug resistance is, as some fear, an irreversible phenomenon. The precautionary principle would justify support for safeguarding trypanotolerant breeds *in situ* or *in laboratory*, as a fall-back option for the worst-case scenario of total resistance to existing trypanocides, combined with failure to develop new drugs.

General discussion of collaboration between developed and developing countries for scientific investigations of disease resistance

Question:

Regarding the project in Guadeloupe: how did you attract farmers to join the programme? Who is paying the breeding costs?

Answer:

Average kid mortality is in most breeds between 15 and 20 %. Therefore, farmers are interested in disease resistant breeds. As Creole meat is very attractive to the consumers, it can be sold under a special label for high prices. The price difference, compared to meat from other goats, pays part of the breeding costs but not all. The rest has to come from increased productivity, lower drug costs (other breeds have to be treated regularly), lower mortality, etc. If a calculation is made based on that, it will show that Creole goats can compete with imported breeds. This convinced farmers to join the programme.

Question:

How are the traits of disease resistance implemented into breeding programs?

Answer:

A nucleus flock at INRA research station is the basis. Beside traits of economical importance, breeding values for parasite resistance are estimated based on an experimental challenge. Earlier studies have shown that there is a good correlation with natural challenge. This helps to standardize the estimates in a nucleus system. The tested bucks are sold to the breeders.

Question:

Regarding the situation in Africa: how attractive are trypanotolerant breeds to farmers?

Answer:

In some regions they are not attractive at all because of undesirable features. For example, in the cotton belt where animals are also used for transport, temperament traits are of high importance. The N'Dama is not easy to handle and farmers prefer the Zebu. In addition, many pesticides are used in cotton areas, and this decreases the incidence of the disease transmitter (Tsetse flies). The situation may change if the use of insecticides for cotton production decreases.

Question:

What are the major problems in breeding for trypanosomosis resistant animals?

Answer:

Disease resistance is not on the top priority list of farmers. As long as drugs work (in their belief) they are happy. Food safety is not a priority either. Therefore, trypanotolerance seems not to pay back. Additionally, financial support and infrastructure are lacking, including animal recording.

Many research projects have been implemented in the tropics, but they were not sustainable; they always ended as soon as the financial support stopped. Often, the duration of the projects is not long enough to show any breeding success.

In many parts of Europe, breeding was until few years ago supported by governments (e.g. performance and progeny testing). In developing countries no strong cooperatives exist which could embark in such programmes. Without external support there is no realistic chance to develop genetic activities further. Animal breeding takes time and it costs!

Question:

Will research play a significant role in this field in the future?

Answer:

The support of trypanosomosis research is decreasing. Donors seem to be more attracted by other diseases which are “in vogue” even if their economic importance is lower. It is difficult to make such subjects attractive to donors for a long term commitment. Economic values, side effects, food safety, environmental damage etc. are of importance.

SECTION 4. TECHNOLOGY TRANSFER BETWEEN DEVELOPED AND DEVELOPING COUNTRIES

What classical technologies could be realistically applied in developing countries for breed development? How can the traits of disease resistance be incorporated into breeding programs? (L. Dempfle)

For any genetic improvement of a population, there is need for:

1. a clearly defined breeding goal,
2. good estimates of the genetic merits of animals,
3. a small ratio of selected candidates to all tested candidates,
4. a short generation interval and
5. appropriate technologies and procedures.

A clearly defined goal

Livestock are kept for making a living and thus their usefulness has to be improved. Disease resistance/tolerance is not the primary goal, but a means to improve their usefulness. A careful analysis of how much emphasis should be put on the various traits is needed. It is doubtful whether diseases which can be reasonably well controlled by other means should be part of genetic improvement programmes. Genetic improvement is usually very slow, particularly in cattle. In the past, efforts have been made to improve the ability to cope with some diseases, but the diseases were then controlled by other means (e.g. bloat in cattle – drenching). That was true for Marek's disease in poultry; great efforts were undertaken in the sixties to reduce the problem by genetic improvement, but a vaccine came out in the early seventies which 'solved' the problem. Today, there is again great interest in genetic improvement, despite the availability of a vaccine.

Good estimates of the genetic merits of animals

The genetic merits of the candidates have to be inferred. The most basic requirement is a functional Pedigree and Performance Recording Scheme, which at least has to include information about the most common and most important diseases. That phenotypic information on the candidates and their relatives might be supplemented by marker assisted selection and/or genomic selection. However, the efforts in time and money that have to be invested to use these techniques should not be underestimated.

A small ratio of selected candidates to all tested candidates

In any genetic improvement scheme, a certain number of breeding males and females is needed. The number of selected males can be markedly reduced by using artificial insemination (AI) (depending on the species) and the number of selected females can be reduced (but much less) by using embryo transfer (ET). However, the impact of embryo transfer is often over-emphasized; in a very well organized dairy cattle breeding scheme, genetic progress can be increased by about 5 % (up to 10 %) using ET. That is not a big amount but it is still a nice increase. However, one has to ask whether the money spent for ET could not be invested in other measures which would increase genetic progress even more.

In a small nucleus, AI is often not needed as a certain number of males is necessary to have a sufficiently large effective population size. The required number of males can easily serve the females by natural service. However, AI is the quickest way to disseminate the genetic progress from the nucleus to the commercial population, at least in cattle. Yet, AI related problems in countries with limited developed infrastructure should not be underestimated. Most of the time, AI is only justified if superior genetics is to be disseminated. Use of deep

frozen semen is usually regarded as the state of the art, however, one should not forget that some very progressive countries and AI stations still make use of fresh semen (e.g. the dairy industry in New Zealand).

A short generation interval

Genetic progress is made at each generation. Thus, in each time period, one should have as many generations as possible. However, that can conflict with the recording of some traits, e.g. mastitis is not so frequently expressed in the first lactation as it is in later ones. When selection decision is based mainly on first lactation, the generation interval is shorter but the mastitis liability would be poor.

Technologies and Procedures

Genetic improvement in poultry and pigs is nowadays mainly done with a scheme comprising nucleus – multiplier – commercial tiers. The nucleus is usually quite small in comparison to the commercial sector, but nearly all efforts (recording) for genetic improvement are concentrated there. Breeding schemes for developing countries are usually designed as nucleus schemes (open or closed, centralised or decentralised, station or village based). Station based nucleus breeding schemes might be easier to manage but there is the danger of genotype by environment interaction. The concept of an open nucleus might be the method of choice for any developing country.

For data analysis, advanced statistical methods (BLUP, REML) are usually utilised. These statistical methods are easy to use and can be used anywhere.

In recent years, marker assisted selection (MAS) attracted lot of attention, but in the meantime emphasis has shifted to genomic selection. For MAS, the search for useful markers can be quite complex and time consuming. ILRAD (ILRI) tried to determine markers for trypanotolerance. The trial started in 1983 and the phenotyping ended in 1998 (Hanotte et al. 2003). It is not very likely that many such experiments will be carried out in the future in developing countries! For genomic selection, the necessary analysis is also quite complex and, at present, it is not very clear how it could be used in a small nucleus population. Whatever will be useful for breeding schemes in developing countries, a functioning Pedigree and Performance Recording Scheme is essential. Having such a scheme, all proven quantitative genetics procedures can be applied. At a later stage, newer techniques like genomic selection can be employed, if and when appropriate.

References

Hanotte, O., Ronin, Y., Agaba, M., Nilsson, P., Gelhaus, A., Horstmann, R., Sugimoto, Y., Kemp, S., Gibson, J., Korol, A., Soller, M. and Teale, A. 2003. Mapping of quantitative trait loci controlling trypanotolerance in a cross of tolerant West African N'Dama and susceptible East African Boran cattle. *Proceedings of the National Academy of Sciences of the United States of America* 100: 7443-7448.

What new technologies could be realistically applied in developing countries for breed development? How can the knowledge be incorporated into breeding programs? (M. Malek)

There is considerable genetic diversity among sheep and goat breeds in the world, but there has been little attempt to exploit this diversity to increase small ruminant productivity. One reason for this is the lack of coherent organized breeding strategies. Small ruminants are a principal source of animal protein in many developing countries. Their biodiversity is often expressed in well-adapted traits that enable them to survive harsh, local environmental conditions or show resistance to endemic diseases where exotic breeds cannot thrive. Unfortunately, since such traits are not sufficiently characterized, they are underutilized in conventional breeding programmes and there is insufficient research on the ways to select breeds or individuals carrying the most advantageous traits. The characterization and mapping of genes controlling such traits and the subsequent use of this information in selection and breeding programmes should make it possible to facilitate significant increases in small ruminant productivity.

Different breeds are anticipated to possess substantial variation in SNP (Single Nucleotide Polymorphisms) profiles due to random mutation, natural selection and genetic drift during periods of geographic isolation. There are new methods for analysis of SNP variability which can be considered as a basis upon which to design molecular characterization and breeding projects. However, the maturity of each method and its feasibility to contribute to the overall objective of the breeding project should be clarified at the start. With availability of 60,000 (or more) SNP arrays for different species at reasonable cost, a researcher can gain access to a large amount of genomic data. This is why the 60K SNP arrays are such a useful tool for assessment of genetic relationships among breeds. There are a number of clear advantages to using the 60K SNP array as a molecular characterization tool.

To fully capitalize on these advantages will require much greater emphasis on the development of structured breeding populations and the collection of detailed and extensive phenotypic information. However, this work may be beyond the reach and resources of many potential collaborators in developing countries. It is important to keep in clear focus exactly what use of new methods such as the 60K SNP array would return to a new project. If structured populations with phenotypic data are not available, the best one may be able to hope for is identifying small sets of SNP (small genomic regions) which require follow-up investigation. Follow-up will often consist of sequence based analysis of candidate gene regions. However, this approach has largely proven to be unsuccessful for complex and intractable traits such as disease related trait. The major reason for this difficulty is the contribution of many genes, each which individually contributes only minor effects and the influence of environmental factors. This is the very reason that prompted researchers to develop genome-wide tools that can evaluate the entire genome in a single experiment.

The utilization of modern molecular and breeding technologies to identify, locate, isolate, and characterize genes of economic importance is an important task. The understanding of the biology of traits related to disease is a complex matter, therefore it is essential to maintain a strong multidisciplinary group (nutrition, reproduction, physiology and production) in order to find a solution for the complex problems of disease. A project to study genetics of disease traits in developing countries will likely be successful only if it can bring together scientists from a range of developing and developed countries in a coordinated setting and to provide access to, and training in use of, modern tools for molecular genetic analysis.

For such a project, the possibility of accessing detailed genetic knowledge available from different resources (databases), will improve the capacity of each country's participating

scientists to understand the genetic potential of their livestock. An eventual goal with respect to disease traits may be to bring resistance into breeds/lines used for small ruminant production or to create lines acceptable for production with resistance.

The logical steps in designing a multi-country project for study of genetics of disease resistance of local breeds in developing countries are the following:

- Identify countries with indigenous breeds of possible interest and characterize the breeds in order to collect detailed phenotypic information for all the important production and adaptability traits.
- Select appropriate technology to apply
- Plan the data collection and analysis
- Collect the data and perform the given analyses
- Interpret the results
- Emphasis on new projects should focus on breed-level comparisons, which is appropriate given available resources and the desire to involve relatively large numbers of investigators from a number of regions and countries. An investment in genotyping of modest numbers of animals from within a fixed array of breeds with 60K chips should provide very interesting information for determination of breed-level genetic relationships but is unlikely to lead to unambiguous detection of useful genetic markers for disease-resistance or other performance traits.

Factors to consider are:

- Before applying any of new technology, the comparison should be done with great attention to the maturity of the technique and implementation as most of these methods are at development stage.
- If a new project(s) has the ability to collect detailed phenotypic information for a number of traits (related to disease or immune response) across all animals, characterize it and bank it properly. Therefore the development of a programme to manage a Genetic Repository Bank on small ruminants is an essential.
- Using new technology may not fulfil all of the goals the project has in terms of laboratory based capacity building. One of the consequences associated with high density SNP arrays and the new sequencing technologies is that the lab work is performed in commercial service labs. This shifts the emphasis away from lab based expertise in Universities and bioinformatics skills needed to manipulate large datasets. This might mean a shift is required in the project in both national and regional level of thinking and what skills it aims to foster as part of the program.
- Most of discussions about genomics stress the importance of good phenotypic data. Therefore, it is an essential for each project to include groups that have their basis in the field and the lab, with good field data or capacity to collect them. Possible candidate countries should be identified and included in new projects.

In animal genetics, the development of bioinformatics and genomics tools continues to form an integral part of the IAEA strategy for providing Member States (MS) with the means for utilising the genetic resources within their national herds or flocks. Therefore the aim of the genetics group of the Animal Production Unit (APU) of IAEA's Laboratory is to develop tools for the use of MS for management of their indigenous livestock. The first is an online programme to manage a Genetic Repository Bank in sheep that will enable scientists to insert their own information into the database and graphically view the origin of samples. This will mean that counterpart laboratories can liaise with APU and be provided with updated information, such as laboratory protocols, standard operating procedures, nuclear and related techniques, methodologies and procedures, detailed genome search and analysis tools, radiation hybrid map information and livestock molecular markers database.

Genetic characterization is another area in which we try to coordinate collaboration of scientists in member states. Genetic characterization is a process where livestock breeds are sampled and genotyped at an established set of loci. The characterization included analysis of both phenotypic and genetic data, including the genotypes of microsatellites from a standard FAO panel. Therefore, by comparing the allelic frequency at common loci across breeds, one can determine the genetic similarity of breeds. Breeds with unique genetics are more valuable for conservation purposes. The information will allow the participants to evaluate local biodiversity both within and across breeds. To help in this collaboration, we are building an on-line database of microsatellite information for characterization of cattle, sheep and goats. Specifically, this database will make available the allelic frequencies for all markers used for genetic characterization, for as many breeds as possible. This will allow users to compare their breeds with breeds from other countries to determine uniqueness. In addition, our intention is to work with scientists to perform a global "meta-analysis" of characterized species, which could be very valuable for conservation activities.

General discussion of technology transfer between developed and developing countries

Question:

What technologies are useful for breeding for disease resistance?

Answer:

Disease resistance is normally not the primary goal in breeding programs. It probably comes along with the main production traits. Embryo transfer brings an advance of about 5 % in breeding progress but the associated cost has to be considered. If infrastructure is available, it might be useful in small populations. Artificial insemination is very useful to disseminate genetic progress. Marker-assisted-selection (MAS) and genomic selection have not yet delivered their expected benefits in practical breeding. Their value has to be proven first in the developed world.

Question:

Can we use the outcome of genome scans for adaptive genetic differentiation in developing countries?

Answer:

The aim of such studies is to identify loci underlying adaptation. This may help to understand mechanisms and identify candidate genes. So far it can not be used for practical breeding; Maybe in the long term.

Question:

Can we use any molecular techniques in developing countries?

Answer:

Molecular techniques are just tools which may help in the future. Furthermore, one have to keep in mind that phenotypic data are always needed to validate molecular data, which is limiting their use in developing countries and in many developed countries as well.

SECTION 5: ACCESS AND BENEFIT SHARING (ABS) AND INTELLECTUAL PROPERTY RIGHTS (IPR)

Access and Benefit Sharing (ABS) and Intellectual Property Rights (IPR): Issues that may arise from finding potential major genes in a local breed and transferring them to highly selected commercial populations, or vice versa. (S.J. Hiemstra)

Animal Genetic Resources (AnGR) exchange flows between countries and regions may change in the future as a result of increasing interest in specific traits or genes. Increasing knowledge about the genetic background of tolerance/resistance to parasitic diseases in ruminants may result in increasing demand for certain breeds or genotypes. This raises questions about the need for a change or strengthening of the international regulatory framework for AnGR, in particular about Access and Benefit Sharing (ABS) and Intellectual Property Rights (IPR). This paper will explain the current policy and regulatory framework relevant for AnGR conservation and sustainable use.

Genetic erosion

Domestic animals supply 30% of total human requirements for food and agriculture and 70% of the world's rural poor depend on livestock as a component of their livelihoods. The global livestock sector consists of a variety of production systems and farm animals are used for a variety of functions. Centuries of selective breeding and exchange of farm animals or germplasm within and across countries have resulted in the development of the current diversity of breeds and within-breed genetic diversity. There is consensus that global AnGR diversity is under pressure. The existence of threats to AnGR is generally accepted, even though debate remains about the severity of genetic erosion.

AnGR exchange patterns

The exchange of AnGR between countries, regions or private parties has played and will continue to play an important role in breed and livestock sector development. Exchange of genetic material between developed countries (North to North) is dominant and – driven by globalization – high performing breeding stock is exported from North to South, which sometimes raises issues about sustainability of introduction of 'Northern genes' into the South. South to South exchange has also been extensive and important for livestock development. However, such exchange has been much less well documented. Movements of livestock germplasm from South to North have been rare in the past century, and in most cases the economic benefits to both North and South have been relatively small. This is in contrast to plant genetic resources, where South to North flows are prominent, mainly driven by the search for new disease resistances and adaptive traits to be incorporated in new plant varieties. The general impression is that AnGR exchange is going rather 'smoothly' and veterinary standards are the most relevant barriers for exchange between regions, countries or breeders. Hiemstra et al. (2006) show that AnGR exchange flows may change in the future, in particular in the context of climate change, developments in biotechnology, disease challenges and other major drivers of change.

FAO, CBD and WTO/WIPO/TRIPS

The FAO Commission on Genetic Resources for Food and Agriculture (The Commission) has recognized the importance of conservation and sustainable use of animal genetic resources for food and agriculture (AnGR). The Commission approved the finalisation of the first Report

on the State of the World's Animal Genetic Resources (FAO, 2007a) and the Global Plan of Action and the Interlaken Declaration were adopted at the First International Technical Conference on Animal Genetic Resources (FAO, 2007b). Since 1995 the Commission covers all Genetic Resources for Food and Agriculture. Among other issues, the Commission included the implementation of the GPA and Access and Benefit Sharing (ABS) in its Multi Year Programme of Work (MYPOW). Although not designed primarily for AnGR, two other groups of international agreements with a general scope also apply to AnGR, i) the CBD and ii) WTO/WIPO/TRIPS. The objectives in the three various policy areas (FAO, WTO/WIPO/TRIPS, CBD) are seemingly conflicting and there is a lack of coherence in the institutional structures.

The Convention on Biological Diversity (CBD, 1992) provides a legal framework for the conservation and sustainable use of biological diversity. According to the CBD, states have sovereign rights over their genetic resources and authority to determine access (and benefit sharing) conditions to them (ABS). The Conference of the Parties (COP) of the CBD decided to develop an International Regime (IR) on ABS to be adopted by COP-10 in 2010. This regime will address access to and benefits derived from genetic resources for food and agriculture, which (also) fall into the mandate of the FAO. A Working Group of the CBD on ABS will develop a proposal, which may or may not include different sub-sectors and possible exemptions.

WIPO, the World Intellectual Property Rights Organisation, promotes the development of measures designed to facilitate the efficient protection of intellectual property throughout the world and to harmonize national legislation in this field.

ABS regime

A future ABS regime may have impact on exchange flows of AnGR. However, there is widespread un-awareness amongst stakeholders in the livestock sector about the CBD and ABS. Major stakeholders are sceptical and feel that there are more relevant issues to work on (Hiemstra et al., 2006; Ivankovic and Hiemstra, 2008). In general they also fear that imposing new legally binding rules could complicate trade and management of AnGR. We also note that stakeholder groups take diverging positions. The 'formal' business sector, mainly interested in profits and access, is strongly in favour of a practical and workable IR on ABS. On the other hand, the 'informal sector' (civil society groups, local communities, livestock keepers) are more concerned about losing incomes, freedom to operate and about rights to tradition and culture. Future scenario's based on climate change, biotechnology developments, horizontal/vertical concentration in the livestock/breeding sector or disease challenges may influence the balance of power between stakeholder groups and will influence the ABS debate.

Protection versus ABS

Access and Benefit Sharing issues are also connected to (Intellectual) Property Rights (IPR) in the livestock sector, governed by WTO/WIPO/TRIPS. The general picture is that AnGR are primarily owned privately (sometimes communally) and are not considered to be in the public domain (in contrast to Plant Genetic Resources gene banks). Currently, the exchange of AnGR is mainly regulated by the transfer of private ownership (by private law contracts and customary law) and is also influenced by zoo-sanitary regulations. It is a general belief that the current exchange of AnGR has generated benefits for both seller and buyer under the present circumstances where private law agreements have been in use. The genetic value of a breeding animal or germplasm should be included in the market price. On the other hand,

AnGR are actually under the state sovereignty (CBD) and may also interfere with IPR over improved AnGR (WIPO).

In general, animal breeders would be in favour of protection of genetic material to assure a fair benefit from genetic improvement and investment. Moreover, breeders need access to genetic resources for further breeding, usually available within breeding populations. The question is, however, how to balance protection, access and benefit sharing in the light of the current and future ABS and IPR regulatory framework. Currently, breeding companies seem to be rather confident that they don't need access and legal protection, but they also realize that future developments may require legal measures, e.g. the need for access to genes, important for new traits such as disease resistance (Oleson, 2009).

Speaking about protection of AnGR it is important to first of all define exactly the resource to be protected, ranging from genes, germplasm, animals to breeds/populations. Moreover, there is a variety of different actors who can claim property to a particular resource, e.g. livestock keepers, breeders, communities, herd books or nations. In current practice there is a whole range of options to 'protect' AnGR, from biological protection (e.g. selling hybrids only) to strong legal protection (e.g. patents). Common in animal breeding is also that breeders intend to stay ahead of their competitors through continuous upgrading. Although current exchange agreements are not very well documented, there are many different types of agreements in use for exchange (of property) of AnGR for research or breeding purposes.

Plant genetic resources

For Plant Genetic Resources for Food and Agriculture, FAO member states ratified the International Treaty on plant genetic resources for food and agriculture (ITPGRFA). Core elements of the ITPGRFA are the inclusion of farmers' rights and the multilateral system of ABS to cover the genetic resources of major food and fodder crops that are under the control of the Contracting Party Governments and the international gene banks. Debates and developments related to international agreements in the crop sector have tended to frame the debate for AnGR as well. In order to assess the need for any specific AnGR policies and regulations, we have to understand the key differences between PGR and AnGR.

Options for strengthening the AnGR policy and regulatory framework

A number of policy and regulatory options was identified by Hiemstra et al. (2006), which could be taken into consideration.

Standard or model MTA

Regardless the form of the future IR for ABS, there is a need to explore the development of a standard or model Material Transfer Agreement (MTA) for AnGR exchange. Such a model or standard MTA may facilitate exchange in the future, could arrange for proper benefit sharing and may contribute to reduction of inequality of negotiation parties (if any). A MTA could also include sustainable use aspects, e.g. genetic impact assessment before introduction of exotic AnGR, and will support responsible exchange of AnGR. So far, a systematic study of the use of agreements for AnGR has not been undertaken.

Sui generis protection for AnGR

It is argued that relationships among stakeholders are becoming increasingly unbalanced. In particular globalization and changes in business organisation (e.g. global sourcing,

standardisation, vertical integration and lengthening supply chains) are generating an increased concern about equity and the position and rights of livestock keepers and smallholders. In addition, we also see an increasing number of (product and process) patents in the livestock sector. Exploration and development of a sui generis protection system for AnGR could be useful, particularly where based on the establishment of breed associations (possibly associated with trademarks), geographical indications, the protection of traditional knowledge and livestock keepers' or breeders' rights.

The fact that the concepts of plant varieties and animal breeds are quite different implies that the present system for plant breeder's rights (for example the UPOV sui generis system) is unlikely to be applicable to the livestock sector in the same way. For a sui generis system to be adequate for the animal sector, the particular needs for legal protection must be further analysed carefully. Legal and political aspects of 'livestock keepers' rights' would also need to be further explored and might contain similar provisions as those on the more well-known concept of 'farmers' rights'.

References

CBD. 1992. Convention on Biological Diversity. www.cbd.org

FAO. 2007a. The first Report on the State of the World's Animal Genetic Resources

FAO. 2007b. The Global Plan of Action and the Interlaken Declaration.

Hiemstra, S.J. 2007. Exchange, use and conservation of AnGR: policy and regulatory options. Publication available on www.cgn.wur.nl

Ivankovic, M. and Hiemstra, S.J. 2008. Analysis of applicability of Access and Benefit Sharing (ABS) principles on Animal Genetic Resources (AnGR). Publication available on www.cgn.wur.nl

Oleson, I. 2004. Strategies and regulations pertaining to genetic resources 2003-2006. Cooperation project funded by FUGE program. Case studies, 2004.

General discussion of Benefit Sharing (ABS) and Intellectual Property Rights (IPR)

Question:

Can patents in animal breeding be prevented? What are the expected consequences?

Answer:

It is tried to change patent legislation exemptions for further use of patented material. So far no monitoring system of the use is established.

Question:

What animals are protected and how are they protected? Breeding lines from poultry and pig industry? What about breeds where major genes have been identified (e.g. Booroola)?

Answer:

With the development of technology like single gene introgression into breeds some breeds may become attractive for commercial use in the future. We also see that species (e.g. Alpacas) are of interest to some countries for various reasons. It is the legislation of the countries to allow export or not.

SECTION 6: CONCLUSIONS AND RECOMMENDATIONS OF THE WORKSHOP

1. There is an urgent need to look for genetically based disease resistance/tolerance in certain breeds in different parts of the world. This trait complex is probably one of the reasons why we still have 'local' breeds in different parts of the world.
2. Disease resistance will especially be of interest where normal control strategies do not work (e.g. too expensive to control disease by drugs or vaccines, no drugs or vaccines available, problems of resistance to the drugs) and it has an impact on flock productivity.
3. Some parasitic diseases (trypanosomosis, nematodes, ticks and tick-borne diseases) meet the criteria under the circumstances mentioned at (2). The most important diseases will be of endemic nature. In a developing country context, these are GI nematodes, ticks (& tick-borne diseases), the various forms of theileria and trypanosomosis.
4. The first priority must be to look for breeds which are located in regions and affected by diseases mentioned at points (2) and (3). Interesting candidate breeds are named in some FAO survey documents and various publications.
5. The identification of the breeds is based on phenotype recording under field conditions, and ideally on the comparison with other susceptible breeds present in the same region. Classical technologies have been and are being used successfully.
6. From a nematode perspective, repeated FEC, PCV/FAMACHA measures are most effective to characterize breeds because they are relatively inexpensive, repeatable and heritable. However, more work to develop simple tools should be given emphasis.
7. Phenotyping requires an investment to: i) build up infrastructure, ii) educate people to do it, iii) buy equipment and access to labs, iv) monitor the animals, v) follow variables linked to the disease diagnosis, vi) measure/characterise phenotypes, vii) data analysis and viii) assess covariables interfering with phenotypes.
8. Breed development can be based on classical “quantitative genetics approach”, with the need to estimate breeding values, through phenotype assessment, selection criteria, and recording pedigrees. Molecular techniques require a lot of infrastructure. They cannot be used yet in the context of developing countries; when they are, it is important that they are sustainable.
9. The perspectives for the sustainable use and development of disease resistant breeds in many developing countries are difficult at the moment. The main problems are due to the absence of infrastructure (e.g. breeders’ organisation, institutional organisation) and policy and financial support.
10. Responsible government agencies must get involved in breed development, and must support farmers in defining breeding objectives and strategies, and establishing a suitable organisation.
11. Funds are needed to undertake proper breed descriptions and breed comparison trials. Results can not simply be transferred because of expected genotype-environment interactions.

12. Most of the resistant breeds are located in the developing world. The identification tools are however mostly in the developed world. So technology transfer and collaboration are needed.
13. Eventually transgenic livestock may be developed which carry resistant genes from tropical breeds. This touches issues of ABS and IPR.
14. There is good scope to identify more indigenous breeds in the tropics that are resistant or tolerant to parasites.
15. It can be expected that some of these breeds will have a lot to offer to production in the developed and developing world. Their economic advantages need to be well documented and promoted. Smallholder farmers in the tropical developing world must become more aware of the value of their local indigenous livestock.
16. Guidelines are needed to support further work in the field of disease resistance.
17. It can be expected that the resistance/tolerance in animals to diseases will have an important impact on the maintenance of animal genetic resources and biodiversity worldwide.

ANNEX 1: DETAILED ANSWERS TO QUESTIONS

During the workshop the following main questions were addressed:

1. Is there a need to look for genetically based disease resistance/tolerance in certain breeds in different parts of the world?
2. What are the breeds (have we already identified “interesting candidate” breeds?) and what are the diseases we should look for?
3. How could classical and/or new technologies realistically be applied to identify the breeds in different parts of the world? What are the requirements and costs?
4. What type of collaboration between developed and developing countries is needed for that?
5. What are the perspectives for the sustainable use and development of such breeds in different parts of the world?

The questions were partly answered during the sessions. However, every participant had the chance to make further comments after the workshop.

Answers from different contributors: SCB – S. Bishop; SoT – S. Thevenon; LB – L. Baker; JM – J. Miller; JoM – John Mugambi, AA – A. Amarante; LD – L. Dempfle; JG – Johan Greeff; MT – Markos Tibbo; NM – Nathalie Mandonnet

1. Is there a need to look for genetically based disease resistance/tolerance in certain breeds in different parts of the world?

SCB: Yes, absolutely. It is the resistance/tolerance/adaptation attributes that are the reason for 'local' breeds remaining successful and appropriate in different parts of the world. If this was not the case, then importations of exotic breeds into Africa and Asia would have worked, and, for example, nearly all the dairy cattle in the world would be Holsteins! At the very least, we need to know the best breeds to use in different places, and have strategies for conserving and exploiting such resources.

SoT: Looking for genetically based disease resistance/tolerance is interesting when the disease is imperfectly controlled by the current available methods:

- no efficient vaccine available
- appearance of resistance of the pathogen agents to the drugs
- drugs residues present in the environment and/or in the milk and the meat
- interest in decreasing the inputs, especially important for low-inputs system

This is feasible when the animal disease is not a zoonosis. Some parasitic diseases (trypanosomosis, nematodes, ticks and tick-born diseases) meet these criteria.

LB: Definitely, but clearly there will be a need to prioritize which breeds to investigate.

JM: I think it is advantageous to find out what breeds are resistant to whatever. The one problem is that they may be resistant under one circumstance (environmental, etc.) and not under another. So importing/exporting such breeds may not result in the expected outcome (genotype-environment interactions).

JoM: Yes, but policies on their conservation must be worked out.

AA: Yes, there is no scientific record about disease resistance in many indigenous breeds of ruminants.

LD: I think that beyond a reasonable doubt there are breeds in West Africa which are much more able to cope with trypanosomosis and, although less well documented, other endemic diseases like Cowdriosis (now called Erlichiosis) and Dermatophilosis. The tolerance is not locally restricted! However, these breeds are not generally more resistant but only to diseases they were exposed to for a long time, so natural selection could have acted on them. There is anecdotal evidence that West African trypanotolerant breeds may be very susceptible to Rinderpest.

JG: There is a strong need to identify breeds that are genetically resistant to diseases across the world. Some of these breeds are disappearing fast and are replaced by, and crossed with "exotic" breeds that are perceived to be more productive. It is imperative that these indigenous breeds should be evaluated to determine whether they are genetically resistant to diseases that are common in their environment. The question, however, of which breeds should be conserved is very difficult to answer because of the lack of information on the breeds, the number of breeds involved and the logistics to access and evaluate the large number of breeds.

MT: Yes there is a need to look for genetically based disease resistance/tolerance in certain breeds. There are breeds that have survived and became productive in disease-ridden environments with limited or no external inputs (pharmaceuticals) for centuries. Fragmented reports mention some breeds as resistant without empirical evidence on them. Some resistant/tolerant breeds are under threat of extinction (e.g. the Sheko cattle breed in Ethiopia).

NM: It is important to look for genetically based disease resistance in indigenous tropical breeds in order to characterize those breeds and convince animal keepers to stop the introduction of exotic specialized breeds that are less adapted and less productive in tropical environment. It is also a source of knowledge for resistance mechanism.

2. What are the breeds (have we already identified "interesting candidate" breeds?) and what are the diseases we should look for?

SCB: The interesting candidate breeds must surely be named in the various FAO survey documents. We cannot study everything and every breed, nor do we necessarily know why some are successful, but the ones that are most likely to be useful will be listed. The only problem is that these are long lists, and cover many countries!

In terms of diseases, we again have the problem of making the appropriate choices. The primary attribute, before any specific disease is even considered, is actual productive output or efficiency. This will capture much of the adaptation & disease resistance attributes. For specific diseases, then we need to focus on a very small number, otherwise we get nowhere. These will be endemic diseases, and in a developing country context must include GI nematodes, ticks (& tick-borne diseases), the various forms of theileria and trypanosomosis. For tropical chickens I am not sure.

SoT: Interesting candidate breeds are - West African taurine cattle (N'Dama, Baoule, Lagunaire) tolerant to trypanosomosis, dermatophilosis and maybe tick-borne diseases and helminthosis. Furthermore, West African hybrid cattle (Borgou) show intermediate levels of trypanotolerance and interesting productive ability. Finally indicus breeds tolerant to ticks and tick-borne diseases.

LB: In some cases there may be interesting candidate breeds. For example, the Djallonke sheep and goats in West Africa are said to be resistant or tolerant to trypanosomosis and haemonchosis. I am not aware of any properly designed breed comparisons to support this and suggest they should be undertaken. In many cases, candidate breeds are identified by the fact that they live and survive in tropical environments without any health interventions (eg drugs or vaccines) while exotic breeds that are imported into these environments drop dead very quickly.

There are usually multiple health constraints in tropical environments and it is important at the outset to prioritize them. For many diseases there are well established control mechanisms (eg drugs or vaccines) and this will often be the best intervention. Initially, we should be most interested in breeds that are resistant or tolerant to those diseases that are difficult or expensive to control by drugs or vaccines (or these do not exist yet) and thus will have the biggest impact on flock productivity.

There was reasonable consensus at the workshop that for sheep and goats at least haemonchosis and GI nematodes in general are a high priority disease constraint in the tropics and world wide. While anthelmintic drugs do exist, there is worldwide evidence of anthelmintic resistance by the parasites. While some new anthelmintic drugs may be on the horizon, it will only be a matter of time before the parasites will be resistant to these as well. There is scope to identify more indigenous sheep and goat breeds in the tropics that are resistant or tolerant to GI parasites. Eventually these breeds may have a lot to offer to sheep and goat production in the developed world as they are doing already in a big way in the USA (i.e. through crossbreeding programs). Eventually transgenic livestock may be developed which carry resistant genes from tropical indigenous breeds.

JM: We have identified a number of breeds that are resistant to something (I am partial to nematodes).

JoM: The presentations had breeds of interest. Diseases that have no effective vaccines or drugs should be of particular importance in this respect.

AA: In South America, we have the Nelore cattle, resistant to ticks (*Rhipicephalus microplus*) and the Santa Inês hair sheep, with resistance to *Haemonchus contortus* infection. Both parasites are very important to cattle and sheep industry, respectively.

LD: N'Dama and West African Shorthorn breeds like Baoule, Lagunaire, etc. against Trypanosomosis (less clear against Cowdriosis, Dermatophilosis, Helminthosis).

JG: I believe we should rank diseases in terms of their importance by quantifying the losses in production that they are responsible for. Those diseases that result in the largest losses should receive priority and breeds should potentially be conserved if they are genetically resistant to these diseases. According to my knowledge nematodes and diseases associated with ticks, mosquitoes, flies, etc. are the most important, followed by the bacterial diseases such as mastitis and footrot. In certain countries Paratuberculosis (Johnes), Brucellosis and Salmonellosis are also very important but I believe are less so than the nematodes and tick borne diseases.

At the moment only a few breeds have been evaluated for disease resistance. The Red Masaai and Barbados Blackbelly are probably the best studied ones and have been shown to be highly resistant to nematodes. Breeds such as these with a proven history of resistance should qualify to be conserved as such. However, for the other numerous breeds where only anecdotal information is available on their level of resistance, I think we should rather focus on conserving the genes that are responsible for their resistance. This is a difficult issue because

we don't understand the mechanisms of disease resistance in the breeds and we don't know which genes are responsible for resistance. To overcome this and because it is impossible to conserve all breeds, I believe we should source a few animals (rams and if possible also ewes) from a number of different populations that have not been evaluated experimentally but where strong anecdotal evidence exist that they may be resistant or resilient to a specific disease. Sourcing different and unrelated populations will generate genetic variation and establishing such a nucleus flock/herd will ensure the genes responsible for resistance to a particular disease will survive. By applying a circular mating system where each sire is replaced by a son and each ewe is replaced by a daughter over say 20 "families" (samples from different flocks/breeds that appear to be resistant to a specific disease). By following a slow replacement policy, such a population can be conserved for a very long time without inbreeding problems while the disease resistant genes will be conserved at the same time.

MT:- For endoparasites: Djallonke sheep, Red Maasai sheep, Sabi sheep, Arsi sheep, Garole sheep, Small East African goats. For trypanosomiasis: Sheko cattle breed, West African taurine breeds (N'Dama, Baoule, etc), Orma Boran cattle, Djallonke sheep.

NM: The interesting breeds are those established in endemic areas for centuries. We must first investigate the most widely spread diseases: strongylosis, trypanosomiasis, cowdriosis.

3. How could classical and/or new technologies realistically be applied to identify the breeds in different parts of the world? What are the requirements and costs?

SCB: You have to start simple, even though it isn't so sexy. Therefore, trait measurement and quantitative analyses have to be the first step. If you want to demonstrate breed differences in a certain region, then do a breed comparison. With molecular techniques, the problem isn't so much the cost (often money can be sourced), but the fact that unless you are careful it can be a complete waste of time - i.e. negligible benefits compared to selecting on phenotype. Further, to routinely implement molecular techniques in a breeding context requires a lot of infrastructure if it is to be sustainable. Possibly this can be done in Brazil, through Embrapa, but it would be difficult in most other developing countries. It is difficult in most 'developed' countries. Particularly because there are very few 'off the shelf' tests that can be used, and none that I'm aware of that are applicable to tropical diseases or performance.

But surely the question to address to each circumstance is what NEEDS to be done?

- It may simply be sufficient to show that one breed truly is more productive than others in the same region

- You may wish to demonstrate the attributes by which one breed is better, e.g. better trypanotolerance or worm tolerance, so that you can then consider using this breed in other regions with similar environments

- Only if sustainable infrastructure is available, a longer-term breeding programme can be considered

- Molecular tools may only be truly appropriate in a very small number of cases. But there may be other reasons for investing in them, including training and maintenance of local expertise (e.g. avoiding loss of local expertise, i.e. 'brain drain'), leverage of funding from organisations such as IAEA, etc. But in this case, the aims for using this technology must be very clear, and NOT sold on a false promise such as 'faster genetic progress'.

SoT: The identification of tolerant breeds is based on the record of phenotypes, and ideally on the comparison with other susceptible breeds present in the same region. The record of phenotypes is carried out in experimental conditions or in the field. Ideally, field records must

be preferred in order to allow for genotype by environment interactions. However, it requires usually a strong investment to: i) monitor the animals, ii) follow variables linked to the disease diagnosis (through direct parasites observation, serological or PCR techniques) since infection date and challenge are not controlled, iii) measure phenotypes (e.g. PCV, growth), iv) assess covariables interfering with phenotypes (co-infection, pregnancy, food supply). Costs are coming from technicians, diagnostic and offsets for farmers.

Added interesting information: genotyping to assess breeds relationship and diversity (microsatellites or SNP).

LB: The first step is to do a comprehensive literature search including the grey literature. For example, I was surprised that I could not find much information on disease resistance in cattle or buffalo in Asia. Admittedly I did not have much time to do this but probably more importantly I did not have the time or resources to search the grey literature. A fairly recent review (Baker and Gray, 2004) includes a comprehensive review of sheep and goat breeds that have been shown to be resistant to GI parasites in Asia and Africa. A large proportion of the literature cited is grey literature. It is possible that some of the literature or information required is contained in either the FAO DAD-IS database or in ILRI's DAGRIS data base (is there any link between these databases yet?) (*Editor comment: unfortunately not*). The DAGRIS database may be more suitable for this search as it contains links to publications rather than just survey data?

Once candidate breeds have been identified that appear to be resistant or tolerant to important diseases, then properly designed breed comparisons should be undertaken to quantify the resistance properly. This assumes that adequate phenotype(s) are available to measure the resistance such as faecal egg counts or packed cell volume for resistance to GI parasites.

JM: For a nematode perspective, FEC, PCV/FAMACHA could go a long way to identify such breeds in many parts of the world. The FAMACHA is relatively inexpensive, but the training to apply it properly would require some extensive manpower (i.e. setting up workshops to extend the technology to as many as possible). The FEC would be more costly and probably not feasible in many areas, but it would be covered as a thing to do where it can be done. The concept would be to train trainers that can then go out and teach producers and also collect data.

JoM: At present the technologies for identification of resistant breeds are expensive. More work to develop simpler tools (even pen-side tests!) should perhaps be given emphasis.

AA: As far I know classical technologies are being used successfully to characterise resistant breeds. They are relatively inexpensive, such as nematode faecal egg counts and body weight gain and can be easily used to study animals raised in contaminated environments. Logically, new technologies can be very useful for the understanding of the molecular and genetic mechanism involved in such resistance.

LD: Differences between breeds have to be identified under field conditions. That is not possible without a sufficiently large recording scheme (sufficiently large trials).

JG: Establishing a unique population by sampling different unevaluated flocks/breeds for each of the diseases that are considered to be the most important, will ensure that the disease resistant genes are conserved. This population should be established, managed and maintained in an environment where the disease is endemic. Production and reproduction traits should be measured and the incidence of the disease be recorded in each population. By also recording pedigrees in each flock, the performance data should be used to continuously select for

disease resistance using classical quantitative genetics. This information will provide the foundation for molecular genetic research to identify SNP markers and potentially the genes that are responsible for resistance to each disease.

MT: Molecular techniques could be useful in identifying resistant populations if supported with phenotypic information. However, this approach is still being tested in developed countries and affordability of this technique for developing countries is questionable. Classical technologies such as the use FEC combined with FAMACHA or PCV are important available tools particularly if implemented in a communally grazed smallholder flocks or herds.

NM: The use of genomic tools is unrealistic in developing countries because it implies large population reference size and high costs. For the moment, it would imply a reliance of the South on the technology and financial resources of the North.

Anyway, performance recording is the basis of genetic identification and improvement and must be conducted in the most sustainable and rigorous way. Collaborations are possible and have to be encouraged on this topic.

4. What type of collaboration between developed and developing countries is needed?

SoT: The collaboration must help the developing countries to promote their breeds and their genetic improvement programs, through:

- Training for researchers, students and technicians, on diagnosis techniques, phenotype assessment, data base elaboration and statistical analyses;
- Capacity building for laboratory analyses (diagnosis techniques), establishment of experimental station;
- Support the establishment of breeders' organisations and institutional organisations to develop sustainable genetic improvement program.

LB: The developing country personnel should be able to undertake the literature review but may need help to access the international reference databases (e.g. like Science Direct). They may also need help and funds to undertake the breed comparison experiments which are not trivial undertakings. In particular, they may need help on the animal health side to measure the disease resistance phenotypes, which may require sophisticated equipment and labs, depending on the disease being studied. They may also need assistance with analysis of the data once collected.

JM: No matter what diseases are considered, it would probably require some extensive collaboration to review, setup and administer such programs to ensure that efforts are reasonable and meaningful data can be acquired.

JoM: Most of the resistant breeds are located in the developing world. The identification tools are however mostly in the developed world. So, we need technology transfer to the third world and collaboration between the two worlds to make the tools cheaper.

AA: Training people from developing countries in PhD programs in institutions with high standard of research could facilitate the collaboration.

LD: Since in many countries the infrastructure is very poor, and sometimes also the scientific capacity, some support is needed for both aspects.

JG: I believe a collaborating partnership should be established between countries that are interested to participate in a project of this nature. Ministers of Agriculture of countries where the important diseases are found, and obviously that have potentially resistant breeds, should be approached and canvassed for their support to establish and manage a unique population that is resistant against a specific disease that is endemic in a country. Those countries that are interested and are willing to participate can make an in-kind contribution to establish a population for each of the major sheep and cattle diseases. A joint meeting should be held to decide which country will host which population. This will be determined by what facilities, resources and expertise are available. Managing and establishing each population will obviously require specific skills which are available in both the developed and developing countries.

MT: The type of collaboration could be bilateral or multi-lateral! North-South, South-South collaboration is needed for initiating multi-country projects (e.g. for Djallonke sheep evaluation). Cost could be shared among countries. In-kind contributions through provision of phenotypic data would be an asset. Animals should however be evaluated in areas where they are finally be used.

NM: Joint effort between developed and developing countries is needed for the conception of breeding schemes adapted for developing country conditions, the choice of traits for disease resistance and financial support until self-reliance of the breeders.

5. What are the perspectives for the sustainable use and development of such breeds in different parts of the world?

SCB: Lets be honest! In many developing countries, the prospects for effective conservation and exploitation are probably quite bleak. Only where there is sustainable infrastructure and governance, proper progress can be made.

SoT: In West Africa perspectives for use and development of such breeds are not good. The main problems are linked to the absence of breeders' organisation and institutional organisation. In Europe, the development of local breeds and their genetic improvement were strongly supported and funded by the state. Currently, no such organization seems present in West African countries and this problem is strengthened by the lack of financial means.

The Ministries of Agricultural must get involved in breed development, and must support farmers in order to propose breeding objectives and establish a suitable organisation (open nucleus system, pedigree record or relationship estimates using molecular markers).

Breeds development can be based on classical "quantitative genetics approach", with the need to estimate breeding values, through phenotypes assessment, selection criteria, and pedigree records, or on new technologies, using MAS or genomic selection. However, in any cases, phenotypes must be recorded, and, for genomic selection, the number of animals that must be phenotyped and genotyped is so high that it seems not achievable yet.

LB: This is a subject which only got cursory attention at the workshop and which in my opinion requires a lot more attention. There is urgent need for smallholder farmers in the tropical developing world to be made more aware of the value of their local indigenous livestock even though they may not be the biggest or most good looking livestock. A good example is the Red Maasai sheep in Kenya. Dorper sheep were imported into Kenya in the 1960s from South Africa and Zimbabwe for their size, colour (white with black heads) and

conformation. It has been clearly shown that in the areas of Kenya with a high endoparasite challenge (e.g. the coast and western Kenya) that the most economically profitable breed of sheep is the Red Maasai while in more arid and semi-arid areas of Kenya the Dorper has a role to play either as a purebred or in a crossbreeding programme (Baker *et al.*, 2004).

Some years ago, FAO was developing breeding plans for smallholder farmers in the tropical developing world. What happened to this endeavour? (*Editorial comment: FAO has just published Guidelines about this topic "Breeding strategies for sustainable management of animal genetic resources - guidelines "which are available under <http://www.fao.org/nr/cgrfa/cgrfa-meetings/cgrfa-comm/twelfth-reg/en> - information documents CGRFA-12/09/Inf.11*). Recently ILRI and partners have also been researching community-based breeding programmes for indigenous livestock.

JM: When I did some work in Haiti, local producers traveled (sometimes many miles) to mate their breeding does with a good buck.

JoM: Their economic advantages need to be well documented. I believe that way livestock keepers will find them attractive to keep. Breeding schemes should also be instituted.

AA: The use of resistant breeds has become essential to keep production viable economically, especially with the increase in occurrence of drug-resistant populations of parasites.

LD: In the low input systems, and under high infestation with tsetse flies, the trypanotolerant breeds will still be used for a long time. However, the herd owner wants to have as much utility as possible from his livestock. Thus, in situations of higher inputs and less tsetse challenge, the livestock owner might quickly switch to more 'productive' but less tolerant breeds. In the cotton area of West Africa, there seems to be a preference for Zebu cattle in spite of the trypanosomosis risk. A possible solution might be to make the trypanotolerant breeds more productive.

JG: It is expected that the micro and macro parasites will become more resistant to the available chemicals. As labour is also becoming a critical issue and animal welfare issues are a major issue in many countries, I suspect that more and more farmers will adopt easy care breeds depending on their unique circumstances. Breeding for disease resistance will become more important, but with the availability of resistant animals, some farmers may replace their existing breed with an alternative type. This is already happening in Australia where many farmers in the extensive regions have replaced the Merino with the recently imported Dorper breed. The main motivation for this replacement is that the Merino is labour intensive and highly susceptible to flystrike whereas the Dorper is a hardy hair breed that does not need shearing, produces an excellent carcass under extensive conditions and is not susceptible to flystrike.

MT: The most important aspect is the sustainable use and development of such breeds or genes. Implementing genetic improvement program and delivery of genetic change remains a challenge of all times for smallholders. For this, there is a need for setting-up community-based genetic improvement programs. This could be used for various projects that attempts to improve and conserve such breeds.

NM: Indigenous livestock breeds are the guarantee of the future livestock production, in the South through implementation of sustainable breeding scheme and in the North through exploitation of their resistance/resilience/tolerance genes (absorption, synthetic breed).

ANNEX 2: WORKSHOP PROGRAM

22 June, 2009

08:45-09:15	Registration
Session 1: Introduction	
09:15 – 10:00	Welcome by the Animal Genetics Division, FAO (Irene Hoffmann) (15 min)
	Workshop program, objectives and expected outputs (Marie-Hélène Pinard-van der Laan) (15 min)
	Self introduction (15 min)
Session 2: Current research and latest findings in the field of breeding for disease resistance in ruminants and host-pathogen interactions	
Facilitator: Badi Besbes	
10:00 – 10:30	A review: Assessing Evidence for Disease Resistance in Livestock (Steve Bishop)
10:30 – 11:00	Coffee break
11:00 – 11:30	A review: latest findings in the host-pathogen interactions in parasitic diseases? Can they be used for practical breeding? (Sophie Thevenon)
11:30 – 12:30	General discussion and recommendations of Session 2
12.30 – 14.00	Lunch break
Session 3: Actual standing and perspectives for the sustainable use and development of resistant or tolerant breeds	
Facilitator: Matthias Gauly	
14:00 – 14:30	Actual standing and perspectives for the sustainable use and development of parasite resistant or tolerant breeds in developed regions: Australia and New Zealand as an example (Johan Greeff)
14:30 – 15:00	Actual standing and perspectives for the sustainable use and development of parasite resistant or tolerant breeds in Asia and other regions (Leyden Baker)
15:00 – 15:30	Actual standing and perspectives for the sustainable use and development of parasite resistant or tolerant breeds in the US (Jim Miller)
15:30–16:00	Actual standing and perspectives for the sustainable use and development of parasite resistant or tolerant breeds in Africa (John Mutua Mugambi)
16:00 – 16:30	Actual standing and perspectives for the sustainable use and development of parasite resistant or tolerant breeds in South America (Alessandro Amarante)
16:30 – 17:00	Actual standing and perspectives for the sustainable use and development of trypanosoma resistant or tolerant breeds (Leo Dempfle)
17:00 – 18:00	Discussion and recommendations of Session 3

23 June 2009

Session 3: Actual standing and perspectives for the sustainable use and development of resistant or tolerant breeds	
Facilitator: Leyden Baker	
8.30–9.15	Recommendations for ways to describe local breeds for disease resistance. What are the needs? (Markos Tibbo)

9.15–10.15	Discussion and recommendations of Session 3
10.15–10.45	Tea/coffee break
Session 4: Collaboration between developed and developing countries for scientific investigations of disease resistance of candidate breeds	
Facilitator: Marie-Hélène Pinard-van der Laan	
10:45–11:15	Example of collaboration and recommendations for beneficial collaboration: Integration of tolerance to gastrointestinal parasites in creole goats into breeding programmes (Nathalie Mandonnet)
11:15–11:45	Example of collaboration and recommendations for beneficial collaboration. Integration of tolerance to trpanosomiasis into breeding programmes (Issa Sidibe)
11:45–12:45	General discussion and recommendations of Session 4
12:45–13:45	Lunch break
Session 5: Technology transfer between developed and developing countries	
Facilitator: Leo Dempfle	
13:45–13:55	Introduction What classical technologies could be realistically applied in developing countries for breed development? How can the traits of disease resistance be incorporated into breeding programs? (Leo Dempfle)
13:55–14:10	A whole genome scan for adaptive genetic differentiation in West African Cattle (Mathieu Gautier)
14:10–14:55	What new technologies could be realistically applied in developing countries for breed development? How can the knowledge be incorporated into breeding programs? (Massoud Malek)
15:00–16:00	General discussion and recommendations of Session 5
16:00–16.30	Tea/coffee break
Session 6: Benefit Sharing (ABS) and Intellectual Property Rights (IPR)	
16.30–17.00	Access and Benefit Sharing (ABS) and Intellectual Property Rights (IPR) issues that may arise from finding potential major genes in a local breed and transferring them to highly selected commercial populations, or vice versa. (Sipke Joost Hiemstra)
Session 7: Discussion, summary and conclusions of the Workshop	
17.00-17.30	Reporting and plenary discussions

ANNEX 3: LIST OF PARTICIPANTS

1. Marie-Hélène Pinard-van der Laan, UMR, Génétique Animale et Biologie Intégrative - bât 211, Equipe Génétique, Immunité, Santé, INRA - Dépt. de Génétique Animale, F-78352 Jouy-en-Josas Cedex, France, email: pinard@jouy.inra.fr
2. Badi Besbes, FAO, Animal Production Officer, Viale delle Terme di Caracalla, 00153 Rome, Italy, email: Badi.Besbes@fao.org
3. Irene Hoffmann, FAO, Chief AGAP, Viale delle Terme di Caracalla, 00153 Rome, Italy, email: Irene.Hoffmann@fao.org
4. Matthias Gauly, Department of Animal Science, University of Goettingen, Livestock Production Group, Albrecht-Thaer-Weg 3, 37075 Goettingen, Germany, email: Mgauly@gwdg.de
5. Johan Greeff, Department of Agriculture and Food Western Australia, Perth, Australia, email: johan.greeff@agric.wa.gov.au
6. Sophie Thevenon, CIRAD, UMR Trypanosomes, F-34398 Montpellier, France, email: sophie.thevenon@cirad.fr
7. R. Leyden Baker, PO Box 238, Whangamata, New Zealand, Formerly at International Livestock Research Institute (ILRI), P. O. Box 30709, Nairobi, Kenya, email: leydenbaker@yahoo.co.nz
8. Markos Tibbo, International Centre for Agricultural Research in the Dry Areas, PO Box 5466, Aleppo, Syria, email: M.Tibbo@cgiar.org
9. Steve Bishop, The Roslin Institute & Royal (Dick) School of Veterinary Studies, University of Edinburgh, Midlothian, EH25 9PS, UK, email: stephen.bishop@roslin.ed.ac.uk
10. John Mugambi, Veterinary Research Centre of Kenya Agricultural Research Institute, P.O. Box 32-00902 Kikuyu, Kenya, Tel +254 20 2519769/2020512, email: jmmugambi@hotmail.com
11. Leo Dempfle, Department of Animal Science, Technische Universität München, Germany, email: Leo.Dempfle@t-online.de
12. Issa Sidibe, Burkina, CIRDES 01 B.P. 454 Bobo-Dioulasso 01, Burkina Faso, email: sambo@fasonet.bf
13. Nathalie Mandonnet, UR143, INRA, 97170 Petit-Bourg, France, email: Nathalie.Mandonnet@antilles.inra.fr
14. Alessandro F.T. Amarante, UNESP – Universidade Estadual Paulista, Brazil, email: amarante@ibb.unesp.br
15. James E. Miller, Department of Pathobiological Sciences, School of Veterinary Medicine, Louisiana State University, Baton Rouge, LA 70803, email: jmille1@lsu.edu
16. Massoud Malek, IAEA, International Atomic Energy Agency, P.O. Box 100, Wagramer Strasse 5, A-1400 Vienna, Austria, email: M.Malek@iaea.org
17. Mathieu Gautier, INRA, UR339 Laboratoire de Génétique Biochimique et Cytogénétique, F-78350 Jouy-en-Josas, France, email: Mathieu.Gautier@jouy.inra.fr
18. Mark Bronsvort, The Roslin Institute & Royal (Dick) School of Veterinary Studies, University of Edinburgh, Midlothian, EH25 9PS, UK, email: mark.bronsvort@ed.ac.uk
19. Didier Boichard, INRA, Head of the Animal Genetics Department F-78350 Jouy-en-Josas, France, email: didier.boichard@jouy.inra.fr

20. Beate Scherf, FAO, Animal Production Officer, Viale delle Terme di Caracalla, 00153 Rome, Italy, email: beate.scherf@fao.org
21. Raffaele Mattioli, FAO, Animal Health Officer, Viale delle Terme di Caracalla, 00153 Rome, Italy, email: Raffaele.Mattioli@fao.org
- Sipke Joost Hiemstra, Centre for Genetic Resources, Netherlands (CGN), Wageningen University and Research Centre, email: sipkejoost.hiemstra@wur.nl