

2006

# Safeguarding Livestock Diversity

## THE TIME IS NOW



ANNUAL REPORT 2006  
INTERNATIONAL LIVESTOCK RESEARCH INSTITUTE



SAFEGUARDING LIVESTOCK DIVERSITY

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INTERNATIONAL LIVESTOCK RESEARCH INSTITUTE

ANNUAL REPORT 2006

ILRI

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Significant contextual information in this report is sourced from the most definitive recent reports in this area, particularly the publication of the Food and Agriculture Organization of the United Nations titled *The State of the World's Animal Genetic Resources on Food and Agriculture*, available online at: <ftp://ftp.fao.org/docrep/fao/010/a1250e/a1250e.pdf>

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## Foreword

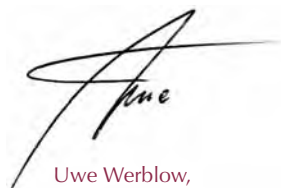
The mission of the International Livestock Research Institute (ILRI) is to help people in developing countries move out of poverty. The challenge is to do so while conserving the natural resources on which the poor directly depend. Among the natural resources important to the world's poor are the 'living assets' people accumulate in the form of their farm animals.

This report describes research helping to characterize, use and conserve our rapidly diminishing livestock genetic resources. As the greatest diversity of the world's remaining farm animals is found in developing countries, our success depends critically on the more than half a billion people in those countries who depend on livestock for their livelihoods.

ILRI and partner research addresses the rapidly evolving challenges the highly dynamic livestock sector is posing to poor people and their environments. The accelerating speed of change within the intensifying livestock systems of developing countries—changes in production, feeding, markets and consumption—means that the diverse indigenous farm animal populations of the developing world have little time in which to adapt to meet the world's changing circumstances. We are at risk of losing these populations forever.

ILRI works with the UN Food and Agriculture Organization (FAO), whose Commission on Genetic Resources for Food and Agriculture is the permanent forum where governments negotiate matters relevant to these genetic resources. The Commission in 1999 requested FAO to coordinate development of a country-driven first report on the *State of the World's Animal Genetic Resources for Food and Agriculture*, which was finalized at a conference in Switzerland in 2007.

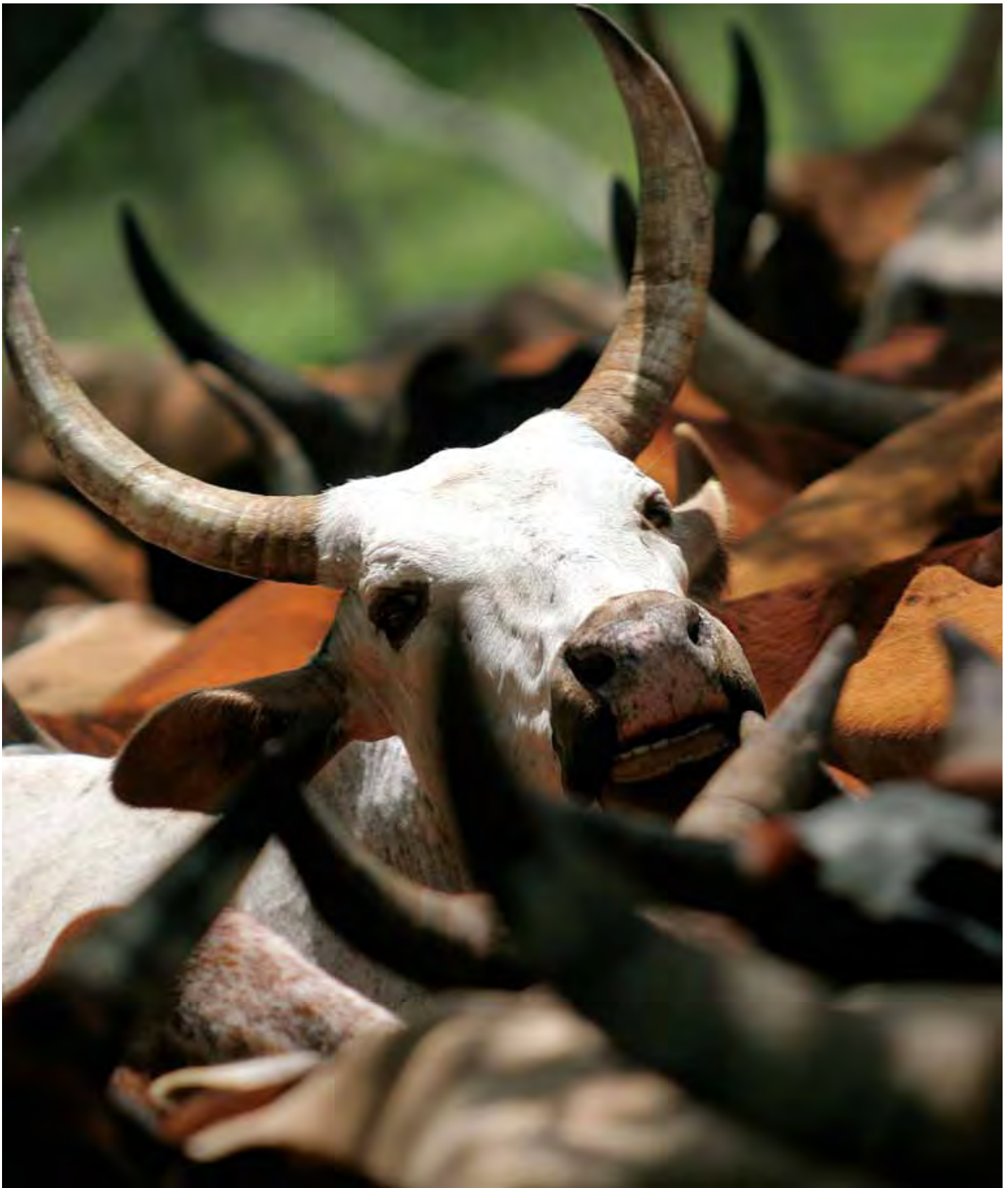
ILRI is working with FAO and many other partners to ensure that the world's poorest people benefit from their husbandry practices that are enriching the whole world—and are likely to do so far into the future.



Uwe Werblow,  
Chairman of the Board of Trustees



Carlos Seré,  
Director General



## Who We Are:

# International Livestock Research Institute

The International Livestock Research Institute (ILRI) works at the crossroads of livestock and poverty, bringing high-quality science and capacity-building to bear on poverty reduction and sustainable development. ILRI works in Africa, Asia and Latin America, with offices in East and West Africa, South and Southeast Asia, China and Central America.

ILRI is a non-profit-making and non-governmental organization with headquarters in Nairobi, Kenya, and a second principal campus in Addis Ababa, Ethiopia. We employ over 700 staff from about 40 countries. About 80 staff are recruited through international competitions and represent some 30 disciplines. Around 600 staff are nationally recruited, largely from Kenya and Ethiopia.

### PARTNERSHIPS

All ILRI work is conducted in extensive and strategic partnerships that facilitate and add value to the contribution of many other players in livestock research for development work. ILRI employs an innovation systems approach to enhance the effectiveness of its research. Fundamental change in culture and process must complement changes in technologies to support innovations at all levels, from individual livestock keepers to national and international decision-makers.

### WHY LIVESTOCK RESEARCH FOR THE POOR?

Farm animals are an ancient, vital and renewable natural resource. Throughout the developing world, they are means for hundreds of millions of people to escape absolute poverty. Livestock in developing countries contribute up to 80 percent of agricultural GDP; 600 million rural poor people rely on livestock for their livelihoods.

Globally, livestock are becoming agriculture's most economically important sub-sector, with demand in developing countries for animal foods projected to double over the next 20 years. The ongoing 'livestock revolution' offers many of the world's poor a pathway out of poverty.

Livestock not only provide poor people with food, income, traction and fertilizer but also act as catalysts that transform subsistence farming into income-generating enterprises, allowing poor households to join the market economy.

Livestock sustain most forms of agricultural intensification—from the Sahelian rangelands of West Africa to the mixed smallholdings in the highlands of East Africa

to highly intensified rice production in Asia. Research is helping farmers exploit the potential of their animals to turn the nutrient cycling on their farms faster and more efficiently.

Holding back livestock development in poor countries are inappropriate policies, scarce livestock feeds, devastating diseases, degraded lands and water resources, and poor access to markets. Research by ILRI and its partners is helping to alleviate these problems by developing new knowledge as well as technological and policy options.

#### POVERTY FOCUS

ILRI's strategic intention is to use livestock as a development tool, one that widens and sustains three major pathways out of poverty: (1) securing the assets of the poor, (2) improving smallholder and pastoral productivity and (3) increasing market participation by the poor. ILRI conducts research in five themes—Targeting research and development opportunities; Enabling innovation; Improving market opportunities; Using biotechnology to secure livestock assets; and People, livestock and the environment—and coordinates the Systemwide Livestock Programme of the Consultative Group on International Agricultural Research (CGIAR).

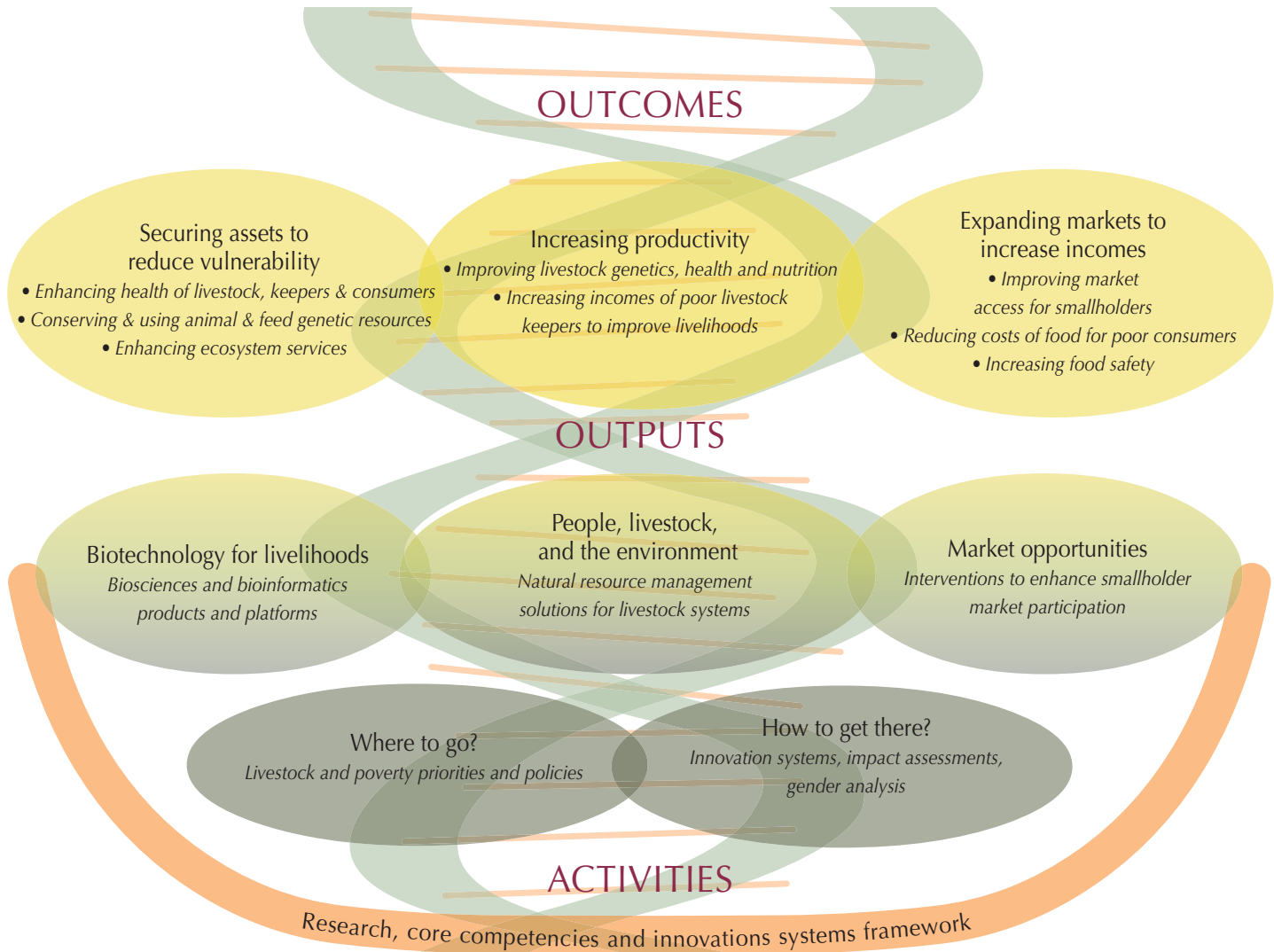
#### GOVERNANCE

ILRI is guided by a board of trustees comprising 12 leading professionals in relevant research, development and management issues. The Institute is supported by the CGIAR, an association of more than 60 governments and public- and private-sector institutions supporting a network of 15 agricultural research centres working to reduce poverty, hunger and environmental degradation in developing countries. The co-sponsors of the CGIAR are the World Bank, the United Nations Development Programme, the Food and Agriculture Organization of the United Nations and the International Fund for Agricultural Development.

#### FUNDING

ILRI is funded by more than 60 private, public and government organizations of the North and South. The institute's expenditure for 2006 was USD35.4 million. Some donors support ILRI with core and program funds; others finance individual research projects. In-kind support from national partners such as Kenya and Ethiopia, as well as that from international collaborators, is substantial and vital. This mix of generic, specific and in-kind resources is essential for the partnership research we conduct.

## KNOWLEDGE TO ACTION REDUCING POVERTY, HUNGER AND ENVIRONMENTAL DEGRADATION



## DYNAMIC LIVESTOCK SECTOR

Increasing demand in developing countries ● More complex pathways and longer market chains ● Supermarket revolution ● Food safety demands ● Pressure on natural resources to double livestock production

### ILRI's value proposition

ILRI and its partners conduct collaborative research to create and integrate knowledge that enables diverse stakeholders to develop and use innovative, livestock-based pathways out of poverty.

### New Tools to Improve Farmyard Biodiversity

ILRI released the second editions of two state-of-the-art information and training resources for managing animal genetic resources in developing countries: the Domestic Animal Genetic Resources Information System, a comprehensive database of local breeds, and a one-stop Animal Genetics Training Resource.

### ICAR-ILRI Plan Collaborations in Delhi

In January ILRI, the Indian Council for Agricultural Research and major development agencies in India conducted a high-level meeting in Delhi to map out future collaboration in livestock research on the sub-continent.



### Doctors and Vets Unite to Fight 'Africa's Oldest Enemy'

In June ILRI, the Doyle Foundation and a research consortium funded by the Wellcome Trust invited medical and veterinary experts to a 4-day workshop to better combat African trypanosomosis, or sleeping sickness, an 'orphan' disease killing people and cattle across a third of the African continent.

### Ethiopian Herders Risk Floods to Save Their Cattle

Heavy rains in Ethiopia followed the Horn of Africa's worst drought in 22 years; Ethiopians stranded on outcrops surrounded by rising waters refused to be rescued without their farm animals.

### ILRI and AU-IBAR Support 37 African Countries to Diagnose Bird Flu

With substantial support from the German Technical Cooperation (GTZ), ILRI and the Africa Union-Interafrican Bureau for Animal Resources provided 80 laboratory staff from across Africa with specialized knowledge in rapid detection of highly pathogenic avian influenza.

### ILRI and ICRAF Align Services

ILRI and its sister Nairobi-based CGIAR institute, the World Agroforestry Centre (ICRAF), are aligning services to increase institutional efficiencies so as to release more resources for their research programs; a joint ILRI-ICRAF Research Methods Group was started this year.



### African Animal Feeds Database Launched

In October the ILRI-led Systemwide Livestock Programme published on the web the most comprehensive and authoritative resource on the nutritional values of African livestock feeds.



### ILRI Facilitates Regional Plan for Eastern and Southern Africa

ILRI continued to lead CGIAR Alliance efforts to develop regional plans by CGIAR centres and their partners for collective action in eastern and southern Africa; four collective flagship research projects are under development.

### Belgian Senators Visit Kenya & ILRI Project

In May a group of Belgian senators visited Kenya's Parliament and toured Belgian-funded projects, including one ILRI conducts with Maasai herders in Kitengela, a wildlife-rich rangeland on the outskirts of Nairobi.

### ILRI Receives Strong Endorsement by External Experts

ILRI's second External Program and Management Review reported in October that ILRI is holistically and effectively addressing livestock-related problems relevant to the poor, an 'orphan component of international agricultural research'.

### LEAD Launches *Livestock's Long Shadow*

At a conference in Bangkok in November, the inter-institutional Livestock, Environment and Development Initiative, on whose steering committee ILRI sits, launched a high-profile report synthesizing information on the environmental and related impacts of global livestock production.



### Beijing Hosts Livestock-for- Development Professionals

In mid-April ILRI supported a Beijing meeting of 500 livestock experts promoting international cooperation in livestock services to enhance rural development; China's livestock production, in big transition, reached USD162 billion in 2005, about 35% of China's agricultural output.

### White Papers Cite ILRI Research Linking Climate Vulnerability and Poverty

A new strategy for the Department for International Development and the UK's Stern Review on Climate Change were among the high-profile White Papers using and quoting ILRI analyses mapping Africa's climate vulnerability hotspots.



### Make Poverty History Stalls

Progress in meeting a series of high-level and highly promoted initiatives launched in 2005 to address poverty and hunger stalled, with many donor agencies failing to honour their financial commitments and suspension of the Doha Round of multilateral trade negotiations working for fairer deals for developing countries.

### ILRI Wins 6 CGIAR Awards

ILRI captured 6 CGIAR Science Awards this year: Outstanding Scientific Article (published in *Science* by ILRI and partners at The Institute for Genomic Research); Outstanding Partnership with a Civil Society Organization (conducted with the Kitengela Ilparakuo Landowners Association, in Kenya); 2 honourable mentions for Outstanding Photography; and, with the CGIAR genebank community and libraries, 1 Outstanding Partnership and 1 Scientific Support prize, respectively.



### ILRI Expands Its Global Footprint

In September, ILRI's new Scottish representative for Asia, Iain Wright, took up residence in New Delhi, replacing Bill Thorpe, who had opened the ILRI Delhi office in 2004; in July a new ILRI representative for southern Africa, Zimbabwean Siboniso Moyo, opened an ILRI office in Maputo while Lucy Lapar, from The Philippines, opened an ILRI office in Hanoi.



### ILRI and IFPRI Call for Bird Flu Task Force

An international conference held in Nairobi in June by ILRI and the International Food Policy Research Institute recommended establishing an international task force to coordinate bird flu research that takes developing-country contexts into account.

### Landmark Paper Published in PNAS

In February ILRI researchers published a landmark paper in the *American Proceedings of the National Academy of Sciences* on their use of state-of-the-art genomics to hunt for proteins of the East Coast fever parasite that are promising candidates for a vaccine against this cattle-killing disease.

### Livestock 'Water Productivity' a Boon to the Poor

A CGIAR and partner report on the *Comprehensive Assessment of Water Use and Management in Agriculture* released during World Water Week in Stockholm in August makes the case for 'livestock water productivity' in developing countries.

### CAAS-CGIAR Strengthen China-CGIAR Partnership

In early April the Chinese Academy of Agricultural Sciences and ILRI and the CGIAR held a high-level consultation that included roundtable discussions on ways to strengthen research partnerships between China and the CGIAR.



### ILRI Bioinformatics becomes Specialist Node of EMBnet

Bioinformatics research and training at ILRI, including a high-performance computing facility managed as a shared facility by Biosciences eastern and central Africa, was strengthened by ILRI's acceptance this year as a specialist node of the prestigious European Molecular Biology Network.

### Canada Releases Second-Phase Funding for BecA

The Canadian Government released funds for the second phase of development of the hub of a new regional research platform, Biosciences eastern and central Africa.

### World's Most Diverse Forage Collection Comes under New Treaty

World leaders in agricultural research on 16 October signed agreements to guarantee long-term access to some of the world's most important collections of agricultural biodiversity, including accessions maintained in the ILRI Forage Genebank.

### ILRI Hosts Consultations on *World Development Report 2008*

In November ILRI hosted two days of consultation on the 2008 edition of the World Bank's flagship publication, *World Development Report*, dedicated to *Agriculture for Development*, a sign that agriculture is back on the front burner of development and political agendas.



### ILRI and Wellcome Develop FMD Roadmap

ILRI and the Wellcome Trust held a workshop in Agra, India, in December, where 55 experts in foot-and-mouth disease met to develop a technology 'roadmap' for better controlling FMD in developing countries.



### Policymakers and Scientists Rethink Pastoral Pathways out of Poverty

At a conference held in Nairobi in June, ILRI brought policymakers and scientists together to discuss ways to promote pastoral pathways out of poverty in East Africa's neglected arid lands.

### World Bank Parliamentary Network Visits Kenya and ILRI Project

Members of a World Bank Parliamentary Network came to Kenya in September and with 7 Kenyan parliamentarians visited ILRI and the World Agroforestry Centre and ILRI's pastoral project in Kitengela and other field projects.



## Introduction

This report describes research conducted by ILRI and partner organizations to improve management of livestock genetic resources in developing countries. ILRI's work in this area consists largely of characterizing local livestock breeds and delivering genetic improvements to smallholder and pastoral production systems.

The building blocks of livestock development have changed little over some 12,000 years: they are the animal genetic resources humans have at hand. Contemporary livestock form an invaluable repository of variation that can be harnessed to match constantly changing farming environments. Those managing these genetic resources today need to account for the particularly dynamic nature of livestock production in developing countries, which is demanding fast responses to fast-changing circumstances.

We regard it as axiomatic that the world must safeguard as much diversity as possible for an unpredictable future. We should also plan for changes that we can predict, such as those accompanying global warming. Many smallholder tropical farming and pastoral systems will be forced to adapt to rising temperatures, increasingly unpredictable rainfall (more droughts and floods), new disease challenges and less fodder and water. That the climate will change faster than our livestock can evolve adaptations to those changes will necessitate in some regions a complete reassessment of the nature and viability of livestock keeping and farming. Certainly how well we adapt to the effects of climate change will depend on the availability of diverse animal genetic resources suited to new conditions.

The characterization, use and conservation of populations of forages and farm animals have many issues in common. Approaches for conserving forage genetic resources, however, cannot be directly applied to animal genetic resources.

In traditional production systems, where locally adapted breeds and varieties predominate, planting seed and breeding animals are drawn from farmers' fields, herds and flocks and genetic diversity within resulting landraces is substantial. Most breeding and development activities are 'participatory' in the sense that decisions regarding the seeds to save for planting and the animals to retain for breeding are made by farmers rather than professional plant and animal breeders. But intensification of agriculture has changed these patterns of genetic resource use and development. Intensification of crop production has generally been accompanied by an institutionalized and centralized seed production sector dominated by publicly funded national and international centres and private firms. Intensification of the livestock sector is much less advanced. The animal breeding sector is far less centralized and institutionalized than the plant seed sector, although there has been substantial movement towards centralization in the poultry, pig and, to a more limited extent, dairy cattle sectors. Direct involvement of farmers in animal breeding remains substantial for the other livestock sectors, and animal genetic resource utilization and further development remains strongly participatory in certain production environments. These different structures have important implications for the conservation of global genetic resources.

Biological differences clearly require different approaches to the conservation of plants and animals but perhaps the most significant difference between the crop and livestock sectors involves institutional capacity for managing genetic resources. Many institutions in the seed sector already maintain extensive collections of plant genetic resources and help both develop and release plant varieties. Establishing a genebank for animals, on the other hand, involves long-term storage of gametes, embryos or somatic cells in liquid nitrogen. Costs to collect, cryoconserve and subsequently reconstitute animal germplasm are many times greater per preserved genome than costs to collect, store and subsequently utilize seed. As a result, those promoting the conservation of animal genetic resources have heavily emphasized *in situ* approaches, although, with the exception of a small number of developed countries, there has been little action to establish *in situ* conservation programs. Institutional capacity for conserving animal genetic resources is also limited, with only a few national *ex situ* collections existing, mainly in developed countries. Among CGIAR centres, only ILRI and the International Center for Agricultural Research in the Dry Areas (ICARDA) actively address issues of better management of animal genetic resources.

Public perceptions of the importance of managing plant and animal genetic resources also differ. It has long been accepted that international genebanks financed by the international community should preserve plant genetic diversity. The Global Trust Fund, for example, is creating a framework for long-term financial support for these genebanks so that they are independent of the short-term financial priorities of their host institutions. And the Norwegian Government is providing a last resort for plant genetic resources in the form of an international seed depository buried in a vault in the Arctic. The global community has been less prepared, however, to safeguard the world's livestock breeds, even though it takes much longer to develop an animal breed than it does to develop a plant variety. Scientists like to say that what matters gets measured, but in the case of livestock genetic resources, we have only just begun to 'measure' our invaluable domestic stock.

The preferred method of conserving animal genetic resources is preservation of live animals, which allows breeds to continue to evolve with their environments. *In vitro* methods, which preserve only current genetic status, provide an important back-up strategy when *in vivo* conservation cannot be established or cannot conserve the necessary population size. *In vitro* conservation may also be the only option in the aftermath of emergencies such as disease outbreaks or wars. The past focus on cryoconservation as a supporting tool for breeding programs has led to technically sound solutions for the main livestock species.

We shall need to reinforce our human and technical capacities for characterizing these resources and implementing measures for their sustainable use and conservation. We need, for example, to combine all available information on breed and species characteristics, origin and geographical distribution. Where possible we should include molecular characterizations.

Safeguarding our barnyard genetic resources to meet the current and future needs of the human population is a global responsibility. Every country on earth has relied for its development on genetic resources for food and agriculture that originated elsewhere; conserving those genetic resources should thus be a common concern of all countries.

Although our information on the world's remaining livestock genetic resources is imperfect, experts agree that we need to take action now rather than wait for substantially better information to become available. The accelerating threats to livestock diversity in recent years demand that we act now before a substantial proportion of those resources are lost to us. The time is now.





## Why conserve farm animal genetic diversity

The world is losing its animal genetic resources at an alarming rate through increasing losses of breeds of farm animals traditionally kept in developing countries. A full twenty per cent of the world's domesticated animals are threatened with extinction.

Research to save the biological capital of the world's poorest peoples is a win-win for all. As modernization loads many farm animal breeds into the dustbin of history, genetic engineers are salvaging priceless relics. Researchers at ILRI and partner organizations, for example, have shown that many of the genes that enable African cattle to survive poor food, little water and tropical diseases are unique because Africa's humpless cattle were domesticated by Neolithic people in Africa. Research has also disclosed that one of Africa's many forgotten flocks, the Red Maasai 'hair' sheep, has unrivalled resistance to the billion-dollar problem of intestinal worms. And other research at ILRI helped confirm that a wild salt-water-drinking camel discovered a few years ago in the Gobi Desert is a new species. The hidden genetic value locked up in these humpless cattle, hairless sheep and salt-water-drinking camels, along with an estimated 7616 other often obscure animal breeds of some 40 livestock species round the world, is of growing importance as modern methods of fighting animal diseases falter, the climate warms and markets change. Saving these breeds will help us cope with the challenges of today and tomorrow.

### History of animal genetic resources

Some 12,000 to 14,000 years ago, humans began to domesticate animals and plants and to spread their Neolithic farming across most of the world's terrestrial habitats. Thousands of years of natural and human selection, genetic drift, inbreeding and crossbreeding have led to the diversity of animal genetic resources we see today, which in turn have sustained animal agriculture in diverse environments and production systems.

Diversity in animal genetic resources is vital to all agricultural production systems. It provides the raw material for breed improvements and for adaptation to changing circumstances. As revealed by recent molecular studies, the diversity found in contemporary local livestock populations and breeds greatly exceeds that found in their commercial counterparts.

### The 'Big Five' Global Species

Remarkably few animal species were ever successfully domesticated. Only 14 of the 40 or so domesticated mammalian and bird species provide 90 per cent of human food supply from animals. On a global scale, just 5 of the 40 species—cattle, sheep, pigs, goats and chickens—are distributed widely and in large numbers. The world has over 1.3 billion cattle—about one for every five people on the planet. The world's sheep population is just over one billion—one for roughly every six people. There are about a billion pigs, one for every seven people, and 800 million goats, one for every eight people. And chickens outnumber humans by 3.5 to 1 worldwide; there are nearly 17 billion of them.

Other livestock species—water buffaloes, yaks, horses, asses, camels, llamas, reindeers, ducks, geese and turkeys—have smaller populations but are crucial to the livelihoods and survival of hundreds of millions of poor livestock keepers in developing countries and in marginal areas. For example, while the number of goat breeds fell drastically in countries of the North during the twentieth century as a result of the increasing importance of cattle, goats remain of major economic and nutritional significance for smallholders of the South, particularly in drylands and mountains and other agro-ecologically marginal areas, where other domestic animals cannot easily be kept.

With the exception of the wild boar (*Sus scrofa*), the ancestors and wild relatives of major livestock species are either extinct or highly endangered. This is a major difference from crop species, many of whose wild ancestors still exist and represent

## Global livestock species domestication events

New archaeological and genetic information is improving our understanding of the origins of livestock species. The first animal to be domesticated was the dog, used for hunting and guarding at least 14,000 years ago. Where the initial domestication took place is unknown, but many maternal lineages have been found in modern dogs, indicating multiple genetic contributions from their wild ancestor, the grey wolf, *Canis lupus*, in the Old World.

Goats were domesticated as early as 10,000 years ago in the Zagros Mountains of the Fertile Crescent. Sheep were also probably first domesticated in the Fertile Crescent, about 8000 to 9000 years ago. Archaeological information suggests two independent areas of sheep domestication in Turkey—the upper Euphrates Valley in eastern Turkey and in central Anatolia. The ancestor of the domestic pig is the wild boar, *Sus scrofa*. Extensive zoo-archaeological findings indicate that pigs were domesticated around 9000 years ago in the Near East. Both archaeological and genetic evidence indicate a second major independent domestication centre for pigs in East Asia (China) and local contributions across the geographic range of the wild boar.

Domestication of cattle has been particularly well documented, with evidence of three initial domestication events from three aurochs (*Bos primigenius*) subspecies. *B. primigenius primigenius*, domesticated in the Fertile Crescent around 8000 years ago, and *B. p. opisthonomus*, possibly domesticated as early as 9000 years ago in the northeastern part of the African continent, are the ancestors of the humpless *B. taurus* cattle of the Near East and Africa, respectively. Humped zebu cattle (*Bos indicus*) are now believed to have been domesticated at a later date, around 7000 to 8000 years ago, in the Indus Valley region of modern-day Pakistan from the subspecies *B. p. nomadicus*. Recently, a fourth domestication centre has been suggested in East Asia, but it is unclear whether it occurred independently or represents local aurochs introgression in cattle of Near Eastern origin.

The ancestor of the domestic water buffalo, *Bubalus bubalus*, is undoubtedly the wild buffalo of Asia. Two main types are recognized, based on their phenotypes, karyotypes and recent mitochondrial DNA work: the river buffalo found in the Indian subcontinent, the Near and Middle East and eastern Europe, and the swamp buffalo found in China and Southeast Asia. The two types hybridize in the northeastern part of the Indian subcontinent. They were probably domesticated separately, with possible centres of domestication of the river buffalo in the Indus Valley and/or the Euphrates and Tigris valleys some 5000 years ago, and of the swamp buffalo in China, where it was domesticated at least 4000 years ago with the emergence of rice cultivation.

There is an ongoing debate as to when and where the horse, *Equus caballus*, was domesticated. The ancestor of the domestic horse is extinct. Substantial evidence from north Kazakhstan supports the view that horses were domesticated in this area during the Copper Age around 3700 to 3100 BC.

Domestication of the donkey, *Equus asinus*, seems to have followed a much simpler process. Mitochondrial DNA studies have confirmed an African origin for the domestic donkey and have ruled out the Asiatic wild ass as a possible progenitor. Two mitochondrial lineages suggest two domestication events. One lineage is closely linked to the Nubian wild ass, *E. asinus africanus*, which is still found living wild in northeastern Sudan close to the Red Sea. The other lineage shows some affinities to the Somali wild ass, *E. asinus somaliensis*. It could, therefore, also have an African origin, although domestication in a neighbouring area (Arabian Peninsula or Fertile Crescent) cannot be excluded. Archaeological evidence from Egypt—which supports an African centre of domestication for the donkey—suggests a domestication date of around 6000 to 6500 years ago.

The domestic yak, *Poephagus grunniens*, is endemic to Central Asia and well adapted to a cold and high altitude. Yak pastoralism is widespread in the Central Asian Highlands, and the introduction of yak pastoralism was crucial to the development of year-round sustainable



occupation of the higher altitude zones of the Himalayan Plateau. It may have been connected with the establishment of Tibetan-Burman populations in this region. Today, some wild yaks, *P. mutus*, are still found on the Qinghai-Tibetan Plateau, but they may have been heavily interbred with feral domestic yak.

As in the case of the yak, the domestication of the reindeer, *Rangifer tarandus*, has allowed pastoral communities to occupy habitats that would otherwise be largely unsuitable for other livestock keeping. The oldest definitive archaeological evidence of reindeer domestication was discovered in the Altai Mountains of Siberia and has been dated to about 2500 years ago; it indicates that reindeer riding was practised at the time.

The domestication of the two-humped Bactrian camel, *Camelus bactrianus*, may have occurred in the area that is now the Islamic Republic of Iran/Turkmenistan, or further east, in southern Kazakhstan, northwestern Mongolia or northern China. The earliest evidence of domestic Bactrian camels is from the site of Sahr-i Sokta in the central part of the Islamic Republic of Iran, from where camel bones, dung and woven fibres dating from approximately 2600 BC have been recovered.

Recent ILRI genetic work indicates that the wild camel, *C. ferus*, populations of the Gobi Desert, which successfully hybridize with the domestic species, are probably not the direct maternal ancestors of domestic or feral camels. The wild ancestor of the one-humped dromedary, *C. dromedarius*, is now extinct. Domestication of the species is believed to have started around 5000 years ago in the southeastern part of the Arabian Peninsula.

The origin of the South American Camelidae has now been unravelled, with the guanaco *Lama guanicoe* and the vicuña *Vicugna vicugna* being the ancestral species of the domestic llama, *Lama glama*, and alpaca, *Vicugna pacos*, respectively. Archaeozoological evidence points to the central Peruvian Andes as the centre of origin of the alpaca 6000 to 7000 years before present. The llama was probably domesticated at the same period in the Andes around Lake Titicaca. Large-scale introgressions between the two domestic species have been



revealed—an ongoing hybridization process that probably began with the Spanish conquest, which destroyed the traditional breeding structures and management of the two species.

The ancestor of Bali cattle is the banteng, *Bos javanicus*, of which three endangered subspecies have been recognized. The domestication of the species did not, in fact, occur on the island of Bali, where there is no evidence for the presence of the wild ancestor. The species could have been domesticated in Java and/or on the Indo-Chinese Peninsula. *B. taurus* and *B. indicus* introgression has been found in Bali cattle, and Bali cattle genetic background has also been inferred in several Southeast Asian cattle breeds, suggesting that the domestic species once had a wider distribution than it has today.

The ancestor of the mithun, *B. frontalis*, is the gaur, *B. gaurus*. As in the case of Bali cattle, the centre of domestication of the species is unknown. Archaeological excavation in northeastern Thailand suggests that both species might have been domesticated as early as 7000 years ago.

The domestic chicken, *Gallus domesticus*, is descended from the wild red jungle fowl, *Gallus gallus*, with five possible progenitor subspecies. While previous molecular studies suggested a single domestic origin in Southeast Asia (Thailand), at least six distinct maternal genetic lineages have now been identified, suggesting more than one domestication centre. Archaeological information indicates a centre of chicken domestication around the Indus Valley 5000 years ago and another in eastern China as early as 7500 to 8000 years ago.

With livestock domestication events having taken place in today's developing regions of the world, these regions host the greatest livestock diversity and resources to help us address current and future challenges of livestock production. The largest diversity is expected to be found at or in close proximity to the centres of domestication events and at the crossroads of major human migratory events. Moreover, the diversity of livestock agro-ecological and production systems of the developing world have led to the emergence of livestock with unique adaptive traits.





an important source of variation and adaptive traits for breeding programs.

That few animals were ever domesticated can be explained by the difficulties of domesticating wild animals. Characteristics for successful domestication include lack of aggression towards humans, a strong gregarious instinct and willingness to ‘follow the leader’, a tendency not to panic when disturbed, the ability to breed in captivity, relatively short birth intervals, large litter size, rapid growth rate and a herbivore diet that can easily be supplied by humans. These characteristics, which encourage taming by humans, are rarely found together in a single animal species, as evidenced by repeated twentieth-century failures to domesticate the oryx, zebra, African buffalo and various species of deer.



The ancestral species of most livestock species have now been identified. Many extant domestic animal populations and breeds originate from more than one wild ancestral population, and in some cases there has been genetic admixture or introgression between species that do not normally hybridize in the wild. These admixture and hybridization events probably occurred after initial domestication and were often linked to human migration, trading or requirements of agricultural societies for new livestock phenotypes. Examples include admixture between taurine and zebu cattle, the presence of cattle genetic background in yaks and Bali cattle, Asian pig hybridization with European breeds, crossbreeding between dromedaries and Bactrian camels, and (as revealed by recent genetic studies) intensive admixture between the two South American domestic camelids (llamas and alpacas).

One of the most exciting areas of intersection between archaeology and genetics has been in documenting the locations of livestock domestication, with archaeology

guiding genetic research and genetics providing support to some controversial archaeological theories or revealing possible new geographic origins for livestock species and their diversity. We now know that nearly all major livestock species are the result of multiple domestication events in distinct geographic areas, often followed by genetic introgression between wild relatives and their domestic counterparts.

Evidence suggests that livestock were domesticated in at least 12 areas of the world. While domestication centres of both crops and livestock are intermingled in the Fertile Crescent and other areas, crop and livestock domestication seem to have occurred largely independently on the African continent and elsewhere. The following geographic areas are important primary centres of origin and, therefore, of diversity of livestock species: the Andean chain of South America (llamas, alpacas, guinea pigs), Central America (turkeys, Muscovy ducks), northeast Africa (cattle, donkeys), southwest Asia including the Fertile Crescent (cattle, sheep, goats, pigs), the Indus Valley (cattle, goats, chickens, riverine buffaloes), Southeast Asia (chickens, Bali cattle), east China (pigs, chickens, swamp buffaloes), the Himalayan Plateau (yaks) and north Asia (reindeer). Additionally, the southern part of the Arabian Peninsula is thought to be the region of origin of the dromedary, while the Bactrian camel may originate from the area that is now the Islamic Republic of Iran, and the horse from the Eurasian Steppes.

Unravelling the geographic patterns and histories of livestock dispersals is essential for identifying areas with high levels of diversity, which represent potential high-priority areas for conservation efforts. Few such mapping-intensive studies have yet been undertaken, however.

Understanding the origin, history and evolution of animal diversity is essential for designing sustainable conservation and utilization strategies. Today's livestock



## Genetic studies of cattle disclose the history of African pastoralism

Recent genetic marker analysis of indigenous cattle populations from all over Africa have now unravelled the major events in the history of pastoralism in Africa (see figure). The earliest African cattle originated within the continent, possibly as early as around 8000 BC. The exact centre(s) of domestication remain(s) unknown, but archaeological information suggests the northeastern part of the continent. These first African cattle were humpless *Bos taurus* animals. They initially dispersed north, as well as south to the borders of the tropical rainforests. Today, the only remaining descendants of these indigenous African taurine cattle are the trypanotolerant West African breeds (e.g. N'Dama and Baoulé), the Kuri of the Lake Chad Basin and the Sheko breed from Ethiopia. All these populations are now being intensively crossbred with zebu cattle (*Bos indicus*), and their unique genetic make-up is disappearing through unbalanced genetic admixture.

Humped zebu cattle arrived in Africa much later. They first appear in the eastern part of the continent perhaps as early as 2000 years ago as a result of early Arab contact or long-distance sea trade; this initial arrival resulted in the first introgression of zebu genes into the humpless African taurine cattle. The major wave of zebu arrival probably started with the Arab settlements along the East Coast of Africa from about the seventh century AD. Inland dispersal of zebu cattle probably followed the movement of pastoralists (e.g. Fulani throughout the Sahel) and was accelerated by the rinderpest epidemics of the late nineteenth century.

Southern Africa was the last area of the continent to acquire cattle pastoralism. The Bantu spread herding southward from the Great Lakes region some 2000 years ago, ultimately to San hunter-gatherers, who acquired livestock from them.

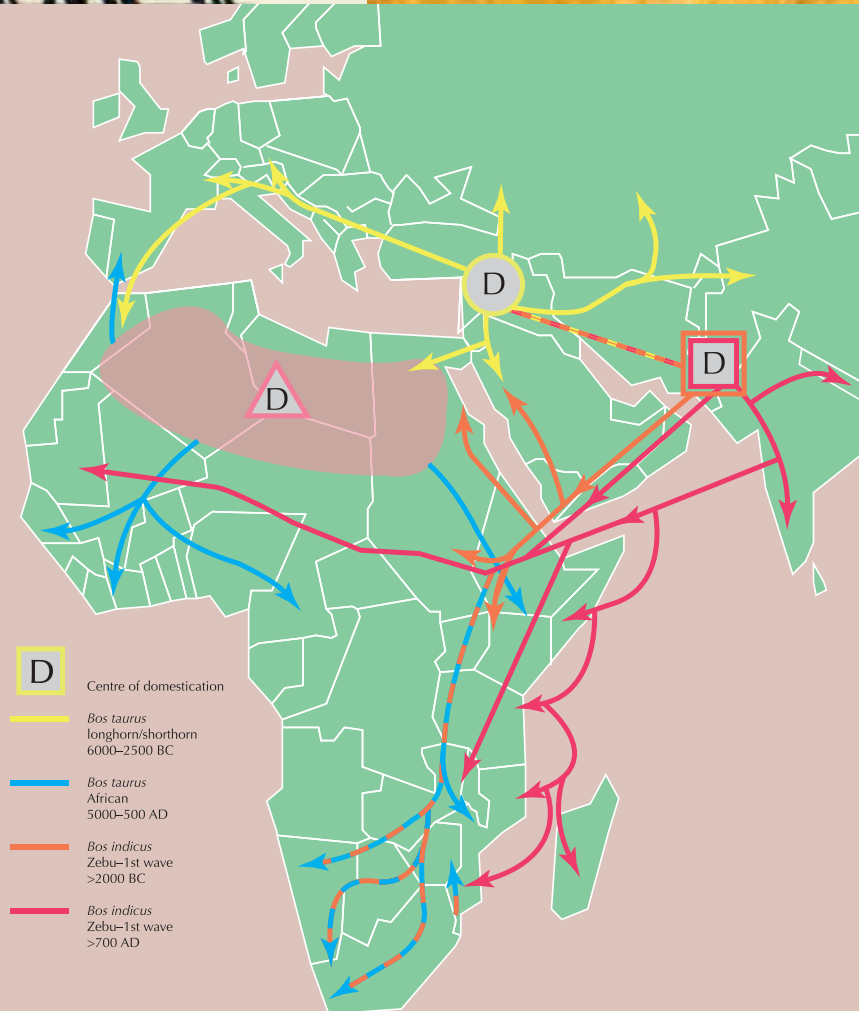


Figure: Origin and migration routes of domestic cattle in Africa

Source: ILRI 2006



## About breeds

Breeds develop in a dynamic process of genetic change driven by environmental and human selection. Both natural and artificial selection, as well as crossing between stocks and replacement of one stock with another, are typical features of breed development in livestock production systems worldwide. Despite recent global endeavours by FAO, ILRI and other organizations, the current status of livestock breeds, particularly in the developing world, remains poorly understood and notoriously difficult to quantify.

For starters, the term 'breed' has no universally accepted biological or legal definition. In developed countries most breeds are characterized by clear definitions, physical characteristics and strict definitions of the purity of their pedigree, typically regulated by a breed society backed by law. In developing countries a breed is commonly defined by local tradition, physical characteristics of the breed, its geographical location, or the ethnic group that developed it.

We use the term 'breed' here to refer a population of animals that share certain defined physical characteristics and that are not routinely bred with other populations. Within a breed there may be 'stocks', 'strains', 'varieties' or 'lines', terms used, often interchangeably, to describe populations within breeds that are phenotypically distinct as a result of human selection.

## Crossbreeding

Local breeds have often been diluted by indiscriminate crossbreeding with imported stock, often without significant gains in production levels or other desirable characteristics. Indeed, well-meaning but ill-advised promotion of such crossbreeding can lead to the total disintegration of local breeds. Moreover, loss of breeds is just one indicator of the loss of genetic diversity in farm animal species: genetic variance *within* breeds may make up to 50 per cent of the total variance. Losses of within breed diversity through indiscriminate crossbreeding can thus be as strong a threat to biodiversity as losses of whole breeds.

## Disappearing breeds

Of all the world's regions, North America has the highest proportion of extinct breeds (25 per cent) among its recorded breeds; this high figure may be related to the greater levels of breed recording in this region. Regions with the highest proportion of their livestock breeds classified as at risk are Europe and the Caucasus (28 per cent of mammals and 49 per cent birds) and North America (20 per cent of mammals and 79 per cent of birds). Europe and the Caucasus and North America are the regions that have the most highly specialized livestock industries, in which production is dominated by only a few breeds.

Problems in other regions may be obscured by the large number of breeds of unknown risk status. In Latin America and the Caribbean, for example, the risk status is unknown for 68 per cent of mammalian breeds and 81 per cent of avian breeds. And we don't know the risk status for 59 per cent of mammalian and 60 per cent of avian livestock species in Africa, where population size has not been reported for over two-thirds of breed populations. And none of these statistics takes into account the erosion of genetic diversity within breeds due to crossbreeding, a problem considered by many experts to be a major and increasing threat to livestock genetic diversity.



diversity, which originated in the wild ancestors of our domesticated farm animals, was shaped by processes of mutation, genetic drift and natural and human selection over the millennia. Although only a subset of the genetic diversity present in the ancestral species survived in their domestic counterparts, genetic diversity has continuously evolved in our domestic stock.

#### *Why conserve farm animal genetic diversity*

The world's livestock gene pool is shrinking. Extinction of any breed or population means the loss of its unique adaptive attributes, which are often under the control of many interacting genes and are the results of complex interactions between the genotype and the environment.

#### *Rates of erosion*

Of the more than 7600 breeds noted by the Food and Agriculture Organization of the United Nations (FAO), 190 have become extinct in just the past 15 years and a further 1500 are considered 'at risk' of extinction. Country reports to FAO's first *State of the World's Animal Genetic Resources*, published in 2007, show that 60 breeds of cattle, goats, pigs, horses and poultry have been lost over the last five years, an average rate of one breed lost each month. Of particular concern are the high rates of loss of indigenous breeds in developing countries, which, coupled with inadequate programs for the use and management of these genetic resources, is reducing livelihood options for the poor.

#### *Causes of erosion*

Over the last hundred years, developed countries have engaged breeding and selection programs designed to maximize the production potential of breeds and strains, often to the point where those breeds or strains require expensive and technologically advanced external inputs to survive. There has not been a similarly focused effort in most developing countries, with the result that most domesticated and semi-domesticated breeds in the South are more genetically heterogeneous and, although having lower output per animal in terms of milk, eggs or meat, are able to survive with fewer inputs. The result is lower but more stable overall production in their typical environments and a wide range of other services provided by the local animals.

One of the most significant contributing factors to the erosion of local breeds is the indiscriminate introduction of exotic breeds and germplasm from developed countries in local production systems in developing countries. Most of the extensive movement of livestock germplasm from North to South has been highly specialized animals or semen used in crossbreeding. Wholesale transfers of intensive poultry and pig production systems have been made in recent years in some developing countries.

ILRI and FAO experts concur that one of the biggest factors reducing farm animal diversity is the globalization of livestock markets. Most of the world's rapidly growing demand for livestock products is being met by intensive production systems based on a few species and breeds of high-input, high-output animals. Intensive production systems often bring with them erosion of local animal genetic resources. When pressure on land resources increases and livestock are kept more intensively, small farmers usually opt for crossbreds that offer higher returns to labour.

Other causes of the erosion of farm animal genetic resources are:

- neglect of multi-purpose animals for single productivity traits such as milk, meat or eggs.
- urbanization and intensification of animal production systems.
- political instability and natural disasters, including disease outbreaks, droughts and famine.
- lack of breed characterization and economic valuation data.

#### *Why erosion matters*

Some 11,000 years of human and natural selection have produced today's more than 7000 genetically diverse breeds within the 40 or so major livestock species. These breeds were carefully selected and nurtured by thousands of cultures to fit a wide range of environmental conditions, tasks and human needs.

The reshuffling of genes at each generation, mutation, and cross-breeding or admixture of different gene pools has offered new opportunities for natural and human selection. This evolving genetic diversity has been the basis of the enormous gains in output achieved in commercial breeds and of the adaptation of indigenous livestock to highly diverse and challenging environments.

Today's vast array of animal breeds, each characterized by its unique adaptive and productive traits, allows farmers to select stock or develop new characteristics or breeds in response to changes in the environment, threats of disease, market conditions and societal needs, all of which are largely unpredictable. Rapid and uncontrolled losses of unique and often uncharacterized or poorly understood animal genetic resources is eroding that foundation for development.

Although the precise value of the vast majority of animal genetic resources is poorly understood by both scientists and policymakers, we know that the diversity of cattle, sheep, goat, pig, poultry and breeds of other farm animal species represents an irreplaceable source of traits for livestock development in response to changing environmental and human needs. The following are among key reasons for conserving farm animal genetic resources.

- to prevent genetic erosion in populations of current value.
- to provide options for adaptation to changing environmental conditions.

## North-to-South livestock gene flows crowd out local breeds

In contrast to plant genetic resources, where genes have moved largely from South to North as industrialized countries search for disease-resistance and adaptive traits to be incorporated into new plant varieties, movements of livestock germplasm from South to North have been rare in the past century.

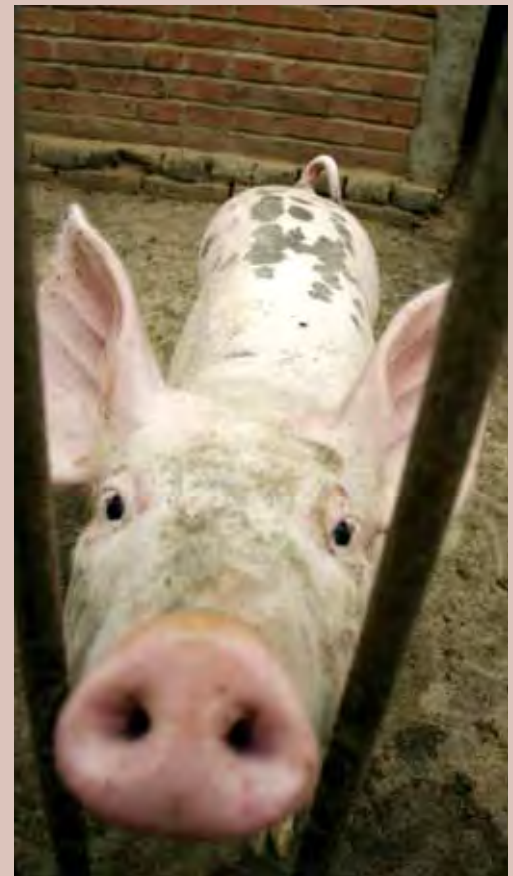
Until the beginning of the nineteenth century, when breeding organizations were first established in the North due to demand for higher producing animals, the movement of live animals caused a slow dispersal of genes largely from South to South and South to North. These flows, starting from the centres of livestock domestication (in western Asia and the eastern Mediterranean as well as Southeast Asia, the Indus Valley, North Africa and the Andes of South America), generally enhanced livestock genetic diversity.

Over the last four to five decades, in contrast, gene flows via both live animals and their semen or embryos have accelerated both among countries of the North and from North to South, propelled by globalization and the commercialization of animal breeding. In the North, technological advances have made it possible to ship semen and embryos in addition to live animals (commercial use of semen started in the 1960s, of embryos in the 1980s, and of sexed embryos in the mid-1990s.)

The ease of movement encouraged large-scale replacement of many traditional local breeds with a few high-performance exotic breeds (called by some 'Formula One animals') and helped reduce livestock genetic diversity. Large White, Duroc and Landrace pigs, Saanen goats, and Rhode Island Red and Leghorn chickens have spread throughout the world, often crowding out local breeds. The black-and-white Holstein-Friesian dairy cow, for example, is now found in 128 countries and in all regions of the world and an astonishing 90 per cent of all cattle in the North are of just six tightly defined breeds. This breed replacement process has already run its course in North America and Europe, where half of all breeds documented are now extinct or in danger of becoming so.

The South now possesses an estimated 70 per cent of the world's known livestock breeds, partly because in most countries commercial breeding has not yet taken hold, breeding stock is still traded without involvement of breeding organizations or companies and many areas still lack artificial insemination coverage. In the face of the ongoing Livestock Revolution, for example, it's probable that the transfer of pig and cattle breeding genotypes and systems will increase in rapidly developing countries of the South. In Vietnam, for example, the percentage of indigenous sows declined from 72 per cent of the total population in 1994 to only 26 per cent just eight years later, in 2002. Of the country's 14 local pig breeds, five are vulnerable, two are in critical state and three are facing extinction. And in some countries, national chicken populations have changed practically overnight from genetically heterogeneous backyard fowl to selected homogeneous stocks raised under intensive conditions. Generally, introduction of Formula One animals continues to be seen by developing countries as a solution to low productivity of local breeds, even in areas where the exotic genotypes are ill-adapted and local breeds outperform crossbreds.

It is alarming that of the nearly 3000 breeds newly reported to FAO between 1999 and 2006 and for which we have population data, 45 per cent are either at risk or already extinct. It is clear that the South, currently rich in its livestock genetic diversity, will be the hotspot of breed losses in the twenty-first century. The crowding out of local breeds is set to accelerate in many developing countries unless special provisions are made for their conservation by providing livestock keepers with appropriate support.



## International frameworks governing livestock genetic resources

The Convention on Biological Diversity (CBD) underlines the importance of conservation and sustainable use of all genetic resources and imposes obligations regarding access and benefit sharing arising from the use of genetic resources. The CBD stipulates that genetic resources be recognized as being under the sovereign rights of countries. Sovereign rights signify that countries may regulate aspects of genetic resources including property right issues and access to the resources at the national level. In 2002 a decision of the Conference to the Parties to CBD led to establishment of a Working Group on access and benefit sharing to elaborate and negotiate an international regime on access and benefit sharing within the framework of the CBD. Continued agricultural progress implies the need for continued access to the global stock of genetic resources for food and agriculture.

The FAO Commission on Genetic Resources for Food and Agriculture is the permanent forum where governments discuss and negotiate matters relevant to genetic resources for food and agriculture. There is an international treaty that regulates plant genetic resources for food and agriculture. It may be useful to analyze this treaty and see whether the animal sector can draw lessons from it, while keeping in mind the differences between plant and animal genetic resources. For example, unlike animal breeds and strains, new plant varieties can be protected by plant breeder's rights. And farm animal breeders are interested in individual animals while plant breeders focus on whole populations of a plant variety (clones). Because simply extending the content and form of the plant genetic resources treaty would be inappropriate, intergovernmental processes under FAO are considering development of voluntary 'soft' instruments to strengthen national policies and actions.

Recognizing the need to create a foundation to underpin decision-making regarding livestock genetic resources, the Commission in 1999 requested FAO to coordinate development of a country-driven first report on the *State of the World's Animal Genetic Resources for Food and Agriculture*. This report was finalized at a First International Technical Conference for Animal Genetic Resources, held in Interlaken, Switzerland, in September 2007. This conference provided the first internationally agreed framework for advancing the conservation and sustainable use of animal genetic resources for food and agriculture.



- to support sustainable animal production systems for food security.
- to provide genetic resources for crossbreeding and development of new genotypes.
- to meet the demands of new markets for livestock products and services.

In developing countries, where livestock are ubiquitous, the current storehouse of livestock genetic diversity is essential. The ‘big five’—cattle, sheep, goats, poultry and pigs—as well as 9 other popular farm animals and 26 or so more specialized species are raised by more than half a billion people either on pastoral rangelands by nomadic herders, or on mixed farms by smallholders who raise crops along with livestock, or in peri-urban areas by people who raise a few animals in their backyards. All of these small-scale livestock enterprises matter to developing-country governments because livestock account for some 30 per cent of their agricultural gross domestic product, a figure expected to rise to 40 per cent by the year 2030.

The diverse livestock production systems, like most crop production systems, are changing in response to globalization, urbanization, environmental degradation, climate change and science and technology. But the fastest changes are occurring within the livestock systems. That’s because the developing world’s rising human populations and household incomes are causing demand for milk, meat, eggs and other livestock foods to soar. As one would expect, livestock markets are growing and changing to serve that growing demand. What’s less appreciated are the changes being wrought by many of the billion-plus small-scale livestock keepers and sellers of the developing world who are changing the way they do business to help meet that growing demand.

The rate of change within the livestock sector is so rapid that many local populations of livestock developed by small-scale farmers over millennia no longer have time to evolve adaptations to their new circumstances or the new needs of their owners. They are simply dying out, and at unprecedented and accelerating rates. FAO estimates that 20 per cent of our uniquely adapted breeds of domestic animals are at risk of extinction.

#### Challenges in managing farm animal genetic resources for development

Conservation of farm animal genetic resources is more challenging than conservation of plant genetic resources. There are still large gaps in our knowledge of the origin, extent and distribution of farm animal genetic diversity, particularly in the developing world, making it difficult to prioritize conservation work. The population size of most developing-country livestock breeds is small. And in the developing world, there is little experience with *in situ* conservation methods, due to the costs of keeping breeds under threat alive on special farms, and there exist only a handful of genebank collections of farm animal genetic resources.



## Africa's 'Big Five' vintage cows

What's at stake in the current 'livestock meltdown' is nothing less than the animal basis for world food security. If we are to adapt food production systems to radically changing conditions in the coming decades, animal as well as plant genetic diversity will be critical resources for doing so. Traditional breeds offer diversity, which is the only base for future selection and adaptation. The ongoing loss of our livestock genetic heritage is tantamount to losing a road map for survival—the key to food security, environmental stability and improving the human condition. Here are five rare 'vintage cows' of Africa that could be part of that road map.

### Sheko

Only some 2,400 Sheko cattle remain alive. These relatively small animals, which are related to West Africa's ancient N'Dama cattle, are found only in the remote corner of southwestern Ethiopia, near the Sudanese border, where the Sheko people bred them for millennia for their natural resistance to disease, particularly tsetse-transmitted trypanosomosis. The Sheko are believed to be among the last remnants of Africa's original humpless shorthorn cattle, which were probably first domesticated in this region of eastern Africa.

### Ankole

There are about 3.2 million Ankole cattle in five countries of East and Central Africa. The Ankole are drought-resistant and beloved by their keepers also for their uncommon gentleness, beauty, rich milk and tasty meat (believed also to be low in cholesterol). Rapidly expanding human populations, infrastructures and markets, however, are forcing more and more farmers to replace their indigenous African Ankole cattle with exotic breeds such as the black-and-white Holstein-Friesians dairy cow, which produces much more milk. At their current rates of decline, these hardy, graceful animals could disappear within the next 50 years.

### Red Fulani

This large bony and typically red-coated animal has extremely long lyre-shaped horns. It is kept by pastoral Fulani people, who herd the animal across open semi-arid rangelands of the Sahel that criss-cross five countries of West and Central Africa. This is a dual-purpose milk and meat animal prized for its ability to cope with heat, ticks, insect bites and water and feed scarcity.

### Kuri

These hamitic longhorn humpless cattle inhabit the hot, humid shores and archipelagos of the Lake Chad Basin in Cameroon, Chad, Niger and Nigeria. They are large-bodied, typically white, and carry highly distinctive bulbous horns. The breed is adapted to the hot and humid climate and can survive long droughts. They are managed under traditional systems, feeding on grass on the small islands of Lake Chad. They are excellent swimmers and follow their herdsman through the water as they travel from one island to another; their bulbous horns are considered useful in floating. The Kuri are highly fertile animals and excellent milk and meat producers. ILRI estimates the remaining population of Kuri, now threatened with extinction, to number only some 10,000 head.

### Improved Boran

The semi-nomadic Borana tribe in southern Ethiopia and northern Kenya herd the Boran, a medium- to large-sized and long-legged zebu animal that has considerable potential as a meat breed. On acquiring them early in this century, Kenyan ranchers judiciously crossed the original Ethiopian Boran with European breeds. This scheme to maximize the potential of an indigenous breed rather than attempt to replace it with exotic types has been highly successful. Today, the Improved Boran is one of Africa's top beef breeds. Docile and well-adapted to hot, dry ranching conditions and to sparse pasture, these valuable animals have been exported from Africa to other continents, such as Australia, and from there to the USA.

## What makes livestock conservation so different from plant conservation?

### Genebanks

Whereas it appears that most countries perceive the value of conserving their plant genetic resources, many countries do not yet appreciate the value of conserving their livestock genetic resources. Establishing a genebank for animals involves long-term storage of semen, embryos or tissues in liquid nitrogen. Costs to collect, cryoconserve and subsequently reconstitute animal germplasm are many times greater per preserved genome than costs to collect, store and subsequently use seeds. Perhaps for that reason, we have no initiative for livestock germplasm comparable to the Global Trust Fund for preserving plant germplasm. And while Norway is completing construction of a seed vault carved out of solid rock inside a mountain in the Arctic as a 'fail-safe' back-up facility for plant genebanks around the world—a vault that will open in 2008 and help ensure a secure and reliable supply of genes of plants, including all of our major crop species, into the distant future—the global community has been much less prepared to make the investments needed to safeguard its livestock heritage. This despite the fact that it generally takes much longer to create a livestock breed than to create a plant variety—for some breeds it has taken centuries—and that it is clearly a global responsibility to ensure that all key resources for food and agriculture are maintained.

### Wild ancestors

With the exception of the wild boar (*Sus scrofa*), the ancestors and wild relatives of major livestock species are either extinct or highly endangered as a result of hunting, changes to their habitats, and in the case of the wild red jungle fowl, intensive crossbreeding with the domestic counterpart. In these species, domestic livestock are the only depositories of the now largely vanished diversity of the wild ancestors. This is a major difference from crop species, in many of which the wild ancestors are still commonly found at the centres of origin and represent an important source of variation and adaptive traits for future breeding programs.

### Gene flows

In contrast to plant genetic resources, where genes have moved largely from South to North, movements of livestock germplasm have been largely from North to South over the last four to five decades.

### Public awareness

Whereas public awareness of the significance of conserving the world's plant and wild animal genetic resources is fairly high, awareness of the need to conserve livestock genetic diversity at the policy level tends to be low. One result is grossly inadequate characterization of local breeds. A second is that development of

livestock genetic resources is left largely to the commercial sector, which focuses on international high-performance breeds. A third result is that people's use of livestock genetic diversity to secure their livelihoods and nutritional health, and the potential to improve on this traditional strategy, is largely unacknowledged in policy areas, international agendas and the work of international and non-governmental organizations.

### Farmer involvement

In traditional production systems, most breeding and development activities are 'participatory' in the sense that decisions regarding the seeds to save for planting and the animals to retain for breeding are made by farmers rather than professional plant and animal breeders. However, the intensification of crop agriculture has brought about institutionalized and centralized seed production sectors dominated by publicly funded firms. The animal breeding sector is far less centralized and institutionalized and direct involvement of farmers in animal breeding remains substantial.

### Institutional capacity

Perhaps the most significant difference between the crop and livestock sectors involves institutional capacity for genetic resource management. Many institutions in the seed sector already maintain extensive collections of plant genetic resources and actively contribute to the development and release of plant varieties. Institutional capacity for the conservation of livestock genetic diversity, in contrast, is scarce, with only a few national *ex situ* collections existing, mainly in developed countries. It therefore appears we shall have to substantively enhance global capacity for conservation and better use of these resources, as well as promote new institutional models and collaboration among public institutions and between public institutions and private farmers.







## How Research can Help

Most of the developing world's indigenous livestock populations will not be able to adapt in time to their rapidly changing environments and circumstances; we'll need new strategies and interventions to improve our conservation and husbandry of these resources. From a research viewpoint, it's clear that if we're going to manage the world's remaining livestock genetic resources well, we'll have to characterize the remaining populations to decide which are worth saving and why, we'll have to find ways of broadening use of those populations deemed useful, and we'll have to conserve the most important livestock genetic diversity for possible future use—by poor and rich farmers alike. It's also clear that advances in several scientific fields promise to give rise to those innovations.

### RESEARCH OPPORTUNITIES

Ongoing breakthroughs in livestock reproductive technologies and functional genomics, for example, as well as in the information fields of bioinformatics and spatial analysis, are being systematically marshaled for the first time to address this challenge. And policy and agricultural systems analysts are today articulating more judicious thinking about the production and funding of global public goods.

ILRI work to characterize animal genetic resources is mapping and quantifying diversity in livestock populations in developing countries. ILRI and its partners are developing protocols for assessing diversity in field sampling, in laboratory work and in data analyses. These protocols are being widely used by the national agricultural research systems in Africa and Asia and form bases of capacity-building initiatives to equip countries to undertake detailed studies of their high-priority local breeds.

### THE TOOLS OF CONSERVATION

To capitalize on the world's livestock genetic resources and halt the loss of valuable genes, conservationists, like animal breeders, need better tools.

#### Breed surveys

Conducting surveys of livestock breeds is time-consuming and logistically complex but essential for conservation work. We need to collect data systematically to identify breed populations and describe their observable characteristics, geographical distribution, number, uses and general husbandry, as well as their production environments. Full baseline surveys need to be undertaken once, with some elements repeated if significant changes occur. In collaboration with FAO, ILRI developed and tested an approach for collecting and analyzing on-farm breed-level information in Zimbabwe, which was then applied in Ethiopia. This work highlighted the need to verify outcomes of multivariate survey techniques with complementary molecular genetic studies. Ideally, the populations so surveyed should then be monitored on a yearly or biennial basis.

#### Information systems

ILRI scientists are facilitating broader use of these products by establishing systems that allow national partners to record and curate their own data and by completing integration of ILRI's high-resolution, research-based Domestic Animal Genetic Resources Information System (DAGRIS) with FAO's complementary country-based Domestic Animal Diversity-Information System (DAD-IS). These web-linked tools provide our national partners and other stakeholders in animal genetic resources with integrated, high-quality and publicly accessible systems for measuring, documenting and evaluating genetic diversity; the information obtained may then be used to inform developing-country genetic resource conservation and use programs. ILRI's current focus is on disease resistance and other livestock traits of critical importance for poor people living in marginal environments.

## Information systems

Database-driven information systems can greatly enhance decision-making, research, training, planning and evaluation of programs. Over the past six years, ILRI has built a unique database called the Domestic Animal Genetic Resources Information System (DAGRIS). DAGRIS synthesizes detailed research-based information on the distribution, characteristics and status of breeds of cattle, sheep, goats, pigs and chickens indigenous to Africa and Asia. DAGRIS is posted on the internet for use by all stakeholders in the livestock development and animal conservation fields, including policymakers, development practitioners and farmers. FAO has built another public-domain electronic information system, the Domestic Animal Diversity Information System (DAD-IS).

The complementary ILRI and FAO systems serve as 'gateways' to each other through electronic links via the internet. National databases of domestic animal diversity are the foundation of these international information systems and serve as essential national planning tools. They present the current state of knowledge on the size, distribution, status and utility value of a country's farm animal genetic resources; help to identify information gaps; and allow access to information on planned and ongoing management activities.

The functionality of the existing information systems is being increased to allow extraction and customized analyses of various categories of information within and between data sources. GIS-based environment and production system mapping will help users predict where there might exist important but poorly documented adaptive traits of interest such as disease resistance and optimal adaptation to the environment (temperature, humidity, altitude).



## The ILRI-FAO complementary global information systems for livestock genetic resources

### DAGRIS

[www.dagris.ilri.cgiar.org/](http://www.dagris.ilri.cgiar.org/)

Knowledge of the extent of existing genetic diversity, characteristics and use of indigenous farm animal genetic resources in developing countries is the basis for their present and future sustainable utilization. A dearth of comprehensive information on indigenous breeds in developing countries prompted ILRI to initiate in 1999 development of the Domestic Animal Genetic Resources Information System (DAGRIS). DAGRIS is a free electronic source of systematic information on indigenous farm animal genetic resources in developing countries.

In addition to containing information, obtained from a synthesis of the literature, on the origin, distribution, diversity, characteristics, present uses and status of indigenous breeds, DAGRIS uniquely includes complete references to, and abstracts of, published or unpublished scientific literature pertaining to the breeds in the system. DAGRIS is designed to support research, training, public awareness, genetic improvement and conservation.

DAGRIS provides users with useful attributes of recognized livestock breeds, including poultry. The first version of DAGRIS focused on cattle, sheep and goats of Africa; the second version, launched in 2006, enlarged the scope of the system to include breeds of selected Asian countries. The database today consists of 23,000 trait records on 152 cattle, 160 sheep, 71 goat, 124 chicken and 121 pig breeds from Asia and Africa, with more breeds and species to be covered in future. The structure and functionality of DAGRIS was designed also to capture breed-level information on geese, turkeys, ducks, yaks, buffaloes and camels and to cover breeds of Latin America and the Caribbean.

DAGRIS is being expanded to cover more species (turkeys, geese and ducks) and more countries in Asia. A new module will allow all users to upload breed-level research information into the database. Development of GIS links in the database will allow geo-referencing of breed-level information. A template for a country module of DAGRIS is also being developed to help country experts further develop and customize the database.

### DAD-IS

[www.fao.org/dad-is](http://www.fao.org/dad-is)

FAO has developed a dynamic, multilingual Domestic Animal Diversity Information System (DAD-IS) providing a summary of national breed-level information on the origin, population, risk status, special characteristics, morphology and performance of breeds as provided by FAO member countries. Each country decides when and what breed data are released through an officially designated contact person, who can enter into the system breed information, images, publications, links to external websites, contact addresses and news. DAD-IS contains more than 14,000 national breed populations from 35 species and 181 countries.

FAO built DAD-IS to help implement its Global Strategy for the Management of Animal Genetic Resources and to help countries and country networks implement their programs. DAD-IS provides countries and regions with tools to set up their own web-based information systems. Although it does not document original research results on breeds, DAD-IS provides a virtual library containing a large number of selected technical and policy documents, including tools and guidelines for research related to animal genetic resources. It offers weblinks to other relevant electronic information resources, such as ILRI's DAGRIS.

### Landscape genomics

To help resource-poor people use the world's extant livestock genetic resources more appropriately, sustainably and cost-effectively, ILRI and partners are exploring the emerging field of 'landscape genomics'. This data-hungry discipline, which integrates bioinformatics with geographical information systems, offers the opportunity not only to understand the function of the genome, but also to predict the genotype most appropriate to a given environment. This approach ambitiously aims to understand in great detail the world's livestock populations as well as the landscapes in which they are maintained and to use that information to match one to the other with unprecedented precision. Today's genomic revolution allows us to know the details of the full complement of an animal's genetic make up. Breakthroughs in systems analyses and information technologies are also enabling scientists to describe in detail the landscapes in which livestock are maintained, including the natural resource endowments and agro-ecological characteristics of those livestock landscapes, the agricultural production and marketing systems used and the cultures and socio-economies these environments encompass. Such detailed information provides scientists with an opportunity to probe genome function in unique ways. Scientists are already employing landscape genomics to understand the distribution of particular arrangements of genes (called 'alleles') in particular livestock populations and to find genetic mutations causing disease in humans. Although research in this new field relies on vast datasets and state-of-the-art data management, this approach has potential to match livestock genotypes precisely to those environments in which they are most likely to thrive or, at the very least, to survive harsh or changing environments.

Outputs of this long-term research work can add value to existing data-gathering exercises, helping us to answer such questions as: 'What genotype or combination of genotypes is appropriate in a milking cow maintained under a given management regime (e.g., free range or stall-fed), facing a given range of disease pressures (fast-killing diseases such as East Coast fever, wasting diseases such as trypanosomosis and Rift Valley fever, or production/marketing diseases such as foot-and-mouth and worm infections) or a given level of disease risk (e.g., high to medium to low tsetse fly challenge), and contending with a given set of physical stresses (e.g., seasonal ploughing, short calving intervals, water scarcity, inadequate amounts or quality of feed).

### Genomics

At the same time, ILRI is continuing to focus on determining the functions of specific genes and sets of genes, such as those controlling disease resistance or tolerance, for application in vaccines, diagnostics and therapeutics. We are expanding our long-term research to understand the genetics underlying trypanotolerance in cattle and helminth resistance in sheep to include two other high-priority diseases, avian influenza and Rift Valley fever.

A better understanding of the disease-resistant trait possessed by many developing-country livestock breeds will help us in many ways. This understanding will, for example, help us learn how these animals survive in harsh and disease-endemic areas, help us stop future infectious disease epidemics that threaten all of the world's animal genetic resources, and help us control the expected spread of tropical diseases to temperate areas due to climate change. The research needed to understand and then exploit the disease-resistant trait requires cooperation between Northern and Southern countries. This collaborative research at ILRI and elsewhere is benefiting from advances in the 'new genetics', particularly genomics, which is leading to the identification of genes or gene families controlling resistance to major diseases and to the unravelling of molecular mechanisms underlying general immune response to disease.

### Reproductive technologies

ILRI is also pilot-testing options for improving livestock production systems. These options involve adapting 'off-the-shelf' technologies, such as artificial insemination and other reproductive technologies and approaches, for smallholder systems. A major constraint to scaling out dairy improvement is the limited supply of appropriate high-quality animals of well-defined genotypes. ILRI researchers are conducting a 'proof of concept' study involving a series of reproductive technologies—*in vitro* fertilization with sexed semen followed by embryo transfer—to produce replacement heifers of well-characterized genotypes for smallholder dairy systems. If successful, this technology could increase the proportion of female calves (or males, depending on the system) and would provide an effective method for delivering first-cross (F<sub>1</sub> generation) replacement animals. It could also triple the rate of recovery from cattle losses following drought or other disasters.

### Community-based management of indigenous farm animal genetic resources

In more marginal livestock production systems, ILRI is working with others to analyze the potential for community-based breeding approaches to deliver long-term genetic change using local breeds as base material. We know we must engage the many poor farming and herding communities that have developed and maintained these local breeds. They are the guardians of much of the world's livestock diversity. Their capacity to continue this role needs to be supported—for example, by ensuring sufficient access to grazing land. At the same time, it's essential that we don't constrain development of livestock production systems by,



## DAGRIS Up Close

Complementing ILRI's DAGRIS are three other globally accessible, public-domain electronic databases on livestock biodiversity:

- (1) The Domestic Animal Diversity-Information System (DAD-IS) of FAO: <http://www.fao.org/dad-is>
- (2) EFABIS, the EAAP Animal Genetic Databank of Europe, related to the FAO global databank on animal genetic resources: <http://efabis.tzv.fal.de/>
- (3) The database of Oklahoma State University on breeds of livestock of the world: <http://www.ansi.okstate.edu/breeds/>

DAGRIS adds value to these other information sources in the following ways.

- (1) It provides key *bibliographic information* to all breed-specific information in the database to lead users to more detailed research-based information.
- (2) It helps identify information gaps in characterization information at breed level.
- (3) By including breed characterization information from *unpublished literature* (research reports, field reports, official documentation, theses), it provides 'local' and non-mainstream information that may otherwise be unavailable.
- (4) It retains the original *integrity of scientific information* by capturing results 'as published' and by providing the original data and their sources.
- (5) Its 'reports' functionality provides summaries of information that *facilitates decision-making* in research and policy formulation. (DAGRIS will offer fully functional decision-support tools in future.)

Country modules of DAGRIS are being pilot-tested in selected African and Asian nations, from which templates for other countries will be developed. The database is also being 'geo-referenced' with GIS links. The standard minimum level of detail for all geographic information in DAGRIS is being compiled for breed distribution and characterization information. This will open up exciting new opportunities for analysis as well as generating new categories of breed-level information. Biophysical GIS information on climate, ecosystems, landscapes, livestock-related resource endowments and disease burdens, for example, when overlaid on breed-level information will provide systematic analyses of adaptive attributes of indigenous livestock and enhance the selection of breeds for given areas and circumstances.

Additional system structures being introduced include a module for uploading and downloading non-curated (any relevant breed-level characterization information that is yet to be reviewed and validated for inclusion in DAGRIS) breed-level research information from the published and grey literatures and a module for presenting molecular genetic information ('DAGRIS-Mol') together with phenotypic information.



## Examples of tropical breeds possessing genetic resistance to disease

### *West Africa's N'Dama cattle*

The short, generally small, thick-set and muscular humpless N'Dama, thought to have been developed in the highlands of Guinea, is kept by farmers in free-range village production systems across 20 countries of West and Central Africa. Over some 7,000 years, these cattle developed resistance to a deadly disease transmitted by the tsetse fly. This disease kills both cattle (trypanosomosis) and people (sleeping sickness) and is said to be largely responsible for holding back development across vast areas of Africa's prime humid and sub-humid regions. The N'Dama and a few other so-called trypanotolerant African livestock breeds (including Ethiopia's Sheko cattle) are well known for their ability to survive and produce milk, meat and other products in tsetse-infested areas, where susceptible zebu and European breeds cannot.



### *East Africa's red Maasai sheep*

Red Maasai 'hair' sheep (they do not produce wool) have traditionally been kept by the pastoralist societies of East Africa. Highly resistant to gastrointestinal parasite infections and other diseases, they thrive in harsh environments ranging from drought-prone savannas to humid zones. These traits make the genes these sheep carry invaluable to the world. Work done by ILRI and partners has provided scientific evidence confirming the existence of genetic resistance to helminth parasites in the Red Maasai sheep and has drawn attention to the importance of this sheep resource. But despite a slackening global demand for wool that is promoting the spread of hair sheep elsewhere, the introduction of Dorper sheep from South Africa has caused, in little more than 15 years, pure-bred Red Maasai to almost completely disappear.



### *Asia's backyard chickens*

Native Asian chicken populations may carry adaptive genetic traits conferring resistance or tolerance to infection with highly pathogenic avian influenza. Asia's scavenging chicken populations have been historically exposed to past avian influenza and so probably possess a variety of adaptive traits, including resistance to this viral infection. Researchers are now exploring links between the genetic background of indigenous chicken populations and their susceptibility to avian influenza.



for example, disallowing breed improvements or replacements. To help address this dilemma, a few community-based conservation and breeding programs have been started. ILRI is conducting one such project.

With scientific as well as financial support from Germany, ILRI scientists are collaborating with national research organizations in Benin, Ethiopia and Kenya to improve community-based management of indigenous farm animal genetic resources. The goal of this GTZ-funded project, which started in 2004, is to reduce poverty and increase food security by supporting local communities in managing their animal genetic resources. Project scientists are focusing on building the analytical, technical, managerial and organizational skills required for such communal management.

The project began by co-developing and -testing with communities in each of the three target countries a framework for community-based management of farm animal genetic resources. By the end of the project, in early 2008, at least one community-based management program will be operational in each country. Project staff are helping the communities to quantify opportunities for selling more local animals and products (e.g., meat, milk, eggs) and to identify institutional barriers to the commercialization and marketing of indigenous livestock and livestock products.

To this end, the scientists and community members are quantifying preferences among livestock producers and consumers of livestock products for alternative livestock genotypes, estimating the costs and benefits of farmers raising those alternative breeds, and using this information to inform policy and development discussions. They are identifying policies that hamper communities in their use and conservation of indigenous livestock and recommending policies that would increase the benefits local communities derive from keeping local farm animals. And they are involving policymakers in their project implementation, in their workshops and in their 'action learning' events to sensitize them to community needs and capacities.

All of the research work—from conducting trait surveys, market appraisals, and evaluations of livestock breeds and products to analyzing data, synthesizing information and writing up reports to monitoring distributions of indigenous stock and interventions for animal health, all of which is done by national project coordinators and researchers, local research teams, technicians and enumerators,

and 12 master's and 4 doctoral students—is strengthening national capacity in using and conserving indigenous animal genetic resources. The project in addition is training the local communities in good husbandry practices (e.g., animal feeding, fattening, breeding, housing, healthcare, marketing) as well as entrepreneurship and community organization (e.g., how to follow national policies and statutes, elect officials, draft constitutions, develop budgets, and create and manage documents needed, for example, to organize cooperatives, trust funds or micro-credit schemes or to register cattle breeder groups).

The participatory ways in which these frameworks for community-based management of farm animal genetic resources have been developed and their operations are being implemented are bearing fruit. On a recent field day in Ethiopia, participating farmers showed off their fattened surplus oxen that had originated from Ethiopia's indigenous Horro cattle. Non-participating farmers rated the steers excellent and the participating farmers estimated their net return at USD100–150 per steer. The turnout on the field day was a remarkably large and mixed gathering of policymakers, national researchers, extension/development agents, farmers, and journalists. The 'show' stimulated everyone to help manage indigenous animal genetic resources through sustainable use. Similar activities are under way in Kenya and Benin.

The third annual planning workshop for this project was held on ILRI's Nairobi campus in September 2006. Proceedings of this workshop are available online at: <http://www.ilri.cgiar.org/Link/Files/2006%20Workshop%20Report.pdf>

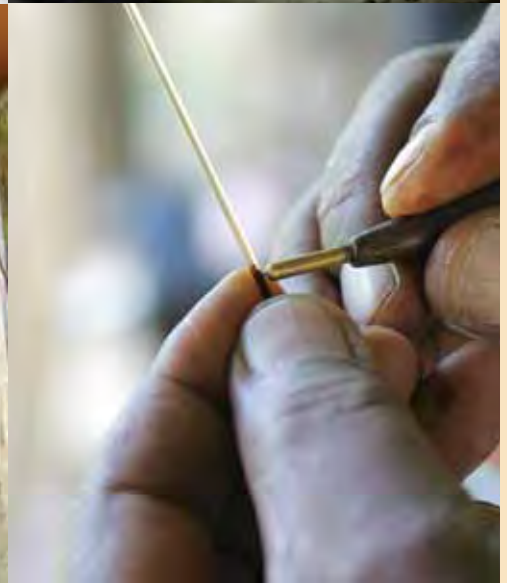
### Genetic markers

ILRI is also assessing the potential of using genetic markers and other genetic information and/or conventional breeding approaches to select animals for disease resistance in developing countries. This work supports development of strategies for using rapidly accumulating information in livestock breeding programs.

### Molecular characterization

Characterization at the molecular genetic level is undertaken to explore in quantitative and qualitative ways neutral and functional genetic diversity within and between animal populations so as to determine genetic relationships and uniqueness. In the absence of comprehensive breed characterization data and documentation of the origin and history of breeding populations, molecular marker information provides the most easily obtainable estimates of genetic diversity.

Molecular characterization is a relatively new biological frontier, involving use of different classes of genetic 'markers' and applying new and fast-evolving disciplines grouped under the generic name of genomics.





## Investigation of genetic resistance to bird flu in native chickens of the South

In developing countries, native chickens in rural areas scavenge for food. This form of poultry rearing, which is a mainstay of the poor across the developing world, has to date featured insufficiently in discussions of bird flu.

Natural selection has played a major role in the survival of these indigenous chickens and their reproductive fitness. It is expected that some, if not all, of African and Asian chicken populations have been exposed to avian influenza and will show signature of selection at genes for a variety of adaptive traits, including resistance to viral infection.

The domestic chicken (*Gallus domesticus*) is descended from the wild red jungle fowl (*Gallus gallus*). New research findings from ILRI point to multiple centers and events of domestication of the chicken in Asia: at least three major independent ones in South China, Indonesia and the Indian subcontinent, and two minor ones in the Indo-China region. Several genetically distinct domestic chicken stocks from the Indian subcontinent and Indonesia dispersed into Africa following different routes and at different periods. Commercial poultry lines (broilers and egg-layers) have a crossbred origin.

We have as yet little understanding of the importance of chicken genetic diversity in maintaining a robust resource in the face of diverse challenges. But it is clear that conflicts, commercial pressures and diseases all threaten this diversity. Highly pathogenic avian influenza is probably now the biggest threat to traditional poultry production and to poultry diversity worldwide.

Although not an entirely new disease, bird flu's causal agent—an influenza virus of the H5N1 subtype—turned aggressive in late 2003, killing whole chicken flocks, spreading to more than 50 countries in Asia, Europe and Africa and attacking people as well as birds. The global response to stop the spread of this disease called for eliminating the virus by culling all domestic birds in infected zones and restricting poultry movements. In this way, over 200 million chickens have died or been destroyed in Asia alone because of avian influenza.

With avian influenza, a pressing case for more genetic diversity and for integrating genetic traits controlling disease resistance is staring us in the face. One of the most frequently cited rationales for maintaining many different animal breeds, including poultry, is the need to

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Recent advances in molecular biology relevant to livestock breeding and the conservation of breeds and genetic diversity include the mapping and sequencing of the genomes of the most important livestock species; new technology to measure polymorphisms at loci spread all over the genome (e.g., large-scale methods to detect single-nucleotide polymorphisms, better known as ‘SNPs’); and development of microarray technology to measure gene expression.

Information obtained through the sequencing of the entire genome (achieved for chickens and almost complete for pigs and cattle), integrated with SNP and DNA microarray technology, is speeding up the search for genes of interest and is facilitating the identification of the complex regulatory pathways of gene expression for traits of interest to livestock breeders and farmers.

ILRI and collaborating laboratories are using DNA markers to distinguish and characterize indigenous breed diversity at the DNA level. In this way, we are quantifying molecular diversity within breeds, mapping livestock diversity hotspots, identifying breeds at risk and prioritizing breeds for conservation and broader use.

ILRI and collaborating laboratories are also using the genomics approach to identify genes of tropical breeds that control resistance to parasitic diseases. Researchers at ILRI and elsewhere have identified a wide range of disease quantitative trait loci (QTLs) with significant influence on production performance. If marker-delimited genome regions that control such traits are identified, the corresponding markers could be used in marker-assisted selection programs. However, ILRI and FAO concur that at present marker-assisted selection should be applied only where well-structured breeding programs are already in place. This is a high priority for developing countries aiming to improve their indigenous livestock resources.

#### Use: Access to appropriate germplasm

Each breed of farm animal suits some areas and situations better than others. Specific local environments include the conditions in which animals are managed (e.g. temperature, feed quality and quantity, disease control regimes) and the purposes for which the animals are raised (e.g. to produce meat, milk or manure, to pull a plough). Not all species are a good economic fit for one of these environments, called by scientists an ‘agri-ecological-marketing zone’, and not all populations or breeds within a species will be a good match either.

The range of substantively different zones or niches is huge, particularly when considering the extent to which farmers can often adapt conditions to suit a particular animal. At one extreme are pastoral and range lands that are inherently difficult to change; all emphasis here is put on selecting animals that best suit the available marginal resources. At the other extreme are large pig and poultry ‘factory-farms’ that can be controlled to optimize profit; here, animals are selected to best suit these human-made controlled environments. Between these extremes

are mixed crop-and-livestock production systems where there exists some scope for modifying both an animal's genetics to suit the system as well as the system itself, particularly through improved feeding systems.

Every zone naturally changes over time with, for example, changing market demands, local environmental conditions and climatic conditions. When the rate of change is slow, it is relatively easy to forecast what the local environment will be like in, say, 10 years' time and thus relatively easy to select from within the current population of farm animals those that will leave offspring best suited to predicted future conditions. When change occurs fast, however, it becomes unrealistic to select breeding animals from within the current populations of farm animals in the hopes of producing offspring with traits that will better suit the new conditions, so a local breed is crossed with another. At some point in this crossing process, a decision must be made whether breed replacement is a better choice than blending existing and new breeds. If replacement is considered the best option, the same breed of exotic sire is used for each generation. If blending is the best option, a crossbred male can be used to achieve the desired mix of local and exotic genes in the fewest number of generations.

A pastoralist faced with erratic rainfall may cope by maintaining a range of diverse genotypes, some of which can survive long dry spells. Animals generated by crossing locally adapted females to an 'exotic' (usually European) sire may be more profitable than their mothers when conditions are good, but the same animals may be the first to die in a drought. Farmers that keep both local and exotic sires can find a balance between high-profit/high-risk and low-profit/low-risk.

Although farmers are astute at picking the most appropriate local species and breeds for their environments and situations, they cannot be expected to know how an animal from another continent will perform in their environs. Responsibility for generating such knowledge officially lies with the national agricultural research systems, such as the United States Department of Agriculture or Brazil's EMBRAPA. In most developing countries, however, scarce resources exist to conduct the needed trials and extension services to disseminate the results tend to be severely limited. Where these services are unavailable, inappropriate genotypes may be introduced by private breeding companies focused more on making a profit than on promoting what is in the best long-term interests of poor farmers. For example, whereas exotic animals will suit some farmers in some high-input production systems, the same animals can prove disastrous in the low-input systems that most poor farmers employ.





combat disease. The diversity of fowl kept by small growers is probably the most important resource we have for future solutions to some of today's most urgent zoonosis problems, including bird flu. There is some evidence, for example, that areas where native chickens dominated, poultry flocks remained largely free of bird flu. But backyard poultry as well as migratory birds have been accused of being the source of the problem, millions of birds belonging to smallholders have been culled and valuable genetic diversity has been lost.



Mass culling of birds threatens poultry genetic diversity not only in the killing operations but also in re-stocking programs that supply inappropriate genotypes. These culling programs, as well as discarding unique diversity, thus risk increasing the susceptibility of re-stocked flocks to viral infections, leading to a descending spiral of infection-cull-infection.

Given their diverse origins, selection under harsh circumstances and known variation to a range of other pathogens, it is unlikely that all chicken breeds of the developing world are uniformly susceptible to bird flu. Ignoring the potential of natural immunity as a component in the management of bird flu would be short-sighted. For this reason, ILRI is conducting research with partners to understand the genetics underlying variation in response to avian influenza. There are likely to be many gene variants affecting a breed's level of disease resistance, including single genes controlling the presence or absence of cell receptors as well as gene groups regulating more general disease response mechanisms, mechanisms that recent ILRI and partner research is demonstrating to have broad applicability across a range of diseases. Other research laboratories can access the project's resources to look for genetic traits in chickens controlling resistance to other important chicken pathogens, such as the virus that causes Newcastle disease.

Most cases of highly pathogenic avian influenza in poultry and humans have been recorded in Southeast Asia, and there have also been outbreaks of the deadly H5N1 strain of bird flu in sub-Saharan Africa. It is now increasingly recognized that local and international poultry trade rather than migratory birds or scavenging chickens probably plays a significant role in the spread of bird flu.

By 25 July 2007, the World Health Organization had registered 319 laboratory confirmed human cases of infection with highly pathogenic avian influenza and 192 cases of deaths caused by avian influenza A (H5N1) in twelve countries, of which 256 and 165 cases are concentrated in South and Southeast Asia, respectively.

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Overlaying maps of genetic diversity on maps of avian influenza outbreaks worldwide and on the chicken genotypes affected (commercial or rural) supports a putative genetic component at population level for resistance or susceptibility to avian influenza. Recent evidence indicates at least one candidate gene, *Mx*, is associated with chicken resistance/susceptibility to highly pathogenic bird flu, with a clear involvement of the MHC class I haplotypes to the resistance/susceptibility trait. A comprehensive geographic and breed survey of the molecular diversity of the *Mx* gene in indigenous chicken populations may allow validation of its function in relation to resistance/susceptibility to infection with the bird flu virus.

A research partnership involving more than 20 national research institutions in Asia and Africa was set up and led by research teams at ILRI's Nairobi laboratories, at Beijing's Joint Laboratory on Livestock and Forage Genetic Resources (run by the Chinese Academy of Agricultural Sciences and ILRI), at the Institute for Animal Breeding in Germany's Federal Agricultural Research Center, and at the Research Center for Biology in The Indonesian Institute of Science.

A total of 1946 samples from 109 indigenous commercial chicken and wild jungle fowl populations from Asia, Africa and Europe were genotyped for a particular single nucleotide polymorphism, or 'SNP', at the *Mx* gene. The findings showed higher resistant allele A frequencies present in white egg-layers compared to broilers and the highest frequency of resistant allele A in indigenous chickens on the Indian subcontinent. Indigenous Chinese and Korean chickens and German fancy breeds had higher frequencies of susceptible allele G. In Indonesia, Papua New Guinea and Vietnam, three countries where highly pathogenic bird flu is endemic and there have been losses of human life, indigenous chickens had intermediate frequencies of susceptible allele G. Indigenous African chickens had a slightly higher susceptible allele G than the resistant allele A. This first extensive geographic survey of a polymorphism at the *Mx* gene supports the expectation of finding different selection pressures against bird flu infections among chicken populations correlating with their geographic domestication, breed origins or history.



Government artificial insemination services in Africa and other developing regions commonly promote insemination from exotic sires, believing it to be unacceptable to offer semen from a crossbred sire. The conventional wisdom is that ‘pure’ breeding is the best choice. It is understandable for people to think that if one generation of exotic bull use is good (which it often is), two generations will be twice as good (which it often is not). For many poor farmers, neither the indigenous nor the exotic animal is ideal. What is needed are new (synthetic) breeds. The many animals imported into developing countries over the last several decades have blended with local cattle and been subjected to strong (natural) selection to form ‘interbreeding crossbred populations’; this gives developing countries an ideal starting resource for selection programs.

ILRI and its partner organizations are working to provide animal breeders with the means of combining livestock genes in new ways that provide livestock owners with fitter farm animals that remain productive under stressful conditions. They are also working to develop appropriate breeding strategies suited to smallholders and pastoralists and helping to promote pilot breeding schemes suitable for low-input systems, particularly sustainable community-based programs.

### Conservation

With the increasing pace of change making it difficult to predict what sorts of circumstances farmers will face in future, it is vital that we conserve genetic samples from a wide range of livestock populations. In our conservation strategies, we must make judicious choice of breeds known to have special traits, such as tolerance of infections with pathogens, to ensure that unique and important genotypes are not lost forever.

### *Reproductive technologies can enhance conservation*

From the early development of artificial insemination in the mid-1940s, reproductive biotechnologies have been instrumental in the transfer of genetic material. The greatly accelerated pace in global movement of germplasm has come largely from the use of artificial insemination, multiple ovulation, *in vitro* fertilization, embryo transfer and the use of frozen semen and embryos. Shipment of semen, ova or embryos is far more practical and less expensive than transporting live animals across continents and oceans.

Although application of these advanced reproductive technologies can be viewed as a threat to genetic diversity, because large numbers of genetically uniform offspring can be produced from only a few parents, they also provide powerful tools for its preservation. Germplasm from endangered breeds, unpopular lines, or populations that are being replaced by other stocks can be retained indefinitely through judicious sampling and cryopreservation of semen and embryos. And animals selected for conservation can be documented at the molecular level to possess desired genetic characteristics. DNA libraries, which possess cloned fragments of an

animal's genome, can also preserve the genetic material of endangered stock for future use or study.

*Cryopreservation.* The discovery in 1949 that semen could be protected from the harmful effects of freezing and thawing was an important development in animal breeding. Considerable progress has been made since then in establishing procedures for freezing and storing the semen and embryos of a wide variety of mammalian species, usually in liquid nitrogen at minus 196 degrees centigrade. Cryopreservation now offers a cost-effective way to retain a sample of the genetic diversity of a population of animals in suspended animation for indefinite periods of time. Current technology permits the cryopreservation of semen for most livestock species. The first cryopreservation of mammalian embryos followed by live birth was reported in mice in 1972. Since then, embryos of many mammalian species have been cryopreserved and the procedures are now routine in cattle, sheep and goats.

Ideally, we should be recording lots of physical measurements (growth, milk yield) of animals whose germplasm we conserve in livestock genebanks for future use. However, it is better to freeze semen or embryos immediately, while recording a minimal amount of such phenotypic characterization information, rather than wait to have better information. Even such little information as the physical location of the animal, with perhaps a digital photograph of it, would suffice. If we wait to have more comprehensive measurements before cryo-banking animals, valuable time will be wasted—and valuable resources lost.

*Multiple ovulation and embryo transfer.* Administration of a follicle-stimulating hormone causes multiple ovulations. After estrus is induced, the donor female is inseminated and multiple embryos (six to eight per cow) are subsequently obtained. A new series of technologies, mainly in cattle, involves the collection and maturation of oocytes and their *in vitro* fertilization. Oocytes can be aspirated from the ovary of a live animal or excised from the ovary immediately after slaughter. The oocytes are then matured and fertilized in an artificial environment and they produce normal embryos to be transplanted into recipient foster mothers for their development.

*Embryo splitting and cloning.* Splitting and cloning embryos has been achieved mainly with cattle and sheep. Although cloning does not increase the amount of genetic diversity, it does enable researchers to evaluate stored samples without reducing the amount of diversity preserved. It can also be used to provide a back-up collection of samples for many users.

*Sexed semen.* It is now feasible to separate X-chromosome-bearing (female) and Y-chromosome-bearing (male) sperm. The discovery was made several decades ago by the United States Department of Agriculture and is now being commercialized (under licence) in different parts of the world. The high cost of sex-separated bull

## Molecular markers up close

Recent major developments in molecular genetics have provided powerful new tools, called molecular markers, that ILRI and collaborating institutions are using to assess the origins of livestock species and the diversity of livestock breeds. DNA-based polymorphisms are now the markers of choice for molecular-based surveys of genetic diversity. Typically, they include D-loop and cytochrome B mitochondrial DNA (mtDNA) sequences (maternal inheritance), Y chromosome-specific single nucleotide polymorphisms (SNPs) and microsatellites (paternal inheritance), and autosomal microsatellites (bi-parental inheritance). Different genetic markers provide different levels of genetic diversity information. Autosomal microsatellite loci are commonly used for population diversity estimations, differentiation of populations, calculation of genetic distances, estimation of genetic relationships, and the estimation of population genetic admixture. MtDNA sequences are the markers of choice for domestication studies, because the segregation of an mtDNA lineage within a livestock population will only have occurred through the domestication of a wild female or through the incorporation of a female into the domestic stock. More particularly, mtDNA sequences are used to identify putative wild progenitors, the number of maternal lineages and their geographic origins. Finally, the study of a diagnostic Y chromosome polymorphism is an easy and rapid way to detect and to quantify male-mediated admixture.



## Recommended livestock germplasm conservation methods

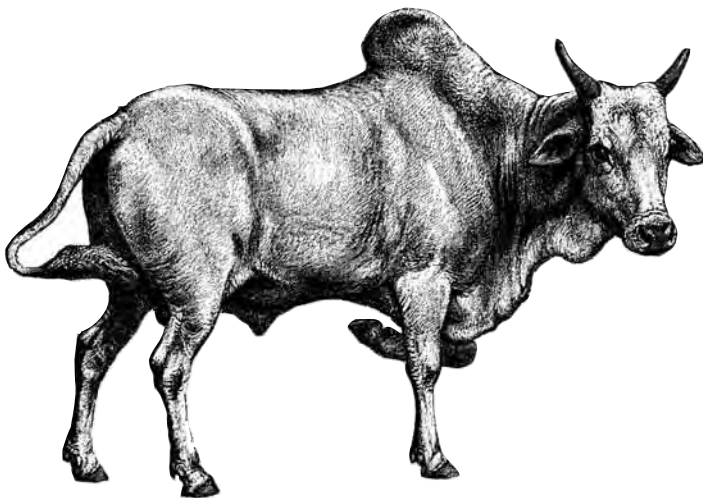
- Promote *in situ* approaches to conserving animal genetic resources as a preventive measure against loss.
- Use *ex situ in vivo* conservation in institutional or community owned herds or flocks to support conservation of breeds of current known value.
- Expand *in vitro* conservation methods to provide a secure back-up for the farm animal genetic resources of the developing world. This will protect against threats that can drive genetic resources to extinction faster than monitoring can identify the threat. Develop capacity for cryopreservation, including development of human and technical resources, in developing countries. Undertake cryopreservation of a wide range of animal genetic resources. Determine the most appropriate system for regional or international cryopreservation programs as a back up for developing world farm animal genetic resources. Make use of technical developments in the cryopreservation of gametes, embryos and somatic cells generated by developed-country research programs.



semen, along with its somewhat reduced fertility, means that it is not going to be widely used soon in the poorest countries. In South America, however, and in some developed countries, the sexed-semen technology has been used routinely for more than five years. The primary role of sex-separated semen is to increase the proportion of female calves for dairying. In many parts of Africa, females are valued as highly as USD240 more than males at birth.

With support from Heifer Project International, ILRI has started a pilot trial of a technology that promises to achieve the same 90–95 per cent female calf crop, but at substantially reduced cost. The pilot project uses eggs taken from abattoirs; many hundreds of these eggs can be fertilized in the laboratory using a single dose of sex-separated semen. In this way the high cost of a dose (currently about USD100 in Africa) can be spread across many female offspring. The same use of abattoir material (including bull testicles) can greatly reduce the marginal cost of stocking a genebank. Fifty males and fifty unrelated females would be a good representative sample of a population. Using current cost estimates, an entire breed could be cryobanked for less than USD5,000.

*Semen screening and embryo washing.* New technologies of semen screening and embryo washing are improving our ability to ensure the healthy status of germplasm. Semen immunoextension involves treating semen with specific antibodies to prevent disease transmission. Embryo washing and treatment remove or neutralize pathogens that may be found around the embryo. It has been effective against most pathogens tested to date.







## Building capacity to manage tropical animal genetic resources

Although animal genetic resources provide a livestock pathway out of poverty for many of the 1.2 billion people in the world living in extreme poverty, in many developing countries few functional breeding programs exist and many others have failed, there is a dearth of national policies impinging on animal breeding, universities have limited and uneven abilities to train students in applied genetics and animal breeding, institutional development is generally weak and access to knowledge in applied genetics and animal breeding restricted, few trained scientists are skilled in animal genetics or breeding and few teaching resources are available. For these reasons, extensive capacity building will be needed to conserve and widen use of livestock genetic resources.

In collaboration with the Swedish University of Agricultural Sciences and supported by the Swedish International Development Agency, ILRI conducted a project to strengthen the subject knowledge as well as the teaching and communication skills of teachers and supervisors of graduate students in animal breeding and genetics in developing countries. Since 2000, this project has trained a total of 95 people, 20 from eastern and southern Africa, 18 from West and Central Africa, 19 from across the continent, 18 from Southeast Asia and 20 from South Asia. The Forum for Agricultural Research in Africa has adopted this project as a model in an initiative known as 'Building African Scientific and Institutional Capacity', or BASIC for short.

One component of the project involved ‘training the trainers’. University teachers and researchers responsible for training bachelor of science, master of science and doctoral students in animal breeding and genetics were given refresher courses, after which those trained passed on their new knowledge to their students and colleagues in their home institutions, who further spread the knowledge. The project also made use of new networks (e.g. AFRIB in Africa and SAGDG in South Asia) that are facilitating development and review of regional research proposals.

The training package produced by this project includes:

- Regional needs assessed via questionnaires and country visits.
- Planning workshop conducted with regional scientists.
- Training materials posted on web and CD-ROM.
- Three-week courses for trainers combining animal breeding and genetic resources with teaching methodologies and science communication.
- Follow-up workshops to share experiences and impacts.

### Animal Genetics Training Resource

This project developed a comprehensive Animal Genetics Training Resource that is now being accessed and used worldwide. This is a unique, one-stop, user-friendly multimedia electronic resource for teachers and supervisors of graduate and post-graduate students in animal breeding and genetics. The training resource consists of core modules on major topics, case studies from developing countries, exercises, tools and a library. It also has links to many other information sources about animal genetic resources, including ILRI’s DAGRIS. It covers established as well as rapidly developing areas, such as gene-based technologies and their application in livestock breeding programs. This resource is empowering university trainers to deliver course content of relevance to developing-country contexts and helping to build capacity of developing-country institutions to utilize their indigenous animal genetic resources to the full.



## Shared research platforms

Better management of the livestock genetic resources of developing countries relies on increasing the capacity of local scientists and institutions in developing countries to conduct relevant and practical research in several fast-evolving genetic disciplines. But financing the construction and maintenance of facilities to conduct genetics research and related data handling and training programs, or to pay salaries that would retain high-quality local geneticists and laboratory and field technicians, is beyond the means of most developing countries.

Groups of institutions in industrialized countries have on occasion solved this problem by sharing research facilities that would otherwise be prohibitively expensive. A typical example is the European Molecular Biology Organization, which has catalyzed inter-institutional collaboration. ILRI is adapting this model in establishing joint biosciences ventures in both Africa and Asia. In Nairobi, ILRI's laboratories are being transformed into the 'hub' of a Biosciences eastern and central Africa (BecA) network sponsored by the New Partnership for Africa's Development (NEPAD). In Beijing, ILRI has teamed up with the Chinese Academy of Agricultural Sciences (CAAS) to establish a Joint Laboratory on Livestock and Forage Genetic Resources. These two advanced biosciences platforms, still in the early phase of their implementation, illustrate how shared research facilities can be established and used by developing countries to address pressing development issues.

### Biosciences eastern and central Africa, Nairobi

Biosciences eastern and central Africa (BecA) is the first of four regional networks of centres of excellence in biosciences supported by NEPAD. BecA consists of a hub, located on ILRI's Nairobi campus, that provides a common biosciences research platform, research-related services and capacity building and training opportunities, as well as a network of regional nodes and other laboratories distributed throughout eastern and central Africa for the conduct of research on high-priority issues affecting Africa's development. BecA is being established amongst a group of cooperating institutions that agree to make their facilities available for regional use. BecA is available for use by the national agricultural research systems of developing countries, regional universities, advanced research institutes in developed countries, and centres of the Consultative Group on International Agricultural Research working on high-priority African problems.

BecA provides biosciences facilities for the African scientific community to address high-priority development problems, including better management of agricultural biodiversity. This shared research platform brings together a critical mass of scientists drawn from national, regional and international institutions in state-of-the-art biotechnology facilities. An important part of its agenda is to enhance the capacity of young African scientists to resource and lead bioscience research addressing regional priorities, to attract investment in biosciences in and for Africa from public and private sectors, and to advise and develop capacity in managing intellectual property and bio-safety issues.

BecA's state-of-the-art laboratories are strong in functional genomics, including micro-array and proteomics facilities, conducted to solve severe problems in African crop and animal production. Since 2003, when its first phase was implemented, BecA has hosted 66 students on attachment, 53 graduate fellows (28 master's and 25 doctoral students) and 12 visiting scientists. This phase was funded by the Canadian International Development Agency through the Canada Fund for Africa.

## Joint Laboratory on Livestock and Forage Genetic Resources, Beijing

ILRI's Nairobi laboratories have been the primary facility for molecular genetics research underpinning collaborative assessment of the genetic diversity of Africa's indigenous livestock populations. For such work in and with Asian countries, ILRI and the Chinese Academy of Agricultural Sciences (CAAS) held discussions on possible collaboration. In May 2004, CAAS and ILRI established a Joint Laboratory on Livestock and Forage Genetic Resources. CAAS built and equipped the Joint Lab, which is run by an ILRI-CAAS geneticist and hosted by the Institute of Animal Science (IAS), in Beijing. Staff of the Joint Lab are developing molecular tools with which to characterize livestock and forage genetic diversity in China and southeastern Asia, as well as training scientists and building capacity for this research in the region. The current project portfolio of the joint Lab includes: molecular characterization of chicken genetic diversity using mitochondrial and microsatellite DNA markers, assessment of the genetic diversity of Asia's small ruminant genetic resources, and linking China's database on domestic livestock diversity (CDAD-CN) with ILRI's Domestic Animal Genetic Resources Information System (DAGRIS). ILRI has also collaborated with the Institute of Grassland Research, which is part of CAAS, in characterizing the genetic diversity of ILRI's 150 collections of the alfalfa plant, and with the College of Grassland Science and Technology of the Lanzhou University to characterize the genetic diversity of ILRI's 50 collections of chickpea varieties.

Work at this Joint Lab has attracted broader collaboration in livestock genetic resources work, such as a research project coordinated by the Joint FAO / IAEA Division (International Atomic Energy Agency) characterizing Asia's small ruminant genetic resources and AVIANDIV (chicken genomics) and ECONOGENE (goat diversity) projects supported by the European Union. The capacity building work of these projects includes fellowships not only for graduate students but also for national scientists to spend short periods in the Joint Lab analyzing their samples with genotyping and data analysis protocols.



## The CAAS-ILRI Joint Lab up close

The CAAS-ILRI Joint Laboratory on Livestock and Forage Genetic Resources (JLLFGR) opened in 2004 at Beijing's Institute of Animal Science of the Chinese Academy of Agricultural Sciences (IAS-CAAS).

Research at JLLFGR targets the indigenous farm animals and forages of China and Southeast Asia. Establishment of JLLFGR has created a new research platform in the region that is providing new opportunities for international cooperation in conserving livestock and forage genetic diversity. In addition to its research work, JLLFGR hosts national and international training courses, workshops and conferences on these topics.

Chinese scientists have been engaged for many years in collecting, storing and researching the country's indigenous livestock and forage genetic resources. This Chinese work has been particularly productive in the areas of survey and investigation, documentation, database and information systems, genetic characterization, *in situ* conservation and *ex situ* preservation and use. In this work, IAS-CAAS established molecular and biochemical genetic laboratories and stored a large number of livestock and forage genetic resources indigenous in China and abroad. This work complements one of ILRI's key research areas, which is the characterization and conservation of livestock and forage genetic resources of developing countries.

*(continues)*



### Global public goods

In recent years ILRI has built infrastructure and expertise to help developing-country partners exploit genetics, genomics, functional genomics, bioinformatics, ruminant humoral and cellular immunology and other frontier biotechnologies. ILRI has established shared biotechnology platforms, notably Bioscience eastern and central Africa (BecA) and a Joint Laboratory for Livestock and Forage Genetic Resources (JLLFGR), in collaboration with the Chinese Academy of Agricultural Sciences. These platforms, which began operating in earnest in 2006, are designed to improve the capacity of ILRI, of partner institutions and of individual scientists undertaking biotechnology research for practical use in developing countries.

### The power of partnerships

ILRI works in strategic partnerships and alliances with a wealth of other organizations worldwide—national, regional and international—to achieve its mission. We place a high priority on helping institutions build their capacity for conducting livestock research addressing significant global challenges and opportunities.

Knowledge is central to this work, particularly for ILRI's research to help characterize the indigenous animal genetic resources of the developing world. All information produced is made freely available to the research and development communities for improving management of our animal genetic resources.

The task of determining the molecular diversity of all livestock populations in developing countries is beyond the ability or capacity of any one institution. Furthermore, although the national agricultural research systems of developing countries are eager to know in detail the extent of the livestock diversity still existing in their countries, many of these countries lack sufficient human and technical capacity to conduct the studies needed to make these assessments. Innovative approaches, with extensive partnerships at their core, were thus needed if we were to begin to map the genetic livestock diversity of the developing world and its countries and facilitate the work of those countries in conserving and improving use of their animal resources.

### Key partners

The organizations that played central roles in this project were, in addition to the national agricultural research institutions and universities of developing countries and ILRI, international organizations such as FAO, the FAO/International Atomic

Energy Agency (IAEA) Joint Division, the International Society of Animal Genetics, advanced research institutes and consortiums, and national and international donor agencies, including the International Foundation for Science, the FAO/IAEA Joint Division, and the Academy of Science for the Developing World.

The partners in this project committed themselves to the following steps.

- Partners reach consensus on the purpose of the project, develop sampling procedures, conduct sampling work and obtain transfer agreements with national governments.
- National institutions collect blood samples of selected livestock populations, retaining duplicates of the samples collected and dispatching the rest to ILRI's Nairobi laboratories.
- A subset of each sample is analyzed with a standard set of molecular markers. Whenever possible, a scientist from the collaborating institution assists in the molecular work and/or data analyses. The molecular analyses are conducted in ILRI's Nairobi laboratories or in the CAAS-ILRI Joint Laboratory on Livestock and Forage Genetic Resources, in Beijing. The Nairobi and Beijing molecular geneticists share their protocols with staff from countries possessing molecular laboratory facilities and capacities and train the staff in data analyses.
- The results of the molecular analyses are input into a global analysis of livestock genetic diversity and made public.

### *Accomplishments*

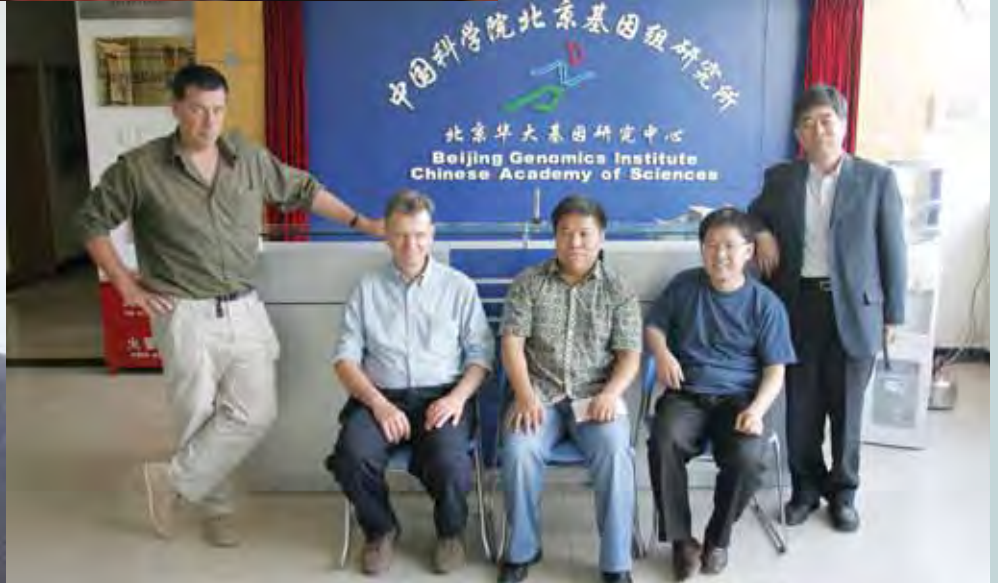
This highly collaborative work, which is built around capacity building as well as analyses of a unique collection of livestock samples, has advanced our understanding of the global distribution of animal genetic diversity. With more than 7,000 cattle, 3,500 sheep, 3,000 goat, 1,000 yak and 2,500 chicken DNA or blood samples from countries in Asia and Africa, the ILRI-hosted sample collection represent a unique resource for present and future studies of livestock diversity. (The samples themselves, however, are not made publicly available because they remain the property of the national research institutions that provided them.)

The collective work by this project succeeded in identifying livestock genetic diversity 'hot spots' and high-priority ecological and geographic areas for the conservation and utilization of livestock diversity. The major work was done on African cattle and African and Asian chickens, with other work started on sheep, goat and other species. A major challenge now is to cover the large geographic regions with as yet unknown animal genetic resources diversity.



JLLFGR research focuses on developing new molecular tools for characterizing livestock and forage genetic diversity in China and southeastern Asia. JLLFGR also trains scientists and supports national agricultural research systems and their research partners in the region in building their capacity to conduct research on genetic resources.

JLLFGR is now a fully functional state-of-the-art facility for relatively low throughput genotyping. ILRI and CAAS assigned one full-time staff member, Han Jianlin, to oversee the Joint Lab and four part-time staff to work there. CAAS and IAS-CAAS financed the construction of a new molecular facility comprising three molecular laboratories. China also financed the purchase of all the modern equipment in JLLFGR, including PCR machines, an automatic DNA analyzer and a co-focus microscope.





Since 1995, more than 50 national scientists from 18 countries in Africa and Asia have been trained at ILRI facilities in molecular genetic analysis of livestock genetic resources. The training periods have varied from a few weeks to several months. This training has been financially supported by national institutions as well as agencies such as the International Foundation for Science, the FAO/IAEA Joint Division and The Academy of Science for the Developing World. Long-term partnerships have also been initiated with institutions such as South Korea's Rural Development Administration, in which a series of scientists will come to ILRI for training over a period of several years.

ILRI scientists have collaborated extensively with the FAO's animal genetic resources group over many years. Out of this collaborative work came development of (1) a global strategy for the sampling of various livestock species, (2) a conceptual framework for assessing the economic value of various animal genetic resources in developing countries and (3) tools for on-farm phenotypic characterization of livestock.

This project in future will continue to exploit South-South as well as North-South synergies. It will continue to integrate research, training and capacity building activities. The methodologies and protocols used by the project will be continually refined. Project staff will remain sufficiently flexibility to accommodate the diverse needs and capacities of all their partners. And all the data generated by the project will remain freely accessible and in the public domain.



## Recommendations

The use, development and conservation of livestock genetic resources are profoundly political as well as development and environmental issues. Many of the central policy questions remain unanswered. With the First International Technical Conference on Animal Genetic Resources and launch of the *State of the World's Animal Genetic Resources* in September 2007, the time is at hand to turn plans into practice and awareness into action. Among the outstanding policy issues that must be addressed are the following.

### Provide traditional farmers with incentives for keeping traditional animals

Traditional pastoralists and mixed crop-and-livestock farmers in developing countries who keep local breeds of farm animals are providing a 'public good'. They should be provided with incentives for continuing to maintain these unique animals, especially in light of increasing pressure for pastoralists and smallholders to replace their traditional breeds with more productive but less resilient animals to make themselves competitive in the expanding livestock markets of developing countries. Examples of such incentives are facilitating access by herders and farmers to niche markets for traditional livestock products, providing breeding programs that increase the productivity of local breeds, better transport for getting livestock products to markets, and other public services in and for livestock-keeping communities.

### Consider biodiversity losses when controlling livestock disease epidemics

It is generally difficult to quantify the impact of disease epidemics on livestock genetic diversity—mortality data are rarely broken down by breed. However, large numbers of animals can be lost and, in some cases, such as during avian influenza outbreaks, it is often the culling measures rather than the disease itself that accounts for the largest number of deaths. It is only recently that threats to animal genetic diversity have been given any consideration in the planning of disease control measures, and they continue to be largely ignored, in part because alternatives to existing approaches (such as ‘mass culling’) have not been developed.

### Consider biodiversity losses when restocking after disasters

The impact of disasters and emergencies on livestock genetic resources is also not well documented. In the initial aftermath of a disaster, collecting data on losses and protecting local farm animal diversity will never be a high priority. Nevertheless, experience shows that post-disaster restocking activities need to be carefully considered to ensure that they do not cause further losses of livestock genetic diversity and that the breeds used to restock depleted herds are appropriate to the local community, environment and production system.

### Develop nuanced ways of valuing livestock genetic resources

Current means of quantifying the value of livestock are largely based on direct-use values, such as yields of meat, milk, eggs and wool. This is despite the fact that other categories of value may often be of equal or greater importance to livestock keepers, especially in developing countries. Among the intangible benefits different livestock species and breeds provide different communities in developing countries are traction for pulling ploughs, transporting goods and fertilizing crop fields, serving as ‘walking’ bank and savings accounts, as insurance against crop loss, medical events and other disasters, as mediators of nutrient cycling and other environmental services, as means of cementing of social ties and fulfilling social obligations, and as expressions of cultural values and social status. ILRI and partner scientists have estimated that approximately 80 per cent of the value of livestock in low-input developing-country systems can be attributed to these non-market functions, while only 20 per cent is attributable to direct production outputs. By contrast, over 90 per cent of the value of livestock in high-input developed-country production systems is attributable to the latter. By focusing largely on direct-use values, the conservation of livestock genetic resources in developing countries is likely to be consistently undervalued.

### Develop policies that safeguard our genetic interdependence

Although most domesticated animals originated in the South (North America and Oceania have no indigenous mammalian livestock species) and today’s livestock genetic diversity is concentrated in the South, no country or region is ‘self-sufficient’ in animal—or plant—genetic resources. Even the most genetically abundant regions of the world look beyond their own borders for at least half of the





germplasm required for their staple foods. Genetic inter-dependence among all nations underscores the need for international cooperation in conserving and using biodiversity. Fortunately, till now, most attempts to limit the spread of livestock genetic resources have failed. New policies will help ensure continued and informed access not only to animal breeds, populations and genes but also to systematic breed evaluations that indicate the potential usefulness of these resources in different environments and circumstances.

### Practical steps to take

From a political viewpoint, we'll need new and appropriate institutional and policy frameworks, as well as lots of policy discussions, to find ways to strengthen national and international programs that support the conservation of livestock biodiversity. While the political issues are being discussed at length at national and inter-governmental fora, four practical things can be started immediately to ensure that the world's remaining livestock biodiversity is conserved for future generations.

#### (1) Keep it on the hoof.

Give local farmers and communities incentives for maintaining local livestock breeds by, for example, improving access by poor farmers and herders to markets, perhaps including niche markets, where they can sell their traditional livestock products.

#### (2) Move it or lose it.

Encourage safe movements of livestock populations within and between countries, regions and continents to widen global access, use and conservation of farm animal genetic resources.

#### (3) Match breeds with environments.

Optimize livestock production by expertly matching livestock genotypes with farmer ambitions, fast-changing environments and specific natural resources, production systems and socio-economic circumstances.

#### (4) Put some in the bank.

Freeze semen, embryos and tissues of local breeds and store them indefinitely to protect indigenous livestock germplasm against extinction due to the on-going declines in livestock diversity and to serve as long-term insurance against catastrophic losses due to wars, droughts, famines and other future shocks.

Whereas societies and countries tend to differ in their short-term interests in livestock production, their long-term interests—such as learning how to cope with unforeseen changes in livestock production systems and their environments—tend to converge. This creates real opportunities for international scientific, environmental and aid agencies to work with developing countries in collective action to conserve the world's remaining livestock genetic diversity.





# Appendices

# Financial investors 2006

## INVESTORS IN CORE AND SPECIAL PROGRAMS

Australia  
Canada  
China  
Denmark  
Finland  
France  
Germany  
India  
Ireland  
Italy  
Netherlands  
Norway  
Republic of Korea  
Sweden  
Switzerland  
United Kingdom  
United States of America  
World Bank

## INVESTORS IN SPECIAL PROGRAMS AND PROJECTS

African Development Bank (AfDB)  
African Union-Interafrican Bureau for Animal Resources (AU-IBAR)  
Asian Development Bank (ADB)  
Association for Strengthening Agricultural Research in Eastern and Central Africa (ASARECA), Uganda  
Australian Centre for International Agricultural Research (ACIAR)

Austria  
Belgium  
BIO-EARN (East African Regional Programme & Research Network for Biotechnology, Biosafety and Biotechnology Policy Development)  
Canadian Food Inspection Agency (CFIA)  
Canadian International Development Agency (CIDA)  
Capitalisation of Livestock Programme Experiences (CALPI), India  
Centre for Tropical Veterinary Medicine (CTVM), University of Edinburgh, UK  
Colorado State University (CSU), USA  
Comart Foundation, Canada  
Common Fund for Commodities (CFC)  
Cooperazione Internazionale (COOPI), Italy  
Cornell University, USA  
Danish International Development Agency (DANIDA)  
Department for International Development (DFID), UK  
Desert Margins Program (DMP)  
Ethiopian Institute of Agricultural Research  
European Development Fund (EDF)  
Food and Agriculture Organization of the United Nations (FAO)  
Foundation for Advanced Studies on International Development (FASID), Japan  
France  
Gatsby Charitable Foundation, UK  
Gesellschaft für Technische Zusammenarbeit (GTZ), Germany  
Global Environment Facility (GEF), USA  
Indian Council of Agricultural Research (ICAR)

Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria (INIA), Spain

Intercooperation (IC), Pakistan and Switzerland

International Atomic Energy Agency (IAEA) Austria

International Development Research Centre (IDRC), Canada

International Fund for Agricultural Development (IFAD), Italy

Japan

Kenya

Kenya Agricultural Research Institute (KARI)

Land O'Lakes Inc, USA

Makerere University, Uganda

Michigan State University, USA

National Graduate Institute for Policy Studies (GRIPS), Japan

Natural Environment Research Council (NERC), UK

Natural Resources Institute (NRI), UK

Netherlands

Netherlands Foundation for the Advancement of Tropical Research (WOTRO)

OPEC Fund for International Development (OFID), Austria

Oromiya Agricultural Development Bureau (OADB), Ethiopia

Republic of Korea

Rockefeller Foundation, USA

Sasakawa Global 2000 Program (SG2000), Japan

Scanagri, Denmark

Statens Veterinärmedicinska Anstalt (National Veterinary Institute, SVA), Sweden

Strengthening Informal Sector Training and Enterprise (SITE), Kenya

Sweden

Swiss Agency for Development & Cooperation (SDC)

Switzerland

Syracuse University, USA

Terra Nuova, Italy

Texas A & M University (TAMU), USA

University of Florida, USA

University of Glasgow, UK

University of Guelph, Canada

University of Nagoya, Japan

University of Nairobi, Kenya

United States Agency for International Development (USAID)

United States Department of Agriculture (USDA)

United States National Science Foundation (NSF)

Urban Harvest (Strategic Initiative on Urban and Peri-Urban Agriculture, SIUPA), Peru

Vétérinaires sans Frontières-Belgique (VSF-Belgium)

Virginia Polytechnic Institute and State University, USA

Wellcome Trust, UK

World Bank, USA

**CGIAR INVESTMENTS IN PROJECTS**

Bioversity International, Italy

Consultative Group on International Agricultural Research (CGIAR), USA

International Center for Tropical Agriculture (CIAT), Colombia

International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), India

International Food Policy Research (IFPRI), USA

International Institute of Tropical Agriculture (IITA), Nigeria

International Rice Research Institute (IRRI), Philippines

International Water Management Institute (IWMI), Sri Lanka

Virtual Academy for the Semi-Arid Tropics (VASAT), India

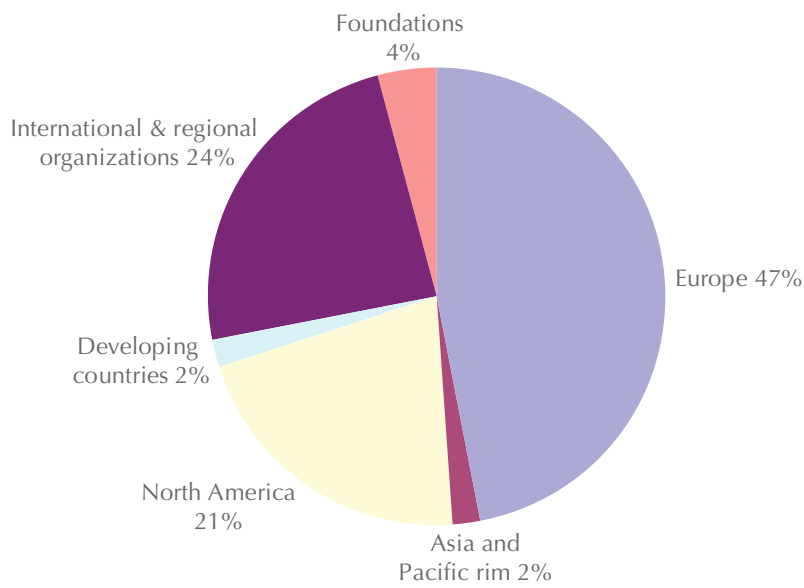
World Agroforestry Centre (ICRAF), Kenya

## Financial highlights 2006

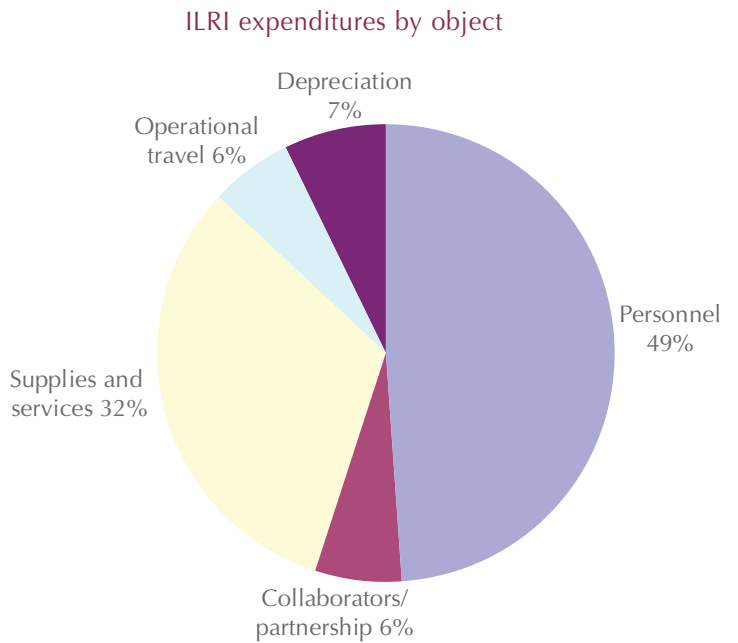
ILRI's revenue in 2006 amounted to USD31.2 million against an expenditure of USD35.4 million, resulting in a deficit of USD4.2 million for the year 2006. ILRI had planned this deficit to allow for the hiring of new scientific staff and for investments in major new projects such as the NEPAD-sponsored Biosciences eastern and central Africa (BeCA) research platform.

Of ILRI's total revenue in 2006, unrestricted funding made up 43% (USD13.44 million), restricted funding 44% (USD13.84 million) and centre income 13% (USD3.91 million). Programmatic expenditure accounted for 74% of all expenses in the year.

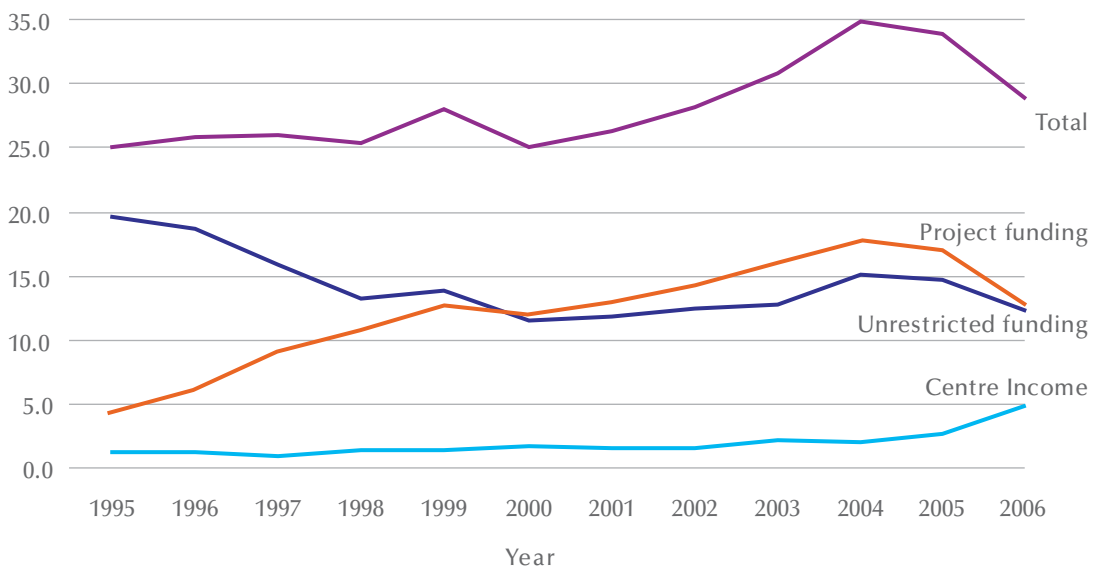
The institute's net assets amounted to USD26.5 million at 31 December 2006, with liquidity and operational reserve levels above CGIAR recommended ranges. This situation helps ILRI adopt a forward-looking perspective in financial and budget matters. Financial indicators at the end of 2006 indicate that the institute's financial health and stability continue to be sound.



ILRI funding by type of donor



ILRI funding trend





## Selected publications 2006

For a full list of ILRI publications, please visit the ILRI website: [www.ilri.org](http://www.ilri.org)

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ILRI (International Livestock Research Institute). 2006. ILRI medium-term plan 2007–2009. Livestock: A pathway out of poverty. ILRI, Nairobi, Kenya. 82 pp.

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Rowlands, J. (ed). 2006. Biometrics and research methods teaching resource version 1. ILRI (International Livestock Research Institute), Nairobi, Kenya. CD-ROM.

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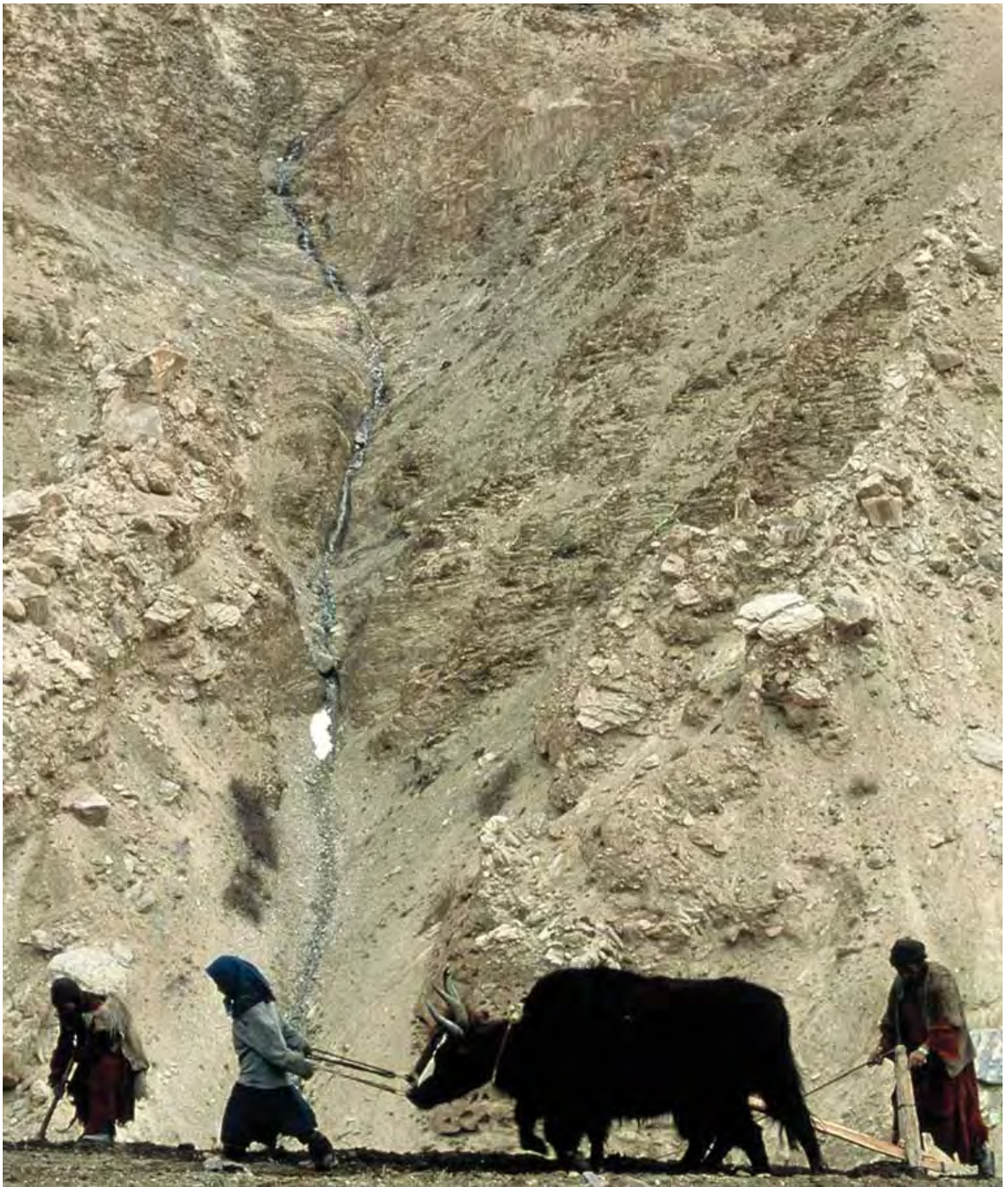
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## Graduate fellows 2006

ILRI supported the following graduate fellows, who were awarded post-graduate degrees in 2006, by providing fellowships, supervising students and facilitating student research in ILRI projects. Some studies were conducted in collaboration with other international agricultural research institutes.

### PhD

**Alpha Madiou Barry**, La Trypanosomose Animale Africaine Chez les Bovine Ndama dans la Prefecture de Mandiana en Zone Cotonniere de Haute Guinee. Institut Supereur de Formation et de Recherche Appliquee (ISFRA), *Université de Mali*, Mali.

**Ameha Sebsibe**, Meat Quality of Selected Ethiopian Goat Genotypes under Varying Nutritional Conditions. *University of Pretoria*, South Africa.

**Aynalem Haile**, Genetic and Economic Analysis of Boran Cattle and their Crosses with Holstein-Friesian in the Central Highlands of Ethiopia. *National Dairy Research Institute*, India.

**Delia Grace**, Epidemiology and Control of Cattle Trypanosomosis in Villages under Risk of Trypanocide Resistance in West Africa. *Freie Universitat Berlin*, Germany.

**Markos Tibbo**, Productivity and Health of Indigenous Sheep Breeds and Crossbreds in the Central Ethiopian Highlands. *Swedish University of Agricultural Sciences*, Sweden.

### MSc

**Abdelhafidh Hassen**, (joint ILRI-ICARDA fellow) The Sustainability of Small Ruminants' Production Systems: a Marketing-Health Approach. *Institute of Agriculture*, Mograne, Tunisia.

**Abdel Rahim Suliman**, (joint ILRI-ICARDA fellow) Sero-surveillance and Impact of Selected Small Ruminant Diseases (PPR and Heartwater) in Gedarif, Blue Nile and El Khowei Areas. *University of Khartoum*, Sudan.

**Abdul Hassan Musa**, The Correlation of Plasma Lipid with Susceptibility of Inbred Laboratory Mice to Experimental Trypanosoma congolense Infection. *University of Nairobi*, Kenya.

**Abonesh Tesfaye**, The Impact of Small-Scale Irrigation on Household Food Security and Assessment of its Management Systems: The Case of Filtino and Godino Irrigation Schemes in Ada Liben District, East Shoa. *Haramaya University*, Ethiopia.



**Ahmed Amdihun**, GIS and Remote Sensing Integrated Environmental Impact Assessment of Irrigation Project in Finchaa Valley Area. *Addis Ababa University*, Ethiopia.

**Alemayehu Abebe**, GIS Applications in Suitability Modeling for Livestock Production in Tana Sub Basin – Blue Nile River Basin. *Addis Ababa University*, Ethiopia.

**Belete Anteneh**, Studies on Cattle Milk and Meat Production in Fogera Woreda: Production Systems, Constraints and Opportunities for Development. *Debub University*, Ethiopia.

**Belete Bantero**, Across Systems Comparative Assessment of Hare Community-Managed Irrigation Schemes Performance. *Arbaminch University*, Ethiopia.

**Dawit Ayalew**, Association of *Cryptosporidium Paruum*, *Giardia*, *Lamblia* and *Entamoeba & Histolytica/dispar* Infection with Drinking Water Sources among Children in Rural Parts of Dire Dawa. *Addis Ababa University*, Ethiopia.

**Emily Kamanthe Muema**, Genetic Diversity and Relationship of Indigenous Goats of Sub-Saharan Africa Using Microsatellite DNA Markers. *University of Nairobi*, Kenya.

**Ephrem Assefa**, Impact Assessment of Rainwater Harvesting Technologies: The Case of Atsbi Womberta Woreda. *Addis Ababa University*, Ethiopia.

**Girma Asfaw**, Evaluation of Failures and Design Practices of River Diversion Structures for Irrigation: Case of Oromiya Regional State. *Arbaminch University*, Ethiopia.

**Hanna Beksissa**, A Study on the Response of Three Genotypes of *Mucuna pruriens* to Different Growth Media for Tissue Culture Differentiation. *Addis Ababa University*, Ethiopia.

**Hillary Kichumba Kipruto**, Evaluation of Genetic Distances Between Lines of Cowpea: Comparison of Amplified Fragment Length Polymorphic DNA (AFLP), Microsatellite and Nutritional Data. *Kenyatta University*, Kenya.

**Joseph Muiruri Kamau**, Fine Mapping of Trypanosomosis Resistance Loci in Murine by Haplotype Approach. *University of Nairobi*, Kenya.

**Nazmi O. Hussein**, (joint ILRI-ICARDA fellow) Epidemiological Studies on Peste des Petits Ruminants (PPR) Disease in Sheep and Goats in Northern Jordan. *University of Science and Technology*, Jordan.





**Rabin Mahmoud Hassan**, (joint ILRI-ICARDA fellow) Review of the Delivery of Veterinary Services with Reference to Small Ruminants and Animal Access to Market. *University of Khartoum*, Sudan.

**Rebeka Amha**, Impact Assessment of Rainwater Harvesting Ponds: The Case of Alaba Woreda. *Addis Ababa University*, Ethiopia.

**Rehima Mussema**, Analysis of Red Pepper Marketing: The Case of Alaba Woreda and Silte in SNNPRS of Ethiopia. *Haramaya University*, Ethiopia.

**Samuel Mbuki**, Characterisation of the Sheep and Goat Breeding Practices of the Pastoralist Gabra and Rendille Communities of Northern Kenya. *Egerton University*, Kenya.

**Victor Atunga Mobegi**, Genetic Characterization of African Chicken Using Mitochondrial DNA D-Loop Sequences. *University of Nairobi*, Kenya.

**Shiferaw Mulugeta**, Survey and Rectification of the Causes of Poor Fertility and Hatchability of Eggs from Rhode Island Red (RIR) Chicken Breeds in Ethiopia. *Alemaya University*, Ethiopia.

**Wakena Totoba**, Developing Optimal Operation Rules for the Cascaded Wadecha-Belbela Reservoir System. *Arbaminch University*, Ethiopia.

**Yoseph Tadesse**, Genetic and Non-Genetic Analysis of Fertility Traits in Holeta and Ada's Berga Dairy Herds. *Alemaya University*, Ethiopia.



## Selected staff 2006

*Unless otherwise stated, staff are located in Nairobi, Kenya, or Addis Ababa, Ethiopia.*

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Rose Ndegwa, Kenya	intellectual property officer
Bruce Scott, Canada	director of partnerships and communications

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## About ILRI and the CGIAR

The International Livestock Research Institute (ILRI) works at the crossroads of livestock and poverty, bringing high-quality science and capacity building to bear on poverty reduction and sustainable development.

ILRI works in partnerships and alliances with other organizations, national and international, in livestock research, training and information. ILRI works in the tropical developing regions of Africa, Asia and Latin America and the Caribbean.

ILRI is one of 15 Future Harvest Centres, which conduct food and environmental research to help alleviate poverty and increase food security while protecting the natural resource base. The Centres are funded by government agencies, development banks, private foundations and regional and international organizations and are supported by the Consultative Group on International Agricultural Research (CGIAR).

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## Our values

### RESPONSIBLE

Our commitment to our mission inspires us, attracts others to our cause and enlarges the world's ambition and capacity to reduce poverty through agricultural research. Integrity is the cornerstone of our business. We maintain ethical standards based on the highest regard for accuracy, fact, truth and transparency and we recognize and reward those who exemplify these qualities.

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We value excellence, initiative and innovation. We are demand driven and outcome oriented. We think strategically and act opportunistically, working across themes, disciplines, departments, systems and scales, linking partners across the research-to-development spectrum, for greatest impacts. We encourage risk taking and regard failure as opportunity. We aim for superior communications, placing high value on the art of listening. We daily take the time and time-out needed to build and maintain exceptional relations with each other and with our partners.

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We treat all people with respect for their opinions, privacy, differences, backgrounds, dignity and natural desire to grow and we distribute resources and opportunities among staff equitably as well as cost effectively. We treat each other as managers of our own work and defer decision making as well as responsibility to front-line workers. We define leadership by how much people help other people develop professionally. We hire, mentor and develop highly motivated professionals, actively recruiting women and men from developing countries. We view our diversity as a central asset to be nurtured and we take particular pleasure, energy and courage from the cultures of the countries in which we work.





## Image Captions and Credits

Unless otherwise noted, all images are by ILRI/Mann.

*Front cover:* A boy rides a buffalo home to his family's farm in northern Vietnam.

*Back cover:* *Left and right:* a pig and a cow and her calf on farms in northern Vietnam; *middle:* a sheep on a farm outside Beijing.

- 3 World livestock map graphic (ILRI/MacMillan and O'Meara).
- 4 *Top:* Widowed crop-livestock farmer Va Thi Chua, near the town of Meo Vac in northern Vietnam. *Middle:* An employee of farmer Bakele Dangne, who adopted tsetse control methods in the Ghibe Valley of southwestern Ethiopia, stands in the doorway of Bakele's homestead, which Bakele improved with the increased income he got by keeping his cattle free of 'sleeping sickness'. *Bottom:* Pigs being transported to market near Taipusi town in the grass rangelands of Inner Mongolia.
- 5 *Top:* One of many new supermarkets coming to the city of Hyderabad, in south-central India's Andhra Pradesh. *Middle:* Young buffalo grazing beside the road between Ha Giang and Tam Son in northern Vietnam. *Bottom:* Buffalo milk is sold at the urban dairy of Anan Thainan in Ramchandrapuram Village, on the outskirts of Hyderabad, in Andhra Pradesh India.
- 6 Maintained by the Yunnan Beef Cattle and Pasture Research Centre, a model farm for pasture management and animal breeding outside Kunming, the capital of Yunnan Province, in southwestern China, this animal is a cross between China's indigenous yellow cattle and Brahmin and Morry Gray breeds.
- 8 Sheko cattle native to Ethiopia's southwestern highlands.
- 11 ILRI 'Knowledge to Action' diagram (ILRI/Persley and Ouma).
- 12 Building facade in the frontier farming town of Meo Vac, in northern Vietnam.
- 13 *Left:* On the mountain road from Meo Vac to Dong Van, in the northern frontier of Vietnam, a farmer carries his piglets to market. *Right:* Australian Texel sheep at the experimental station of the Institute for Animal Science, in Beijing, China.
- 14 Two donkeys eating their mid-day forage rations from nose-bags in the Atlas Mountains outside Marrakesh, Morocco (Michael Rubinstein).
- 15 *Left:* Goats on the farm of Worku Mengiste in the Ghibe Valley of Ethiopia's southwestern highlands. *Right:* Cattle being inspected at a livestock market in Zhang Bei town, in Inner Mongolia, China.
- 16 Corner of a farmhouse kitchen in the Atlas mountains outside Marrakesh, Morocco (Susan MacMillan and Michael Rubinstein).
- 17 *Left:* Cow and her calf kept on a 'biodiversity farm' near the town of Meo Vac in northern Vietnam. *Right:* Worker at Lung Pu School, in the farming community of Dong Van Province, in northern Vietnam.
- 18 Sheep belonging to farmer Wang Cheng in Shunyi County, outside Beijing, China.
- 22 Mr Jiang, of China's Yunnan Province, with a one-month-old Brahmin calf he is hand-feeding because it is not suckling its mother's milk.
- 25 *Top:* A boli object of a vaguely bovine form, covered with chicken and goat blood and other sacrificial coatings, which once played a central role in the ritual life of a Bamana village (Rand African Art); *Middle:* Crying Cows (Les Vaches qui Pleurent), ancient Saharan rock engraving photographed by David Coulson (courtesy of the Trust for African Rock Art). *Bottom:* Head detail of a large auroch, the wild ancestor of domesticated cattle, in the famous Hall of the Bulls in the Lascaux Cave, France.
- 26 *Top:* Water buffalo on the outskirts of Hyderabad, India. *Bottom:* A Guizhou pony native to southern China, a tough animal used for traction in forests, kept at the Experimental Station of the Chinese Institute for Animal Science, in Beijing.
- 27 *Top:* Wild Mongolian camel and baby discovered in the Gobi Desert (Alex Timson). *Bottom:* Engraving of one-humped dromedary and two-humped Bactrian camel.
- 28 Scavenging chicken in the mountains of southwestern Ethiopia.
- 29 *Top left:* Nubian chiefs bring gifts of humpless African cattle to their Egyptian Pharaoh, 18th Dynasty, New Kingdom. Detail from a 14th-century-BC wall painting in the necropolis of ancient Thebes, Luxor, Egypt. *Top right:* Proto-Fulani prehistoric rock art of people with their oxen at Tassali-N'Anger, in the Sahara, about 6,000 BC. *Map figure at bottom:* ILRI/Olivier Hanotte.
- 30 Modern chicken farm, Andhra Pradesh, India.
- 33 A pig on a farm in Shunyi County, outside Beijing, of Du Shuhai and Liu Guiyang, who work their farm together alone after their three daughters left to live in the city.
- 34 Mr Kyalo, a dairy farmer in Machakos, Kenya, manages a fine herd of high-milk-producing exotic Hostein cows (Brad Collis).

- 36 *Top:* Red Fulani cattle in Niger (ILRI/Elsworth). *Middle:* Improved Boran bull, from Kenya (ILRI/Elsworth). *Bottom:* Ankole cattle from Tanzania (Julie Ojango).
- 39 *Top:* A Mong Cai pig native of northern Vietnam. *Middle:* A youth walks his family's herd of native buffalo home in northern Vietnam. *Bottom:* A group of native Sheko cattle in the Ghibe Valley of southwestern Ethiopia.
- 40 A native 'black pig' on a biodiversity farm near the town of Meo Vac, in northern Vietnam.
- 43 *Top:* Farmer Ma Thi Puong feeds her pigs on her farm in Meo Vac Province, northern Vietnam. *Middle:* 57-year-old farmer M Durgaiah stands with some of his cows in Burhaiah Thanda Village, Andhra Pradesh, India. *Bottom:* A farmer feeds his goat outside Chengdu, Sichan Province, in southwestern China.
- 47 *Left:* Farmer Wang Cheng feeds his sheep in Shunyi County, outside Beijing, China. *Right:* A scavenging pig in a Hyderabad neighbourhood, in Andhra Pradesh, India.
- 48 *Top:* An ancient humpless N'Dama animal from West Africa (ILRI/Elsworth). *Middle:* The 'hair' red Maasai sheep of East Africa (Brad Collis). *Bottom:* Native black chickens, which have black legs and meat, from northern Vietnam.
- 51 ILRI disease and breeding research in the Ghibe Valley of southwestern Ethiopia.
- 52 *Top:* Chickens at a farm near the town of Meo Vac in northern Vietnam. *Bottom:* A girl carries a chicken in the Mekong Delta of Vietnam (Jim Holmes).
- 55 *Top:* African artefact in the collection of Keith Sones. *Bottom:* Youth holding duck in Bangladesh (Jim Holmes).
- 56 *Top:* Pig and chicken farmer Liu Guiyang Liu feeds her chickens in Shunyi County. *Bottom:* Boy with his chickens at his homestead in Kenya (Panos).
- 59 Min piglets raised at the experimental station of the Institute for Animal Science, in Beijing, China.
- 60 Improved dairy cow eating maize stover (ILRI/Elsworth).
- 61 Improved Boran, a hardy meat breed from Kenya.
- 62 Youth holds chicken at a poultry centre in Senegal (Panos).
- 66 Plaque outside the Chinese Academy of Agricultural Sciences (CAAS)-ILRI Joint Laboratory for Livestock and Forage Genetic Resources (JLLFGR), in Beijing, China, and livestock geneticist Han Jianlin, inside the Joint Lab.
- 69 Staff of the CAAS-ILRI Joint Laboratory for Livestock and Forage Genetic Resources (JLLFGR), in Beijing.
- 70 *Clockwise from top left:* ILRI partner Harry Noyes (University of Liverpool) and ILRI scientists Sung Jong Oh and Steve Kemp visit Beijing's CAAS-ILRI Joint Laboratory for Livestock and Forage Genetic Resources (JLLFGR); CAAS-ILRI geneticist Han Jianlin, who manages the JLLFGR; Bin Liu, senior scientist at the Beijing Genomics Institute of the Chinese Academy of Sciences; Kemp, Noyes, Jianlin, Liu and Oh in the lobby of the Beijing Genomics Institute; ILRI geneticist Steve Kemp at the Beijing Genomics Institute; ILRI's Han Jianlin giving a seminar at the CAAS-ILRI JLLFGR.
- 72 A cow and her calf at a 'biodiversity farm' in northern Vietnam.
- 75 A pig from northern Vietnam (ILRI/Mann), a cow from southwestern China (ILRI/Mann), an Ankole animal from Tanzania (Julie Onjango).
- 76 A pig peers out of his pigsty on a farm southeast of Beijing (Iain Wright), a buffalo is walked to market outside Chengdu, in China's Sichuan Province (ILRI/Mann).
- 78 Children of a family manging a biodiversity farm near Meo Vac, in northern Vietnam.
- 84 Woman and sheep in Latin America (Cliff Ward).
- 86 Yaks used for traction in the Himalayas (Cliff Ward).
- 88 Ethiopian student and administrative assistant Rahel Mesganaw and Chinese student He Feng, son of Shunyi farmer He Wenyuan.
- 89 Indian student and research assistant Kirti Danwar working in ILRI's Delhi office and Vietnamese student Kien Van Nguyen, working at the Truong An poultry farm near the town of Dong Van, in northern Vietnam.
- 90 ILRI liaison officer for China Xianglin Li, Shunyi County farmer He Wenyuan, ILRI representative for Asia Iain Wright, and ILRI manager of capacity strengthening Anandajayasekaram Pooniah.
- 94 At ILRI's the upper Ghibe Research Station, cattle stand in a crush ready for bleeding and weighing.
- 98 Near Woliso town south of Addis Ababa, Ethiopia, Gizau Wonchi tends young cattle .
- 100 Ankole cattle are herded by young boys in Rwanda (Panos).
- 102 Sheep grazing in Inner Mongolia, China.



