Animal genetic resources and resistance to disease

1 Introduction

Livestock diseases adversely affect animal production throughout the world. Livestock keepers and other stakeholders involved in promoting animal health can draw on a number of approaches to reducing these negative effects. Options at the herd level include chemotherapy, vaccination, the control of disease vectors, and appropriate management methods. However, there are often constraints to the sustainability of such disease control strategies. Problems include the environmental and food safety-related impacts of chemical treatments; the affordability and accessibility of treatments to poorer livestock keepers; and the evolution of parasite resistance to the treatments applied. Examples of the latter problem include widespread resistance of nematode parasites to anthelmintic drugs; bacterial resistance to antibiotics; resistance to antiprotozoal drugs such as those used in the treatment of trypanosomiasis; the evolution of virus resistance to vaccines for diseases such as Marek's disease; and acaricide resistance in ticks. In the case of antibiotics, there are also concerns regarding residues in the food chain, and the implications for human health of the emergence of antibiotic-resistant micro-organisms (BOA, 1999).

For many livestock diseases, evidence has been found for genetic variation in the extent to which host animals are susceptible. Two distinct phenomena must be distinguished in relation to the genetic management of disease. On the one hand, "resistance" refers to the ability of the host to resist infection. One the other, "tolerance" refers to a situation where the host is infected by the pathogen, but suffers little adverse effect.

The distinction can be important. For example, where the objective is to prevent the spread of the disease to other populations (as in the case of zoonotic diseases) disease resistance rather than tolerance is required.

Managing genetic resources in order to enhance the resistance or tolerance found in livestock populations offers an additional tool for disease control. A number of advantages of incorporating genetic elements in disease management strategies have been recognized (FAO, 1999) including:

- the permanence of genetic change once it is established;
- the consistency of the effect;
- the absence of the need for purchased inputs once the effect is established;
- the effectiveness of other methods is prolonged as there is less pressure for the emergence of resistance;
- the possibility of broad spectrum effects (increasing resistance to more than one disease);
- the possibility of having less impact on the evolution of macroparasites such as helminths, compared to other strategies such as chemotherapy or vaccination; and
- adding to the diversity of disease management strategies.

A number of approaches to the genetic management of disease can be applied, depending on the nature of the problem and the resources available. Strategies may include choosing the appropriate breed for the production environment; cross-breeding to introduce genes

TABLE 31

Selected studies indicating breed difference in resistance or tolerance to specific diseases

Disease/Parasite	Breed(s) showing greater resistance	Compared to which breed(s)	Experimental conditions	Results	Reference
Trypanosoma congolense	Djallonke sheep	Djallonke × Sahelian cross-breeds	Artificial Infection	Lower parasitaemia level, a longer prepatent period and a higher antibody response than the cross-breeds, but the cross-breeds were still heavier and grew faster	Goosens *et al.* (1999)
Ticks (*Amblyomma variegatum*; *Hyalomma spp.*)	N'Dama cattle	N'Dama × Zebu	Field conditions in the Gambia	Fewer ticks	Mattioli *et al.* (1993)
Ticks (various species)	N'Dama cattle	Zebu	Village herds in the Gambia	Fewer ticks	Claxton and Leperre (1991)
Theileria annulata	Sahiwal cattle	Holstein-Friesian	Artificial infection	Less severe clinical symptoms	Glass *et al.* (2005)
Anaplasma marginale; ticks (various species)	N'Dama cattle	Gobra Zebu	Field conditions in the Gambia	Lower serological prevalence of *A. marginale*; fewer ticks.	Mattioli *et al.* (1995)
Haemonchus contortus	N'Dama cattle	Zebu	Village herds in the Gambia	Fewer abomasal worms, lower FEC*.	Claxton and Leperre (1991)
Haemonchus contortus	Red Masaai sheep	Dorper	Lambs kept under field conditions in subhumid coastal Kenya	Lambs showed lower faecal egg count for *H. contortus*, higher PCV**, lower mortality then Dorper lambs. Estimated to be 2 to 3 times as productive as Dorper flocks under these conditions.	Baker (1998)
Haemonchus contortus	Small East African goats	Galla		Kids showed lower faecal egg count for *H. contortus*, higher PCV, lower mortality then Galla kids. Estimated to be 2 to 3 times as productive as Galla flocks under these conditions.	Baker (1998)
Haemonchus contortus	Santa Ines sheep	Ile de France, Suffolk	Lambs grazed on pastures in São Paulo State SE Brazil	Lower FEC, higher PCV, lower worm counts	Amarante *et al.* (2004)
Fasciola gigantica	Indonesian Thin Tailed sheep	Merino	Artificial Infection	Lower number of flukes recovered from liver; differences in immune response	Hansen *et al.* (1999)
Fasciola gigantica	Indonesian Thin Tailed sheep	St Croix	Artificial infection	Fewer parasites recovered from liver	Roberts *et al.* (1997)
Sarcocystis miescheriana	Meishan pigs	Piétrain	Artificial Infection	Less severely affected in terms of clinical, serological, haematological and parasitological indicators.	Reiner *et al.* (2002)
Ascaridia galli	Lohman Brown chickens	Danish Landrace	Artificial Infection	Lower worm burdens and egg excretion	Permin and Ranvig (2001)
Foot rot	East Friesian × Awassi cross-bred sheep	Pure-bred Awassi	Natural outbreak in Israel	Lower prevalence.	Shimshony (1989)
Foot rot	Romney Marsh, Dorset Horn, Border Leicester sheep	Peppin Merino, Saxon Merino	Natural transmission on irrigated pasture in Australia	Less serious lesions, faster recovery	Emery *et al.* (1984)
Newcastle Disease virus, Infectious Bursal Disease	Mandarah chickens	Gimmazah, Sinah, Dandrawi (native Egyptian breeds)	Artificial Infection	Lower mortality rate than the other breeds	Hassan *et al.* (2004)

* FEC = faecal egg count.
**PCV = packed cell volume.

into breeds that are otherwise well adapted to the required purposes; and the selection for breeding purposes of individuals that have high levels of disease resistance or tolerance. The latter approach can be facilitated if molecular genetic markers associated with the desired traits have been identified.

The starting point for all these strategies is the genetic diversity of the livestock populations. If genetic resources are eroded, potentially important means of combating disease may be lost. Moreover, there is evidence, from simulation studies, to show that populations that are diverse in terms of the number of distinct genotypes conferring disease resistance are less susceptible to catastrophic disease epidemics (Springbett *et al.*, 2003). The maintenance of diversity in terms of the genes underlying resistance provides an important resource for combating the effects of possible future pathogen evolution.

2 Disease resistant or tolerant breeds

There is much anecdotal evidence pointing to the greater disease resistance of livestock breeds indigenous to environments where they face a heavy disease challenge. When countries enter details of their livestock breeds in FAO's DAD-IS system, they have the opportunity to indicate whether the breeds have any particularly interesting or valuable characteristics – including disease resistance. In most of these cases the claims made for specific breeds have not been subject to scientific investigation. However, for many of the diseases in question, evidence is available in the scientific literature for differential disease resistance or tolerance among livestock breeds (see examples in Table 31). The following discussion highlights the information made available in DAD-IS regarding the resistance or tolerance of particular breeds, focusing on the diseases for which there is also scientific evidence that there is a genetic component to susceptibility. Table 32 presents an overview of the entries in DAD-IS that report disease resistance in mammalian breeds, and Tables 33 to 39 list the breeds reported as being resistant or tolerant to specific diseases or disease types.

TABLE 32

Mammalian breeds reported to DAD-IS as having resistance or tolerance to specific diseases or parasites

Disease	Buffalo	Cattle	Goat	Sheep	Pig	Horse	Deer
Trypanosomiasis		17	4	4			
Tick infestation/burden	1	17		1			1
Tick-borne diseases (unspecified)		4					
Anaplasmosis		2					
Piroplasmosis/Babesiosis		4				1	
Heartwater/Cowdriosis		1		1			
Internal parasites/worms	1	2	1	9	1	2	1
Fascioliasis	2			1			
Bovine leukosis		9					
Foot rot (*Bacteroides nodusos*)		1		14			
Total*	4	59	6	33	3	5	2

*Total number of entries related to disease resistance or tolerance (some breeds are reported to show resistance or tolerance to more than one disease).

2.1 Trypanosomiasis

Trypanosomiasis transmitted by tsetse flies is one of the most important animal health problems in Africa – occurring mainly in West and Central Africa, and in parts of East Africa. Other types of trypanosomiasis are significant problems both in Africa and in other regions. Parasite resistance associated with control based on trypanocidal drugs, and sustainability problems involved in the implementation of tsetse control programmes, have increased interest in the use of integrated control methods including the utilization of disease tolerant breeds of livestock (FAO, 2005). The most trypanotolerant breeds include N'Dama and West African Shorthorn cattle, as well as Djallonke sheep and goats. Despite smaller size, studies have shown that these breeds are more productive than susceptible animals under moderate to high tsetse challenge (Agyemang *et al.*, 1997). Table 33 shows the breeds reported in DAD-IS as being resistant or tolerant to trypanosomiasis.

TABLE 33

Breeds reported to DAD-IS as showing resistance or tolerance to trypanosomiasis

Species/ Subregion	Number of breeds	Most common name of breed
Cattle		
North & West Africa	15	N'dama (20), Baoulé (4), Lagune (Lagoon) (6), Bourgou (2), Muturu (2), Dahomey (Daomé) (2), Somba, Namchi, Kapsiki. Kuri, Toupouri, Ghana Shorthorn, Keteku, Somba
East Africa	2	Sheko, Jiddu
Sheep		
North & West Africa	4	Vogan (2), West African Dwarf (4), Djallonké (10), Kirdimi
Goat		
North & West Africa	4	West African Dwarf (16), Djallonké (2), Kirdimi, Diougry

Figures in parenthesis = number of countries reporting if more than one.
Note that there may be other breeds for which there is evidence of disease resistance or tolerance but for which this has not been reported to DAD-IS.

2.2 Ticks and tick-borne diseases

Ticks are a widespread problem for livestock producers, particularly in the tropics. Ticks themselves weaken animals by the withdrawal of blood, cause tick paralysis through the injection of toxins secreted in their saliva, damage hides, and provide sites for secondary infections. Moreover, they also spread a number of serious diseases, the most notable being anaplasmosis, babesiosis, theileriosis and cowdriosis (heartwater). The presence of specific tick species varies with agro-ecological conditions, some being more widely distributed than others. Resistance or tolerance to ticks, and to a lesser extent to tick-borne diseases, is well documented. For example, a number of studies indicate that N'Dama cattle show a higher resistance than Zebu animals to ticks (Claxton and Leperre 1991; Mattioli *et al.*, 1993; Mattioli *et al.*, 1995). Another example is provided by a study in Australia which found that pure-bred *Bos indicus* cattle were less susceptible to babesiosis than were cross-bred *Bos indicus* × *Bos taurus* animals (Bock *et al.*, 1999). In the case of theileriosis caused by *Theileria annulata*, Sahiwal calves, a breed indigenous to India, were found to be less adversely affected than Holstein-Friesian calves when infected with the disease (Glass *et al.*, 2005). Tables 34 and 35, respectively, show the breeds reported in DAD-IS as showing resistance or tolerance to ticks and tick-borne diseases.

2.3 Internal parasites

Helminthosis has been recognized as one of the most serious animal health constraints affecting poor livestock keepers (Perry *et al.*, 2002). Resistance or tolerance to *Haemonchus contortus*, an ubiquitous nematode worm that infests the stomachs of ruminant animals, has been subject to many studies (see examples in Table 31). The Red Maasai sheep breed, for example, is noted for its resistance to gastrointestinal worms. A study conducted under field conditions in subhumid coastal areas of Kenya found that lambs of the Red Maasai breed showed lower faecal egg counts (FEC) for *Haemonchus contortus*, and

TABLE 34
Breeds reported to DAD-IS as showing resistance or tolerance to tick-burden

Species/Subregion	Number of breeds	Most common name of breed
Cattle		
Southern Africa	8	Nguni (2), Angoni, Sul Do Save, Pedi, Bonsmara, Shangaan, Kashibi, Tswana
Southeast Asia	4	Pesisir, Limousin, Javanese Zebu, Thai
Europe & the Caucasus	1	Zebu of Azerbaijan
South America	1	Romosinuano
Southwest Pacific	3	Australian Friesian Sahiwal, Australian Milking Zebu, Australian Sahiwal
Sheep		
Southern Africa	2	Nguni (3), Landim
Buffalo		
Southeast Asia	1	Thai
Deer		
Southeast Asia	1	Sambar

Figures in parenthesis = number of countries reporting if more than one.
Note that there may be other breeds for which there is evidence of disease resistance or tolerance but for which this has not been reported to DAD-IS.

TABLE 35
Breeds reported to DAD-IS as showing resistance or tolerance to tick-borne diseases

Species/Subregion	Disease	Number of breeds	Most common name of breed
Cattle			
North & West Africa	Tick-borne diseases (unspecified)	2	Baoulé, Ghana Shorthorn
Southern Africa	Tick-borne diseases (unspecified)	1	Angoni (2)
Europe & the Caucasus	Anaplasmosis	2	Cinisara, Modicana,
North & West Africa	Piroplasmosis	2	N'dama, Noire Pie de Meknès
Europe & the Caucasus	Piroplasmosis	1	Modicana
Europe & the Caucasus*	Heartwater (Cowdriosis)	1	Creole (also dermatophilosis)
Sheep			
Southern Africa	Heartwater (Cowdriosis)	1	Damara (2)
Horse			
Europe & the Caucasus	Piroplasmosis	1	Pottok

Figures in parenthesis = number of countries reporting if more than one.
Note that there may be other breeds for which there is evidence of disease resistance or tolerance but for which this has not been reported to DAD-IS.
*Guadeloupe, Martinique.

TABLE 36
Breeds reported to DAD-IS as showing resistance or tolerance to internal parasites

Species/Subregion	Number of breeds	Most common name of breed
Cattle		
Southern Africa	1	Madagascar Zebu
Southeast Asia	1	Javanese Zebu
Goat		
Near & Middle East	1	Yei goat
Sheep		
Southern Africa	2	Madgascar, Kumumawa
Southeast Asia	3	Garut, Malin, Priangan
Europe & the Caucasus	1*	Churra Lebrijana (fascioliasis)
Latin America & the Caribbean	3	Criollo (8), Criollo Mora, Morada Nova
Near & Middle East	1	Rahmani
Buffalo		
Southeast Asia	3*	Papua New Guinea Buffalo, Kerbau-Kalang (fascioliasis), Kerbau Indonesia (fascioliasis)
Pig		
Southeast Asia	1	South China
Deer		
Southeast Asia	1	Sambar
Horse		
Southeast Asia	2	Kuda Padi , Bajau

Figures in parenthesis = number of countries reporting if more than one.
Note that there may be other breeds for which there is evidence of disease resistance or tolerance but for which this has not been reported to DAD-IS.
*Figures include breeds reported to be resistant to fascioliasis.

lower mortality than Dorper lambs (another breed widely kept in Kenya). The Red Maasai flocks were estimated to be two to three times as productive as the Dorper animals under these subhumid conditions favourable to the parasites (Baker, 1998). Similarly, greater resistance and higher productivity was found in Small East African goats a compared to goats of the Galla breed under the same conditions (ibid.). There is also some scientific evidence for resistance or tolerance to the liver fluke *Fasciola gigantica*, which is a widespread parasite. For example,

Indonesian Thin Tailed sheep have been found to show greater resistance than sheep of the St. Croix and Merino breeds (Roberts *et al.*, 1997). One sheep breed and two buffalo breeds are reported in DAD-IS as showing some resistance or tolerance to fascioliasis (Table 36).

2.4 Foot rot
Foot rot is a contagious bacterial disease of hoofed animals which causes severe lameness. It is a serious economic problem, particularly for sheep producers. It occurs more often in

temperate zones. There is evidence that some breeds are more resistant to foot rot than others. A study conducted in Australia revealed that when exposed to natural infection on irrigated pastures, the British breeds Romney Marsh, Dorset Horn and Border Leicester showed less susceptibility to foot rot (manifested by relatively benign lesions and a more rapid resolution) than did Peppin and Saxon Merinos (Emery *et al.*, 1984).

Similarly, Shimshony (1989) reports that East Friesian × Awassi cross-bred sheep showed lower prevalence of the disease than pure-bred Awassi during an outbreak of the disease in Israel. It appears that breeds originating from wetter areas where the disease is more common are less susceptible. Breeds reported in DAD-IS as showing resistance or tolerance to foot rot are shown in Table 37.

TABLE 37
Breeds reported to DAD-IS as showing resistance or tolerance to foot rot

Species/Regions	Number of breeds	Most common name of breed
Cattle		
Europe & the Caucasus	1	Sayaguesa
Sheep		
North & West Africa	1	Beni Ahsen
East Asia	2	Large Tailed Han, Small Tailed Han
Europe & the Caucasus	10	Kamieniecka, Leine, Swiniarka, Polskie Owce Dlugowelniste, Churra Lebrijana, Lacha, Bündner Oberländerschaf, Engadiner Fuchsschaf, Rauhwolliges Pommersches Landschaf, Soay
Southwest Pacific	1	Broomfield Corriedale

Note that there may be other breeds for which there is evidence of disease resistance or tolerance but for which this has not been reported to DAD-IS.

TABLE 38
Cattle breeds reported to DAD-IS as showing resistance or tolerance to leukosis

Subregion	Number of breeds	Most common name of breed
Central Asia	1	Bestuzhevskaya
Europe & the Caucasus	7	Krasnaya gorbatovskaya, Istobenskaya, Kholmogorskaya, Suksunskaya skot, Yakutskii Skot, Yaroslavskaya, Yurinskaya, Sura de stepa

Note that there may be other breeds for which there is evidence of disease resistance or tolerance but for which this has not been reported to DAD-IS.

2.5 Bovine leukosis
Bovine leukosis is a blood-borne disease caused by the bovine leukosis virus (BLV). The disease causes considerable economic losses as a result of trade restrictions, mortality and lost production, and condemnation of carcasses at the slaughterhouse. There appears to be a genetic component to susceptibility to the disease. Petukhov *et al.* (2002), for example, report differences between breeds, families, and bulls' daughters in terms of the frequency of BLV infection among cattle in West Siberia. Table 38 shows the breeds reported in DAD-IS as showing resistance or tolerance to bovine leukosis.

2.6 Diseases of poultry
Outbreaks of Newcastle disease and gumboro (infectious bursal disease) frequently devastate village chicken flocks. Both diseases have a worldwide prevalence. Outbreaks of Newcastle disease have been reported for at least a century. Four panzootic waves occurred during the twentieth century. Gumboro was first described in 1962 and epidemic outbreaks have been reported since the 1970s.

TABLE 39
Breeds reported to DAD-IS as showing resistance or tolerance to avian diseases

Species/Subregion	Disease	Number of breeds	Most common name of breed
Chicken			
North & West Africa	Newcastle disease	1	Poule De Benna
Southern Africa	Newcastle disease	1	Nkhuku
Southeast Asia	Newcastle disease	1	Red Jungle Fowl
Central America	Newcastle disease	1	Gallina criolla o de rancho
Southeast Asia	Marek's disease	1	Ayam Kampong
Europe & the Caucasus	Marek's disease	4	Borky 117, Scots Dumpy, Hrvatica, Bohemian Fowl
Duck (domestic)			
North & West Africa	Newcastle disease	2	Local Duck of Moulkou and Bongor, Local Duck of Gredaya and Massakory
Guinea fowl			
North & West Africa	Newcastle disease	2	Numida Meleagris Galeata Pallas, Djaoulés
Muscovy duck			
North & West Africa	Newcastle disease	1	Local Muscovy Duck of Karal and Massakory
Turkey			
North & West Africa	Newcastle disease	1	Moroccoan Beldi

Note that there may be other breeds for which there is evidence of disease resistance or tolerance but for which this has not been reported to DAD-IS.

A study comparing the effects of infection with Newcastle disease and infectious bursal disease virus on four Egyptian chicken breeds found that Mandarah chickens (a dual purpose breed developed through cross-breeding) showed less susceptibility than the other breeds to both diseases – indicated by significantly lower mortality rates following artificial infection (Hassan *et al.*, 2004). Similarly, there is evidence for genetic resistance to Marek's disease. Lakshmanan *et al.* (1996), for example, report that a study of Fayoumi and White Leghorn chickens revealed the former to show greater resistance to the development of tumours (see below for a further discussion of breeding for resistance to Marek's disease). Table 39 shows the avian breeds reported in DAD-IS as showing resistance or tolerance to specific avian diseases.

3 Opportunities for within-breed selection for disease resistance

Selective breeding to take advantage of within-breed variation in disease resistance is an important strategy in the control of a number of diseases. For endemic diseases, which are a continuously present in the relevant production systems (e.g. mastitis, helminthosis) selection based on phenotypic response to disease challenge is possible. In the case of mastitis, somatic cell count in milk (an indicator of bacterial infection) or clinical cases of the disease can be used as phenotypic indicators of susceptibility. These indicators are routinely recorded in dairy herds, and their variation has been found to have a large genetic component (Rupp and Boichard, 2003). The existence of an antagonistic relationship between genetic merit for production traits and susceptibility to the disease has promoted interest

Box 14
Genetic resistance to African swine fever

African swine fever (ASF) poses a serious threat to the global pork industry. ASF is a highly contagious disease causing rapid haemorrhagic death of domestic pigs. No effective vaccine is available and the only effective control strategies are strict regulation of the movement of animals and their products and rapid identification, slaughter and disposal of infected animals. Alternative approaches are critically needed.

In contrast to the severe disease observed in domestic pigs, African swine fever virus (ASFV) infection causes no clinical effects in wild native African pigs, the common warthog (*Phacochoerus africanus*) and bushpig species (*Potamochoerus spp.*). Such naturally occurring species-specific genetic resistance is valuable to the study of molecular mechanisms integral to the pathogenesis of this disease.

Breeding for genetic resistance to ASF has been attempted by cross-breeding domestic pigs with resistant species. Despite anecdotal evidence to suggest that this may be possible, interbreeding has had limited success. Alternatively, it may be possible to breed for ASFV resistance by breeding domestic pigs that have survived natural ASFV challenge. Approximately 5–10 percent of domestic pigs survive ASFV infection. Unfortunately, survivors usually succumb to eradication measures following an outbreak. Such an approach would allow study of the nature of genetic resistance and could provide founder animals for resource families that could be used to confirm and quantify genetic variation in resistance or tolerance to ASFV and for identification of associated genetic markers or QTL (quantitative trait loci).

Molecular and genomics-based studies have identified key cellular targets of ASFV proteins that are essential for virus replication or contribute to virus evasion of immune defence mechanisms. Comparative analysis of DNA sequences of these genes from pig species with varying susceptibilities may reveal mutations (single nucleotide polymorphisms or SNPs) that are associated with genetic variation in resistance. Transcriptome analysis of ASFV-infected macrophages using microarrays will provide new candidate genes that are differentially regulated during infection. Such candidate genes could be used for development of DNA marker tests for selection of animals with reduced susceptibility to disease.

Conservation of resistant breeds is critical for progress in genetic resistance to ASFV. Animals, tissues and DNA are vital resources for researchers.

Although breeding for increased resistance to ASFV may be possible, there are several factors to be considered before embarking on such a programme. One consideration is that resistant pigs that are unable to be infected by ASFV will be difficult to achieve. It is more likely that pigs will express a phenotype that is "tolerant" to the clinical effects of ASFV. While tolerant pigs may not express clinical disease, they may become infected and could shed ASFV into the environment. As such, these pigs could pose a risk to susceptible pigs in the area or undermine control strategies.

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Provided by Marnie Mellencamp.

in selection for resistance (ibid.). Many dairy cattle breeding programmes, therefore, include increasing resistance to mastitis as an objective.

Parasite resistance to anthelmintic drugs is as a major problem for the livestock sector in many parts of the world, particularly in the case of small

ruminant production. Control strategies based almost entirely on the frequent use of dewormers are increasingly regarded as unsustainable given the emergence of multiple drug resistant parasites (Kaplan, 2004). The need for alternative methods of control is highlighted by the fact that

no major new class of anthelmintic drug has been launched for around 25 years, and there appears to be little immediate prospect for the emergence of new candidates (ibid.). Interest is growing in integrated parasite management (IPM) programmes, of which breeding for genetic resistance is a component. Selective breeding of sheep on the basis of FEC has been shown to be an effective means of reducing the need for treatment with anthelmintics and of reducing the contamination of pastures with the eggs of nematode parasites (Woolaston, 1992; Morris *et al.*, 2000; Woolaston and Windon, 2001; Bishop *et al.*, 2004).

For epidemic diseases, alternative approaches have to be adopted. It is necessary to develop techniques for selection based on marker alleles associated with enhanced disease resistance (Bishop and Woolliams, 2004). In the case of Marek's disease (a viral disease of chickens), vaccine use has apparently increased the virulence of the disease. As such, breeding for resistance to the disease will become increasingly important in poultry production systems. Selection for resistance based on specific B alleles within the major histocompatability complex (MHC) (Bacon, 1987) has been used for many years to assist in the management of the Marek's disease. More recently, researchers have also identified a number of quantitative trait loci (QTL) associated with resistance to the disease (Vallejo *et al.*, 1998; Yonash *et al.*, 1999; Cheng, 2005). Other diseases for which markers for disease resistance have been identified include dermatophilosis in cattle (Maillard *et al.*, 2003), diarrhoea caused by *E. coli* in pigs (Edfors and Wallgren, 2000) and scrapie in sheep (Hunter *et al.*, 1996).

4 Conclusions

It is clear that there is a strong case for the inclusion of genetic elements within disease control strategies, particularly in the light of constraints to the sustainability of many other methods. There is well-documented evidence for

variation within and between breeds in terms of susceptibility to many important diseases, and in a number of cases this element has been incorporated within breeding programmes. However, research into the genetics of resistance and tolerance to livestock disease is rather limited in terms of the diseases, breeds and species investigated. If breeds become extinct before their disease resistance qualities have been identified, genetic resources which could greatly contribute to improving animal health and productivity are lost for ever.

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