The 10th NIAS INTERNATIONAL WORKSHOP ON GENETIC RESOURCES

Present Status and Genetic Variability of Animal Genetic Resources in Asian Region

Independent Administrative Agency
National Institute of Agrobiological Sciences (NIAS)

December 11-12, 2002

Sponsored by National Institute of Agrobiological Sciences

In corporation with
National Institute of Livestock and Grassland Science (NILGS)
and
The Society for Researches on Native Livestock

NIAS
National Institute of Agrobiological Sciences

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Proceedings of the 10th NIAS Ineternational Workshop on Genetic Resources

December 11-12, 2002
Tsukuba, Japan

Printed in Japan by Sato Printing Co., Ltd, Tsukuba, Japan
Pubulished by National Institute of Agrobiological Sciences, Tsukuba, Japan
ISBN 4-931511-10-4
March 2004

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Keynote Address

Chairperson MIYAZAKI, S

Welcome Address

OBATA, Taro

Director of Genome and Biodiversity Research,
National Institute of Agrobiological Sciences
Nataional Coordinator of Animal Genetic Resources

Distinguished guests and participants, on behalf of the National Institute of Agrobiological Sciences, it is a great pleasure for me to welcome you all to the MAFF International Workshop on Genetic Resources.

This is just the 10th workshop since the first one was organized by MAFF in 1994. The aims of this workshop are to invite researchers from overseas to exchange research information and to promote collaboration for the development of new genetic resource technologies for evaluation, conservation and usage.

During the past nine years, many researchers have attended this workshop to discuss plants, microbes and animals. As a result, this workshop has created a great variety of networks between researchers in each of these fields.

Recently, the genetic diversity of animals has been reducing dramatically as a result of various environmental changes. According to FAO statistics, of the 5,330 mammalian species and the 1,043 bird species, the proportion of breeds that have become extinct has increased from 23% to 35% and from 51% to 63%, respectively. This is quite a serious problem.

The situation is particularly alarming in the Asian and Pacific Rim areas, where modernization has been rapidly expanding and more than one-fifth of all the animal genetic resources in the world are concentrated.

In order to pass the world's genetic resources on to the generations that follow us, it is very important to strengthen research activities on animal genetic resources and it is also necessary to build up international and regional networks among researchers in this field. I think it is our responsibility to do these things for future generations.

Fortunately, FAO has planned the publication of reports on the animal genetic resources that are being conserved throughout the world. These will be very important materials and should clarify the current situation. Based on these reports, new strategies regarding the world's animal genetic resources are likely to be developed.

With this in mind, today's workshop plans to focus on two major points. The first is the current situation of animal genetic resources in the Asian region and the second is the current research activities on gene analysis of the genetic diversity of Asian livestock.

In order for us to have an informative workshop, we have invited special guests from overseas today. Dr. Hans Wagner will present the keynote address regarding FAO activities for animal genetic resources around the world.

Dr. Guixiang Zhang from China, Dr. Kumar Taneja from India, Dr. Thi Thuy from Vietnam and Dr. Omer Faruque from Bangladesh will be giving us presentations. In addition, we have also invited some special commentators. Thank you all very much for joining us today in spite of your busy schedules.

Furthermore, I would like to express our sincere gratitude to Professor Amano, who is the vice-president of the Society for Research on Native Livestock, for assisting in the planning of this workshop.

Finally, I would like to extend a warm welcome to all of our participants. I believe that today's workshop can play a vital role in achieving new forms of research collaboration on animal genetic resources.

Again, everyone, thank you very much for your kind cooperation.

Keynote Address

Present Status of Asian Animal Genetic Resources and the Role of the First Report on the State of World's Animal Genetic Resources

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FAO Regional Office for Asia and the Pacific
Bangkok, Thailand

Introduction

The Asia Region is characterized by a large range of agro-ecological zones ranging from the mountainous areas of the Himalayan Region to the Atolls and small islands of the Pacific, and from deserts in India, China and Australia to tropical rainforest in Malaysia and Indonesia. Many species of animals are now domesticated throughout this vast region. Among the first were goats (*Capra hircus*) and sheep (*Ovis aries*), which were domesticated about 10,000 years ago. The domestic goat's ancestor is the bezoar goat from West-Asia, while sheep are descendent from the mouflon sheep which was found in West and Central Asia. The wild ancestor of the domesticated pig is *Sus scrofa* and domestication has occurred in several regions in the World, including Chinese breeds in East Asia and a particularity breed, the Sulawesi Warty Pig (*Sus celebis*) in Sulawesi and other parts of Indonesia. Other important domesticated animals come from the bovinae family, broadly divided into the humped cattle (*Bos indicus*) domesticated in the Indus valley region and humpless (*Bos taurus*), the Yak (*Bos grunieinsis*), the Mithin or Gaur (*Bos frontalis*) the Banteng (*Bos javanicus*) and the buffalo (*Bubalus bubalis*) About 6000 B.C. chickens were domesticated in India from the jungle fowl and are now by far the most common domestic animals (estimated at 5 billion worldwide) Environmental diversity, as well as the effects of variable feed bases, disease stresses, mutations and selective breeding have resulted in the development of a large number of breeds.

The Asia region contains more than one-fifth of the world's animal genetic resources, with more than 1,200 domestic animal breeds recorded (the number is based on information provided by countries for DAD-IS and considered an under-estimate) The majority of the world's buffaloes and yaks, almost half of its muscovy ducks, pheasants and partridges, one-third of its pig breeds and one quarter of its goat breeds are found in the region. (Table 1)

Livestock sector trends and implications on AnGR

Population growth, urbanization and increased purchasing power have triggered an increased demand for livestock goods and products worldwide with Asia accounting for the highest growth rates. Livestock production is growing faster than any other agricultural sub-sector and it is predicted that by 2020, livestock will produce more than half of the total global agricultural output in value terms. This process has been referred to as the 'livestock revolution' (Delgado et al 1999) The output from the livestock sector in Asia is increasing by 3.3 percent per annum, compared with 1.4 percent per annum for crop production. While the growth in Asia as a whole outpaces that of other regions, the rates differ significantly among subregions of Asia because of the varying availability of resources, systems of agriculture, culture and climate among other factors.

Livestock production is changing from a system that mobilizes surplus and waste resources (backyard scraps, remote pastures, and grasses, all of which are indigestible to humans) to a livestock sector which actively seeks new feed resources for the production of human food products (Steinfeld, de Haan, and Blackburn 1997) As a consequence, most of the future demand for livestock products will have to be met through the intensification of resource-rich mixed crop/livestock production environments, by increasing the productivity of land and livestock. In addition, peri-urban industrial-type livestock production, particularly of pigs and poultry, is mushrooming.

In the process of intensification, the environmental constraints to animal production are alleviated or removed, as more and better resources, housing and veterinary care are provided. This process is inevitably associated with marked changes in the genetic resources required since some species and breeds can make better use of these high potential and much less variable production environments. As a consequence more and more exotic germ-plasm is been used. The many widely differing, lower input production environments require highly adapted animal genetic resources developed in each particular environment, to be able to realize good outputs in a sustainable system.

While some loss of animal genetic resources is inevitable, and should be planned for, the process of intensification is not always driven by rational principles, nor is it always accompanied by appropriate technologies. First, there is a systematic and almost ubiquitous policy bias favouring exotic breeds against indigenous breeds and only limited efforts are made to develop the latter. In attempts to compare productivity of exotic and indigenous breeds, the breeds are not competing on a level playing field. Governments often favour the introduction and spread of particular breeds, farmers may preferentially feed and otherwise more intensively care for the exotic animals (sometimes for years before they realize the drawbacks) Sometimes a serious natural disaster such as a drought must occur to initiate awakening to these biases, for the exotic animals are often the first to die under adverse conditions. In addition, it is often the case that the full costs are not paid for exotic genetic material Superior livestock semen is provided to developing countries free of charge, without progeny testing and disregarding the specific production environment in which the semen is to be used. Genetic material is donated or given at low cost to speed up genetic progress in developing countries. Furthermore, artificial insemination (AI) services to developing countries are often provided initially free of charge or real costs are not fully recovered. This provides access to exotic genotypes at a lower cost than would be applied for AI of indigenous breeds if the mechanisms were in place.

Producing food and agriculture from high-input, short-lifecycle exotic breeds implies a different cost structure to those using indigenous breeds. In many countries, there are subsidies on feed and other inputs which tend to favour exotic breeds as they make more extensive use of it At a lower level, there may be subsidies on production inputs, such as fuel and fertilizer to produce concentrate feed. Preferred credit schemes are likely to have a similar effect Other factors that may affect breed choice include economy-wide policies and determinants such as exchange rates, producer prices, inflation and interest rates. These trends favour loss of the indigenous animal genetic diversity beyond the rate that would occur without distorting the food and agriculture production intensification process. The FAO World Watch List for animal diversity indicates (based on data provided by countries) the number of breeds for mammals (Table 2) which are at risk. The relatively high numbers of breeds at risk for the species of commercial importance to food production (pigs, sheep, goats and cattle) are an expression of the changes in the livestock sector described above. The decline in horse breeds can be attributed to increased mechanization. Please note, the changes from 1995 to 1999 are not necessary an indication of a true increase in breeds at risk but more the result of more and better information due to improved reporting procedures.

The re-establishment of indigenous breeds to meet the demand of the people has been repeatedly demonstrated to be extremely difficult Very often the adapted genetic material for the required production environment has been decimated and cannot be found in the neighbouring countries, and if it is found it is generally only in very small numbers.

FAO's Role

Global Strategy for the Management of Farm Animal Genetic Resources

Country recognition of the importance of animal genetic resources, of the need to sustainably use, develop and conserve these essential resources, and of the poor state of their current management, led the governing bodies of FAO to request the development of the Global Strategy for the Management of Farm Animal Genetic Resources (FAO 1999) (Global Strategy) The priority action is aimed at further enhancing awareness of the many roles and values of animal genetic resources; providing a framework for local, national, regional and global efforts to better use, develop and conserve these resources; and mobilizing the necessary financial support to further development and implement the Strategy One of the activities within the Global Strategy was the development of a first Report on the State of the World's Animal Genetic Resources.

Asia's Pilot Function

The first Regional Project to address the issue of genetic erosion was funded by the Government of Japan. It started in 1994 covering 12 Asian countries The objective was to evaluate thoroughly the particular characteristics of the different breeds and strains; to strengthen, by appropriate breeding programmes, and by adjustments to the husbandry systems to which they are particularly adapted, their prospects of survival, and to contribute to the balanced evolution of the farming systems which are the basis of human food production in Asia. The Development Objective was to identify, characterize and conserve Animal Genetic Resources so as to maintain biological diversity for sustainable agriculture. The project was successful in providing training in the area of animal genetic resources management, in supporting countries' activities in conserving breeds which are in danger of extinction and particularly in raising broad awareness of the role and the importance of the value of indigenous animal genetic resources. All of these countries have developed comprehensive animal genetic resources management plans and in some countries attempts are been made to put them into practice.

The First Report on the State of the World's ANGR

Recognizing that animal genetic resources are of crucial importance for the sustainable utilization of many production systems, and are essential components for achieving global food security and rural development, the Commission on Genetic Resources for Food and Agriculture suggested that FAO should coordinate the development of a country-driven Report on the State of the World's Animal Genetic Resources (8th Regular Session 19-23 April 1999),

The specific outcomes pursued through the preparation of Country Reports and the first Report on the State of the World's Animal Genetic Resources are:

- A detailed assessment of the state of genetic resources in the farm animal sector covering utilization and conservation, as well as the related techniques being used (state of the art), taking into account the production systems and socio-economic conditions of each country.
- An analysis of the changing and growing demands on the farm animal sector and the implications for future national policies and programmes concerning the sustainable utilization and conservation of farm animal genetic resources.
- A detailed review of the state of national capacities related to farm animal genetic resources and an overall assessment of capacity-building requirements.
- Identification of the priorities for the development of an enhanced national programme of sustainable utilization and conservation of animal genetic resources in the farm animal sector. National priorities may refer to animal species and breeds, to short-term and long-term needs for institution building, research, information system development, policy development, legislation, and regulations.
- Recommendations for international co-operation, priority areas, levels and modes of co-operation that the country would wish to pursue, and proposed country contributions and requirements to ensure sound strategic interventions to achieve the sustainable use and conservation of animal genetic resources.

FAO has committed the Animal Production and Health Division (AGA) as the Global Focal Point for Animal Genetic Resources to coordinate the overall preparation of the first Report on the State of the World's Animal Genetic Resources. The Global Focal Point (consisting of the Animal Genetic Resources Group in AGA) has been mandated to facilitate the preparation of the Country Reports. All countries were invited by the Director-General of FAO in March 2001 to join in this process and to submit to FAO, a government-endorsed Country Report As of November 2002, 137 countries have indicated that they will prepare such a Report Negative replies have only been received from Brunei and DPR Korea. A few countries have not officially replied to the invitation but have initiated the in-country process.

FAO has developed training programmes and materials, and through a Global Orientation and Training Workshop held in Rome, in March 2001, has established a group of expert facilitators to support the regional workshops. A set of definitions has been developed and distributed to promote and achieve universal use of key terms. Between 2001 and 2002 14 regional training workshops have been held involving 176 countries and providing training for 320 professionals. The training of professionals and provision of relevant materials to them provided a solid foundation for ensuring country reporting in all regions. The total cost of the regional training workshops was US $785,000, with the majority of the extra-budgetary funding being provided from the Government of the Netherlands, with significant contributions from the Government of Finland and the Nordic Gene Bank.

Significant efforts have been undertaken to keep stakeholders informed of progress in the process for preparation the first Report on the State of the World's Animal Genetic Resources. The Second Ad Hoc Session of International Stakeholders in Animal Genetic Resources was convened in Rome in June 2001 Participants were informed of the process for developing the first Report on the State of the World's Animal Genetic Resources, and were advised of opportunities for stakeholder involvement throughout the process. Additional sessions will be convened as required to keep stakeholders informed of progress, and to encourage their continued participation in the State of the World process. FAO is also making efforts to more broadly enhance understanding of the need for, and process for developing, the first Report on the State of the World's Animal Genetic Resources. An FAO publication called Animal Genetic Resources Information Bulletin (AGRI) is being used to inform and update a diverse readership of progress in the overall development of the Global Strategy, and now serves as a key instrument in informing readers of progress in the preparation of the first Report on the State of the World's Animal Genetic Resources. The Guidelines for Country Reports were published in AGRI in all FAO languages (except Chinese) to assist in gaining understanding of the scope of Country Reports, and to encourage participation in their development The Domestic Animal Diversity – Information System is also being used to convey understanding of the process for developing the first Report on the State of the World's Animal Genetic Resources, as well as communicating progress through development of a new element within the System.

Government endorsed final Country Reports (CR) are now expected to be submitted to FAO by August 2003. Based on draft CRs (which are submitted already now), it is intended to organize regional meetings to identify regional needs for animal genetic resources and to reach agreement on priorities for action at the regional level Identified regional priorities will enable preparation of the Strategic Priority Action Report - a preliminary global report on the state of animal genetic resources and the capacity to management them. These findings will be presented to the Commission at its Tenth Session in 2004. This regional approach will not only make it possible to provide an advance report on the state of animal genetic resources to the Commission, it will also be extremely beneficial in determining priorities for countries and donors for improved sustainable use and development of these genetic resources in full consideration of all available production environments. The regional process will also enable establishment of conservation priorities and identification of appropriate measures for conservation taking into account local needs and conditions

It is proposed that the Intergovernmental Technical Working Group on Animal Genetic Resources for Food and Agriculture meet in 2003 to review overall progress in the preparation of the first Report on the State of the World's Animal Genetic Resources focusing on the review of the Strategic Priority Actions Report and options for a Follow-Up Mechanism. The Working Group will also provide recommendations to the Tenth Session of the Commission on the content and format of the first Report on the State of the World's Animal Genetic Resources.

The Strategic Priority Actions Report is intended to identify both capacity building requirements, and specific needs for urgent action. The Report will provide a basis for the CGRFA to consider an appropriate implementation or follow-up mechanism to ensure effective and timely response to the first Report on the State of the World's Animal Genetic Resources when it is completed in 2006. Perhaps most importantly, preparation of the Strategic Priority Actions Report will assist governments to further develop and elaborate the first Report on the State of the World's Animal Genetic Resources, as well as provide a solid foundation for responding to high priority areas of common interest and concern before completion of the first Report on the State of the World's Animal Genetic Resources.

Following the review of the Strategic Priority Actions Report by the ITWG and with direction from the Commission on the content and format on the first Report on the State of the World's Animal Genetic Resources, preparation of the Report will commence and continue through the 2004-2005 period. This will require further synthesis of Country Reports and Regional Priority Reports, and review of reports from organizations and expert groups. The final Report is expected to be negotiated at the tenth meeting of CGRFA in 2006.

Conclusions

Asia is a vital area for world animal genetic resources, with over 1,200 domestic animal breeds recorded. The majority of the world's buffaloes and yaks, almost half of its Muscovy ducks, pheasants and partridges, one-third of its pig breeds and one quarter of its goat breeds are found in the region. The current and predictable dramatic increase in demand for livestock products of the growing population, urbanization and purchasing power will result in a change of the livestock sector to intensified and industrialized production systems with the use of exotic germ-plasm.

Achieving and maintaining "Food for All" will require sustainable intensification of agriculture. The genetic make-up of an animal is the key to how they will respond to different aspects of the total production environment, but particularly to climate, feed and water, exposure to disease and type of husbandry.

The process of preparation of the first Report on the State of the World's AnGR, in addition to a strong capacity building effect, will increase national and international awareness of the roles and values of animal genetic resources for food security, and heighten the concern for their rapid loss. The Strategic Actions Report will be the basis for effective action at the local, national, regional and global levels.

Table 1 Total Population Size and Number of Breeds of the Major Livestock species in the Asia and the Pacific Region and Their Share of the World Total

	Population size ('000)	Number of breeds	Share of World Total	
			Population (%)	Breeds (%)
Buffalo	125 400	61	93	70
Cattle	461 200	236	35	19
Yak	n/a	9	98	69
Goat	390 450	146	55	26
Sheep	408 100	233	39	18
Pig	525 600	184	55	37
Ass	14 890	12	34	12
Horse	14 860	83	25	11
Camel	2 815	14	15	22
Chicken	6 182 000	124	45	18
Duck	717 800	45	92	45
Turkey	2 140	6	1	18
Goose (dom)	189 450	13	90	20

Source FAOSTAT (estimates 1999 live animal populations) and WWL-DAD

Table 2 Risk status of Mammalian breeds for Asia and the Pacific 1995 - 1999

	Risk status unknown		Extinct		At Risk[1]		Not at Risk	
	1995	1999	1995	1999	1995	1999	1995	1999
Ass	8	4	0	0	1	2	8	6
Bactrian Camel	0	0	0	0	1	1	4	4
Buffalo	15	14	0	0	1	4	41	43
Cattle	72	76	11	19	12	28	106	132
Dromedary	0	0	0	0	0	0	9	9
Goat	30	29	1	1	6	8	90	109
Horse	29	21	4	2	17	19	26	43
Pig	44	60	12	14	15	16	98	108
Sheep	71	68	6	7	15	21	140	144
Yak	0	1	0	0	0	0	6	8

[1] includes risk categories critical, critical maintained, endangered and endangered and maintained

Source World Watch List for Animal Diversity 3rd Edition

Obata: When we consider the conservation of AnGRs, how is it possible to determine the priorities for the long term or short term conservation of AnGRs? Would you give us some points to consider

Wagner: One of the top priorities is to get the SW-AnGRs reports completed by 2006. This does not mean that we do not look at other activities in the area of AnGRs. FAO has quite a number of activities that are looking into the sustainable development of local breeds, particularly in the poultry sector and in the pig sector. The important part is, or the important aspect is to test or to develop sustainable breeding programs. Looking over the developing world, which means Asia, Africa and South America, there are only very few sustainable breeding programs that have been sustained over a period of years and that have shown annual genetic progress. So if we want to improve livestock production and if we want to improve livestock productivity, we have to improve individual animal productivity. The increase in the cattle sector, in terms of output for example, here in Asia and also in Africa, is mainly due to the increase in the number of animals, and it is not an increase of productivity. So what we have to do in the future is to look at reducing the number or, at least keeping number stable, but increasing the productivity of these animals However, to increase productivity you have two major means, one is breeding and one is feeding. So let us choose the one that we are working on in animal breeding; we should look at breeding programs and development programs within the livestock sector. Since it is also an issue, a long discussion issue, you cannot carry out breeding without feeding, and you cannot carry out breeding without improving management So you have to address the whole complex of aspects of livestock improvement The industry in the livestock sector and commercial sector will take off by itself. There are market forces and there are monetary forces that drive this sector. But it has to be mentioned that livestock is a way out of poverty for many poor people, and these people should be able to keep their indigenous breeds or breeds suited to the local environment. However, we also have to help them to develop these indigenous breeds, and this is one of our priorities in the near future.

Taneja: What is the expected change, in terms of the contribution of livestock to agriculture as a whole, from now to 2020 or in terms of retracing the last 20 years to look at the changes? The second issue is that when we talked about the use of livestock manure, if you translate this in terms of its fertilizer value - nitrogen, phosphorous, and potassium - this comes out to be more than four times the actual values that were estimated. If you have some useful information it would greatly help in building up a case for the better management of resources.

Wagner: The present contribution of livestock to agriculture in terms of GDP is about 30-40%. It varies very widely between countries. In certain African countries it was over 90% and in other countries down to 10%. The fact is that the livestock sector will increase dramatically in the Asian region and we have examples of this in Thailand, the Philippines, Indonesia, Malaysia, and to a lesser extent perhaps, also now in Vietnam. The major industrialized sectors of these countries and their major commercial companies are also impacting on other neighboring countries such Laos and Cambodia and so on, so it is just a question of time before this sector will become established. Perhaps a small piece of information and a small indication for research here is that we think that intensified and industrialized production will be necessary to supply food items. But we also realize that this industrialized production is completely detached from the soil and creates dramatic problems regarding the environment and pollution. We have areas in Thailand with a phosphorous and nitrogen overload of 400-500%. The industrialized sector is able to produce at lower prices than the traditional sector can. But the industrialized sector is polluting and is doing damage to the environment for which they are not paying. So we are currently launching a project that is called area wide integration. We are looking at the issues of industrialized production compared to small scale production. If the resulting policy creates a level playing field between the traditional producers and the industrialized producers, then perhaps traditional producers can compete better than they can at the moment So this is the issue we are addressing in the Asian region in particular.

Miyazaki: From the point of view of AnGRs, ancestral or wild relatives of domestic animals are also very important Do you have any program on these animals?

Wagner: FAO does not have such a specific program, but we know that quite a number of countries have programs that look at these issues and at the wild ancestors of domestic species.

1. Present situation of Animal Genetic Resources in Each Asian Country

Chairpersons SASAKI, Y
IZAIKE, Y

Present Situation of Domestic Animal Genetic Resources in China

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1 Introduction

China is one of the countries that have the richest animal and poultry breed resources as a gene pool in the world. The genetic diversification of domestic animal species in China, especially the excellent germplasm characters of native breeds, was left over by our ancestors under several thousand years' diversification in natural and ecological environment These native breeds were playing an important role in history, for example, Chinese native pig breeds were introduced to Rome as early as two thousand years ago, Chinese Langshan Chicken were introduced to the United Kingdom in 1970s. More than 30 Chinese superior domestic animal and poultry breeds such as Beijing Duck, Meishan Pig, Guanzhong Donkey, and Qinchuan Cattle have been exported to some countries in Asia, Europe, America and Oceania. These native breeds exert a profound influence on the development of the genetic diversification of domestic animal and poultry breeds and animal husbandry industry throughout the world. They are essential raw materials in developing new types and new breeds and will be contributing to the sustainable development of animal production in the future.

According to "Animal Genetic Resources in China and Asia" by Changxin Wu in 1996, the livestock and poultry genetic resources in China mainly include the following 12 species pig, yellow cattle, yak, water buffalo, sheep, goat, horse, donkey, chicken, duck, goose, special fowl, totaling 282 breeds (Table 1, the figure comes from "Animal and Poultry Breeds in China" in 1986, not including other breeds from provinces of the country), of which, there are 194 native breeds (accounting for 68.8%), 45 developed breeds (accounting for 16.0%) and 43 introduced exotic breeds (accounting for 15.2%)

2 Status of the Diversification Conservation of Domestic Animals

2.1 Status of threat to domestic animal species and breeds

The genetic resources of China's domestic animals have certain changes in 20 years. The population of 41.9% of native breeds has decreased by different extent The extinct animal and poultry resources are as follows: In 1993, The Ministry of Agriculture (MOA) had confirmed 10 extinction breeds. In 1999, MOA had confirmed 7 extinction breeds, 11 critical breeds and 40 endangered breeds.

There are many factors that are responsible for the population decline of domestic animal genetic resource. For example, the production performance of some native breeds could not meet the demand of current market as well as an inadequate recognition of the special characters of some native resources, therefore, the people introduced foreign exotic breeds to simply substitute or blind cross with native breeds for improvement As such, it caused the quantity and homogeneity of the population decline of some native breeds or even caused crisis in some native breeds. Once a breed disappears, the loss would be invaluable. Therefore, it is essential to adopt powerful conservation measures for preservation of them, otherwise, a relatively big risk exists in the conservation of Chinese native animal and poultry breeds.

2.2 Policies Concerning Domestic Animal Conservation

The genetic resource preservation of domestic animals is a long-term, public welfare and social cause. First of all, the Chinese Government has actively given support by enlisted it into the development plan of national economy and social development, encourages enterprises and individuals to take part in the conservation and scientific development of animal genetic resources. Secondly, it is overall arranged and is responsible by governments at different levels. The central government and local governments should formulate perfect, practical plans for animal and poultry breed resources conservation and development Thirdly, the conservation work is combined with development and utilization, with preservation as the major objective and combining conservation with utilization and promoting conservation by utilization. Fourthly, combination of traditional means with modern biotechnology, it is essential to bring into full play the roles of the conservation farms and conservation areas while unfold conservation work by making use of embryo, sperm, DNA and other modern conservation technologies and methods.

At present, MOA is drafting the “Animal Husbandry Law”, which has integrated the conservation of animal and poultry genetic resources as an important content in the Law. It has concrete stipulations on the legal responsibility of conservation work, and this has made the conservation work to follow legal procedures. Meanwhile, MOA has formulated the “Plan of Animal and Poultry Genetic Resource Conservation”, conscientiously implementing and improving the system and science of our breed conservation work.

2.3 Progress of Animal and Poultry Genetic Resources Work

The Chinese Government has always attached great importance to the work of animal and poultry breed resource conservation.

In order to clarify the animal and poultry germplasm in China, the Chinese Government had started animal and poultry breed resource survey in the 1950s. Through 9 years of efforts, China had clarified the breed resource status in developed areas and published “Pig Breeds in China”, “Cattle Breeds in China”, “Sheep and Goat Breeds in China”, “Poultry Breeds in China” and “Horse and Donkey Breeds in China” In the past 20 years, China has unfolded systematic research on germplasm characters of some animal and poultry breeds and genetic distance estimation, and achieved certain results in the theory of systematic conservation of animal and poultry breeds and conservation methodology This has provided scientific support for the unfolding of conservation work of animal and poultry breed resources.

In order to strengthen the conservation of native breeds, the Chinese Government has input large quantities of funds and established a big batch of excellent native breed resource farm and bull stations in various parts of the country.

In order to transfer the advantages of rich Chinese animal and poultry breed resources into economic advantages, while strengthening conservation work, we have given focus on the breeding and industrialization of animal and poultry breeds. In recent 20 years, we have used modern breeding techniques and means in developing a huge batch of specialized lines and new breeds. During the period of 1996-2001, the State had examined and approved a total number of 17 new animal and poultry breeds. Meanwhile, the methods of animal and poultry recourse development and utilization move to the orientation of integration of breeding, production and processing. Thus this has enabled China to keep the excellent characters of many local native animal and poultry breeds and improved the production performance by a big margin.

2.4 Methods of Animal and Poultry Genetic Resource Conservation

At present, the conservation of animal and poultry breed resources in China has mainly adopted three methods, i.e., living body conservation, cell conservation and gene conservation. The three methods are complementary with each other, and composed of the main body of animal and poultry genetic resources conservation at present time in China.

— **living body conservation:**

The living body conservation is undertaken by the method of constructing conservation farm and conservation areas in the original producing place or other established place of animal and poultry genetic resources, for example, the Poultry Conservation Gene Bank in Jiangsu Province has conserved 21 chicken breeds, with conservation scale of 200-300 chickens in each breed. These places of genetic resources is responsible for formulating corresponding conservation policies, such as forbidding cross with exotic breeds, formulating scientific and effective breeding programs, avoiding inbreeding and other technical measures, etc. At present, this method are fairly popular and play an active role in resource conservation work. In order to further select and purify the quality of native breeds, the producing areas of various species have established numerous selection breeding farms for horse, cattle, sheep and poultry through special funds allocated by the government Meanwhile, China has also divided some corresponding conservation areas. Through years of breeding and purification work, the quality of native breeds has been improved significantly. These breeds have not only conserved, but also performance tested, which has enabled China to further understand the characters of these breeds.

— **Cell conservation:**

MOA established the Center of Preservation and Utilization of Germplasm Resources of Domestic Animals and Forage in 1996. The center develops conservation technologies very rapidly.

At present, it has conserved frozen embryos and frozen semen of 16 breeds of cattle, sheep and other animals. Each breed has conserved 1500 ampoules of frozen semen and 100 frozen embryos. There are two yak breeds in conservation, storing about 1500 ampoules of semen in each breed.

— Gene Conservation

In the Center of Preservation and Utilization of Germplasm Resources of Domestic Animals and Forage, we have preserved the blood samples of 58 Chinese native pig breeds, corresponding extracted DNA samples of nearly 3600 individuals, some genetic materials of ear tissues and the blood samples of 56 Chinese native cattle breeds including yellow cattle, yak and water buffalo. Awareness of the value of genetic resources has stimulated the molecular level study of the genetic diversity of indigenous breeds in recent years. In June of 2002, the center finished the project "Measurement of Genetic Distances between Chinese Indigenous Pig Breeds" Its objectives are to confirm the order of conservation among these breeds, to propose effective methods to maintain and utilize them, and to estimate the diversity and genetic relationships of local pig breeds by means of twenty-seven microsatellite recommended by the International Society of Animal Genetics (ISAG) and the Food and Agriculture Organization (FAO) Measurement of genetic distances between Chinese indigenous cattle breeds are still going on.

2.5 Breed Special Character Identification

The domestic animal and poultry breeds of China have varied good performance characteristics such as meat output, milking, wool and cashmere production, egg production, draft, high reproduction, small body size, medicinal purpose and ornamental purpose, etc. Many breeds are well known in the world for producing traditional style products.

We shall describe the characters of China's native domestic animal resources as follows:

Pig: Most of the Chinese pig breeds are dual-purpose pigs. They are classified into large-, medium- and small-types. Jinhua Pig has the characters of thin skin, fine bone and tender pork. It is the raw material for making Jinhua hams. Gilts can be mated at the age of 3 months (body weight of 20 kg) with a litter size of 14.25 piglets for sows. Wuzhishan Pig has small body weight and good resistance, with a body weight of 35 kg for adult pig, lean meat percentage of 47.3%, litter size of 6-8. It can be used as laboratory material for life science, nutrition science, birth control and comparative medicine. Tibetan Pig is suitable to be used for all-year-round grazing and has the characters of small in body size, thin skin and high lean meat percentage with an average body weight of 40 kg for adult pigs. Rongchang Pig has the characters of good quality strong white coarse and long bristles with a length of 11-15 cm and a maximum length of 20 cm. The output of bristle is 250-300 grams per pig. Taihu Pig has the characters of big litter size and quality pork, with a litter size of 14.9 piglets for sows. The pre-slaughter weight is 61.5 kg with a dressing percentage of 66.7%, lean meat percentage of 43.9%. It has good reputations for its high fecundity in the world.

Yellow Cattle: Famous excellent native breeds include Qinchuan Cattle, Luxi Cattle, Nanyang

Cattle, Jinnan Cattle and Yanbian Cattle. Nanyang Cattle and Yanbian Cattle are located in hilly regions, and the other three breeds are distributed in plains. These native cattle breeds are high in confirmation and very strong with good draft capacity, fine meat performance. They are the basis for developing and cultivating China's beef cattle.

Water Buffalo: China has a population of more than 20 million buffaloes. All of them belong to Swamp type, but they are divided into four categories. Some of them are produced in Jiangsu, Zhejiang and coastal regions, and are called Haizi water buffalo. Some of them are beach-lake buffaloes produced in Boyang Lake, Dongting Lake and Honghu Lake regions, with strong constitution, suitable for working in paddy field in South China. Wenzhou Buffalo has good milking performance and high butter fat percentage.

Yak: Yaks are produced in the high frigid region above the altitude of over 3000 m in the Qinghai-Tibetan Plateau and has the characters of dual-purpose of milk and meat, pack transportation and producing hairs. It is very essential animal for herdsmen in Qinghai-Tibetan Plateau frigid pastoral region. It is not only a production means but also living means. The white yak, produced in Tianzhu Prefecture, Gansu Province, is a rare yak breed. According to statistics of 2001, China has a total population of more than 14 million yaks, accounting for 95% of the world yak population.

Sheep: We have sheep breeds of wool purpose (carpet wool), meat purpose (coarse wool and fat tail), fur purpose and lamb skin purpose. Of which, the Tibetan Sheep produced in Qinghai-Tibetan Plateau and the Hetian Sheep from Xinjiang have the characters of long wool and good elasticity and belong to sheep breeds of quality carpet wool Aletai Sheep from Xinjiang has well-developed fat rump and the Tan Sheep from Ningxia produces white fur coat after first shear, which is famous worldwide. In addition, the Black Fur Sheep from Qinghai and Gansu, Hu Sheep from Jiangsu and Zhejiang are famous breeds producing lambskin. Hu Sheep and Small-Tail Han Sheep have the characters of early maturity, multiple lambs and high fertility.

Goat: The famous goat breeds include Zhongwei Goat, Liaoning Cashmere Goat, Jining Black Goat, Inner Mongolia Cashmere Goat, Chengdu Ma Sheep. Zhongwei Goat produces white fur coat after first shear with beautiful curl and evenly arranged wool Liaoning Cashmere Goat has the characters of high cashmere output with long cashmere. Qingshan Goat from Jining has a hair coat of black and white mixture with a color of black, pink black or iron black, with quality black fine long wool and a productivity rate of 270% per lambing and two lambings per year. Chengdu Ma Goat has a milk production of more than 150 kg per lactation, with milk fat of 6.47%, dense wool, durable and can be divided in layer for use. The lambing percentage is 210% with two lambings per year.

Horse: Chinese horses belong to dual-purpose type. Mongolian Horse is high in speed during short distance. Kazak Horse has good milking performance. Wuzhumuqin Horse is a dual purpose of riding and drafting, adapted to hard conditions among the Mongolian Horses. It is good in walking with strong forces and working sustainable. Hequ Horse is suitable for working as a shaft horse. Its draught force is equivalent to 80% of the body weight and sustainable. Yushu Horse is adapted to plateau climate, and can walk freely in swamp, steep slopes, and narrow winding trail In Yunnan, Guizhou and Sichuan provinces as well as Baise Prefecture, Guangxi Zhuang Autonomous Region, most of the adult horses has a height of about 1 meter, and is called short horse. These horses have been used in developing urban tourism.

Donkey: The famous donkey breeds include Guanzhong Donkey, Dezhou Donkey and Jiami Donkey. Guanzhong Donkey can be used as draft, ride and pack purpose. Male donkey has a draught force of 93.8% of the body weight while female donkey can be used in pack and riding in mountainous road.

Poultry: Most of the poultry breeds belong to dual-purpose breeds. Of which, some breeds, such as Beijing You Chicken and Huiyang Chicken, have the characters of thin skin, fine bones, tender meat and good flavor, and can be used as broiler breeds. Beijing Duck is a large-size meat purpose duck famous in the world and can be used as the raw material for making "Beijing Roast Duck" Gaoyou Duck can be used to make pressed salted duck, and is famous for its double yolk egg. China has many excellent native breeds of egg layers, Xianju Chicken has an annual egg output of 200 with egg weight of 50 grams; Shao Duck has an annual egg output of 280-300 with egg weight of 60-65 grams; and Huo Goose has an annual egg output of 100-120 with an egg weight of 128 grams. In addition, we also have Taihe Silk Fowl, which is a precious breed using as medicine. The Chinese Fighting Fowl is used as ornamentals.

In the aspect of animal and poultry breed character identification, in addition to conventional distribution, population, confirmation and production performance investigations, China has unfolded germplasm study of major native poultry breeds. The study has systematically measured the physiological and biochemical targets: meat quality, fat composition and carcass composition and studies on some other flavor related materials. In recent 10 years, related research institutions have conducted molecular level research on major animal and poultry genetic resources in China, and found some genetic labeling of major economic characters. For example, the genetic labeling includes the high fertility of Taihu Pig, quality flavor of native chicken breeds, and high fertility of Small-tailed Han Sheep and microsatellite DNA genetic diversity on different breed of animal species. This has provided scientific basis for the conservation, development and utilization of genetic resources.

3 Development and Utilization Situation of Domestic Animal Genetic Resources

Domestic animal genetic resources are an important basis for livestock industry development Over a long period of time, China has always followed the principle of combining development and utilization with conservation in the aspect of development and utilization of domestic animal genetic resources.

MOA is responsible for the administration of genetic resources of domestic livestock and poultry, with corresponding administrative institutions established in different provinces, autonomous regions and municipalities and with the bureaus and stations of animal husbandry established in different prefectures, cities, counties and towns. The National Examining and Approving Committee for Livestock and Poultry Breeds has been established by MOA and the corresponding committees have also been established in some local areas, which are responsible for examining and approving new breeds and new lines.

In order to continuously develop and improve the quality and performance of domestic animals, MOA has established associations, technical organizations and breeding centers of breeding committee for some breeds. These organizations of association and breeding committees have played an important role in improving the quality of domestic animal breeds in China.

By using the techniques of computer and Internet and on the basis of the supplementary survey on animal and poultry breed resources, we have established the "China Information System of Domestic Animal Genetic Resources" The Animal and Poultry Breed Resource Dynamic Monitoring Center" is now under construction. The software package of the information system can be applied in the administration of animal and poultry genetic resources throughout the country.

Here, the Chinese Government is willing to unfold cooperative research in the domain of domestic animal genetic resources, and spare common efforts in the conservation and utilization of global domestic animal genetic resources and for a sustainable development of livestock industry.

Table 1 Status of China's Animal and Poultry Genetic Resources[1]

	Original native breeds	Developed breeds	Introduced exotic breeds	Total
Pig	48	12	6	66
Yellow Cattle	28	4	7	39
Yak	5	0	0	5
Water Buffalo	1	0	0	1
Sheep	15	7	8	30
Goat	20	2	1	23
Horse	15	11	7	33
Donkey	10	0	0	10
Chicken	27	9	11	47
Duck	12	0	2	14
Goose	13	0	0	13
Special fowl	0	0	1	1
Total	194	45	43	282
% in the total	68.8	16.0	15.2	100.0

[1] According to "Animal Genetic Resources in China and Asia" in 1996

Sasaki: In terms of living animals, is conservation being implemented in selected breeding farms? Is the conservation of cattle on a private basis or is it supported by the government?

Zhang: They are private farms supported by farmer's associations.

Izaike: You mentioned the gene conservation program for pigs from this year. What is the purpose of collecting ear tissue?

Zhang: For molecular analysis and cryopreservation.

Present Situation of Animal Genetic Resources in India[1]

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Abstract

An analysis of present and future use of Animal Genetic Resources (AnGR) in the changing production environment has been made. Issues relating to management of AnGR have been identified. Present status of livestock resources has been discussed. Strategy and an action plan for optimum management of AnGR has been formulated and is being discussed with various stakeholders. The human resource and capacity needs for characterization and conservation of AnGR have been identified.

The diverse animal genetic resources in India include a broad spectrum of native breeds of cattle, buffaloes, goats, sheep, equines, camel and poultry (Table 1) Other animal species viz., mithun, yak, elephant, ducks, geese and quails are important component of animal wealth. No specific breeds of pigs are available. A large number of non-recognized strains/breeds perhaps variants of the recognized breeds also exist The country has some of the best breeds of draught cattle, dairy buffaloes, carpet wool sheep and prolific goats.

The animal breeding and production strategies in recent times have been used to increase milk, meat, wool and egg production to meet the market demands. This has led to the development of some highly productive breeds/strains for extensive use and hence the local adopted breeds capable of producing under low input are getting replaced with high producing genotypes. In poultry, local breeds have totally been replaced with exotic germplasm. The usefulness of a breed now is judged on its present economic viability and not on its real genetic worth. It is difficult to postulate as to what breed types would be needed in future and hence the need to conserve and manage all diverse animal types as a part of genetic security. An attempt has been made to analyze the present and future use of animal genetic resources in the changing production environment and suggest strategies and an action plan for optimum management of animal genetic resources.

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[1] Paper presented at "The 2002 NAAS International Workshop on Genetic Resources, Present Status and Genetic Variability of Animal Genetic Resources in Asian Region", 11-12 December, 2002, Tsukuba, Japan.

Table 1 Biodiversity in animal genetic resources: names of accredited breeds

Cattle	**Gir***, **Sahiwal***, Red Sindhi, **Deoni***, **Nagori***, **Bachaur***, Kenkatha, Malvi, **Kherigarh***, Hallikar, Amritmahal, Khillari, Bargur, Kangayam, **Ponwar***, **Siri***, Nimari, Dangi, **Hariana***, Mewati (Kosi), **Rathi***, **Ongole***, Gaolao, Krishna Valley, **Tharparkar***, **Kankrej***
Buffalo	Murrah, **Bhadawari***, **Jaffrabadi***, Surti, **Mehsana***, Nagpuri or Ellichpuri, **Nili-Ravi***, **Toda***
Sheep	Chokla, Nalli, Marwari, Jaisalmeri, **Pugal***, Malpura, Sonadi, Pattanwadi, Muzaffarbagari, Jalauni, Hissardale, Deccani, Nellore, Bellary, **Hassan***, **Mandya***, **Mecheri***, Kilarkarsal, Vembur, Coimbatore, Nilgiri, Ramnad White, Madras Red, Tiruchy Black, Kenguri, Chhotanagpuri, Shahabadi, Belangir, Ganjam, Tibetan Sheep, Bonpala, Gaddi, Rampur Bushair, **Bhakarwal***, Poonchi, Karnah, Gurez, Kashmir Merino, Changthangi
Goats	Sirohi, Marwari, Jhakrana, **Beetal***, **Barbari***, Jamunapari, Mehsana, Gohilwadi, Zalawadi, Kutch, Surti, Sangamneri, **Osmanabadi***, Kannai Kadu, Malabari, Ganjam, Bengal, Gaddi, Changthangi, Chegu
Camel	Bikaneri, Jaisalmeri, **Marwari***, Kutchi, Sindhi, Shekhawati, Jalori, Mewati
Horses	Kathiawari, Marwari, Bhutia, Manipuri, Spiti, Zanskari
Poultry	**Aseel***, Ankaleshwar, Busra, Brown Desi, Chittagong (Malay), Daothigir, Danki, Ghagus, Harringhatta Black, Kadaknath, Kalasthi, **Kashmir Faverolla***, **Miri***, Naked Neck, Punjab Brown, Tellichery, Titri, Tani, **Nicobari***

* **Information on management practices, physical, economic and genetic parameters has been generated through surveys and breed descriptors developed.**

Among non-accredited breeds, information has been generated on Vechur, Punganur, Umblachery and Kangayam cattle; Tarai and Swamp buffaloes, Garole sheep; Kodi Adu goat

Animal Production Systems and Genetic Resources

The livestock production systems and management practices are greatly influenced by agriculture cropping pattern, climate and topography. The existing animal production systems can broadly be classified as (i) small holder production with little or no land, and (ii) commercial production more relevant to poultry and to some extent dairying with crossbred cows and buffaloes especially in peri-urban areas. Although small holder animal production systems are ecologically sustainable and economically viable, these cannot meet the growing food requirement of large human population (Bhat and Taneja, 1998)

Sheep, goat, camel and to some extent cattle are raised on natural range lands, community grazing lands and crop stubble. This system is coupled with low efficiency and is mostly unorganized. The effects of migratory system on sheep, goat and cattle breeds need to be studied. The underlying issues responsible for poor efficiency of this system should be addressed.

The animal genetic resources (AnGR) have also undergone changes due to introduction of innovative technologies, fast changing production systems and industrialization. The impact of these changes on animal genetic resources needs to be studied. In order to optimally utilize the AnGR, the SWOT analysis of the resources across productive systems should be made for their present and future use and strategies developed for their optimum management and utilization.

Issues and Concerns

It is true that AnGR are crucial to food needs, employment, have social and religious value and therefore should be managed. The major question is as to who (farmer vs. Government), how (*in situ* and *ex situ*) and how long to conserve AnGR. The issues of conservation also need to be deliberated in view of too many low producing populations, shortage of feeds and fodder and high cost of conservation of AnGR.

Information on performance parameters (growth, production, reproduction and survival) of indigenous breeds in relation to their native ecology, feed resources, prevalent management, processing and marketing systems, economics and improvement programs is not available. This needs to be generated through surveys to examine their use in the present and future production systems. The methodologies to identify superior herds/flocks/individual animals to be utilized in the breed improvement programme and conservation need to be worked out

Intermixing among the indigenous breeds and introduction of exotic germplasm for crossbreeding for quick genetic improvement has led to dilution of breeds. The effects of crossbreeding program on native breeds have not been meticulously studied, although it has been held that they are among the casual factors for the degeneration of native germplasm.

The buffalo and crossbred cattle male calves are generally considered inferior as working animals and willfully neglected to die. The slaughter of milch buffaloes after completion of lactation in metropolitan cities is an endemic problem. The magnitude of this problem and its impact has not been assessed.

Status of Animal Genetic Resources

Information on management practices, physical, economic and genetic parameters on some important breeds generated through surveys involving a number of State Agriculture Universities and NGO's has been documented and breed descriptors developed. Monographs on some of the breeds have also been published. The methodologies for surveys have been standardized for different species of livestock and poultry breeds. The questionnaires included information on morphological and performance parameters and genetic profile including production system and socio-economic status of farmers. The questionnaires are as per guidelines of FAO and modified for Indian situation. An information system (AGRI-IS) has been developed for storing and retrieval of information on AnGR of the country. Cytogenetic profile of various breeds of cattle, buffalo, sheep, goats, pigs, poultry, yak and mithun have been established. Blood typing and biochemical polymorphism studies on proteins and enzymes have been completed for some of the breeds. Molecular genetic characterization using microsatellite markers is in progress.

The status of AnGR has been discussed in detail by Taneja and Sahai (1995) and Taneja and Nivsarkar (1998) Species wise information in brief has been presented below.

Cattle: The cattle of Indian sub-continent are characterized by the presence of prominent hump, long face, upright horns, looping ears, dewlap and slender legs. The duly accredited breeds have been classified on functional utility as milch, draught and dual purpose. A number of crossbred genotypes viz., Sunandni, Karan Swiss, Karan Fries and Frieswal have been evolved and breed descriptors developed. Information on physical and economic parameters of important cattle breeds has been discussed by Taneja et al (2002) Selection program for improving milk yield through progeny testing in Sahiwal, Tharparkar, Gir and milk and draft in Ongole and Hariana are in existence. Breed improvement programs for Rathi and Red Sindhi are also being initiated. Around 1000 breedable females of each of these breeds spread over 3-4 locations are included in the programme and 10-15 bulls are tested in each cycle (Taneja, 1999) A national programme on cattle and buffalo improvement with focus on improvement of indigenous breeds is in existence. Breeding farms for some of the important cattle and buffalo breeds are being strengthened to provide quality bulls. A national cattle and buffalo breeding policy is being formulated.

A number of new strains viz., Panganur, Red Kandhari, Vechur, Bhagnari, Dhenani, Lohani, Rojhan, Bengal, Chittagong Red, Nepalese Hill, Kchaha Siri, Tarai, Lulu and Sinhala have been reported. Possibility of some of these being only phenotypic variants getting different names cannot be ruled out Most of these breeds have shown decline in numbers. Punganur, Kangayam and Vechur cattle breeds have special features of small size (Table 2) Long term conservation programs both in situ and ex- situ for these breeds have been initiated.

Table 2 Important Parameters of Vechur, Kangayam and Punganur cattle

	Vechur*	**Kangayam****	**Punganur*****
Adult body weight (kg)			
Female	128.6	128.1	178.0
Male	166.5	151 1	244.0
Age at 1st calving (days)	1080	1541	1110
Milk yield (kg)	561	678	546
Lactation length (days)	242	285	263
Fat %	6.3	3.9	5.0

Source: * Final Report (1993-98) ICAR adhoc scheme on conservation of germplasm of Vechur cattle of the coastal area and dwarf cattle of the high range of Kerala CAS, KAU, Mannuthy, Thrissur

** Final Report (1993-97) ICAR adhoc scheme "A Survey of Kangayam Cattle TNVASU, Namakal

*** Final Report (1993-97) ICAR adhoc scheme on "Preservation and Improvement of Punganur breed of cattle ANGRAU, Palamner, Andhra Pradesh.

Buffalo: Both river and swamp buffaloes are available. Swamp buffaloes are found principally in parts of Assam. The river buffaloes are distributed throughout the country and have been developed for milk production. Murrah has been used as the major improver breed for grading non-descript and other low producing buffaloes throughout the country. The information on physical and economic characteristics of various buffalo breeds have been discussed by Bhat and Taneja (1987) and issues relating to buffalo breeding research by Taneja (1998). Information on population dynamics, physical and economic parameters of swamp and Toda buffaloes has been presented in Table 3. The indiscriminate crossing of Surti with Murrah is seriously affecting the population of Surti in its native tract Similarly, Bhadawari buffaloes known for high fat content are being upgraded with Murrah. Toda buffaloes are also facing extinction through large scale crossing with Murrah. Breeding strategies to conserve the affected breeds have been suggested. Systematic progeny testing programs for Murrah, Jaffrabadi, Mehsana and Surti are in existence. In addition, herd registration programs for Murrah, Surti and Jaffarabadi having minimum lactation yield of 2000, 1600 and 1600 kg have also been taken-up to support conservation and improvement efforts (Taneja et al, 2002)

Table 3 Important parameter of Toda and Swamp buffalo

	Toda*	**Swamp****
Birth weight (kg)	28.0	32.1
Age at 1st calving (days)	1460	1695
Milk yield (kg)	500	506
Lactation length (days)	218	283
Fat %	8.2	8.5
Calving interval (months)	14-18	14-15

Source: * Final Report (1993-96) ICAR adhoc scheme on "Evaluation and Conservation of Toda Buffaloes" TNVASU, Sandynallah, Tamil Nadu.

** Final Report (1993-98) ICAR adhoc scheme on "A Field Survey on the Performance of Swamp Buffaloes of Assam" AAU, Khanapara, Guwahati, Assam.

Small Ruminants

Sheep and goat breeds have been classified and described according to geographical distribution (Acharya, 1982; Khan and Taneja, 1996) There is a large inter-mixing among the breeds in the region where two or more breeds exist There are no breed societies or agencies to register breed-wise animals, maintain flock books or records and ensure purity of the breed. Improvement programs for some of the indigenous breeds viz. Marwari, Chokla, Magra, Changthangi, Deccani, Malpura, Mecheri, Muzzaffarnagari, Nali, Pattanwadi, Madras Red, Mandya and Kashmir Merino are in progress. Open nucleus breeding system approach is being used to improve these breeds for wool and body weights. Breeds that are getting endangered and showing decline in numbers are Gurej, Karnah, Bhakarwal, Jhakharana, Poonchi - all in Jammu and Kashmir and Nilgiri, Muzaffarnagri, Malpura, Chokla, Jaisalmeri, Munjal, Chengthangi, Bonpala and Mandya. Garole sheep though not in breed books has higher litter size (Table 4) and is believed to have famous Borola gene. A project on genetic evaluation of this breed is in progress.

Table 4 Important parameters of Garole sheep

Parameters	Male	Female
Body characteristics (adult)		
Body weight (kg)	15.1 ± 1.4	11.7 ± 0.78
Body length (cm)	45.8 ± 0.7	43.0 ± 0.6
Height at wither (cm)	44.0 ± 0.8	43.7 ± 0.6
Chest girth (cm)	59.7 ± 1.5	55.9 ± 1.2
Reproductive performance		
Age at puberty (days)		226.7 ± 7.9
Age of first conception (days)		252.7 ± 10.4
Lambing interval (days)		205.5 ± 2.2
Lambing rate		173.6 per 100 ewes
Type of birth		
Single		41.6
Twin		43.4
Triplet		14.8
Quadruplet		0.2
Wool production and quality		
Annual wool yield (g)	150.0	
Staple length (cm)	5.1	
Fibre diameter (μ)	67.8	
Medulation (%)	75.2	
Hairy (%)	57.8	

Source: Bose, S (1996) Studies on the productive and reproductive performance of sheep in the saline and semi saline belt of West Bengal Ph.D. Thesis, West Bengal University of Animal and Fishery Sciences, Kolkata.

Crossbreeding of some of the sheep indigenous breeds with exotic viz. Rambouillet and Merino for improving wool production and quality and Dorset and Suffolk for improving feed efficiency and growth have resulted in production of new strains viz., Bharat, Merino, Avivastra, Nilgiri Synthetic (Sandyno), Patanwadi Synthetic and Avikalin for wool and Avimanns for mutton. Indian karakul, through crossing of Marwari, Malpura and Sonadi with Karakul, imported from erstwhile Soviet Union, was also developed for pelt production. Most of these strains, however, have existed at the research farms and not done well with the farmers due to lack of input and expertise available under field conditions.

Goats of temperate Himalayan region (Gaddi, Changthangi, Khasi and Chegu) produce good quality fibre and fine under coat called Cashmere or Pasimna. All the milch goat breeds (Jamunapari, Beetal, Surti and Jharkhana) are found in north-western region in the country. The southern and western regions mainly possess dual purpose breeds (milk and meat) The small sized meat breeds viz., Black Bengal and Assam Hill goats known for their high prolific attributes need to be further studied A breeding policy for goats which did not exist for long time is being put in place. Some of the indigenous breeds viz. Beetal, Surti, Chegu and Jamunapari have shown decline in numbers. Efforts are being made to conserve and improve these goat breeds.

Camel: Camel in India are mostly single humped (Camelus dromedaries), although few double humped camels (Camelus bactrianus) are also present in Nubra Valley of Jammu and Kashmir. Population structure, breed characteristics, management practices, disease incidence and draught capacity of double humped camel have been studied. Females attain puberty at 3-4 years and the reproductive life may continue unto 16-18 years. Annual hair production of adult camel varies from 3-4 kg. Milk production varies from 500-1254 litres in a lactation period 14-18 months The number of double humped camel has gone up from 76 in the year 1996 to 105 in 2000 (Sahni, 2001) Information on economic parameters for important camel breeds has been given in Table 5.

Table 5 Body weight (kg), reproductive parameters (days) and hair production (g/yr) in some camel breeds

	Bikaneri		Jaisalmeri		Kachchhi	
	Male	Female	Male	Female	Male	Female
Birth weight	42.1 + 0.8	38.8 + 0.6	36.9 + 1.2	34.7 + 1.9	33.9 + 1.0	31.5 + 1.9
Weight at 1 year	229.2 + 4.0	223.0 + 7.4	226.0 + 23.8	201.2 + 13.5	202.0 + 4.7	201.8 + 7.2
Adult weight	617.3 + 17.0	577.8 + 9.8	574.0 + 12.7	537.0 + 11.6	576.7 + 44.7	563.7 + 14.7
Age at first service	–	1425.0 + 41.4	–	1412.0 + 16.1	–	1094.5 + 3.4
Calving interval	–	741.9 + 9.8	–	676.0 + 19.4		738.4 + 10.7
Annual hair prod.	1225.2 + 0.2		1089.1 + 0.4		1165.4 + 0.5	

Source: Khanna, N.D., Rai, A.K., Tandon, S.N. and Sahni, M.S. (1993) Camel Genetic Resources in India. Proc. Nat Sem. Agr & Cons 1993.

Pig: Systematic efforts for documentation of pig breeds have not been made. Some breeds based on geographical distribution viz. Ankamali, Deshi, Andman & Nicobar and Indian wild boar have been reported in literature. A number of exotic breeds namely Yorkshire, Landrace, Hampshire and Poland China were introduced for crossing with local pigs. Crossbreds with 50% and 75% exotic inheritance are being used for synthesis of the new genotypes suitable for commercial pig farming. Information on comparative performance of local, exotic and graded pigs is given in Table 6.

Equines: The Zhanskar, Spiti, Manipuri and Bhutia horses are well adapted to hilly terrains. The Marwari and Kathiawari breeds found in Rajasthan and Gujarat are showing decline in numbers due to widespread crossbreeding and lack of incentive to breeders for keeping purebred animals. Descript breeds of donkeys are not known.

Table 6 Comparative performance of local, exotic and graded pigs

Traits	Genetic groups of pigs		
	Local	Hampshire	Upgraded
Litter size at birth	5.5 + 0.5	7.8 + 0.4	7.6 + 0.3
Litter weight at birth (kg)	2.6 + 0.5	10.2 + 0.3	8.90 + 0.3
Litter size at weaning	3.1 + 0.5	5.4 + 0.4	7.2 + 0.3
Litter weight at weaning (kg)	15.4 + 0.5	53.1 + 0.4	74.2 + 0.3
Individual weight at weaning (kg)	5.0 + 0.2	10.0 + 0.2	10.3 + 0.2
Post weaning growth (g/day)	42.3 + 0.2	180.0 + 0.3	130.0 + 0.3
Weight at 120 days (kg)	7.5 + 0.4	20.8 + 0.3	18.1 + 0.3
Weight at 180 days	11.4 + 2.2	31.5 + 1.9	30.0 + 1.7
Age at first farrowing (days)	367.5 + 8.3	441.3 + 11.3	335.0 + 9.2
Inter-farrowing interval (days)	194.5 + 9.5	227.6 + 10.3	192.0 + 8.2

Yak: The yaks are distributed mainly in Arunanchal Pradesh, Sikkim, hilly areas of Uttar Pradesh, Himachal Pradesh and Ladakh region of Jammu & Kashmir. These have not been evaluated from the standpoint of genetic homology, diversity and categorized into breeds. The yaks in Arunanchal Pradesh, Sikkim and Ladakh are quite distinct in their phenotypic characteristics Nivsarkar et al (1997) discussed the history of domestication, distribution, husbandry practices, present perspective and future possibilities of Yak. Milk production in Yak varies from 130-150 kg in a lactation period of 90-170 days. The fat content varies from 5.0 to 11.0%. Pure breeding of yak is practiced at high altitudes (3000 m and above), while at lower altitudes (2000 and 3000 m) where farming is carried out, yaks are usually crossed with local cattle. Among the offspring, the female crossbreds are fertile whereas males are sterile. The crossbred females are superior to pure yak in milk production and fertility.

Mithun: Mithun, the heavy bodied semi-domesticated animals are found in north-eastern states of India usually below 3000 m. Information on the performance parameters of four strains of Mithun is given in Table 7. A large variation in body weights was observed; Arunachalee and Nagamese Mithun were heavier than Manipur and Mizoram thus suggesting that Arunachalee and

Table 7 Some production and reproduction on traits of Mithun

Traits	Mithun strains			
	Arunanchalee	Nagamese	Manipur	Mizoram
Birth weight-male (kg)	20.33	2.00	–	16.62
Birth weight-female (kg)	19.85	19.85	18.00	14.25
Adult weight-male (kg)	540.00	433.00	234.5	265.00
Adult weight-female (kg)	353.00	353.3	278.0	239.8
Av. peak milk yield (ml)	991	441	662	1133
Dry period (days)	131	118	–	–
Calving interval (days)	395	388	–	349

Source Annual Report (2000-2001) NRC on Mithun, Jharnapani, Nagaland.

Nagamese strains could be developed for meat production. There has been extensive crossbreeding of Mithun with local cattle. The crossbreds produce more milk than pure Mithun and are docile. The crossbred males are named 'atsa' while the females are termed 'jatsamin' The Indian Council of Agricultural Research has established a National Research Centre on Mithun in Nagaland. A farm devoted to Mithun production has also been set up at Kamki in West Siang district.

Poultry: A wide variation among chicken breeds in relation to physical and production parameters has been reported. Although exact information on the status of most of the chicken breeds is not available, various reports suggest that indigenous poultry breeds are declining in numbers and many of these are facing extinction. Late sexual maturity, poor egg production, slow growth and small egg size are some of the disadvantages of native birds. Information on performance parameters of Aseel breed under scavenging conditions has been presented in Table 8. Most of the indigenous poultry breeds are well adapted and resistant to many diseases. Hence, there is an urgent need to properly document these breeds.

Table 8 Important parameters in Aseel breed of poultry

Age	Body weight (g)
0 day	29 ± 0.05
4 weeks	107 ± 0.11
8 weeks	234 ± 0.14
24 weeks	1133 ± 1.52
48 weeks	2590 ± 17.18
Egg weight (g)	41
Hatching (%)	
Total Egg Basis	73.97
Fertile Egg Basis	85.11
Fertility (%)	84.28
Age at first egg (weeks)	28.9 ± 0.3
Yearly egg production	33.17
Feed conversion efficiency	5.0 ± 0.44
Management	Scavenging with supplemental feeding

Source: Network Project on Aseel - Final Report (1999)

Strategy and Action Plan

In an ultimate analysis all strategies for conservation of animal genetic resources should be linked to their sustainable utilization. The livestock development programs should be organized to enhance productivity while maintaining genetic purity of the breeds. This can be achieved through (a) evaluation and monitoring of AnGR, developing breed improvement programs, preparing a country report and a national plan for management of AnGR, (b) training of manpower specifically for surveys, genetic characterization, cryogenic storage and data management, (c) addressing issues related to legal framework, IPR and sharing of benefits and (d) creating mass awareness about relevance and use of AnGR. In order to address the above issues relating to AnGR , the National Bureau of Animal Genetic Resources (NBAGR) was established in 1984 with mandate of "identification, evaluation, characterization and utilization of livestock and poultry genetic resources" As breed wise census is not carried out, the limited option available is to generate required information through surveys in the shortest possible time and use the information for developing an action plan for optimum management of AnGR and to identify breeds that need immediate conservation. In a general situation of constraints of funds, it would be difficult to suggest whole hog conservation of every single breed population in the country. The immediate priority should be to conserve useful genotypes facing extinction. Conservation per force will have to be done by the farmers with some scheme of incentives by the Government for economic losses sustained by the farmers in conserving uneconomic but useful breeds. India has agreed to participate in the first report on the State of the World's Animal Genetic Resources, an initiative taken by FAO and a country report on status of AnGR is being prepared. The country report would clearly bring out the present usage of AnGR, their economics, future possible use, institutional strengths and research and developmental priorities relating to management of AnGR including building capacity and human resource. Some of the issues that merit immediate consideration are as follows:

Evaluation of AnGR and Preparation of Country Report

Information on some of the breeds has been generated and a database developed including identifying factors threatening their status in the breeding tract The need is to generate information on the remaining breeds in the shortest possible time, identify gaps and address them on priority in a given time frame.

A number of variants of a given breed have been reported over time. These though phenotypically different may be genetically alike. Such genotypes are being screened for differences if any using DNA fingerprinting. A task force to develop parameters for accreditation of new breeds is being set up. Valuation of breeds in their native environment is being taken up to assess their strength in the changing production environment The model population size needed for *in situ* and *ex situ* (semen, embryo) conservation of breeds in Indian context is being worked out National policy for management of animal genetic resources with clear aims and objectives based on analysis of livestock population and resources, breeding and health status, availability of feeds, production systems and present and future market demands has been developed and is being discussed with various stake holders. It is generally held that warning signals on the loss of bio-diversity emanate when considerable damage has already taken place. To avoid this situation, a country watch list on the pattern of FAO, based on reports of surveys/studies is being published and updated

Many of the native breeds are said to have advantages of fast growth, high prolificacy, disease resistance, adaptability, hardiness and survival under low inputs. These qualities have not been genetically demonstrated. The focus of research now is to identify genes for fast growth, adaptability, disease resistance and fertility in indigenous breeds so that these could be exploited for higher livestock productivity.

Human Resource Development and Capacity building

Human resource to address research priorities in the area of genetic characterization, long term *in-vitro* storage and revival is being strengthened. Training courses on surveys, estimation of population, semen sampling, embryo collection, establishment of live gene banks and health regulations are being organized. Scientific and technical manpower is also being adequately trained to correctly record the required parameters for developing breed descriptors. A course on awareness and management of AnGR is being introduced in agricultural schools.

Legal Framework, IPR and Sharing of Benefits

The legal measures relating to conservation of animal genetic resources are grossly inadequate. Appropriate legal instruments are being worked out to cover all aspects of breed utilization, conservation, trade and marketing. It would be necessary to have a legal frame to regulate mandates and operation of livestock farms and declare some of them as National Gene Banks. In the new WTO structure and IPR regime, access to genetic resources and its transfer is becoming restrictive. The ban on export of genetic resources has to be considered in a manner that access to genetic resources is not denied. Similarly, the possible access to technology has to be examined so that access to new technology is not denied. The AnGR are owned by communities and farmers and hence the issues and mechanisms relating to sharing of benefits from AnGR and traditional knowledge also need to be addressed.

Awareness of AnGR

Mass awareness programs about the present and future use of AnGR for food security need full government support and people's participation. Educational and mass media, electronic media and internet should be the corner stone of this campaign. Farmers who are the real custodian of animal bio-diversity must be involved in the campaign. Breed societies, trusts and herd books should be supported technically and financially. Farm women play a major role in feeding, management and product utilization of livestock. They can greatly help in conservation of livestock resources and should, therefore, be involved in decision making.

It is a matter of common knowledge that information on AnGR currently available is scanty, scattered and needs consolidation and documentation. In this context, publication of monographs on native breeds assumes considerable significance. This activity can also generate global interest in some unique breeds and promote their market value. Country newsletter on animal genetic resources has been introduced on the pattern of animal genetic resource information bulletin of FAO.

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Present Situation of Animal Genetic Resources in Vietnam

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Key words: Vietnamese Animal Diversity and Conservation, Genetic Resources, Sustainable use

A. Introduction

Vietnam is situated in the South-Eastern Asia Vietnam is in Southeast Asia, border with China in the North, Laos and Cambodia in the West, looks out on the Pacific Ocean. Vietnam is one of the highest population density of Agricultural country in the world. The population of about 78 millions going at a rate 2.2% per year and has a mean density of 220 people per km^2

Being not big in territory, having a superficies of over 330,000 km^2, but Vietnam is one of 15 countries in the world richest in genetic resources. This wealth is brought about by the natural and socio-cultural reason.

Natural conditions Vietnam stretches over 15 latitudes, from 8°30' to 23°30' N, so the climate varies and differs distinctly from the North to the South. North Vietnam is located in the tropical zone, but has cold winter due to monsoon influence, the climate, as a result, has sub-tropical feature while the high mountainous areas are of temperate character. Vietnam topography is varied and complex, mountains are of three fourths of the territory superficies, with steep mountains in the north, the Central Highland is pretty flat and the fertile plains in the North and the South. The variety in climate and geography is the main cause to the variety in agro-forestry biodiversity in Vietnam. Vietnam is situated on the Indochina peninsular, the conjunction of the China and India continents, so possesses a lot of species of plant and fauna on these two great continents. Vietnam is on the conjunction of the Pacific and the Indian Oceans, thus in its development history, a great deal of plant and fauna species from other continents have immigrated to Vietnam by sea.

Socio-cultural conditions Vietnam is a multi-ethnic country, of 54 different ethnicities. The particular taming process of plants and animals and the habits of farming, utilizing products of different ethnicities are the important causes to the abundance in agro-forestry biodiversity, of remarkable notice is the diverse ethno-botany knowledge. Vietnam is acknowledged as a country of early developed agricultural civilization, which is another cause to the agro-forestry diversity.

During the past 10 years, owing to government's renovation guideline started from the changes of agricultural policies in the early 1980s, Vietnam's agricultural and rural economy has been developing at rapid rate. It has also been the source supplying foodstuff to society, materials and markets to many industries. This process has been developing in two directions: either more prosperous or erosion. Thank to agricultural development and cultural exchange, animal genetic resources have got more diversified. Numerous commercial animal breeds have been introduced into Vietnam. Many of the local breeds are facing extinction or endanger because their performance, food conversion efficiency or lean meat percent are much lower than that of imported breeds and Vietnamese producers are therefore unwilling to keep them.

The purpose of this paper is to appreciate the present situation of animal genetic resource and their conservation, utilization, to give remaining problems, general directions and solutions for management animal genetic resources in the coming years.

B. Present situation of Animal Genetic Resources

Vietnam fauna is known of 275 species and sub-species of animals, 1,026 species and sub-species of birds, 260 species of reptiles, 32 species of amphibious, 500 fresh water fishes, about 2,000 sea water fishes, and dozens of thousands of non-spine fauna. Endemic Vietnamese fauna are numerous, including dozens of mammals, 10 species of birds, 60 fishes, etc. Since 1992, Vietnam has discovered five more species of mammals unrecorded before, namely *Pseudoryx nghetinhensis, Meganumtiacus vuquangnesis, Pseudonovilos spiralis, Canimientiacus truongsonesis and Muntiacus piliatensis*

Vietnam is considered as one of the world ancient animal domestication area. The husbandry animals here include 12 species, namely *Sus scrofa dom, Bos taurus, Carpa hircus, Ovis aries, Cervus nippon, Cervus unicolor, Oryctolgus cuniculus, Gallus domesticus, Anas platyrhynchos, Cairina moschata, Anser anser dom and Columba livia dom.*

In total, 60 species of local animal species are found with the density of 1.520 spec/km^2, a high one compared to the world density of 0.098 spec/km^2 They generally maintain adapting characteristics to the living environment (harsh and special ecological condition), which may provide useful or potentially useful genes or combinations of gene for future needs. For example, prolifically and early maturity, heat tolerance, disease resistant, flavor meat

So far more than 100 races of different breed animals have been introduced into Vietnam, adaptable to the natural conditions and making great contribution to Vietnam's animal husbandry.

1. Roles of Animal genetic resource in food security and poverty alleviation in Vietnam

At present, indigenous breeds play an important role for country's socio-economic development

1.1. Poverty Alleviation

* **Income earning:** Sale of animals and products (meat, milk, egg, manure, etc.) Create many jobs in rural areas and from that has come more income for the farmers. Crop production using animals for draft power, transport, and manure for maintaining soil fertility. Prize animals such as fighting cock, fighting bull, fancy chickens and birds. Part of agro-tourism such as elephant, etc.

* **Reducing expenses:** Minimum use of chemical fertilizer in crop production. No large investment in purchase of tractor and farm implements. Little use of petroleum for farm production.

* **Socio-economic benefits:** Offer productive role for women, children, and the elderly e.g. in pig, poultry and goat due to it links with work in the home. Use of animals in traditional ceremonies

e.g. use of chicken for ancestral worship. Use of animals in sports, shows or recreation such as fighting cock, fighting bull, Socio-economic status. Loan collateral Other uses such as for dowry or inheritance.

1.2. Food Security

* **Major component in crop production e.g. rice production for family consumption:** Draft animals power for land preparation and transportation. Animals manure for fertilizer. Utilization of crop residues to produce more foods from animals.
* **Increase steady food supplies on family farm e.g. Backyard chickens provide daily meat and eggs:** Duck raising provides eggs and meat Goats and dairy cows provide meat and milk. Preserved meat and traditionally processed animal products such as salted duck eggs, dry beef, pork rind.
* **Provision of family food assurance in case of crop failure due to natural hazards such as flood, drought, crop pests or diseases**

Sale of animals to buy rice or other foods. Our farmers do not usually send crops directly (paddy, cassava, sweet potato etc.) to the market but use the surplus crops as animal feed to produce animal product to gain more money. The different expenses of life: food (a part), clothes, educational fee for children, medicine, weddings, funerals. almost all of them come from the income from animal husbandry.

2. Livestock production

This occupies 20% of agricultural output value. The importance of livestock production and the annual increase of the populations can be seen from following table

Table 1 Livestock population in Vietnam from 1990-2001

Year	Buffalo	Cattle		Pig	Chicken	Water fowl	Goat
	(1000 heads)	Total (1000 heads)	Milk (ton)	(1000 heads)	(1000 heads)	(1000 heads)	(1000 heads)
1990	2,854.1	3,116.9	11,000	12,260	80,184	23,636	372.3
1992	2,886.5	3,201.8	13,080	13,891	99,627	32,041	312.2
1994	2,977.3	3,466.8	16,500	15,587	99,627	32,041	427.8
1996	2,953.9	3,800.3	22,563	16,921	112,788	38,617	512.8
1998	2,951.4	3,987.3	26,645	18,132	126,361	41,529	514.3
1999	2,955.7	4,063.5	29,401	18,886	135,760	43,563	516.0
2000	2,897.2	4,127.9	34,982	20,194	147,050	50,996	543.9
2001	2,819.4	3,896.0	41,241	21,741	158,037	57,973	569.4

National Statistical Sources 2002

With the development of economy, intensification is increasingly developed to meet the demands of higher living standards of growing population. To do this well, agriculture and rural economy has not only to achieve high growth but also to develop sustainably, to enhance the quality of products, efficiency and competitiveness.

Table 2. Perspective of livestock population of period of 2000-2001-2005 and 2010

Breed	Unit	2000	2001	2005	2010
Pig	1000 heads	19,500	20,000	24,000	30,000
Poultry	1000 heads	197,000	220,000	297,000	350,000
Cattle	1000 heads	4,146	4,220	4,200	4,600
In which Dairy	1000 heads	32	33	100	200
Buffalo	1000 heads	2,950	2,960	3,000	3,000
Goat	1000 heads	500	530	650	800
Bee	1000 herds	300	340	500	800
Silkworm	1000 little	420	450	850	1,200

Sources Extension Dept-MARD 2002.

3. Review of animal genetic resources in Vietnam

3.1. Pig genetic resources.

In Vietnam Pig is the most important in livestock production. It is estimated 74% of total meat production. There are 20 pig breeds currently exist in Vietnam in which 14 breeds are native breeds. They are: Black I, Rough I , Mong cai, Ba Xuyen, Thuoc nhieu, Meo, Soc, Muong Khuong, Mini, SonVi, Ban, Lang hong, Co, H'mong pig breeds. Main of native breeds is Mong cai Exotic breeds are: Landrace, Yorkshire, Duroc, Pietrain, Hampshire, Berkshire.

3.2. Cattle genetic resources: 5 in 21 breeds are native cattle.

Yellow Cattle, U dau riu, H'mong, Phu Yen, Thanh hoa, Nghe An, Ba Ria, Coc, Laisind cattle, most of them is Yellow cattle. Exotic cattle breeds includes: Red Shind, Holstein Frisian, Ongole, Sahiwall, Hereford, Simmental, Limousine, Crimousine, Santa Gertrudis, Red Brahman, Grey Brahma, Brown Swiss, Charolais, Drought master, Jersey cattle. Native breeds are raised for draft, meat, exotic are raised for milk and meat

3.3. Buffalo genetic resources: They are kept for draft, meat

Small Buffalo (Re buffalo), Big buffalo (Ngo buffalo), Indian Murrah Buffalo. The Vietnam buffalo breed had crossed with Murrah for milk.

3.4. Horse genetic resources. They are kept as pack and riding animals that include: Vietnam White, Grey horse and Russian Carbading horse.

3.5. Chicken genetic resources.

There are 16 native breeds: They are Ri, Te, Mia, Ho, Dong Tao, Tau Vang, Ac, Oke, H'mong Brown, H'mong White, H'Mong Black, Van Phu, Tre, Choi, Lun, Rhode Ri. About 85% of native chicken is Ri chicken All native chickens are reared in scavenging backyard system with house waste in the rural areas. They are characterized by broodiness. Their meat is said to be tastier than broiler breeds.

13 Exotic breeds were introduced to Vietnam in recent years: Tam hoang 882, Tam hoang Jiangcun, Kabir, Luong Phuong, Egyptian, Hungari Golden, Leghorn, Rhode Island, New Hampshire, Goldline, Sao Chicken. The exotic chickens are use for improving native chicken by crossbreeding

schemes.

3.6. Duck genetic resources.

There are 5 native duck breeds and 3 exotic breeds in Vietnam but most of them are "Co" duck (it occupies 78-80% of duck breeds) All of them are raised for egg and meat. Bau quy, Bau ben, Co, Ki Lau, Hoa ducks. Exotic are: Cherry Valley, Khaki Campbell, Pekin ducks.

3.7. Muscovy duck genetic resources. There are three native Muscovy duck breeds in Vietnam. They are called according to their feather color: Namely "Re" (white color), "Trau" (black color) and "Sen" (mixed white and black color) French Muscovy: R31, R51, R71, and French weighty Muscovy ducks. They are raised for meat

3.8. Goose genetic resources: Two of them are native. De, Co geese and three of them are exotic: Lion, German Rheinland, French Landest geese. They are kept for meat, and liver.

3.9. Goat genetic resources. There are "Co" goat (grass goat) with different color, white, black, gray and mixed black and white, and Bach Thao goat They are raised for meat Three of exotic are used for milking: Barbary, Jamnapari, Beatle goats.

3.10. Rabbit genetic resources: Vietnam Black and Grey rabbit breeds and New Zealand, California Rabbit breeds. They are raised for meat

3.11. Sheep genetic resources. The Phan rang sheep breed is the only sheep that survived in Vietnam. The wool is white. They belong to meat type.

3.12. Sika deer genetic resources. Sika deer is in extinct in the wild in Vietnam, but about 10.000 heads are kept in the central North part of Vietnam. The biological character has been described. They are kept for velvet and meat

3.13. Sambar deer genetic resources. They are kept for meat and velvet

3.14. Pigeon genetic resources. They are kept for meat There is only one native Pigeon breed and two exotic: French Titan and French Mimass pigeon.

3.15. Ostrich genetic resources. They are were imported to Vietnam for meat production. There are African and Australian ostrich.

3.16. Turkey genetic resources. They are kept for meat Vietnam Turkey and French white and black Turkey.

3.17. Crocodile genetic resources. They are kept for meat and skin: Vietnam Crocodile and Cuba Crocodile.

4. Animal genetic conservation program

The Vietnam Government and scientists have applied much effort to the conservation of animal genetic resources since 1989 and the action plan for sustainable conservation of biological diversity was also established.

4.1. Objectives conservation program

The conservation duty focuses on protection and strengthening of production sustainability and minimization of risks in animal raising; maintenance of gene pool to create new breeds for animal husbandry; maintenance of gene pool to meet the demand for breeding new animal races in the future. The main issues are rehabilitate and maintain animal races that are in extinction risk, prevent races extinction; improve *in-situ* conservation in native areas, promote conservation through use; maintain *in-vitro* genetic materials of specially necessary races to avoid inbreeding when the herd in maintaining is too small, and to provide genetic materials for direct use breeding new races as below:

* To survey for collecting informative data on physiology, genetic and economic related traits for characterization of native breeds. Developing alternative stocks with characteristics of native breeds for meeting a wide variety of market production condition.
* To help farmers to *in-situ* conservation, establish small farms for conservation the species that really endangered.
* To establish systematic *ex-situ* conservation for genetic materials: semen, embryos, somatic cells and DNA samples.
* To step by step using bio-techniques to analysis animal genetic resources for identifying:
  - The genetic relations within and between breeds for animal classification
  - Economic important traits and unique traits for today and future use.
* To census, survey existing breeds, exploit unknown breeds for establishment information system
* Internal and external information exchange.

4.2. Achievements

4.2.1 Rescued some breeds were threatened of extinction such as: I pig, Ho chicken and 20 other livestock breeds are given in protection network.

4.4.2. Some breeds had been recovered and developed to supply market demand: Phan rang sheep, Mong cai pig, Ac chicken, Bach Thao goat

4.2.3. Creating new products having both high productivity and high quality by crossbreeding between exotic and indigenous breeds (for example, Dong Tao x Tam Hoang chicken, Mia x Kabir chicken, Co x Bau duck, Mong cai x Landrace pig.)

4.2.4. New genetic resources have been found by surveys: Udauriu cattle, H'Mong cattle, Mini pig, H'mong chicken, Hoa duck.

4.2.5. A data base for breeds in Vietnam following FAO standard and has been built

4.2.6. It has been built – Conservation network whole country
  - National conservation policies
  - Data base for breeds in Vietnam following FAO standard.

4.2.7. A conservation farm at NIAH has built for *ex-situ* live conservation and keeping endangered breeds.

4.2.8. *Ex-situ* conservation system has been established for conservation: semen, oocytes, embryos, somatic cells. The genomic DNA samples and somatic cells of 32 native animal and poultry breeds were preserved. Animal Molecular Genetic Lab. for genetic study has been established and started studying on DNA polymorphisms.

4.2.9. Published WEB site and two books on animal conservation.

5. About conservation of wildlife gene sources

Wildlife has been rapidly draining out, and many species have become extinct due to illegal hunting and trading. This leads to the mission of wildlife gene sources conservation executed by the Forest Control Department under MARD, starting in 1997. Wildlife is protected, i.e. *in-situ* conserved, at National Parks, Natural Conservation Areas, and Specific Forests. Wildlife *ex-situ* conservation in combination with scientific research and tourism development has drawn more investment in two big zoos in Hanoi and Ho Chi Minh City.

At present, Vietnam has three Programs on Wildlife Conservation of Top Importance: *Elephas maximus, Trachypithecus sp. and Phanthera tigris* conservation.

C. Approaches to conservation and exploitation, sustainable utilization of animal genetic resources in Vietnam in the period of 2001-2010

Animal diversity is invaluable treasure for agricultural development particularly and socio-economic development generally. Today, for sustainable development, among natural resources, it is necessary to highly value *animal genetic resources as much as land resources* and *water resources* Contradicts often appear between conservation and development An overlook of diversity situation in some developed countries: unawareness of solution to such contradicts and abiding market-oriented benefits have resulted in deteriorated animal biodiversity to the extent unrecoverable. Vietnam has taken such lessons and promoted advanced technologies of the present technological revolution to effectively conserve its own biological resources in order to serve the national socio-economic goals and share the world benefits.

Genetic resources are those of reproduced ones, which can be made more diverse and richer if they are properly exploited. Therefore, in the long term, to minimize contradicts between conservation and exploitation of animal diversity, Vietnam highly respects approaches of conservation through use so as to ensure sustainable exploitation of his own. For genetic resources, conservation usually includes preservation or maintenance, characterization, evaluation and utilization. Some particular approaches are presented as follows:

1. Social Approaches

The measures in details are below:

* ***Raising community awareness of position and importance of animal biodiversity.***

This can be done by means of

- Promoting constant propaganda on mass media,
- The conservation should be placed within the framework of a measure towards sustainable agricultural development and food security. Conservation of animal diversity must become a common issue attracting relevant attention when working out policies for agricultural development in particular and socio-economic development in general at all levels from the central to the localities.

- Contents of agro-forestry biodiversity conservation should be introduced to educational programs at different levels, from general secondary education to university in the facilities of agriculture and biology

Linking animal biodiversity conservation to national culture conservation

National cultural diversity is a major cause to the animal diversity, which is most obvious in mountainous areas. Therefore, to effectively conserve biodiversity, it is necessary to link it to the cultural conservation. This is suitable to the current direction of Vietnam in rehabilitating and preserving traditional cultures. Practical contents of conservation should be made in details so as relevant policies and measures can be worked out

Defining proper economic mechanism and regulation for agro-forestry biodiversity conservation

Market-oriented economy is the main factor to decrease animal diversity. It is normally perceived that diversity is linked to backward. But it is perceived by all that this biodiversity decreasing and draining has caused instability in development process and progress making. To preserve animal genetic resources and animal husbandry systems, animal products must possess economic significance. In detail, outlets for these products must be found. Variety of foods is the major factor to reinforce health and alleviate diseases. Cut down on food stuffs means dependence on actual conditions and is human habit rather than interests. Therefore, warning of varied foodstuffs, food from fauna to create outlets for products is feasible, which is to seek relevant economic mechanism for animal biodiversity conservation.

Developing and perfecting legal documents on agro-forestry biodiversity conservation

Presently, Vietnam Government issued Decree 07-CP and Decree 08-CP in 1996 on Management of Crop Varieties and Animal Husbandry Races, Decision 845/ TTg in 1995 passed by Prime Minister on Actions for Biodiversity. These are most important documents related to the agro-forestry biodiversity conservation in general and animal diversity in particular in Vietnam. However, many detailed regulations are needed to bring conservation to order. Defining agro-forestry biodiversity conservation is the task controlled by the Government, requiring relevant investment policies. Vietnam is inclined to improve management, decrease medium agents, avoid overlapping assignments to promote investment efficiency.

2. Technical Approaches

* Scientific training program relevant to the science and technology in identification of genetic variation between breeds having different locations as well as economic important and unique traits for today and future use.
* Establishment and enhancing of facilities for cryo-preservation of animal genetic materials. Developing the National Animal Genebank, special concentration to equip the modern laboratory for molecular genetic research.
* Enhancing of conservation network from officials to grassroots. Improving of the genetic resources information system whole the country for surveying and monitoring population size of animals as well as reducing the loss of domestic diversity.

* Transforming market potential breeds in to production by political supports for long-term breeding programs. Diversity gene pool in animal production is the most important measure to realize conservation through use of genetic resources. This work is to promote sustainability of production and efficiency in agricultural environmental protection. Diversifying gene pool in production needs to be made through detailed agro-promotion missions in the national agriculture extension policy.

* Publishing Domestic Animal Diversity Information System (DADIS) on Internet standardized by FAO.

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Furukawa: Recently, your country found a new species of mammal in a mountainous area. Do you have any collaboration with such wildlife researchers? You have some breeds kept solely by minorities. Do you have programs to support minorities for the in situ conservation of breeds husbanded by such minority groups?

Thuy: We have discovered five new species since 1992. At the moment, we only work for the national purpose, but are promoting a research program from 2003 or 2004. It is just a proposal to the government If our research proposal is accepted, we will start research from next year.

We have found minority breeds in mountain areas. In situ conservation in some areas, including native pig breeds, is supported by the Vietnamese government and US$60,000 is provided annually for all species.

Present Situation of Animal Genetic Resources in Japan

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Japan is located between longitudes 123° and 149° east and latitudes 24° and 46° north. Situated in East Asia, the country is made up of a group of islands surrounded by the Pacific Ocean to the east and the Japan Sea to the west, extending far longer in the south-north direction than in the east-west direction. It has a natural land area of 378,000 km^2 The climate differs greatly between the southern and northern regions; some regions belong to the subarctic zone while others are subtropical Rice cropping is mainstream in Japanese agriculture though the form of cultivation varies from region to region.

Agricultural production in Japan is valued at 9.12 trillion yen, 72.3% of which is accounted for by field husbandry. That is to say, 26.9% (2.45 trillion yen) of the value of total production is generated by livestock farming, which exceeds the figure for rice production (25.5%)

The population of Japan is 127 million, with 47.06 million dwellings (2000) Of these, the farming population totals 13.46 million people with 3.12 million dwellings, while households involved in livestock farming account for 160,000 dwellings. Agricultural households account for 10.6% of the population and 6.6% of all dwellings, while households involved in livestock farming account for 5% of these figures, which is equivalent to 0.7% of the total national figure.

1. The historical features influencing animal production in Japan

The history of the raising of domestic animals for practical food production in Japan is extremely short compared to that of Europe.

Domestic animals, such as pig, cattle and chicken had been introduced in late Jomon Era (-BC 500) to Yayoi Era (BC500-AD300) However, government banned slaughtering of animals, such as cattle, horse and chicken, during the period from 650 to 750, because Buddhism had been introduced and prohibited the eating of meats. Those forbiddances suggested meat were eaten by people of the period. After the prohibitory edict, the use of meat and milk became less common. Main purpose of animals breeding was for transportation of goods, farming, or military power such as horse and manure production and utilization of animal products had not become popular until Meiji era (1868-1912)

In regions south of Kyushu, however particularly in Okinawa, pigs and goats have been bred for food for centuries even before Meiji era. Okinawa, on which Japan's feudal government in Edo era had little influence, has used pigs for rituals and goats for special events for food. A culture peculiar to Okinawa has evolved through these customs and rituals. From the Tohoku region to Hokkaido, hunting provided some animal meat for food.

Though meat has been consumed in central part of Japan only for about 130 years, which was the beginning of the Meiji era, it has only reached widespread popularity in the last 40 years. Therefore, Japanese livestock breeds were not subject to improvement techniques for milk and meat production before the mid 1950's.

While the necessity for draft animals become lower by prevalence of farm machinery, the age of smallholder where small numbers of livestock were reared for farm work was terminated.

The demand to animal products increased along with a rapid growth of Japanese economy, and legislation, such as Law for Improvement and Increased Production of Livestock and Agricultural Basic Law, the measure and the basis of a lending facility based on it, consistently promoted scale expansion of farm.

2. Assessing the state of conservation of domestic animal diversity of Japan

Breeds covered in livestock-related statistics and other native species and populations include: 9 beef cattle breeds, 7 dairy cow breeds; 12 pig breeds (including wild boars and counting Kagoshima Black Pig and Berkshire separately), 12 horse breeds and populations; 3 goats breeds and populations; 2 sheep breeds; one breed of rabbit, and 6 other mammal species (Table 1-1) There are 38 chicken breeds and 6 other bird species, of which quail is the only animal species that has been domesticated in Japan (Table 1-2) Lots of species and breeds of livestock and poultry have been introduced into Japan, but breeds other than major breeds of cattle, pigs and chickens have decreased in number and have not played an important role in animal production. There are some breeds included in the statistics that cannot be said to have become well established in Japan, and their introduction at this point would have to be regarded as tentative.

2.1 Present status of Japanese native breeds

Cattle: Since the Meiji era, exotic cattle breeds have been introduced and crossbreeding between Japanese cattle and exotic breeds have been promoted in most regions nationwide. As a result, there are only two cattle populations that escaped hybridization with exotic breeds, Mishima Cattle, which have survived in Mishima Island off the coast of Hagi city in Yamaguchi Prefecture and Kuchinoshima Cattle living on Kuchinoshima of the Tokara Islands in Kagoshima Prefecture. Cattle other than the above-mentioned populations were categorized into 4 breeds depending on the types of exotic cattle introduced into the region; Japanese Black, Japanese Brown, Japanese Shorthorn, and Japanese Polled were developed through crossbreeding.

Pigs: Before Japanese people began to eat pigs nationwide, a native pig called Shima-buta or Aguh existed in Kagoshima and Okinawa. At present Black Pig (it is thought to be of Berkshire origin) has gained popularity as a special brand product in Kagoshima Prefecture. In the case of Aguh, almost all of native Aguh disappeared due to ground fighting in Okinawa at the end of the World War II and the donation and introduction of exotic breeds having high productivity after the war. Given these circumstances, the collection and conservation of a few barely surviving individuals having a shape similar to the native Aguh was carried out As a result, the population increased to 100, and the F_1 is now being marketed as a brand pig. Ohmini is being preserved by private businesses and the F_1 of Ohmini is being marketed as a laboratory animal

Chickens: The cutting off of Japan from outside contact in the Edo era (from 17th to the mid-19th century) had a significant impact on the establishment of the Japanese Chicken as birds either for pets or cockfighting. The Japanese Chicken as a chicken for practical use came about under the influence of exotic breeds introduced in the Meiji period. Since the liberalization of imports for breeding chickens in 1960, native chickens for practical use have fallen into a disastrous condition.

Some native chickens are now being used to breed brand chickens. Brand chickens using native chickens are referred to as Jidori (Japanese old style native), a name that helps consumers to differentiate this chicken from the others on offer. Chickens permitted to use the Jidori label are limited to chickens containing at least 50% of the blood of 41 native breeds designated by the Japan Chicken Association (38 native breeds according to JAS) The major native chicken breeds including these Japanese old-style natives are Rhode Island Red (44.8%), Nagoya (3.8%), Shamo, Hinaidori, Barred Plymouth Rock, and Satsumadori These 6 breeds account for 58% of all native breeds.

Horses: After World War II, farm horses that had been actively raised till then and native horses used for conveyance lost their roles, resulting in a corresponding decline in their numbers. In spite of this, 8 native populations comprising Hokkaido Horse, Kiso Horse, Noma Horse, Tsushima Horse, Misaki Horse, Tokara Horse, Miyako Horse, and Yonaguni Horse are left and all are protected by conservation groups.

Goats: As native goats, there are Tokara Goat and Shiba Goat The Japanese Saanen breed has been produced by successive crossbreeding with a native goat The Shiba Goat is bred as a laboratory animal in universities and research institutes. Its present status is 'endangered-maintained' With regard to Tokara Goat, 35 purebred individuals exist at Kagoshima University and Hirakawa Zoo. Toshima village, the birthplace of Tokara Goat, has opened a goat farm. However, even here, there are only a few purebred individuals. The present status of Tokara Goat is 'critical-maintained'

Quail: Quail are the only indigenous poultry species that have been domesticated in Japan. There are about 7.71 million quail being bred focusing on the use of eggs (2000)

2.2 The state of conservation of farm animal

· Ministry of Agriculture, Forestry, and Fisheries Genebank Project

The MAFF genebank project started in 1985 as a nationwide network. From 2001, the National Institute of Agrobiological Sciences has been the main body conducting research and collection of genetic resources both inside and outside Japan, along with implementing characterization and conservation of resources.

The conservation of livestock and poultry is practiced at the National Institute of Agrobiological Sciences, the center-bank, and independent administrative institutes such as the National Agricultural Research Organization, the National Institute of Livestock and Grassland Sciences, the

National Institute of Animal Health, and the National Livestock Breeding Center, as sub-banks. The center bank is involved with cryo-preservation, mainly focusing on frozen semen. The sub-banks are concentrating more on maintaining live animals, in combination with cryo-preservation. Collection and conservation are being carried out focusing on breeds and strains that have been established in Japan, and approximately 200 accessions have been conserved.

- **Conservation of animals**

Nineteen varieties of livestock and poultry native to Japan have been designated as natural monuments. All of these are chickens except for Mishima Cattle and the Misaki Horse. Of these, only Onagadori in Tosa has been conserved as a special natural monument Moreover, financial assistance to support measures for strain conservation was provided targeting the Hokkaido horse and 14 chickens that are kept for research in three universities. A liaison meeting for the project to conserve 8 native horse groups including Misaki Horse hosted by the Japan Horse Council has been held every year since 1977.

2.3 Techniques for reproduction used in domestic animal production

Artificial insemination (AI): According to 2000 statistics, the prevalence rate of AI is 99% and the frozen semen is used in all the case of AI for 2.48millions cows in total the rate of artificial insemination for dairy cows is 99.4%, with frozen semen being used exclusively. For beef cattle the percentage for AI is 97.8%, and again only frozen semen is used in this procedure. Contrast this with pig and horse, where the corresponding figures are less than 10%.

Embryo transfer (ET): the embryo transfer was carried out for 62 thousands cows which corresponds to 2.5% of artificial insemination of cattle including Japanese Black in which ET was conducted the figure corresponding to 6.3% of 740thouthands AI.

Clone livestock (May, 2002): Cattle, fertilized-ovum clone, in 40 organizations, 629 animals, somatic cell clone, 293 in 38; Pig somatic cell clone, in one organization, five animals; goat, somatic clone, in one organization, two animals are produced.

2.4 Characterization of basic, economic, quantitative and molecular genetic traits

For livestock and poultry within Japan, data has been accumulated on fundamental and production-related traits from all the studies ever conducted, while NIAS genebank project is also promoting characterization of animal genetic resources held at the genebank. Genetic relationships among domestic animal breeds and populations have been studied by using molecular information, polymorphism of protein, blood type, mitochondrial DNA, and genomic DNA markers. Individual identification and parentage tests that have conventionally been conducted using blood groups and protein polymorphisms is shifting after a trial period to tests using microsatellite DNA polymorphisms. DNA diagnosis of inherited disease is started on 5 genes of cattle and one gene of the pig. Moreover genome research, genetic map and QTL analysis on livestock and domestic-fowls are also performed.

3. The state of utilization of farm animal genetic resources

Beef cattle: In 1999, the population, excluding cattle for fattening, totaled 669,000, 93% of which are Japanese Black. With regard to other breeds, Japanese Brown constitutes 4.8%, Japanese Shorthorn 1.2%, and other species constitute less than 1% in total Cattle being fattened for beef production totaled 1.84 million head. Holstein and its cross are also included in the statistics, accounting for 57.7% of the total Japanese Black accounts for 39.8%.

Dairy cows: In 1999, Holstein totaled 1.73 million head, accounting for almost 100%, while the second most common breed was Jersey with only 9,202 head, and species other than Holstein totaled 10,287 head, accounting for less than 1%

Pigs: Although there is the high popularity breed, the Kagoshima Kurobuta in Japan. In addition to this breed, three way cross hybrids among Large White, Landrace, and Duroc, and partially among Large White, Landrace and Berkshire (in place of Duroc), or commercial pigs, which have been produced utilizing imported parental hybrids stocks pigs imported from foreign pig breeding companies

Chickens: For chicken production, meat production using broilers produced from imported parental hybrid stocks imported accounts for 89.4%. Adding waste chickens (9.0%) to this figure takes the percentage to 98.4%. For eggs, White Leghorn and other laying chicken breeds account for 7.21 million fowls, while native chickens and other breeding chickens for meat and eggs account for 340,000 fowls in total (probably used mainly for meat)

4. Recent trends in animal production of Japan

4.1 Self-sufficiency rate of animal products

Beef cattle: The percentage of Japanese Black in beef cattle breeds is increased after the import liberalization of beef started in 1991 As a result, the proportion of Japanese Black among beef breeds, which accounted for approximately 85% from around 1970 to 1991, rose to 93% in 1999, resulting in the sharp decrease in other breeds. In 2000, beef production amounted to 3.64 million tons and of which derived from breeds reared specifically for beef accounted for 1.67 million tons, with national self-sufficiency for beef being 33.5%.

Dairy cattle breeds: Domestic milk production amounted to 8.41 million tons in 2000, with the imported volume in the form of dairy products amounting to 4.00 million tons on a fresh milk basis, 70% of which is cheese.

Pig: Consumption of pork produced in Japan is currently 8.78 million tons and consumption of the imported pork amounts to 6.51 million tons, with a 57.4% rate of self-sufficiency.

Chicken: Domestic production and self-sufficiency rate of chicken and egg in 2000 were 1,195,000 ton (67.6%) and 2,540,000 ton (95.5%), respectively.

4.2 Analyzing future demands and trends

The consumption of livestock products in Japan is one-third lower than the USA, and half that of the EU. However, the Japanese people eat a lot of fish and shellfish, so the intake of animal food compares favorably with developed western countries.

In terms of the demand for livestock products, dairy products such as cheese are expected to increase, but fresh milk, meat and eggs are unlikely to increase due to a leveling off or downward trend in the population. However, in terms of quality and in response consumer needs, there are increasing efforts to expand production and consumption through product differentiation. The trend among consumers is to purchase fresh, safe, palpable and healthy livestock products rather than just focusing on the price. Accordingly, livestock producers are endeavoring to meet consumers' needs by developing brand livestock and products.

Brand products are being produced from beef, pork, chicken and eggs, with 141, 178, 158, 636 brands known respectively. There are a few brands that use native breeds as a point of difference. Native breeds such as Mishima Cattle, Kagoshima Berkshire, Aguh, Hinaidori, Tosa Jidori, Nagoya, Gifu Jidori and Shamo are being utilized to produce brand products, a situation which is greatly contributing to the conservation of these breeds at the present time.

4.3 Outline of future national policies on environmental and self-sufficiency issues

The stock feed self-sufficiency rate in 1998 was 22% in N terms and 25.1% on a TDN basis. If limited to concentrated feed, feed produced within Japan provides only10% (2.00 million tons) of the total demand of 20 million tons. Approximately half of the 33.71 million tons of grain consumed (including human use) is for domestic livestock.

Such imported feed is excreted as feces and urine by livestock, most of which is then applied to farmland. The quantity estimated to be applied to farmland is already exceeded the acceptance capacity due to decline in areas under cultivation.

The Basic Law on Food, Agriculture, and Rural Areas was enacted in 1999. In accordance with the Basic Law, the Basic Plan for Food, Agriculture, and Rural Areas in 2000 was established. Japan's food self-sufficiency (1999) has declined to 41% in terms of supplied calories and 28% for grains. The Plan sets up production goals that take into consideration the nutrient balance of food to increase self-sufficiency to more than 50% in terms of supplied calories, in addition to ensuring a basic food supply. Goals for 2010 are 9.93 million tons of raw milk, 630,000 tons of beef, 1.35 million tons of pork, 1.25 million tons of chicken meat, 2.47 million tons of egg. For the 2010 forage crops, the Basic Plan set the goal of 5.08 million tons (TDN) (4,461kg/ha for a single-year harvest), with cultivated areas totaling 1 10 million ha.

In 1999, the "Law concerning appropriate management and the promotion of use of livestock excretion" was enacted and the "livestock individual identification system" started full operation from FY 2002.

5. National priorities for the conservation of Animal Genetic Resources

Since research into other livestock by veterinarians and zoologists is broadly based, it is important to increase the number of personnel that have an interest in these areas and are involved in genetic resource studies and projects, rather than mere capacity building.

The Ministry of the Environment released the New National Strategy of Japan on Biodiversity in March 2000. The Ministry of Education, Culture, Sports, Science and Technology released the "National bio-resource projects" that aims at the improvement of bio-resource systems such as those for laboratory animals and plants These projects assume the viewpoint of the comprehensive promotion of bio-resources. The NIAS genebank projects are required to review how effective measures to conserve genetic resources have been, utilizing the characteristics of individual projects and linking these projects and systems effectively to take the entire nation into consideration.

6. Reinforcing conservation efforts

Many of Japanese native livestock are in a critical situation. As an auxiliary means for *in situ* preservation by live animals population, *ex situ* preservation by live animal, frozen embryo and frozen semen are being conducted. The conservation of frozen embryos and semen is not necessarily satisfactory because the number of individual being able to collect is limited and freezing technologies have not been well established in some species. The leading technologies of the next generation applicable for *ex situ* and *in vitro* preservation should be somatic cell cloning in the mammals and primordial germ cell (PGC) for producing chimeras in the reproductive cell line in avian species.

The associations of native livestock and domestic fowls are playing an important role. Policies need to be prepared to provide further incentives to the Conservation Group to continue its efforts. In addition, it is necessary to provide detailed information on livestock location wherever possible, particularly for chickens, by ongoing research on the locations where these breeds can be found and their conservation status.

Kurosawa: The water buffalo is almost extinct in Okinawa. However, farmers still use buffaloes for cultivation and also as a tourist attraction.

In Japan, crossbreeding between pigs and wild boar has recently been pursued quite actively. In many cases, farmers have failed to commercialize them and hybrid individuals have been released into mountain areas. Such hybrids are thought to have a genetic impact on wild boars and many researchers and local people are worried about this phenomenon. I hope that government organizations and researchers will work with on this issue.

Minezawa: The problem of hybridization between local and exotic species has occurred not only in the case of the wild boar. Many problematic cases are known among primates, such as between the Japanese monkey and rhesus or Formosan monkeys. However, the issue of hybridization is still controversial in the Primate Society. In the case of pig-boar hybrids, we should deal with the problem carefully. Thanks for your information on the present status of the Okinawan water buffalo.

Wagner: Is it correct that there were no domestic animals in Japan in the years before Christ and that they came from mainland Asia?

As for the issue in developed countries, what are the priorities for AnGR conservation or how should we consider the priorities for AnGR conservation?

Table 1-1 Animal Genetic Resources and Species and Breeds Found in Japan

	Species	Breeds	Present Main Uses	Native or Exotic	Risk Status	Conservation Effort or Program	Conservation			
							Live	Frozen Semen	Frozen Embryo	Frozen Somatic Cell
Mammals	Cattle	Japanese Black	Meat Production	Native	Not at Risk	–	–	–	–	–
		Japanese Brown	Meat Production	Native	Not at Risk	–	–	–	–	–
		Japanese Poll	Meat Production	Native	Critical	Yamaguchi Prefecture	○	○		
		Japanese Shorthorn	Meat Production	Native	Not at Risk	–	–	–	–	–
		Aberdeen-Angus	Meat Production	Exotic	–	–	–	–	–	–
		Hereford	Meat Production	Exotic	–	–	–	–	–	–
		Charolais	Meat Production	Exotic	–	–	–	–	–	–
		Holstein	Milk Production	Exotic	–	–	–	–	–	–
		British-Friesian	Milk Production	Exotic	–	–	–	–	–	–
		Jersey	Milk Production	Exotic	–	–	–	–	–	–
		Guerrsey	Milk Production	Exotic	–	–	–	–	–	–
		Airshire	Milk Production	Exotic	–	–	–	–	–	–
		Brown Swiss	Milk Production	Exotic	–	–	–	–	–	–
		Red Danish	Milk Production	Exotic	–	–	–	–	–	–
		Mishima Cattle	Meat Production	Native	Critical-Maintained	Natural monument	○	○	○	○
		Kuchinoshima Feral Cattle	Meat Production	Native	Critical-Maintained	University	○			
	Pig	Middle White	Meat Production	Exotic	–	–	–	–	–	–
		Berkshire	Meat Production	Exotic	–	–	–	–	–	–
		Land race	Meat Production	Exotic	–	–	–	–	–	–
		Large White	Meat Production	Exotic	–	–	–	–	–	–
		Hampshire	Meat Production	Exotic	–	–	–	–	–	–
		Duroc	Meat Production	Exotic	–	–	–	–	–	–
		Spotted	Meat Production	Exotic	–	–	–	–	–	–
		Chester White	Meat Production	Exotic	–	–	–	–	–	–
		Kagoshima Berkshire	Meat Production	Native*	Not at Risk	–	–	–	–	–
		Aguh (Shimabuta)	Meat Production	Native	Critical-Maintained	Okinawa (Kagoshima)	○			
		Ohmini	Laboratory Animal	Native	Critical-Maintained	Laboratory Animal Supplie	○			
		Wild Pig/Hybrid	Meat Production	Wild, Hybrid		–	–			
	Horse	Percheron and Its Cross	Meat and Banei**	Exotic	–	–	–	–	–	–
		Breton and Its Cross	Meat and Banei	Exotic	–	–	–	–	–	–
		Thoroughbred and Its Cross	Horse Race	Exotic	–	–	–	–	–	–
		Arab and Its Cross	Horse Race	Exotic	–	–	–	–	–	–
		Dosanko	Horse Riding	Native	Not at Risk	Conservation Association	○	○		
		Kiso	Horse Riding	Native	Endangered-Maintained	Conservation Association	○	○		
		Noma	Horse Riding	Native	Critical-Maintained	Conservation Association	○			
		Tsushima	Horse Riding	Native	Critical-Maintained	Conservation Association	○	○		
		Misaki	Horse Riding	Native	Endangered-Maintained	Conservation Association	○			
		Tokara	Horse Riding	Native	Endangered-Maintained	Conservation Association	○	○		
		Miyako	Horse Riding	Native	Critical-Maintained	Conservation Association	○	○		
		Yonaguni	Horse Riding	Native	Endangered-Maintained	Conservation Association	○			
	Goat	Japanese Saanen	Milk Production	Native	Not at Risk	NLBC	○	○		
		Chubby	Laboratory Arimal	Native	Endangered-Maintained	NLBC, NIGLS, Other	○			
		Tokara	Meat Production	Native	Critical-Maintained	University, Zoo	○			
	Sheep	Japanese Corriedale	Wool Production	Native	Not at Risk	–	○			
		Suffolk	Meat Production	Exotic	–	–	–	–	–	–
	Rabbit	Japanese White	Laboratory Animal	Native	Not at Risk	–	○	–	–	–
	Mink		Hide Production	Exotic	–	–	○	–	–	–
	Shika Deer		Meat, Velvet and Horr	Wild	Not at Risk	–	○			
	Red Deer		Meat, Velvet and Horr	Wild, Exotic	–	–	–	–	–	–
	Samber		Meat, Velvet and Horr	Wild, Exotic	–	–	–	–	–	–
	Fallow Deer		Meat, Velvet and Horr	Wild, Exotic	–	–	–	–	–	–
	Taiwanese Shika Deer		Meat, Velvet and Horr	Wild, Exotic	–	–	–	–	–	–

* Kagoshima Berkshire has 70 years history from the first breeding pair has been introduced

** Draft Horse Race, limited in Hokkaido Region (http://www banei-keiba or jp/information/banei-race%20English.htm)

Table 1-2 Animal Genetic Resources Species and Breeds Found in Japan

	Species	Breeds	Present Main Use	Native or Exotic	Risk Status	Conservation Effort or Program	Consarvation	
							Live	Frozen Semen
Bird	Chicken	White Leghorn	Egg Production	Exotic	Not at Risk	–	–	–
		Barred Plymouth Rock	Hybrid Production	Native	Not at Risk	–	–	–
		Rhode Island Red	Hybrid Production	Native	Not at Risk	–	–	–
		New Hampshire	Hybrid Production	Exotic	Not at Risk	–	–	–
		Nagoya	Meat Egg. Hybrid Production	Native	Not at Risk	–	–	–
		White Plymouth Rock	Hybrid Production	Exotic	Not at Risk	–	–	–
		White Cornish	Hybrid Production	Exotic	Not at Risk	–	–	–
		Shamo	Cook Fighting. Fancy. Hydrid	Native	Not at Risk	Natural monument	○	○
		O-shamo	Cook Fighting. Fancy. Hydrid	Native	DD	Natural monument		○
		Ko-shamo	Fancy	Native	DD	Natural monument		○
		Ygido	Fancy	Native	DD	Natural monument	–	
		Kinpa	Fancy	Native	DD	Natural monument Akita Pref	○	○
		Hinai-Dori	Fancy, Hybrid	Native	Not at Risk	Natural monument Akita Pref	○	○
		Satsuma-Dori	Cook Fighting. Fancy. Hydrid	Native	Not at Risk	Natural monument	○	○
		Japanese Long-tailed Fowl	Fancy	Native	DD	Natural monument Kochi Pref Nankoku-	○	
		Totendo	Fancy	Native	DD	Natural monument	○	○
		Japanese Rumples Bantam	Fancy	Native	DD	Natural monument	○	
		Japanese Long-Saddled Bantam	Fancy	Native	DD	Natural monument	○	
		Koeyoshi	Fancy	Native	DD	Natural monument	○	○
		Tomaru	Fancy	Native	DD	Natural monument	○	○
		Minohiki	Fancy	Native	DD	Natural monument	○	
		Jidori or Japanese-Old type	Fancy. Hybrid	Native	DD	Natural monument	○	○
		Gifu-jidori	Fancy. Hybrid	Native	Not at Risk	Natural monument Gifu Pref		
		Tosa-jidori	Fancy. Hybrid	Native	Not at Risk	Natural monument Kochi Pref		
		Shokoku	Fancy	Native	DD	Natural monument	○	
		Japanese Bantam	Fancy	Native	DD	Natural monument	○	○
		Katsura-chabo	Fancy	Native	DD	Natural monument		
		Shojo-chabo	Fancy	Native	DD	Natural monument		
		Ukokkei	Fancy	Native	DD	Natural monument	○	○
		Kawachiyakko	Fancy	Native	DD	Natural monument	○	
		Jittoko	Fancy	Native	DD	Natural monument	○	
		Kurokashiwa	Fancy	Native	DD	Natural monument Yamaguchi Pref	○	
		Tosa Cochin	Fancy	Native	DD	NLBC	○	○
		Kumamoto	Fancy	Native	DD	NLBC	○	
		Kureko-Dori	Fancy	Native	DD	–	–	
		Gankei	Fancy	Native	DD	–	–	
		Utai-Chahn	Fancy	Native	DD	–	–	
		Okinawa Hige-Jidori	Fancy	Native	DD	–	–	
		Miyaji-Dori	Fancy	Native	DD	–	–	
		Ingii	Fancy	Native	DD	–	–	
		Mikawa	Fancy	Native	Not at Risk	Aichi Pref NLBC	○	○
		Sado Hige-Jidori	Fancy	Native	DD	–	○	
	Duck/Hybrid		Meat Hybrid Production				○	
		Osaka-Duck	Meat Production	Native	DD	Osaka Prefecture		
	Turkey		Meat Production	Exotic	–	–	–	–
	Quail		Meat Production	Native	–	–	–	–
	Goose		Meat Production	Exotic	–	–	–	–
	Guinea Fowl		Meat Production	Exotic	–	–	–	–
	Pheasant		Meat Production	Wild	–	–	–	–

DD: Data Deficient

Note The species and breeds adopted in this table are Japanese native breeds and the breeds Which was shown their statistics in the “Annual Animal Breeding Related References”

Minezawa: Wild boar and the mallard duck inhabited Japan from ancient times. However, other domestic animals did not exist in Japan in the B.C. period. Improvement in productivity was the major priority for Japanese animal production and this contributed in various ways to the lives of Japanese people, such increased life expectancy and improvements in physique. However, these contributions have reached their limit and we are now in the stage of managing new Japanese priorities in animal production issues. Many issues have arisen and need to be solved, such as environmental problems and niche markets.

However, it is not easy to find the solutions to these questions and they are problems to be solved in the future together with all of you.

2. Status of Genetic Diversity in Each Asian Livestock from Genetic Survey in Asian Countries

Chairpersons NAMIKAWA, T (Cattle)
AMANO, T (Water Buffelo)
MAEDA, Y (Pig)
TSUJI, S (Goat)
YAMAMOTO, Y (Chicken)

Genetic Diversity of Native Cattle in Asia

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Abstract

The presence of wild species of *Bos* is a unique characteristic of the genetic resources of cattle in Asia. The wild species of *Bos* consist of banteng (*B. banteng*), gaur (*B. gaurus*), yak (*B. mutus*), and kouprey (*B. sauveli*) The kouprey is now very rare and little is known of its present status. No concrete genetic or reproductive data on the kouprey is available to compare with that of the related species. There are some domesticated forms of wild species, for example, domestic gaur (gayal or mithan) in hills of separate India, Bhutan, Myanmar and Bangladesh, domestic yak in Nepal to highland China,, and domestic banteng (Bali cattle) in Indonesia. It is possible that domestic cattle in tropical and subtropical Asia have acquired some genes from such wild species, because they can interbreed with domestic cattle and, though mostly male offspring are sterility, female hybrid offspring are fertile. However, because of the quite limited distribution of the domestic forms of *Bos* spp., the native cattle in Southeast Asia was generally regarded as humped cattle (Zebu, *indicus*) or crossbred between humpless (*taurus*) and humped cattle in various rates, and gene flow from the wild species was thought to be not so common. In this paper, we elucidate phylogenetic relationships of wild *Bos* spp. and some evidence of inflow of genes from the wild species to domestic cattle in Southeast Asia.

Phylogenetic relationships of wild *Bos* spp.

The 1140 bp cytochrome b gene was sequenced for banteng, gaur, yak, Bali cattle, mithan, and American bison. And then, phyogenetic tree of these *Bos* species was constructed using the neighbor-joining method, in which Asian buffalo (*Bubalus bubalis*) and African buffalo (*Synceros caffer*) sequences were placed as outgroup. In the dendrogram, (Fig. 1), the genus of *Bos* (including the American bison) were divided into three clusters, one is cluster of *indicus* and *taurus* cattle, another is of banteng, gaur, Bali cattle and mithan, and the other is of yak and American bison. This classification agrees with the comparative morphological analysis by Groves (1981) According to the fossil record the divergence time between *Bos* and *Syncerus* (or *Bubalus*) is approximately 10 million years (Savage and Russell, 1983) Using this divergence time, the coalescence time for the present *Bos* species was estimated as approximately 5.5 million years. As the divergence time within the domestic cattle is less than 1 million years, present wild Bos species can be used as

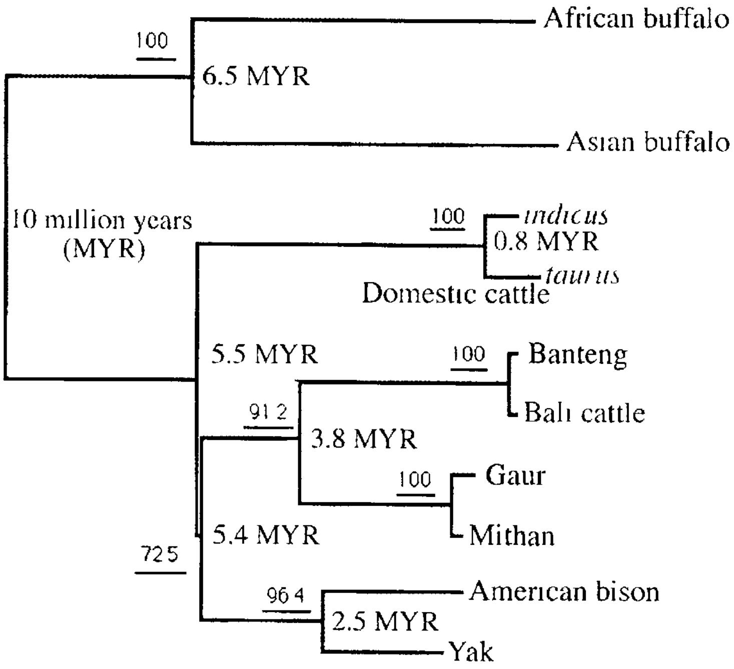

Figure 1 A phylogenetic tree of cytochrome b gene sequences in the genus *Bos* by using the neighbor-joining method. Numerals on internal branches are the bootstrapprobabilities (%) from 1.000 trails

much diverged genetic resources for the cattle.

Paternal gene flow between the *taurus* and *indicus* cattle in Southeast Asia based on variation in *SRY* gene

Domestic cattle in the world (excluding Bali cattle and mithan) were generally classified into two types, that is, *taurus* (humpless or European-type), and *indicus* (humped or Zebu) thought intermediate-type cattle were raised in Southeast Asia and in some African countries (Phillips, 1961) A number of studies have contributed to understand phylogenetic relationship of *taurus* and *zebu* cattle. These studies have suggested that the *taurus* cattle and the *indicus* cattle were differentiated at the subspecies level and the domestication of the two types of cattle occurred independently (Loftus *et al*, 1994; Kikkawa *et al*, 1995) The intermediate-type cattle were considered to have a hybrid origin between the *taurus* and the *indicus* cattle in various ratios. Indochina native cattle called Yellow Cattle was considered as this intermediate-type. The Y chromosome of cattle can be clearly divided into *taurus* and *indicus* by its shape because the Y chromosome of the taurus-type is submetacentric while it of the indicus-type is acrocentric (Halanan and Watoson, 1982) Thus, studies of polymorphisms of Y-linked genetic marker can be used as a powerful tool to investigate the introgression or gene flow between the *taurus* and the *indicus* cattle in the intermediate-type population through the male. The gene for *SRY* (sex-determining region Y) is one of the well studied genes on the mammalian Y chromosome (Gubbay *et al*, 1990) A total of 200 blood or tissue samples of male cattle were collected in Vietnam, Laos, and Myanmar. The

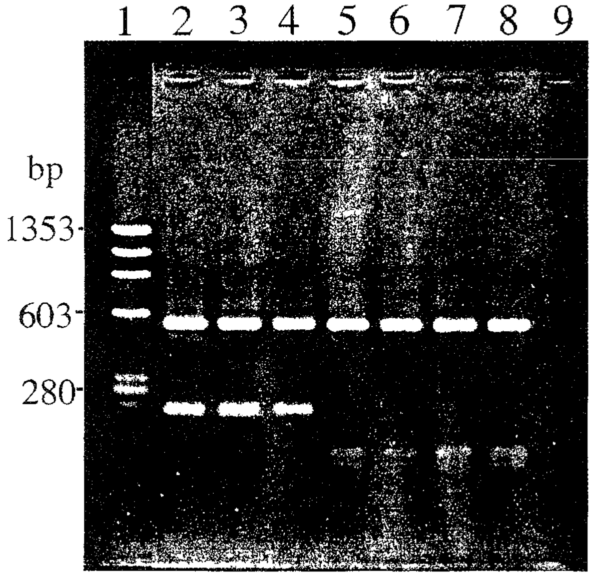

Figure 2. Comparison of restriction fragment patterns for PCR products for the bovine *SRY* gene by *Mse*I Lane 1, a size maker (ϕ 174 DNA-*Hae*III digest), lane 2 to 4, *taurus*-type; lane 5 to 8, *indicus*-type; lane 9 female.

DNA sequence for *SRY* gene of *taurus* has been reported by Kato *et al* (1995) Since sequence of indicus-type cattle was not available, we isolated and sequenced whole length of protein coding region of *SRY* gene (690-bp) from a male cattle which had acrocentric Y chromosome by karyotyping (Tanaka *et al*, 2000) Comparing these DNA sequence, one base substitution was found between the taurus-type and indicus-type (641st base G→T; 214th codon TGT→TTT, 214th amino acid Cys→Phe) As the substitution position was contained in a cleavage site by *Mse*I, PCR-RFLP method was carried out to identify the taurus-type and the indicus-type. PCR primers for amplification of *SRY* gene were 5'-TTAGAACGCTTACACCGCATATTACT-3'and 5'-AGTAGTAAAATTGAGATAAAGAGCGCCT-3' As shown in Fig. 2, electrophoration pattern of MseI digested PCR products of the *SRY* gene could clearly be distinguish the two types on the gel *SRY* gene of the 200 male cattle were examined. Of all of them, 193 cattle had *indicus*-type cleavage pattern and the rest 7 cattle had *taurus*-type. Thus, most of the paternal backgrounds of these cattle were considered to be the indicus cattle. Lan *et al*, (1995) reported that the Yunnan native cattle in China had an acrocentric (indicus-type) Y chromosome. This report supports our present results of *SRY* gene analysis, suggesting that the gene flow from the *taurus* to Southeast Asian cattle is a small minority composing only a few % of the whole.

Cytogenetics analysis of cattle in Southeast Asia

Robertsonian translocation, also called centric fusion, is the most common abnormalities in bovine karyotype. The first detected and most widely reported example is the 1/29 translocation described by Gustavsson and Rockborn (1964) After this report, many other Robertsonian translocations have been reported: rob(7;21), rob(15;25), rob(5;22), rob(4;10), rob(16;18), rob (16;20) (Hanada *et al* 1981, Iannuzzi *et al* 1992; Rubes *et al* 1996) However most of the Robertsonian translocations were reported in the European breed of cattle while cytogenetic analyses in Southeast Asian cattle were very limited. However, Fischer (1971) reported a centric fusion between a large and a small acrocentric in one animal out of four indigenous Thai cattle. In our study of karyotyping of cattle in Southeast Asia, we found an abnormal karyotype of a male calf that consists of only 59 chromosomes (57 acrocentric and 2 large submetacentric) (Tanaka *et al* 2000) R-banding revealed that the phenotypically normal male calf (2n=59) has an acrocentric Y chromosome and is a heterozygous carrier of a centric fusion involving chromosomes 2 and 28 (Fig. 3) It is quite interesting that the rob(2;28) chromosome is the same combination of a biarmed autosome pair in the 2n=58 karyotype of gaur and mithan (Fig. 4) Although, the calf analyzed in this study was not a direct hybrid between cattle and gaur, the rob(2;28) chromosome may have acquired from the gaur or its domestic form mithan, because they can interbreed with domestic cattle producing fertile female offspring, and had a wide distribution in South and Southeast Asia within historical times.

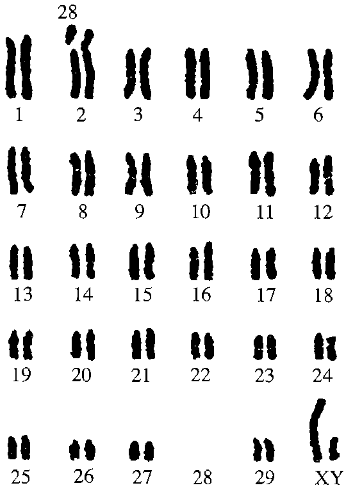

Figure 3. RBG-banded karyotype of a male calf carring ic fusion involving chromosomes 2 and 28.

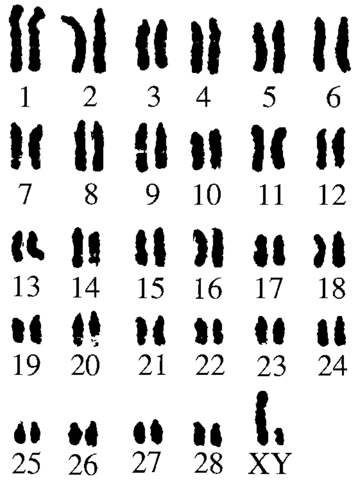

Figure 4. RBG-banded karyotype of a mithan bull in Myanmar

Distribution of β globin alleles in native cattle populations in Southeast Asia.

The hemoglobin-β chain (Hbb) polymorphism is one of the most intensively investigated genetic characters in cattle. Distribution of the Hbb variants is therefore a powerful too to estimate genetic relationships among the various cattle populations all over the world (Namikawa, *et al,* 1984) In Southeast Asia, most of the cattle populations were polymorphic with three electrophoretic bands: Hbb-A, -B, and -X with the three alleles, A, B, X at *Hbb* locus When analyzed by using isoelelectric focusing (IEF) method, pH range 5-8 with 8 M urea, the Hbb-X band can be divided into two polymorphic bands, we temporarily call them X1 and X2 from the higher PI (Fig. 5) The X1 band was confirmed to be identical with the Hbb of mithan, on the other hand, the X2 band showed no difference in the pI from the previous X (X^{Bali}) band of Bali cattle. Figure 6 shows the geographical distribution of Hbb alleles in Indochina area. Hbb-X1 appeared at highest frequency

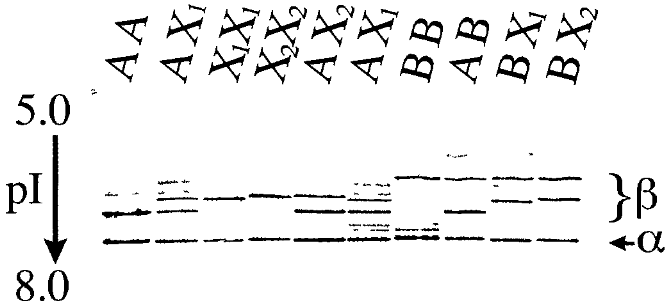

Figure 5. Electrophoretic polymorphisms at *Hbb* locus in Southeast Asian cattle by isoelectric focusing. The X_2X_2 is the standard from Bali cattle.

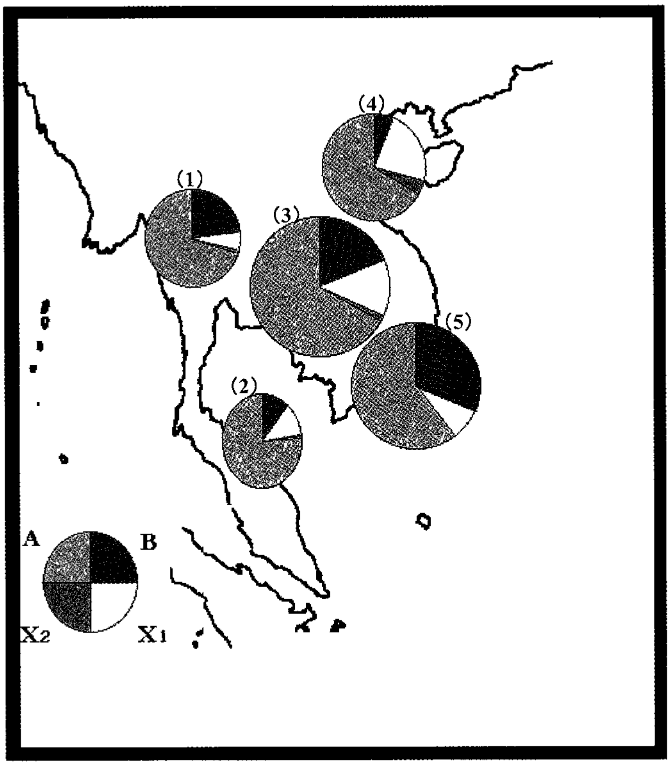

Figure 6. Geographical distribution of *Hbb* alleles by isoelectric focusing of native cattle in Indochina.
(1) Thailand (northern area), (2) Thailand (southern area), (3) Laos,
(4) Vietnam (northern area), (5) Vietnam (southern area)

of 27.8% in the northern area of Vietnam where we can not see any domestic gaur in this district, while Hbb-X2 is a minor allele in Indochina (Okada *et al* 2000) This result suggests that gaur has played an important role of gene souse for cattle in Indochina.

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Nozawa: In Bali, Java, and Sulawesi, there was found to be a high frequency of the X Bali variant of the hemoglobin-beta-chain. Is there a possibility of the existence of an X1 variant in these isles?

Tanaka: All the Bali cattle examined had an X2 variant

Nozawa: What is the distribution of X1 in Mithan or Gayal?

Tanaka: I analyzed seven individuals of Gayal All the individuals have an X1 variant

Wagner: From your study, can you give any advice or deduce any conclusions for conservation activities, in a sense, which breed or lines, or what do?

Tanaka: One of the most important populations comprise the cattle in northern Vietnam to Laos, and some states of Myanmar. They are of a smaller size and have a different genetic constitution to other regions and are thought to have substantial gene flow from wild gaur. I am not familiar with Indonesian cattle, however, the Bali cattle population of Indonesia is also thought to be important

Thuy: As for the location of the sampling, from which parts of Vietnam did you collect samples? From the south or the north? This is important since many differences are found between the regions in Vietnam. In the southern provinces, there are Banteng cattle and minority groups enclose cattle in this area and arrange mating with Banteng cattle.

Tanaka: I collected samples at Hamyen City, 200 km north of Hanoi and also around Ho-Chi-Minh City.

Genetic Diversity of Asian Water Buffalo

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Abstract

Domestic water buffaloes are valuable animal genetic resource of Asia. Asian water buffaloes can be classified into two types - swamp buffalo and river buffalo. The morphology of two types differs in respect to coat colour, horn shape and size. There is variation in their utilization too. The variation in morphology and utility is reflected in the genotypes of buffaloes. There are chromosome polymorphisms, blood protein polymorphisms and DNA polymorphisms between two buffalo types and also within different geographical populations. The studies made so far indicate that two types of water buffaloes have been domesticated from different origins and differentiated at full sub species level The haplotypes of swamp buffaloes and river buffaloes are distributed east and west as Bangladesh forms a geographical boundary area between these two types.

Introduction

Buffaloes belong to family *Bovidae* The Asian buffaloes originated from Asian wild buffalo, *Bubalus bubalis* that are still found in different parts of India, Sri Lanka and Bhutan.

Domestic water buffaloes have been classified into two types - swamp buffalo and river buffalo. This classification has been made on the basis of their morphological, behaviour and geographical distribution (Macgregor, 1941) Buffalo was domesticated in India about 5000 years ago and in China about 4000 years ago (Zeuner, 1963; Cockrill, 1981) Chen and Li (1989) however suggest domestication of buffalo in China at least 7000 years ago. Two types of buffaloes spread then in different regions of the Asia as well as different continents and have eventually acquired their own identity. This paper addresses about the genetic diversity of domestic buffalo of Asia. The genetic diversity study is important for conservation program as well as for taking decision of breeding program. The study of genetic diversity of Asian buffaloes will, therefore, help in their conservation and to take proper buffalo breeding program in this region.

Distribution

Domestic water buffaloes are found in Asia, Africa, Europe and Latin America. There were 162 million water buffaloes in the world in 1999 (FAO, 2000) Of the total number of buffalo, approximately 96% are observed in Asia and Pacific region. Over the last decade (1988 - 98), the number of water buffalo in the world increased slightly 1.30% per year. In 1998, there were 156.7 million buffaloes distributed in 16 countries of Asia (Table 1) From the table, it appears that buffalo number is decreasing in countries of Southeast Asia but increasing in Pakistan, India, Nepal and Bangladesh.

Domestic water buffaloes are valuable animal genetic resource of Asia. There is diverse use of water buffaloes in Asia. River buffaloes are distributed in Bangladesh, Nepal, India, Sri Lanka, Pakistan, Arabian Peninsula and Mediterranean region. Swamp buffaloes are found in Southeast Asia extends northward as far as Yangtze Valley in China and westward as far as Assam (Macgregor, 1941) River buffaloes have a number of recognized breeds and used mainly for milk production. River buffaloes account for more than 70% of the total buffalo in the world whereas swamp buffaloes represent 30%. Swamp buffaloes have no breed and used mainly for draught purpose. Buffalo raising in Asia has been traditional among small farmers and reared under subsisting system in crop and livestock mixed cultivation system. The production systems may be extensive, semi intensive or intensive.

Table 1 Distribution of buffaloes in Asian countries and in the world in 1988 to 1998
(000 heads)

Country	1988	1995	1998	Average Annual Growth Rate 88-98
1 Bangladesh	698	885	854 F	1.9 %
2 Bhutan	4	4F	4 F	-0.9 %
3 Cambodia	709	765	770 F	0.6 %
4 China	20,859	22,928	20,818	0.1 %
5 India	77,470	88,375	91,784 F	1.8 %
6 Indonesia	3,194	3,112	3,145	-0.5 %
7 Iran	436	447	465 F	0.7 %
8 Laos	1,041	1,191	1,093	1.4 %
9 Malaysia	213	157	150 F	-4.2 %
10 Myanmar	2,245	2,203	2,337	1.0 %
11 Nepal	2,952	3,278	3,400 F	1.5 %
12 Pakistan	16,518	19,711	21,213	2.6 %
13 Philippines	2,890	2,708	3,004	0.4 %
14 Sri Lanka	963	764	721	-3.2 %
15 Thailand	5,708	3,710	1,951	-5.2 %
16 Viet Nam	2,807	2,963	2,951	0.5 %
SUB-TOTAL	1,38,706	1,53,200	1,56,708	1.3 %
REST of THE WORLD	4,883	5,538	5,655	1 1 %
WORLD	1,43,589	1,58,738	1,62,363	1.3 %

Source: FAO, 2000
F: FAO estimate

Morphological variation

The Asian buffaloes have a variety of Morphology There is distinct variation in coat colour, horn shape, body size and conformation between river buffaloes and swamp buffaloes. River buffaloes are usually black have curled/spiral or sickle shape horns, medium to large in size and usually dairy type. Swamp buffaloes are dark gray have circular or semicircular horns, small to medium in size and have barrel shape body. Some swamp buffaloes have white coat colour (albinoid) The frequency of white buffalo varies from country to country (Mason, 1974) Nozawa and Ratanadilok (1974) mentioned that frequency of white buffalo in Thailand ranged from 0 to 15%. Amano *et al* (1983) mentioned that frequency of white gene in Indonesian buffaloes ranged from 19 to 49% (1983) Piebald (black and white) buffaloes are found in some islands of Indonesia but their frequency is less than that of white buffalo (Amano *et al* 1983) White stocking and one or two chevron are common in swamp buffaloes. White stocking and chevron are not found in river buffaloes except in 'Surti' breed. Walleye and white spotting in face, forehead, leg and tail switch is common in 'Nili Ravi' The coat colour, spotting pattern and white marking vary in crossbred buffaloes depending upon the level of crossing.

The size of different types of buffaloes varies depending upon breed and locality. Table 2 represents the height, length and heart girth of swamp buffaloes in Far East Such type of body measurement has been conducted by Society for Researches on Native Livestock, Japan in different Asian countries (Amano *et al* 1983, Amano *et al* 1995a, Namikawa *at al* 2000) Their findings are more or less similar to that report of Chantalakahana (2001) Bhat (1992) mentioned the height of male and female Murrah buffaloes in India as 150 and 140 cm respectively.

Table 2. Mature weight and size of swamp buffaloes

Countries	Weight (kg)	Height (cm)		Length (cm)		Heart girth (cm)	
		Male	Female	Male	Female	Male	Female
China	400-500	129	124	143	132	188	179
Indonesia	450-500	130	125	–	–	–	–
Malaysia	364-545	129	121	123	121	183	180
Philippines	364-545	127	120	–	–	196	184
Taiwan	400-500	129	124	141	135	186	190
Thailand	404-600	121-137	121-126	141-148	132-137	186-209	181-183

Source: Chantalakhana, 2001

Genetic variation

The wide variation in the morphology of Asian water buffaloes is also reflected in their genetic make up both in chromosomal make up and gene constitution. Extensive works on chromosome polymorphisms and blood protein polymorphisms have been done in Japan, India, Malaysia and

Thailand. Studies on the buffalo DNA, especially on the mitochondrial and microsatellite DNA polymorphisms, are in progress in Japan, India, Thailand, Malaysia and China. Little work has been done on the blood group systems of buffaloes.

Chromosome polymorphisms: Prakandze (1939) was the first to work with buffalo cytogenetics in Asia giving a brief account on the chromosome number Later Makino (1944) reported correctly the chromosome number of swamp buffalo of Taiwan and he mentioned it as 48. Ulbrich and Fischer (1967), and Fischer and Ulbrich (1968) were the first to report about the details of buffalo karyotypes. Since then many researchers in Japan (Amano and Martojo 1983, Amano *et al* 1987), India (Gupta and Ray Chaudhury 1978, Chakrabarti and Benjamin 1980, Yadav and Balakrishnan 1982), Sri Lanka (Scheurmann *et al* 1974), Malaysia (Harisah *et al* 1989), China (Youjun *et al* 2001) and Thailand (Chavananikul, 1989) have conducted work on cytogenetics of Asian buffaloes. From their studies, it now clear and well established that river buffaloes and swamp buffaloes differ in their karyotypes. The diploid chromosome number of river buffaloes is 50. Their karyotypes consist of 5 pairs of submetacentric chromosomes, 19 pairs of acrocentric chromosomes and a pair of acrocentric sex chromosomes. On the other hand, karyotypes of swamp buffaloes consists of a single pair of large metacentric chromosomes, 4 pairs of submetacentric chromosomes and 18 pairs of acrocentric chromosome and a pair of acrocentric sex chromosome. These two types also differ in fundamental number. The fundamental number of river buffaloes and swamp buffaloes is 60 and 58 respectively. The cross between two types produces a number of chromosome polymorphisms in F_1 and F_2 The details of chromosome polymorphisms have been presented in Table 3.

Blood protein polymorphisms: Giri and Pallai (1956), Vella (1958) and Lyopetjra (1962) for the

Table 3. Chromosome number of the offspring produced from different types of mating between swamp and river buffaloes

Type of mating	Chromosome number
1 Purebred cross mating	
Swamp x River	Parent (2n) 48 x 50
Meiosis	Gamete (n) (24) + (25)
F_1 crossbred	Offspring (2n) 49
2. Backcross to swamp	
F_1 x Swamp	Parent (2n) 49 x 48
Meiosis	Gamete (n) (24), (25) + (24)
BIS	Offspring (2n) 48 or 49
3. Backcross to river	
F_1 x river	Parent (2n) 49 x 48
Meiosis	Gamete (n) (24), (25) + (25)
BIR	Offspring (2n) 49 or 50
4. Inter se mating	
F_1 x F_1	Parent (2n) 49 x 49
Meiosis	Gamete (n) (24), (25) + (24), (25)
F_2	Offspring (2n) 48, 49 or 50

Source Chavananikul, 1989

first time reported the hemoglobin and transferrin polymorphisms in Indian and Thai Buffalo. Later Khana and Breand (1968) reported about the albumin polymorphisms. Since then many investigators in different parts of Asia, especially the Japanese, Indian and Malaysian scientists, have conducted extensive works on the blood protein polymorphisms of Asian buffaloes using many protein loci (Amano 74, 78; Amano *et al* 1980, 1981, 1982, 1983, 1984, 1986, 1987, 1995a, 1998; Sen *et al* 1966, Khana 1969, Tan *et al* 1989, 1991, 1992, 1993; Barker *et al* 1997a; Takahashi *et al* 2000) All the investigators reported about polymorphisms for a number of blood protein and enzyme loci in buffaloes for different populations and types. There are, however, variations in methodology applied and nomenclature used by them. Amano and his associates examined 25 blood protein and enzyme loci of 40 buffalo populations of Asia and mentioned about polymorphisms of serum albumin, transferrin, alkaline phosphatase, cell hemoglobin, carbonic anhydrase, peptidase B and NADH diaphorase (Table 4) The Indian scientists reported about the polymorphisms of albumin, transferrin, hemoglobin, amylase, carbonic anhydrase and ceruloplasmin in Indian buffalo population. Barkar and associates, however, mentioned more polymorphic loci for blood protein and enzymes of buffaloes of Asia. Out of 53 blood protein and enzyme examined, they obtained 25 polymorphic loci for blood protein and enzyme in 17 buffalo populations of Asia. From their studies, it appears that river buffaloes and swamp buffaloes differ genetically for these loci For example, AlbX and TfA have been detected only in the swamp buffalo. On the other hand, Alb^{B} and Tf^{E} have been reported only in the river buffaloes (Amano *et al* 1987, 1995a)

Table 4. Gene frequencies of blood protein loci of 40 buffalo populations

Locus	Allele	VTN	TVC	VT1	PH1	PH2	PH3	PH4	PHC1	PHC2	PHR	WJ1	WJ2	WJ3
Alb	A	0.132	0.08	0.28	0	0.037	0.056	0	0.134	0.028	0.119	0.739	0.679	0.733
	B	0.855	0.92	0	1	0.963	0.944	1	0.333	0.528	0	0.261	0.321	0.267
	X	0.013	0	0.72	0	0	0	0	0.533	0.444	0.881	0	0	0
Tf	A'	0	0	0	0	0	0	0	0	0	0	0	0	0
	A	0.224	0.16	0.019	0.05	0.047	0.056	0.048	0.1	0.083	0	0.478	0.25	0.3
	D	0.776	0.84	0.077	0.95	0.953	0.944	0.929	0.467	0.5	0.262	0.522	0.75	0.7
	E	0	0	0.904	0	0	0	0.023	0.433	0.417	0.738	0	0	0
Hb-α	1	0.921	0.960	0.981	1	1	1	1	1	1	1	1	1	0.967
	0	0.079	0.077	0.019	0	0	0	0	0	0	0	0	0	0.033
Hb-β	1	0.961	1	1	1	1	1	1	0.967	1	1	1	0.928	0.834
	2	0.039	0	0	0	0	0	0	0.033	0	0	0	0.036	0.133
	3	0	0	0	0	0	0	0	0	0	0	0	0.036	0.033
Alp	F	0	0	0	0	0	0	0	0	0	0	0	0	0
	0	1	1	1	1	1	1	1	1	1	1	1	1	1
CA	F	0.289	0.34	0.865	0.617	0.74	0.69	0.643	0.9	0.794	0.881	0.109	0.071	0.167
	S	0.711	0.64	0.135	0.383	0.26	0.31	0.357	0.1	0.206	0.119	0.891	0.929	0.833
Pep-B	1	0	0	0	0	0	0	0	0	0	0	0	0	0
	2	0.789	0.96	1	0.933	0	0.139	0.786	0	0.029	0.905	0.317	0.75	0.7
	3	0.221	0.06	0	0.067	1	0.861	0.214	1	0.971	0.095	0.783	0.25	0.3
	4	0	0	0	0	0	0	0	0	0	0	0	0	0
Dia	1	1	1	1	0.983	1	1	1	1	1	1	1	1	1
	2	0	0	0	0.017	0	0	0	0	0	0	0	0	0

Table 4. Continue

Locus	Allele	WJ4	CJ	NS	WS	SST	SU1	SU2	BL1	BL2	INC	TLD	LAN	MUR
Alb	A	0.775	0.841	0.4	0.412	0.464	0.583	0.579	0.896	0.9	0.625	0.129	0.457	0.1
	B	0.225	0.259	0.05	0.588	0.536	0.417	0.421	0.104	0.1	0	0.843	0	0
	X	0	0	0.55	0	0	0	0	0	0	0.375	0.028	0.543	0.9
Tf	A'	0	0	0	0	0	0	0	0.125	0	0	0	0	0
	A	0.525	0.277	0.15	0.305	0.4	0.269	0.316	0.167	0.35	0	0.229	0	0
	D	0.475	0.733	0.2	0.667	0.6	0.731	0.684	0.708	0.65	0.475	0.771	0.309	0.2
	E	0	0	0.65	0.028	0	0	0	0	0	0.625	0	0.691	0.8
Hb-α	1	1	1	1	0.84	1	1	1	0.979	1	1	1	0.968	1
	0	0	0	0	0.16	0	0	0	0.021	0	0	0	0.032	0
Hb-β	1	1	1	1	1	1	1	0.974	1	1	1	1	0.691	1
	2	0	0	0	0	0	0	0.026	0	0	0	0	0.245	0
	3	0	0	0	0	0	0	0	0	0	0	0	0.064	0
Alp	F	0	0	0	0	0	0	0.027	0.021	0	0	0	0	0
	0	1	1	1	1	1	1	0.973	0.979	1	1	1	1	1
CA	F	0	0.341	0.85	0.118	0	0	0	0.083	0.3	0.75	0.429	0.904	0.85
	S	1	0.659	0.15	0.882	1	1	1	0.917	0.7	0.25	0.571	0.096	0.15
Pep-B	1	0	0	0	0	0	0	0	0	0	0	0	0.032	0
	2	0.15	0.727	0	0.118	0.107	0.25	0.868	0.812	0.75	0	0.829	0.904	0.9
	3	0.85	0.273	1	0.882	0.882	0.75	0.132	0.188	0.25	1	0.171	0.065	0.1
	4	0	0	0	0	0	0	0	0	0	0	0	0	0
Dia	1	1	1	1	1	1	1	1	1	1	1	1	1	1
	2	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 4. Continue

Locus	Allele	BDC1	BDC2	BDW	BDE	NPK	NPT	NPP	CHD	CHB	TWN	ITA	OKI	WLD
Alb	A	0.475	0.275	0.417	0.35	0.187	0.362	0.395	0.143	0.041	0.054	0.143	0.083	0.7
	B	0.100	0.05	0	0.35	0.063	0	0.026	0.857	0.959	0.946	0	0.917	0
	X	0.425	0.675	0.583	0.30	0.750	0.638	0.579	0	0	0	0.857	0	0.3
Tf	A'	0	0	0	0	0	0	0	0	0	0	0	0	0
	A	0	0	0	0.05	0	0	0	0.4	0.216	0.161	0	0.333	0
	D	0.15	0.175	0.167	0.35	0.063	0.241	0.158	0.557	0.784	0.839	0.786	0.667	0.1
	E	0.85	0.825	0.833	0.60	0.937	0.959	0.842	0.043	0	0	0.214	0	0.9
Hb-α	1	1	1	1	0.99	1	1	0.947	1	1	1	1	1	1
	0	0	0	0	0.01	0	0	0.053	0	0	0	0	0	0
Hb-β	1	0.925	1	0.971	0.94	1	0.914	1	0.986	0.889	1	0.857	1	1
	2	0.075	0	0.029	0.05	0	0.086	0	0.140	0.111	0	0.143	0	0
	3	0	0	0	0.01	0	0	0	0	0	0	0	0	0
Alp	F	0	0	0	0.041	0	0	0	0	0	0	0	0	0
	0	1	1	1	0.959	1	1	1	1	1	1	1	1	1
CA	F	0.825	0.85	0.623	0.56	0.75	0.897	0.789	0.671	0.111	0.5	1	0.5	0.9
	S	0.175	0.15	0.177	0.44	0.25	0.103	0.211	0.329	0.889	0.5	0	0.5	0.1
Pep-B	1	0	0	0	0	0.02	0	0	0	0	0	0	0	0.1
	2	1	1	1	1	0.85	0.875	1	0.974	0.9	0.714	0.857	0.833	0.9
	3	0	0	0	0	0.12	0.125	0	0.026	0.1	0.250	0.143	0.167	0
	4	0	0	0	0	0.01	0	0	0	0	0.036	0	0	0
Dia		1	1	1	1	1	1	1	1	1	1	1	1	1
		0	0	0	0	0	0	0	0	0	0	0	0	0

Source: Amano *et al* 1998

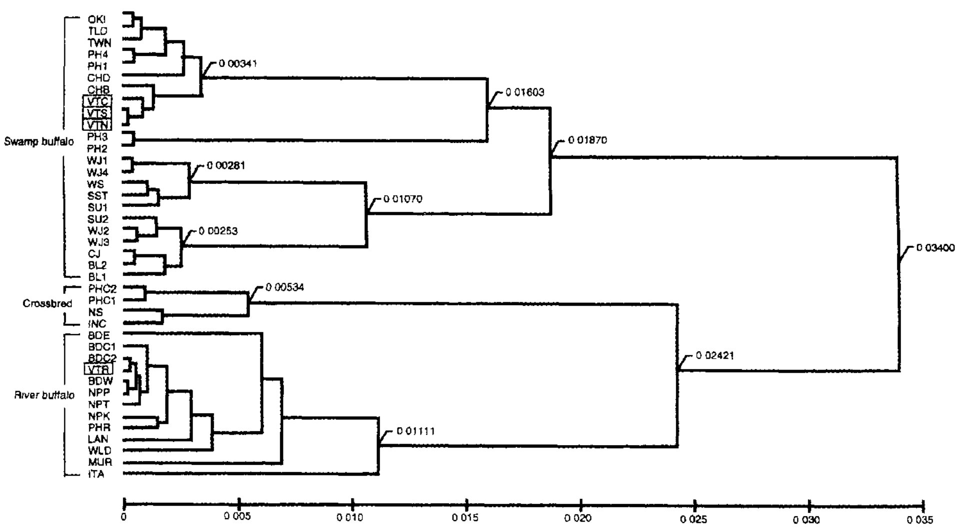
Amano *et al* (1998) estimated the genetic variability of 40 buffalo populations in Asia. This has been presented in Table 5. The highest heterozygosity ($\overline{H}$) value was obtained in population of Bangladesh-East (0.0821 ± 0.0378) and the lowest value in Philippines -2 (0.0218 ± 0.0158) Nei's genetic distance and principal components analysis done by them have been shown in Figure 1 and

Table 5. Genetic variability (P_{Poly} and $\overline{H}$) of 40 water buffaloes populations

Population	P_{Poly} ± S.E	$\overline{H}$ ± S.E.
Vietnam - North	0.2400 ± 0.0854	0.0625 ± 0.0256
Vietnam - Central	0.2000 ± 0.0800	0.0422 ± 0.0212
Vietnam - South	0.2000 ± 0.0800	0.0565 ± 0.0238
Vietnam - River	0.2000 ± 0.800	0.0340 ± 0.0192
Philippines - 1	0.1600 ± 0.0733	0.0290 ± 0.0195
Philippines - 2	0.1200 ± 0.0650	0.0218 ± 0.0158
Philippines - 3	0.1600 ± 0.0733	0.0351 ± 0.0197
Philippines - 4	0.1600 ± 0.0733	0.0372 ± 0.0226
Philippines - Crossbred-1	0.1600 ± 0.0733	0.0566 ± 0.0327
Philippines - Crossbred-1	0.1600 ± 0.0733	0.0590 ± 0.0322
Philippines - River	0.1600 ± 0.0733	0.0391 ± 0.0195
Indonesia - West Java - 1	0.1600 ± 0.0733	0.0568 ± 0.0280
Indonesia - West Java - 2	0.2000 ± 0.0800	0.0582 ± 0.0265
Indonesia - West Java - 3	0.2400 ± 0.0584	0.0744 ± 0.0297
Indonesia - West Java - 4	0.1200 ± 0.0650	0.0441 ± 0.0254
Indonesia - Central Java	0.1600 ± 0.0733	0.0586 ± 0.0279
West Sumatra	0.2000 ± 0.0800	0.0652 ± 0.0289
North Sumatra	0.1200 ± 0.0650	0.0522 ± 0.0289
South Sulawesi - Toraja	0.1200 ± 0.0640	0.0467 ± 0.0277
South Sulawesi - Ujungpandang - 1	0.1200 ± 0.0650	0.0502 ± 0.0280
South Sulawesi - Ujungpandang - 2	0.1200 ± 0.0650	0.0501 ± 0.0264
Bali - 1	0.2400 ± 0.0854	0.0488 ± 0.0226
Bali - 2	0.1600 ± 0.0733	0.0572 ± 0.0281
Indonesia - Crossbred - 1	0.1200 ± 0.0650	0.0489 ± 0.0278
Thailand	0.1600 ± 0.0733	0.0559 ± 0.0271
Sri Lanka - Native	0.2400 ± 0.0854	0.0718 ± 0.0308
Sri Lanka - Murrah	0.2000 ± 0.0800	0.0606 ± 0.0282
Sri Lanka - Wild	0.1600 ± 0.0733	0.0384 ± 0.0199
Bangladesh - Central - 1	0.1600 ± 0.0733	0.0486 ± 0.0267
Bangladesh - Central - 2	0.2800 ± 0.0898	0.0404 ± 0.0233
Bangladesh - West	0.1600 ± 0.0650	0.0444 ± 0.0242
Bangladesh - East	0.1600 ± 0.0733	0.0821 ± 0.0378
Nepal - Kali Gandaki	0.1600 ± 0.0733	0.0444 ± 0.0228
Nepal - Terai	0.1600 ± 0.0733	0.0468 ± 0.0242
Nepal - Pokhara	0.2000 ± 0.0800	0.0503 ± 0.0255
China - Dali	0.2000 ± 0.0800	0.0569 ± 0.0285
China - Banna	0.2000 ± 0.0800	0.0418 ± 0.0187
Taiwan - Kaoshun	0.1600 ± 0.0733	0.0519 ± 0.0273
Italy - Naples	0.1600 ± 0.0733	0.0429 ± 0.0273
Japan - Okinawa	0.1600 ± 0.0733	0.0550 ± 0.0281

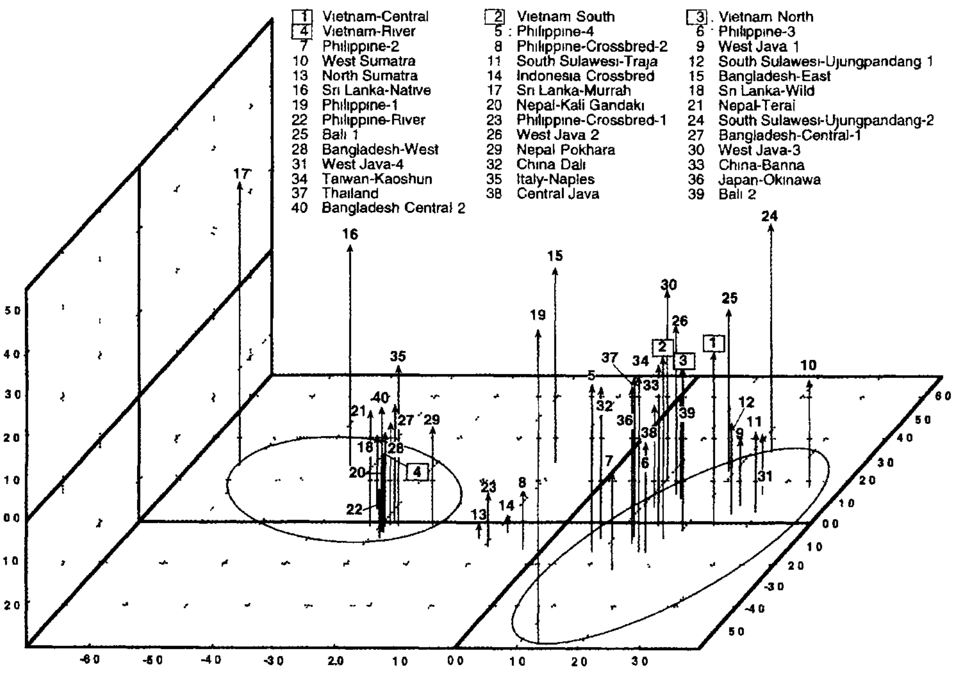
Source: Amano *et al* 1998

Figure 2. Their study reveals larger genetic distance between river buffaloes and swamp buffaloes. They concluded that swamp buffaloes could be classified into two groups - one the swamp buffaloes of Indonesia and other the swamp buffalo of main land of Southeast Asia (China, Laos, Vietnam, Thailand, and The Philippines) They further suggested that swamp buffaloes and river



OKI	Japan-Okinawa	CHB	China Banna	WS	West Sumatra	PHC1	Philippine Crossbred 1	NPP	Nepal Pokhara
TLD	Thailand	VTC	Vietnam Central	SST	South Sulawesi Traja	PHC2	Philippine Crossbred 2	NPT	Nepal Terai
TWN	Taiwan Kaoshun	VTS	Vietnam South	SU1	South Sulawesi Ujungpandang 1	INC	Indonesia-Crossbred	NPK	Nepal Kali Gandaki
PH1	Philippine 1	VTN	Vietnam North	SU2	South Sulawesi Ujungpandang 2	BDE	Bangladesh East	PHR	Philippine River
PH2	Philippine-2	WJ1	West Java 1	CJ	Central Java	BDC1	Bangladesh Central 1	LAN	Sri Lanka-Native
PH3	Philippine 3	WJ2	West Java 2	BL1	Bali 1	BDC2	Bangladesh Central 2	WLD	Sri Lanka Wild
PH4	Philippine 4	WJ3	West Java 3	BL2	Bali 2	BDW	Bangladesh West	MUR	Sri Lanka Murrah
CHD	China Dali	WJ4	West Java 4	NS	North Sumatra	VTR	Vietnam River	ITA	Italy Naples

Fig. 1 Dendrogram drawn from Nei's genetic distance estimated by gene frequency of blood protein types of 40 water buffalo populations (Amano *et al* 1998)



1	Vietnam-Central	2	Vietnam South	3	Vietnam North
4	Vietnam-River	5	Philippine-4	6	Philippine-3
7	Philippine-2	8	Philippine-Crossbred-2	9	West Java 1
10	West Sumatra	11	South Sulawesi-Traja	12	South Sulawesi-Ujungpandang 1
13	North Sumatra	14	Indonesia Crossbred	15	Bangladesh-East
16	Sri Lanka-Native	17	Sri Lanka-Murrah	18	Sri Lanka-Wild
19	Philippine-1	20	Nepal-Kali Gandaki	21	Nepal-Terai
22	Philippine-River	23	Philippine-Crossbred-1	24	South Sulawesi-Ujungpandang-2
25	Bali 1	26	West Java 2	27	Bangladesh-Central-1
28	Bangladesh-West	29	Nepal Pokhara	30	West Java-3
31	West Java-4	32	China Dali	33	China-Banna
34	Taiwan-Kaoshun	35	Italy-Naples	36	Japan-Okinawa
37	Thailand	38	Central Java	39	Bali 2
40	Bangladesh Central 2				

Fig. 2 Three-dimensional projection of 40 buffalo populations by principal components analysis (Amano *et al* 1998)

buffaloes have domesticated from different origins. Their findings are in agreement to those of Barker *et al* (1997a), Lau *et al* (1998) and Takahashi *et al* (2000) and indicated in Figure 3, Figure 4 and Figure 5.

DNA polymorphisms: Mitochondrial DNA (mtDNA) is maternally inherited. Changes in the nucleotide sequence of mtDNA occur faster than nuclear DNA. So analysis of mtDNA provides useful information regarding relationships between and within populations/breeds/species.

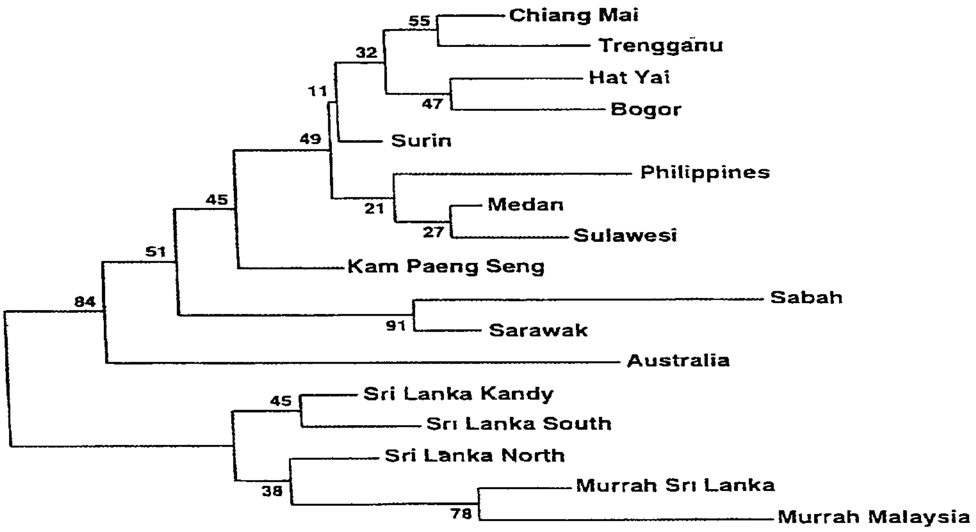
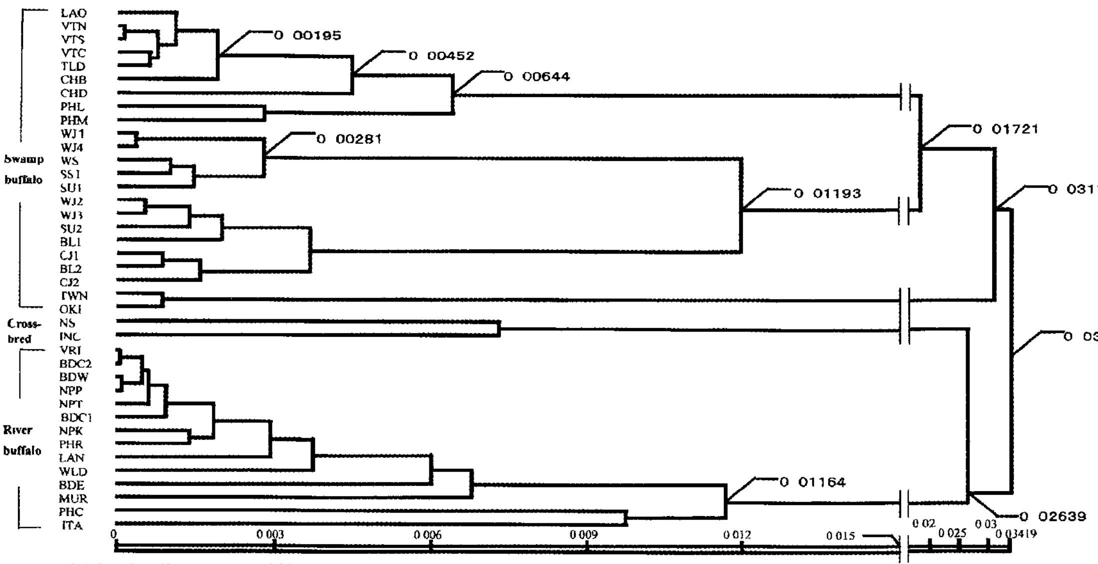


Fig. 3 Dendrogram of relationships among 17 water buffalo populations (Barker *et al* 1997a)



LAO	Laos Vientiane	WJ4	West Java 4	CJ2	Central Java 2	NPK	Napal Kali Gandaki
VTN	Vietnam North	WS	West Sumatra	TWN	Taiwan Kaoshun	LAN	Sri Lanka Native
VTS	Vietnam South	SST	South Sulawesi Toraja	OK1	Japan Okinawa	WLD	Sri Lanka Wild
VTC	Vietnam Central	SU1	South Sulawesi Ujungpandang 1	VR1	Vietnam River	BDE	Bangladesh East
TLD	Thaland	WJ2	West Java 2	BDC2	Bangladesh Centeral 2	MUR	Sri Lanka Murrah
CHB	China Banna	WJ3	West Java 3	BDW	Bangladesh West	PHC	Philippines Crossbred
CHD	China Dari	SU2	South Sulawesi Ujungpandang 2	NPP	Napal Pokharal	ITA	Italy Naples
PHL	Philippines Luson	BL1	Bali 1	NPT	Napal Terai	NS	North Sumatra
PHM	Philippines Midanao	CJ1	Central Java 1	BDC1	Bangladesh Centeral 1	INC	Indonesia Crossbred
WJ1	West Java 1	BL2	Bali 2	PHR	Philippines River		

Fig. 4 Dendropgram drown from the Nei's genetic distance estimated by gene frequencies of blood proteins of 39 water buffalo populations (Takahashi *et al* 2000)

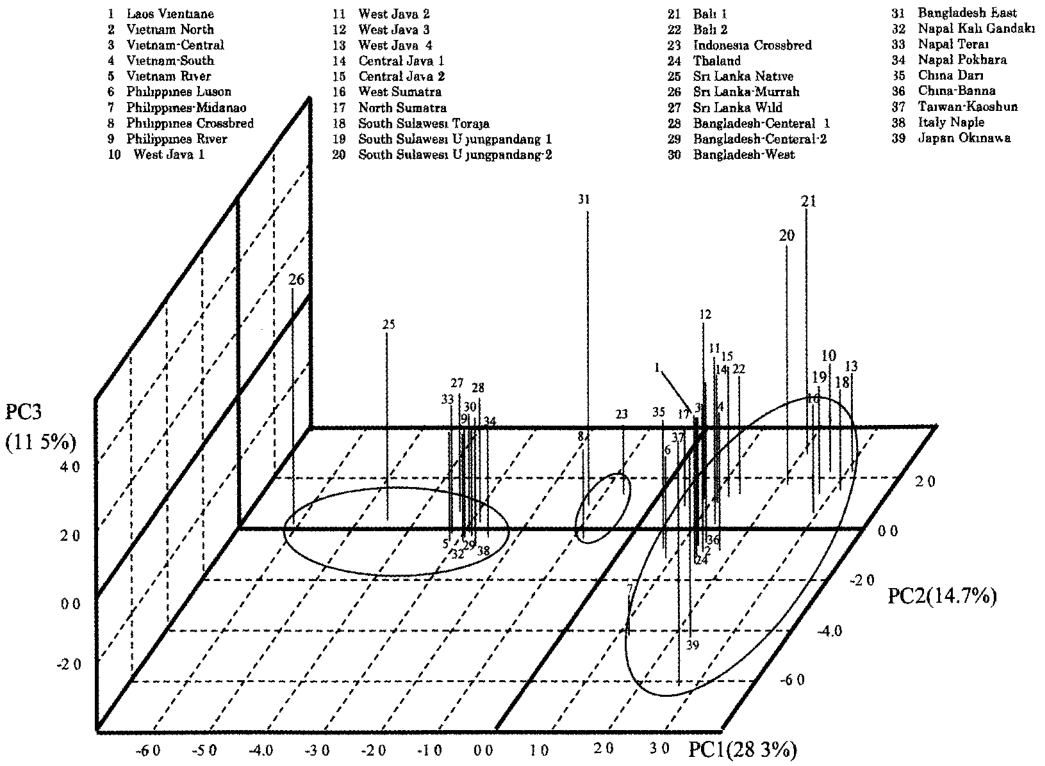


Fig. 5 Three dimensional projection of 39 buffalo populations by principal components (Takahashi *et al* 2000)

Amano *et al* (1995b) reported the genetic variants of ribosomal DNA and mtDNA between river buffaloes and swamp buffaloes and concluded that only mtDNA provides adequate means for classification of water buffaloes. Simple sequence repeat (microsatellite) loci have been found to be common in all eukaryotic genomes with frequencies as high as one every 6 kb (Beckmann and Weber, 1992) Since microsatellites are highly polymorphic, they are also useful genetic markers for comparative studies of genetic variation (MacHugh *et al* 1994) Restriction endonuclease cleavage analysis, nucleotide sequence data of polymorphic sites of mtDNA, and microsatellite loci analysis of DNA are the tools to study such relationships and genetic variability among the organisms. As compared to cattle, little work has been done on buffalo DNA -for both nuclear DNA and mtDNA. However DNA polymorphic work on buffaloes are in progress in different institutes of Asia.

Bath *et al* (1990) described the cleavage pattern of mtDNA of Indian Murrah buffaloes. Out of 13 restriction endonuclease enzymes tested, only one enzyme viz., Bg/I had polymorphic sites. Hu *et al* (1997) described the restriction endonuclease patterns of mtDNA of three local type buffaloes of Yunnan province of China. They tested 18 enzymes and identified polymorphisms for *BamHI*, *EcoRI* and *ScaI* sites. From their result, they concluded that Chinese water buffaloes belong to swamp type with genetic variance among different local buffalo populations. The findings of Bath *et al* (1990) and Hu *et al* (1997) agree to the findings of Pancin and Kamonpatana (1998) and Tanaka *et al* (1995) Pancin and Kamonpatana (1998) used 5 endonuclease enzymes and found polymorphisms for only *BamHI* and *EcoRI* in Thai swamp buffalo population. Tanaka *et al* (1995) used 15 enzymes for swamp buffaloes and river buffaloes. They identified 5 restriction cleavage sites - 2 for river buffaloes and 3 for swamp buffaloes (Fig 6) The additional site they mentioned is *PstI*. The restriction endonuclease cleavage analysis of mtDNA makes it clear that genetic variability exists in different buffalo populations of Asia.

Tanaka *et al* (1995) also calculated the nucleotide diversities (ND) among those buffalo populations of Asia. The ND ranged from 0.2 to 0.6% within swamp and river type, and 1.9 to 2.4% between swamp and river type (Fig. 7) In another study on the sequencing of mtDNA cytochrome b gene (mtcytb), Tanaka *et al* (1996) confirmed such genetic diversities between river buffaloes and swamp buffaloes suggesting a divergent time of 1.7 million year between these two types and concluded that these two types have differentiated from each other at sub species level This finding accords with Kikkawa *et al* (1997) Kikkawa *et al* (1997) observed pair wise nucleotide sequence divergence of two types of buffaloes is to be 2.67% suggesting a divergent time of approximately 1.0 million year Kikkawa *et al* (1997) obtained 15 haplotypes of mtcytb- 7 for swamp buffaloes of Japan, Thailand, Indonesia, Philippines, Bangladesh, and - 8 for buffaloes of Bangladesh, Sri Lanka, Pakistan and Italy. The haplotypes of swamp buffaloes and river buffaloes were distributed east and west as Bangladesh forms a geographical boundary area between these two types. They further observed base substitutions at 5 specific positions (nts 495, 498, 703, 753 and 1053) for river buffaloes and 10 specific position (nts 9, 66, 213, 354, 358, 492, 736, 807, 954 and 1080) for swamp buffaloes in 1140 bp sequence of mtcytb. In another study conducted by Lau *et al*

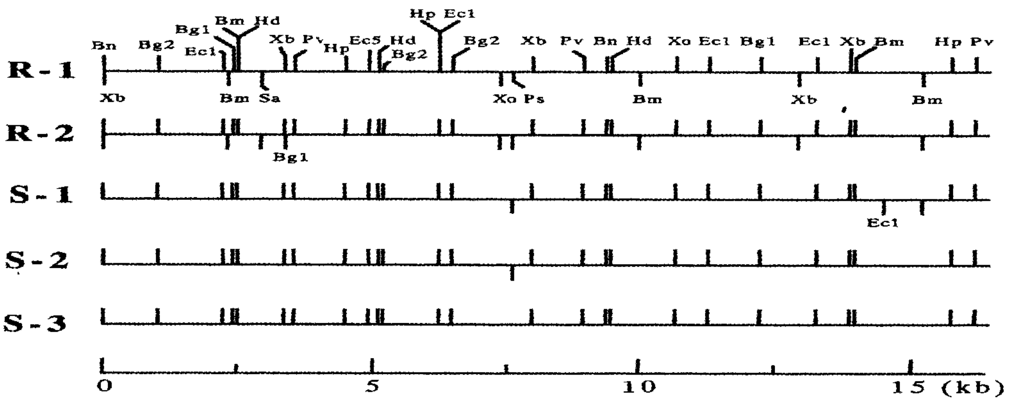


Fig. 6 Restriction endonuclease site maps of 5 mtDNA of the buffaloes (Tanaka *et al* 1995)

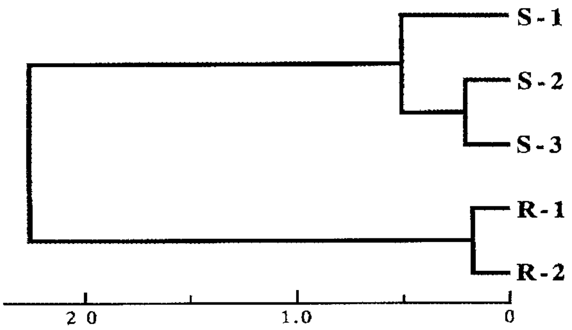


Fig. 7 Dendrogram of mtDNA types of buffaloes (Tanaka *et al* 1995)

(1998) determined mtcytb haplotypes by sequencing 303 bp. They found 5 haplotypes- One for river buffaloes and 4 for swamp buffaloes. One haplotype (swamp 1) was common in all swamp buffalo population of Asia but the rest three were present only in main land swamp buffalo. They also studied the mtDNA D-loop of Asian water buffaloes. Haplotypes and nucleotide diversities of mtDNA D-loop of different buffalo population of Asia has been presented in Table 6 and Figure 8.

Table 6. Haplotype diversity (h) and nucleotide diversity (π) estimated from mtDNA D-loop sequence for each population of swamp and river buffalo

Buffalo type/population	Number of haplotypes	Haplotype diversity (h + SD)	Nucleotide diversity
Swamp	25	0.9135 ± 0.0224	0.0561
Surin	7	1.0000 ± 0.0764	0.0749
Trengganu	3	0.5238 ± 0.2086	0.0487
Sabah	4	0.7500 ± 0.1391	0.0355
Sarawak	5	0.7857 ± 0.1508	0.0545
Philippines	7	1.0000 ± 0.0764	0.0380
Bagor	3	0.5238 ± 0.2086	0.0169
Surawesi	5	0.7222 ± 0.1592	0.0518
Australia	4	1.0000 ± 0.1768	0.0714
River	10	0.7984 ± 0.0667	0.0203
Sri Lanka	4	0.6429 ± 0.1841	0.0195
Murrah Sri lanka	5	1.0000 ± 0.1265	0.0192
Murrrah Malaysia	4	0.5333 ± 0.1801	0.0079
Overall	33	0.9174 ± 0.0157	0.0526

Source: Lau *et al* 1998

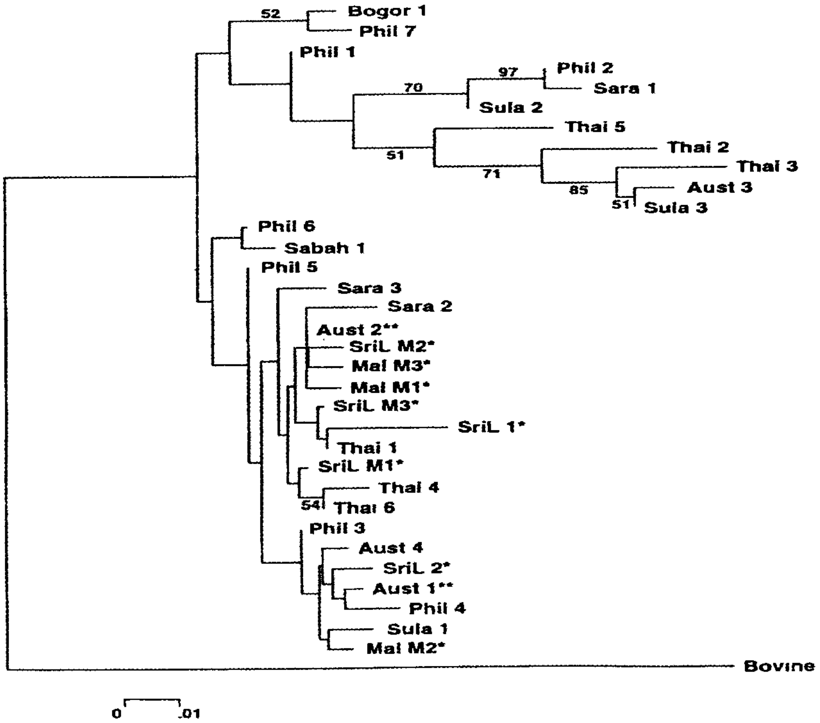


Fig. 8 Neighbour - joining tree for 33 mtDNA D-loop haplotypes of water buffalo with the bovine sequence as an outgroup (Lau *et al* 1998)

Table 7. Number of microsatellite alleles at each locus in swamp and river buffalo, number shared between the two types and average gene diversity within populations

Locus	Number of alleles				Average gene diversity
	Total	Swamp	River	Shared	
CSSM008	7	5	7	5	0.555
CSSM013*	5	5	2	2	0.499
CSSM015	2	2	2	2	0.406
CSSM019	15	14	5	4	0.640
CSSM022	6	5	6	5	0.431
CSSM029	11	10	5	4	0.532
CSSM032	9	7	6	4	0.549
CSSM033	11	9	7	5	0.601
CSSM038	13	6	9	4	0.486
CSSM041	11	7	5	1	0.514
CSSM043	12	9	9	6	0.683
CSSM045	7	6	4	3	0.249
CSSM046*	6	5	4	3	0.506
CSSM047	20	9	1	7	0.711
CSSM057	11	10	7	6	0.652
CSSM060	15	8	9	2	0.508
CSSM061	12	9	10	7	0.594
CSSM062	8	5	6	3	0.541
BRN	10	9	6	5	0.443
HMH!R*	3	2	2	1	0.104
Mean/locus (SE)	9.57 (0.94)	7.10 (0.62)	6.48 (0.76)	4.00 (0.39)	0.514

* Same allele is at highest frequency in both types
Source: Barker *et al.*, 1997b

The phylogenetic relationships of 33 haplotypes showed 2 major clusters, 11 found in swamp buffaloes only and remaining 22 that includes haplotypes found in swamp only, river only and in both river and swamp only. Statistical analysis showed significant differences between the swamp and river types, and among populations within swamp types. The genetic relationships among the 11 populations, based on nucleotide divergence for the D-loop haplotypes, do not accord with their relationships derived from microsatellite (Barker *et al.* 1977b), but accord with Bath (1992) who mentioned no nucleotide variation for microsatellite in Murrah buffaloes of India. Barker *et al.* (1997b) analyzed 21 microsatellite loci in 11 populations of Asian water buffaloes (8 swamp and 3 river type). The number of microsatellite alleles at each locus in swamp and river buffalo, number shared between two types and average gene diversity within population has been presented in Table 7. From their study, they concluded that there was significant differentiation between swamp buffaloes and river buffaloes and also among populations of each type. The topology of swamp buffalo populations' microsatellite tree was in consistent with their geographical distribution. They however estimated much lower time for divergence for two buffalo types (10,000 - 15,000 yr). John and Ali (1997) used synthetic base DNA marker and found variation among different breeds of river buffalo of India. The Toda breed belonged to a group rather than Murrah, Mehsana and Surti (Figure 9).

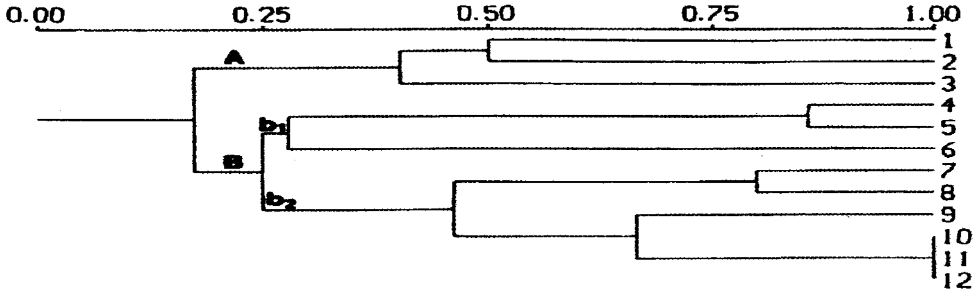


Fig. 9 The phylogenetic tree using UPGMA average of four different breeds of buffaloes based on their DNA profile with OAT15- *Mbo* probe- enzyme (autoradiograpg not shown). Sample 1,2,3 Toda breed, Cluster A; Sample 4,5,6, Murrah breed, Cluster B(b_1); sample 7,8,9 Surti breed and Sample 10,11,12 , Meshana breed, cluster B (b_2) (John and Ali, 1997)

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Chang: There is a considerable genetic distance between the river and swamp buffalo. Is there any possibility of differentiation at the subspecies level? Which group is the origin of the domestic buffalo?

Faruque: Differentiation occurred long before from the advent of domestication. The two types of water buffalo could be considered to have differentiated at the subspecies level. Dr. Tan found almost the same genetic distance between two Malaysian water buffalo groups and calculated that it had been 1 million years since the two populations had separated.

Taneja: Did you come across any fertility problems between the two groups?

Faruque: No.

Amano: The Philippines, China and Vietnam imported improved river buffalo from Pakistan and produced F_1 hybrids for the development of their dairy production. They used only the F_1 females, and the F_1 males were castrated at an early age. There was no problem with the reproductivity of the F_1 females. However, we cannot yet ascertain the fertility of the F_1 males and must check.

Faruque: The studies on F_1 male fertility are ongoing in China. They are checking the characteristics, for example semen, chromosomes, etc., and are preparing a final report. We need to wait for this report to come to any conclusions.

Amano: East Bangladesh is a mixed area where the genes from both types of water buffalo have been found. How is the situation in neighboring countries? Dr. Nyunt, do you have any information?

Nyunt: We used mostly swamp buffalo at agricultural sites and there are very few river buffalo, perhaps 10% of the total, used for dairy production in Myanmar.

Taneja: We use mainly the river buffalo bred in India, except in Assam bordering Bangladesh. Swamp buffalo are mainly used as draft Animals. In Assam, crossing between river and swamp buffalo is taking place under a controlled program. The problem is with the fertility in the crossbred male due to the differential chromosome number. Part of the data, from China and Vietnam, indicate that the hybrid classes crossed to the river type are surviving. As for the male line, they are contributing to hybrid fertility. Some populations in the south resemble more the swamp type. However, their chromosome profile is of the river type.

Distribution and Genetic Diversity of Domesticated Native Pigs in Asia, Focusing on the Short-eared Pig

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Introduction

There are many types of domesticated native pigs in Asia. They are descendants of the local wild pig species (*Sus scrofa* L.), which was domesticated independently in various parts of Asia. Many of the resulting breeds occur in China, where pig breeding has a long history. In recent years, due to the shortage of pig breeding resources, many countries have been looking at Chinese pigs on the basis of their high rate of reproduction (Cheng, 1985).

On the other hand, the realities of native pig production in large areas of South and Southeast Asia are not well known, though there are general introductory reports on native pig research (Fischer and Devendra, 1964; Porter, 1993; Tanaka, 1990). Most of the pigs in these areas are characterized by a straight snout and small ears, and are morphologically different from the typical Chinese pig with a concave face, and large, pendulant ears. This local pig is referred to as the "Short-eared pig" or "Small-eared pig" (Fig. 1).

There has been much debate concerning the precise origin of pig domestication in Asia. It is said that Short-eared pigs were domesticated mainly from several subspecies of wild pig, e.g. the Southeast Asian and Indian wild pigs (*Sus scrofa vittatus and Sus scrofa cristatus*), etc. These native pigs have broad genetic diversity and are important as genetic resources. However, the amount of scientific data on the Short-eared pig is still limited at the present.

Geographical Distribution

In most of the South and Southeast Asian countries, the Short-eared pig is kept mainly by minority ethnic groups in remote regions, such as in mountainous areas or island communities. The geographic distribution of this pig extends from areas of South China to the Tibetan plateau (Phillip and Hsu, 1944; Cheng, 1985). Moreover, historical research confirms that the Short-eared pig was kept in Japan by the mid-nineteenth century (Kurosawa, 1996).

Short-eared pigs in remote regions are usually kept in a loose housing arrangement, although traditional methods differ in some regions. Especially interesting is the breeding of pigs by nomadic, non-Islamic people who live in Muslim countries such as Bangladesh (Kurosawa, 1996).

The number of Short-eared pigs remaining in each country is insignificant. In recent years, their number has been declining due to hybridization with imported foreign breeds. In some areas, particularly Southeast Asia, the Chinese pig and Short-eared pig are sometimes found in the same community. In areas where both the Chinese pig and Short-eared pig are kept many variations in pig breeds can be observed as a result of interbreeding. Examples include pigs with varying sizes of ears and coat coloring, pigs with concave faces, and pigs with sagging backs whose bellies drag along the ground during pregnancy.

Morphological characteristics

The morphological characteristics of the typical Short-eared pig are a narrow head and long, pointed snout, small, erect ears and five pairs of nipples (Fig. 1). This pig is relatively small, with some isolated mountain or island populations averaging a mere 40 kg. According to field surveys it is sometimes difficult to distinguish between wild and domestic pigs at first glance. This is the case in areas with a limited pig population such as Bangladesh, Nepal, Malaysia and Indonesia, etc. (Kurosawa *et al.*, 1992; Tanaka, 1990; Tanaka *et al.*, 1983). Pigs with coat coloring that is similar to wild pig are frequently found in these areas. Like the wild pig reported by Nachtsheim (1925) and Kurosawa (1983), many display five nipple pairs.

One interesting discovery from our survey was the variation in nipple patterns among the native pigs of Asia. The nipple pattern of the typical Short-eared pig ranged from four to six pairs. Other native pigs like the Chinese type and Western breeds varied from six to eight pairs. More specifically, a pattern of five pairs was most frequent in the former, while seven or eight pairs were common in the latter. The nipples of the Short-eared pig were attached to the abdominal and inguinal areas, spaced evenly and symmetrically; furthermore, a supernumerary teat is not found in this pig. These features were observed not only in the populations of the typical Short-eared type, but also in those of the Asian wild pig (Kurosawa *et al.*, 1992). This suggests that there is a close morphological connection between the Short-eared pig and the wild pig with regards to the nipple pattern, and that the degree of pig domestication is low in comparison with Chinese pigs and Western breeds.

Genetic continuity between domesticated and wild pigs

In many areas, wild pigs, particularly feral pigs, interbreed regularly with domestic pigs. Indeed, it is known that there is a case of this in New Guinea (Oliver *et al.*, 1993). Naturally, the pigs in these areas are the typical Short-eared type, and their external characteristics are similar to that of the wild pig. It is thus conceivable that a gene flow from wild pigs is occurring into the domesticated pig population. In addition, hybridization of the domesticated pig and wild species other than the Wild pig (*Sus scrofa*), such as the Warty pig (*Sus verrucosus*) or the Bearded pig (*Sus barbatus*), occurs in the islands of Southeast Asia (Kurosawa *et al.*, 1989, Oliver *et al.*, 1998). We carried out genetic research on a pig population that had interbred with the Philippine Warty pig (*Sus verrucosus philippensis*) kept by the Mangyans in the hills of Mindoro island (Fig. 2).

The emergence of the Short-eared pig in Southeast Asia may well be a result of such cross breeding between *Sus scrofa* and other wild species like those mentioned above.

1) Nomadic pigs in Bangladesh

2) Nepalese native pigs

3) Lao native pig

4) Small-Thai native pig

5) Karo native pig, Sumatra island, Indonesia

6) Toraja native pig, Sulawesi island, Indonesia

7) Ankang pig, China

8) Bamei pig, China

Fig. 1. Photos showing comparison of various types of a female Short-eared pig and two types of a female Chinese pig

Fig. 2. A domestic native sow crossed with the Warty boar (*Sus verrucosus philippensis*) and their hybrid piglets in Mangyan, Mindoro island, the Philippines. The sow shows the black coat color, and the piglets show the dark brown color with longitudinal yellowish stripes which is the typical coat color of the young wild pig (Kurosawa *et al.*, 1989).

Genetic Diversity

Blood type and protein polymorphism research has shown that the gene frequencies of studied genetic loci differed between Asian native pigs and Western breeds (Tanaka, 1990). Similar results have been reported on several subspecies of *Sus scrofa*, including Asian and European wild pigs on the Eurasian continent and adjacent islands (Kurosawa, 1995). In recent years, detailed molecular genetics studies have confirmed that several wild pigs from Asia are genetically similar to the domesticated pigs from that area, whereas the typical wild species of Europe are close to the Western breeds (Okumura *et al.*, 2001; Ozawa *et al.*, 2000).

Asian native pigs show remarkable biochemical polymorphism in comparison to Western breeds. This is evidenced particularly by electrophoretically analyzed differences in gene frequencies at each locus for serum transferrin (*Tf*) and amylase (*Am-1*). There are likewise significant differences between the populations of Short-eared pigs in South and Southeast Asia in the gene frequencies of both these loci. For example, comparisons of the gene frequencies of South Asian and Southeast Asian island pig populations show that Tf^{B} and $Am\text{-}1^{C}$ tend to be more common in the former, while the genes Tf^{C} and $Am\text{-}1^{A}$ show greater frequency in the latter. Furthermore, Southeast Asian island Short-eared pigs differed from northern Chinese native pigs.

These results support the hypothesis that Asian native pigs were independently domesticated in various locations, and that they are polyphyletically derived from several subspecies of Wild pig or other wild species.

In the process of domestication, Asian native pigs, which have geographically diverse origins and continued genetic connection with several species of wild ancestor, should be considered to possess broad genetic diversity. However, the number of purebred Short-eared pigs traditionally kept mainly by minority ethnic groups in remote mountainous or insular regions is drastically decreasing as modernization leads to crossbreeding with Chinese and Western pigs. In the future, Short-eared pig preservation will need to focus not simply on genetic resources, but also on taking into account the traditional culture and social structures of the ethnic groups that are keeping these pigs.

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Nozawa: Compared to other livestock species, the pig is a typical species that is considered to be a polyphiletic domestic animal. We need to be cautious, especially in the case of the pig. The pig is monophiletic at the species level. However, at the breed or subspecies level, the pig is polyphiletic. How many clusters do you think are polyphyletic throughout the world as deduced from your dendrogram? We should assume that a few clusters or more than hundreds of clusters are polyphiletic.

Kurosawa: There are two major classes, the Western type and the Asian type. In Asia, however, we have two different types, those from the islands of South East Asia and those from mainland Indochina, or Chinese pigs. As reported today, Chinese native pigs significantly influenced the South East Asian coastal and plain region populations. Pure small-ear type breeds are still being maintained in many countries, however, they are localized in small mountainous areas. These days it is not therefore possible to separate the Asian pigs clearly, such as into an island type or a South East Asian type. It is very important to know whether the samples or pigs were collected from pure native populations or not. Otherwise, we cannot come to a precise conclusion.

Mitochondrial DNA Diversity in Asian Goats

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Introduction

Conservation of animal genetic diversity is essential to protect our genetic resources for the future. Recently it has been found that almost 600 breeds of domestic animals are at risk of extinction and there is the possibility of further erosion of many traditional and locally adapted breeds.

The goat is probably the earliest ruminant to be domesticated (Zeuner, 1963; Mason, 1984). Evidence shows that the nomadic people of the Middle East tended goats as early as 10,000 years B.C. The goat has been very prominent in world agriculture. Goats are found throughout all regions of the world except for the arctic regions. In fact, approximately 75% of the world's populations drink goat's milk. The goat is widely used as a source of meat especially in Middle-Eastern Countries. Goat milk is also made into cheeses, butter and yogurt. Goats can provide many other products such as Mohair and Cashmere, which is made into cloth and carpet as well as hides for fine leather. History reveals that goats were often carried on ships as a source of fresh milk by early explorers to the New World, including Captain Cook and Christopher Columbus.

Genetic background of domestic goats

The wild goats of the world are divided into three major groups: bezoar (*Capra aegagrus*), markhor (*C. falconeri*) and ibex (*C. ibex*). These are closely related to the modern domestic goat (*C. hircus*). Harris (1961) and Zeuner (1963) have proposed that bezoar is the most likely ancestor of domestic goats. In addition, Harris (1962) has suggested that markhor and ibex might have genetically affected the domestic goats domesticated in Western and Eastern Asia, respectively. However, the hypotheses have not been proven until now.

Analyses of mitochondrial DNA in goats

Characteristics of mitochondrial DNA (mtDNA) studies in livestock species provide valuable information about genetic diversity, phylogenetic relationships and the process of domestication (Loftus *et al.*, 1994; Mannen *et al.*, 1998). Analyses of mtDNA have the advantages that are the clonal transmission, geographic temporal inertia of a particular mt-lineage, the pre- and post-domestication patterns from the rates of substitution accumulation, concluding that domestic mt-lineage is the result of physical capture of a wild female animal (MacHugh & Bradley, 2001).

Recently, we described two ancestral mtDNA haplotypes (*mt-lineage A* and *B*) in Laotian goat, suggesting it is unlikely that single local domestication could explain (Mannen *et al.*, 2001). In same year, Luikart *et al.* (2001) presented more comprehensive data set with more than 400 samples throughout the world by mtDNA analyses. This result also reveals the multiple maternal origins and weak phylogeographic structure in domestic goats. They found three highly divergent mtDNA lineages (*mt-lineage A - C*) in domestic goats. However, most of their samples were from Europe Africa and Middle East, but less from Eastern Asia.

Therefore, in order to understand the genetic diversity of domestic goats in Asia, we have investigated mtDNA diversity in Asian goats samples. In this workshop, I would like to show our recent results of mtDNA diversity in Asian domestic goats. Until now, we analyzed goat mtDNA of Southeastern Asia (Laos, Myanmar, Vietnam), Eastern Asia (Mongol, China), and Southern Asia (Pakistan) (Sultana *et al.*, submitted). We sequenced the hypervariable I region (HVI) of mitochondrial displacement loop (D-loop). The nucleotide length is 579-bp. Using the sequence data set, we constructed phylogenetic trees, analyzed sequence diversity, and estimated genetic frequencies in each country.

Mitochondrial lineages in domestic goats

Figure 1 shows the mitochondrial phylogenetic tree of Asian domestic goats. The mtDNA of Asian domestic goats were classified into four distinct *mt-lineages A, B, C* and *D. Mt-lineage D* has not been detected before our study. *Mt-lineage C* and *D* and was observed in Pakistan, Mongol and China, but in Southeastern countries. *Mt-lineage A* is major mitochondrial lineage and next is *mt-lineage B*.

This phylogenetic topology was further supported by analysis of cytochrome *b* gene sequences.

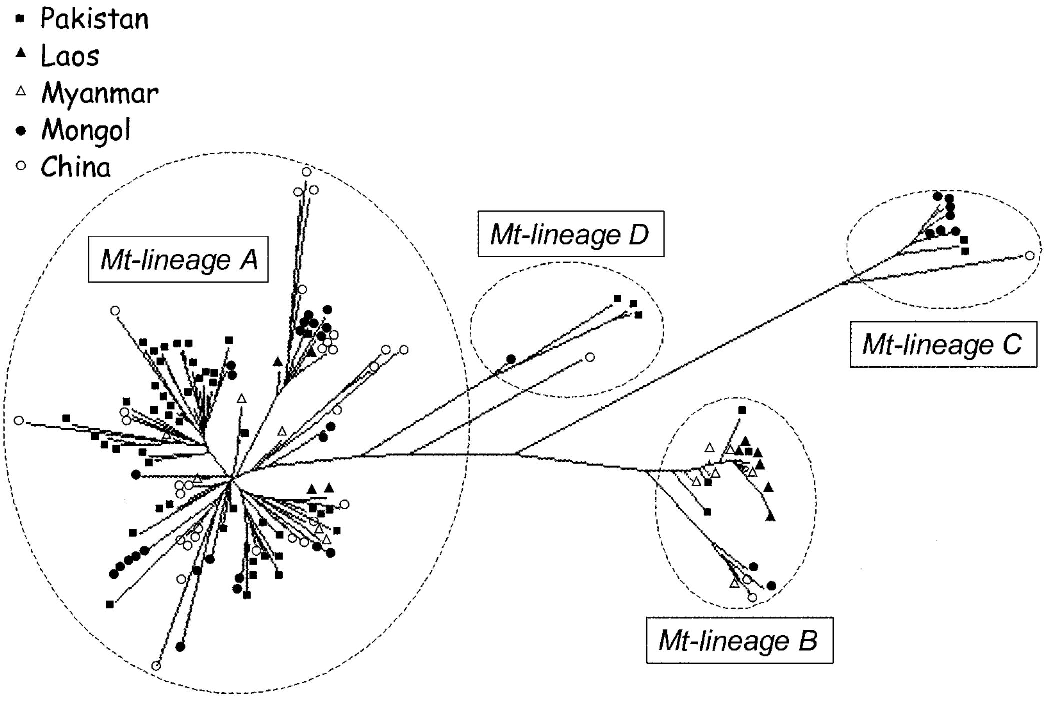

Figure 1 A neighbor-joining tree for D-loop haplotypes of the Asian domestic goat breeds.

Divergence times of goat mitochondrial lineages

Subsequently, Cytochrome *b* gene sequences of the four domestic goat and wild goat mt-lineages were used to estimate the divergence time using divergence time between sheep and goat of about 5 million years ago from the fossil record (Carroll, 1988). The estimated the approximate time to the most common recent ancestor (TMCRA) of the domestic goat lineages was 427,007 YA. Calibrated divergence time between *mt-lineages A* and *D* was 265,040 YA (Table 1).

Thus, estimates from the cytochrome *b* data were significantly different from the domestication time of 10,000 years ago. These results suggest pre-domestic maternal origins of four distinct ancestral mitochondrial lineages.

Table 1 Estimated divergence times among mtDNA lineages (years)

	Lineage B	Lineage C	Lineage D	Wild goat
Lineage A	242,950	375,470	265,040	1,634,400
Lineage B		397,560	375,470	1,744,830
Lineage C			507,990	1,700,660
Lineage D				1,855,270

Genetic frequencies of mitochondrial lineages in Asia and the domestication center of goat

Figure 2 shows genetic frequencies of the four mt-lineages in six countries. In Eastern Asia (Mongol, China) and Southern Asia (Pakistan), *Mt-lineage A* is predominant and the other lineages reveal low frequencies. In contrast, genetic frequencies of *mt-lineage B* are quite high in Southeast Asia (Laos, Myanmar, Vietnam) and *mt-lineage C* and *D* are not observed. This result suggests the hypothesis of multiple maternal origins and multiple domestication centers. One plausible domestication center has been described in Middle East (Taurus, Southeastern Turkey and West Zagros, Iran). However, the domestication center of *mt-lineage B* is unlikely in these areas because the *mt-lineage B* was not observed in Europe, Africa and Middle East and was major in Southeast countries. The domestication center of *mt-lineage B* might be Balukistan in Pakistan or much further eastern area.

Analyses of mitochondrial DNA provide understanding of the diversity or ancestral origin(s) of domestic goat. However, additional molecular studies will lead us to know the origin(s) of domestic goats. Especially, analyses using Y chromosome and autosomal genetic markers (probably microsatellite markers) are required to understand the genetic diversity in domestic goats.

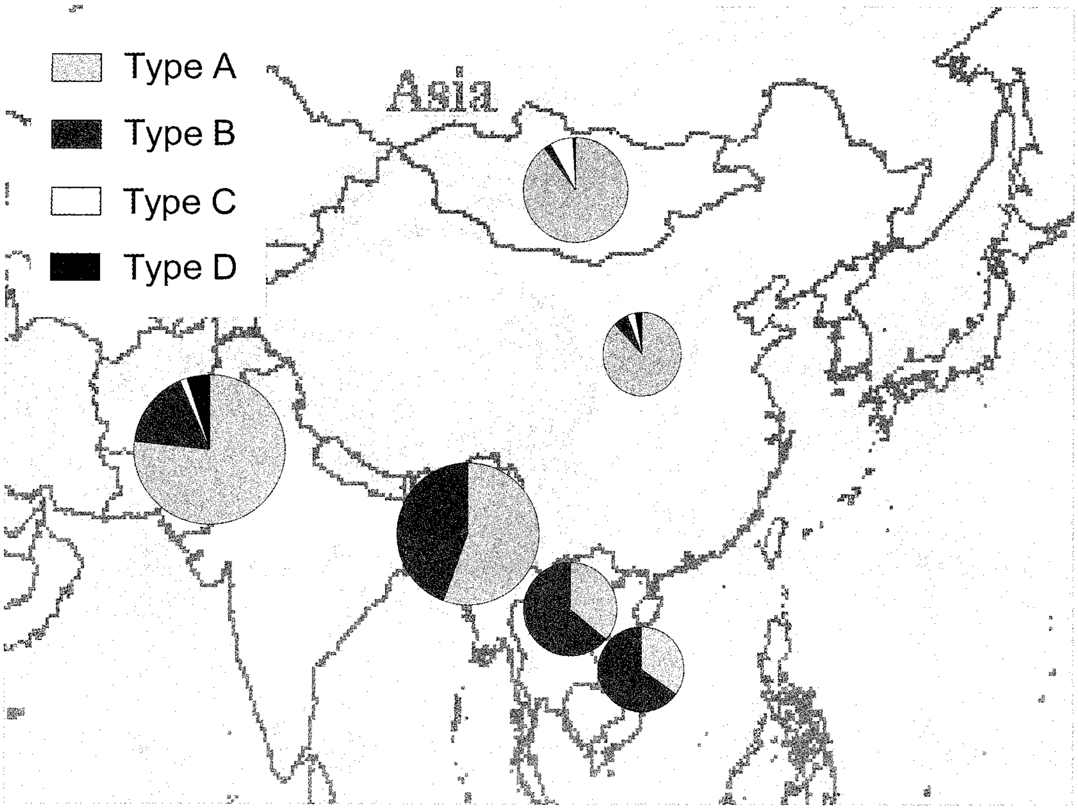

Figure 2 Geographic distribution of the four mtDNA lineages in. The area of the circle is proportional to the total number of samples (n) in each country; Mongol (n=98), China (n=33), Myanmar (n=180), Laos (n=75), Vietnam (n=60), and Pakistan (n=202).

Acknowledgement

This experimental work was done by my students in Kobe University; Y. Nagata, S. Sultana and M. Misako. I thank to Dr. S. Tsuji (Kobe University), Dr. K. Nozawa (Kyoto University) and Dr. D.G. Bradley (Trinity College) for helpful suggestions, Dr. T. Namikawa (Nagoya University), Y. Maeda (Kagoshima University) and many colleagues for sampling trip in Laos and Myanmar. I also thank the Society for Researches on Native Livestock.

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Sasaki: Bezoar found in the Middle and Near East are thought to have been domesticated there first and then to have moved to the west and east. Did Marchor influence the Besoar? In the case of migration, usually it is the males that migrate to another region. Could you deduce this influence from the results of the mitochondrial DNA data set.

Mannen: The French group reported that domesticated goats and three wild goat species had been allocated to completely different groups. If Marchor had influenced the domesticated goat population, it was likely through male wild goats being crossed with a small proportion of domesticated females. We may have to study the Y-chromosome not the mitochondria. From the phylogenic tree, its topology indicates that Besoar is the mainstream. From the findings of mitochondrial studies, it is difficult to trace back any influence from the Marchor or that from Ibex.

The Genetic Diversity of Chicken

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The chicken is an animal with many varieties, next of the dog. About more than 200 varieties of chicken are being raised in the world. We have been interested in the origin of domestic fowls.

In the genus *Gallus*, there are four species of jungle fowls. These are the Red jungle fowl (*Gallus gallus*), the Grey jungle fowl (*Gallus sonneratii*), the Ceylon jungle fowl (*Gallus lafayettii*) and the Green jungle fowl (*Gallus varius*). Concerning what species of the jungle fowl is the ancestor of the domestic fowl, there are two kinds of theories suggested. The one is the monophyletic origin that the Red jungle fowl is the sole ancestor of domestic fowl, and the other is the polyphyletic origin that more than one species of jungle fowl contribute to the formation of domestic fowl.

The studies on the relationship between the jungle and the domestic fowl have been done from ecological, morphological, biochemical and chromosomal viewpoints. Since 1971, a Japanese research group has been doing research activities in Southeast Asia with interest in the evolution and domestication of jungle fowls. Two species, the Red and the Green jungle fowls, still inhabit in the Java and the Bali Islands. From hearing survey, the habitat of the Red jungle fowl was limited to the deep forest, while the Green jungle fowl lived even in a small bush near the cultivated field besides in the forest (Nishida *et al.*, 1980). Nishida *et al.* (1992) made a map of distribution of 5 subspecies of the Red jungle fowl based on the results of their field investigation and on other publications. By examining gene frequencies at four blood group and seven electrophoretic loci, Okada *et al.* suggested that the average genetic distances between the domestic fowl and jungle fowl were small for the Red jungle fowl, intermediate for the Grey jungle fowl, and very large for the Ceylonese and the Green jungle fowls. Hashiguchi *et al.* (1993) suggested that from the results of analyzing of blood protein polymorphisms the Grey jungle fowl was genetically similar to the Ceylonese jungle fowl, and the Green jungle fowl was genetically remote from the other jungle fowls and the native fowl. The diploid chromosome number of the jungle and the domestic fowl is 78, but in their karyotypes No.3 chromosomes showed a morphological difference (Okamoto *et al.*, 1988).

Recently, Akishinonomiya *et al.* (1996) suggested that a continental population of *Gallus gallus gallus* sufficed as the monophyletic ancestor of all domestic breeds, by determining mtDNA sequences of the D-loop regions.

Like the above, various information is being accumulated on the domestication of the chicken at present. The ideas of researchers not always agree, but their results all showed that the Red jungle fowl has the most genetically near relation to the domestic fowl. In addition, it is considered that the Red jungle fowl has the widest habitat in the jungle fowls. From these facts, it is suggested that the Red jungle fowl might do the considerable contribution in the evolutional process in formation of the chicken. But, on the relation with other 3 kinds of jungle fowls, it is supposed that their information is yet insufficient.

This study introduces some works of the genetic analysis in the chicken done mainly in my laboratory, in order to clarify the genetic relationship between the jungle fowls and domestic fowl.

1. Blood Protein Polymorphisms

Blood samples collected in Southeast Asia and Japan were separated into plasma and erythrocyte and stored separately in a freezer (−40℃). Seventeen loci controlling 14 kinds of blood protein were usually screened for genetic variation by starch gel or agar gel electrophoresis. The list of the genetic loci analyzed is given in table 1. The genetic variability within population was quantified by measuring the proportion of polymorphic loci, P_{poly}, and average heterozygosity. The genetic distances were calculated by Nei's formula (Nei, 1972). From the matrix of the genetic distance values, the dendrograms was drawn by the unweighted pair-group method of clustering in numerical taxonomy (Sokal and Sneath, 1963).

Table 2 shows the gene frequencies of polymorphic loci of native fowl in Laos. The three surveyed areas, Viangchan, Louangphrabang and Pakxe, showed almost the same gene frequencies in all loci. Of the 17 loci analyzed by electrophoresis, polymorphisms were detected at 7 loci. The remaining 10 loci, *Amy-3, LDH, PGM, PHI, To, MDH, Es-D, Hb-1* and *Hb-2,* were monomorphic. Maeda *et al.* (1992) indicated that the gene frequency of Amy-1A is gradually decreasing from

Table 1. List of blood proteins examined.

Symbol of locus	Name of blood protein	Cited from
Es-1	Plasma esterase	Okada *et al.* (1980)
Amy-1	Plasma amylase	Hashiguchi *et al.* (1970)
Amy-3	Plasma amylase	Hashiguchi *et al.* (1970)
Akp-akp	Plasma alkaline phosphatase	Okada *et al.* (19810)
Akp-2	Plasma alkaline phosphatase	Okada *et al.* (1980)
Alb	Plasma albumin	Mclndoe (1962)
Tf	Plasma transferin	Stratil (1968)
Pas	Plasma post albumin	Kuryl and Gasparska (1976)
LD	Erythrocyte lactate dehydrogenase	Manwell and Baker (1969)
6-PGD	Erythrocyte 6-phosphogluconate dehydrogenase	Bengtsson and Sandberg (1973)
PGM	Erythrocyte phosphoglucomutase	Bengtsson and Sandberg (1973)
PHI	Erythrocyte phosphoheose isomerase	Bengtsson and Sandberg (1973)
To	Erythrocyte tetrazolium oxidase	Baur and Schorr (1969)
MDH	Erythrocyte malate dehydrogenase	Davidson and Cortner (1967)
Es-D	Erythrocyte esterase	Watanabe *et al.* (1977)
Hb-1	Hemoglobin	Washburn (1968)
Hb-2	Hemoglobin	Washburn (1968)

Table 2. Gene frequencies of polymorphic loci of native fowl in Laos.

Locus	Area Viangchan (57)	 Louangphrabang (44)	 Pakxe (35)	Total (136)
Es-1^{A}	0.254	0.205	0.257	0.239
Es-1^{B}	0.746	0.795	0.743	0.761
Es-1^{C}	0.000	0.000	0.000	0.000
Es-1^{D}	0.000	0.000	0.000	0.000
Amy-1^{A}	0.228	0.261	0.171	0.224
Amy-1^{B}	0.772	0.739	0.829	0.776
Amy-1^{C}	0.000	0.000	0.000	0.000
Amy-1^{D}	0.000	0.000	0.000	0.000
Akp	0.054	0.108	0.044	0.069
akp	0.946	0.892	0.956	0.931
Akp-2^{a}	0.516	0.542	0.455	0.509
Akp-2^{0}	0.484	0.458	0.545	0.491
Alb^{A}	0.000	0.000	0.000	0.000
Alb^{B}	0.851	0.852	0.914	0.868
Alb^{C}	0.149	0.148	0.086	0.132
Alb^{D}	0.000	0.000	0.000	0.000
Tf^{A}	0.000	0.000	0.000	0.000
Tf^{B}	0.939	0.977	0.986	0.963
Tf^{C}	0.061	0.023	0.014	0.037
Pas^{A}	0.121	0.121	0.014	0.093
Pas^{a}	0.879	0.879	0.986	0.907

( ): Number of bird.

south to north. In this study, it is also recognized that Amy-1A gene is decreased in order of Indonesia (0.816), Laos (0.224) and Nepal (0.184). By including this data and the previous data of protein polymorphisms in Bangladesh (Okada *et al.*, 1988), Nepal (Maeda *et al.*, 1992) and Indonesia (Hashiguchi, *et al.*, 1993), the dendrogram among native fowls and jungle fowls was illustrated in figure 1. Laos native fowl was genetically close to Bangladesh native fowl, and the genetic distance between them was estimated as 0.01. And, these populations and Nepal native fowl were clustered in one group.

2. Karyotype

Blood was drawn from the cutaneous vein of the elbow with a heparin-wetted syringe, and centrifuged at 400 r.p.m. for 5 minutes. Lymphocyte rich supernatant fluid was used as a sample. The culture medium was composed of 4.0 ml of RPMI-1640, 0.1 ml of antibiotic solution (penicillin & streptomycin), 0.1 ml of phytohemagglutinin (PHA; Wellcome) and 0.2-0.5 ml of sample. Incubation was over, the cell was treated with hypotonic solution (0.075 M KCl) for 10 minutes. As

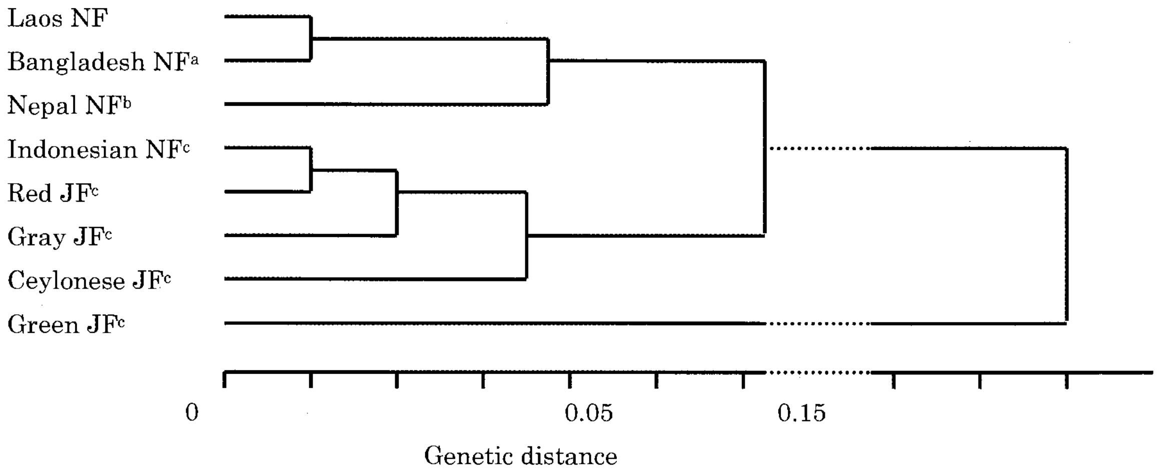

Figure 1. Dendrogram showing genetic similarities among native fowls and jungle Fowls.
NF: native fowl, JF: jungle fowl
a: Okada *et al.* (1988), b: Maeda *et al.* (1992), c: Hashiguchi *et al.* (1993)

repeating the fixation more than three times, three drops of cell suspension were placed on the center of a slide and held momentarily over steam. Steam-dried chromosome preparations were then stained with 5% Giemsa solution.

It was observed that the metaphase cells of jungle fowls and domestic fowl lymphocytes consisted of macrochromosomes and microchromosomes. Careful counting on the metaphase plates from each fowl made it clear that the diploid chromosome number of the jungle and the native fowls is 78. Their chromosomes were arranged into 39 pairs according to decreasing size, and were divided into 10 pairs of macrochromosomes and 29 pairs of microchromosomes. The karyotypes of the four species of jungle fowls looked almost the same (table 3). Macrochromosomes were identified unequivocally according to the size and position of the centromere. Microchromosomes were too minute to distinguish each other. but they may be acrocentric. It was observed that there was no difference in ten pairs of macrochromosomes between the Red jungle fowl, the Grey jungle fowl, the Ceylonese jungle fowl and the domestic fowl. On the other hand, No.3 chromosomes of the Green jungle fowl showed subtelocentric that was a different type from the other jungle fowls and the domestic fowl.

Table 3. Analysis of the karyotype of jungle fowls and F_1.

Chromosome No.	R, G, C, c	Gr	F_1
1, 2,	Submetacentric	Submetacentric	Submetacentric
3	Acrocentric	Subtelocentric	Acrocentric and Subtelocentric
4	Subtelocentric	Subtelocentric	Subtelocentric
5, 6, 7, 9	Acrocentric	Acrocentric	Acrocentric
8, Z, W	Metacentric	Metacentric	Metacentric
10 ~ 38	Acrocentric	Acrocentric	Acrocentric

R: Red jungle fowl; G: Grey jungle fowl; C: Ceylonese jungle fowl; c: domestic fowl;
Gr: Green jungle fowl; F_1: Green jungle fowl-Gifu native fowl hybrid.

3. Mitochondrial DNA Polymorphisms

We sequenced mitochondrial DNA (mtDNA) to assay genetic variation. Initially we compare cytochrome b sequences (cyt b) among four Red jungle fowl subspecies and four Asian native fowl populations (table 4). DNA from blood was extracted by means of a standard phenol/chloroform protocol (Sambrook *et al.* 1989). 1143bp of cyt b region were amplified from whole DNA via the polymerase chain reaction (PCR). We estimated the number of haplotypes and segregating sites, and the gene diversity from the aligned sequences. Distances were calculated by the Kimura's two-parameter model (Kimura, 1980) and the neighbor-joining option (Saitou and Nei 1987) in the PHYLIP 3.5c package (Felsenstein 1993) was used for distance analyses. Nucleotide diversity and its standard error were estimated using the program Arlequin package (Schneider *et al.* 2000). Population structure was also analyzed by performing analysis of molecular variance (AMOVA) by Arlequin. For the AMOVA, we make assumptions that samples from each country represent populations.

Table 5 shows a summary of genetic structure including nucleotide diversities (π) and mean

Table 4. List of samples examined in this study.

Population			Number of Individuals
	G.g.gallus	Thailand	6
		Vietnam	5
Red Jungle Fowl	*G.g.spadiceus*	Vietnam	10
	G.g.jabouillei	Vietnam	7
	G.g.bankiva	Indonesia	2
Green Jungle Fowl	*G.varius*	Indonesia	7
		Indonesia	10
Native Fowl	*G.domesticus*	Sri Lanka	11
		Thailand	11
		Vietnam	10
Total			79

Table 5. Genetic Variability of the study populations.

	n	No.of haplotypes	Total sites	Polymorphic sites	No.of Subustitutions	No.of transitions	No.of transversions	Mean no.of pairwise difference	Nucreotide diversity
Red jungle fowl	30	15	1143	40	41	35	6	5.871264	0.005137
G.g.gallus	11	5	1143	4	4	1	3	0.982816	0.000860
G.g.spadiceus	10	3	1143	5	5	3	2	2.005780	0.001755
G.g.abouilleij	7	7	1143	10	10	8	2	3.012159	0.002731
G.g.bankiva	2	2	1143	1	1	1	1	1.000879	0.000876
Native Fowl	42	14	1143	29	29	19	10	2.854908	0.002498
Indonesia	10	6	1143	11	11	3	8	3.725173	0.003259
Sri Lanka	11	8	1143	8	8	7	1	3.401186	0.002976
Thai Land	11	6	1143	11	11	11	0	2.584830	0.002261
Vietnam	10	4	1143	3	3	2	1	0.600555	0.000525
G.varius	7	5	1143	4	4	2	2	1.619048	0.001416
Total	79	34	1143	103	107	81	26	12.877838	0.011267

number of nucleotide differences. Analysis of sequences showed 107 polymorphic positions, representing 9% of the total sequence obtained. 75.7% of mutations detected corresponded to transitions. In the red jungle fowl populations, the average nucleotide diversity of *G.g.gallus* was lower than the other two subspecies. The Vietnam native fowl in the study population have also low nucleotide diversity than the other populations.

The haplotypic neighbor-joining tree is shown in figure 2. Two main clusters of haplotypes can be recognized. *G.g.bankiva* was classified into the cluster separated from others. However, neighbor-joining analysis showed no clear relationship among the three red jungle fowl subspecies (*G.g.gallus, G.g.spadiceus and G.g.jabouillei*) and the four native fowl populations.

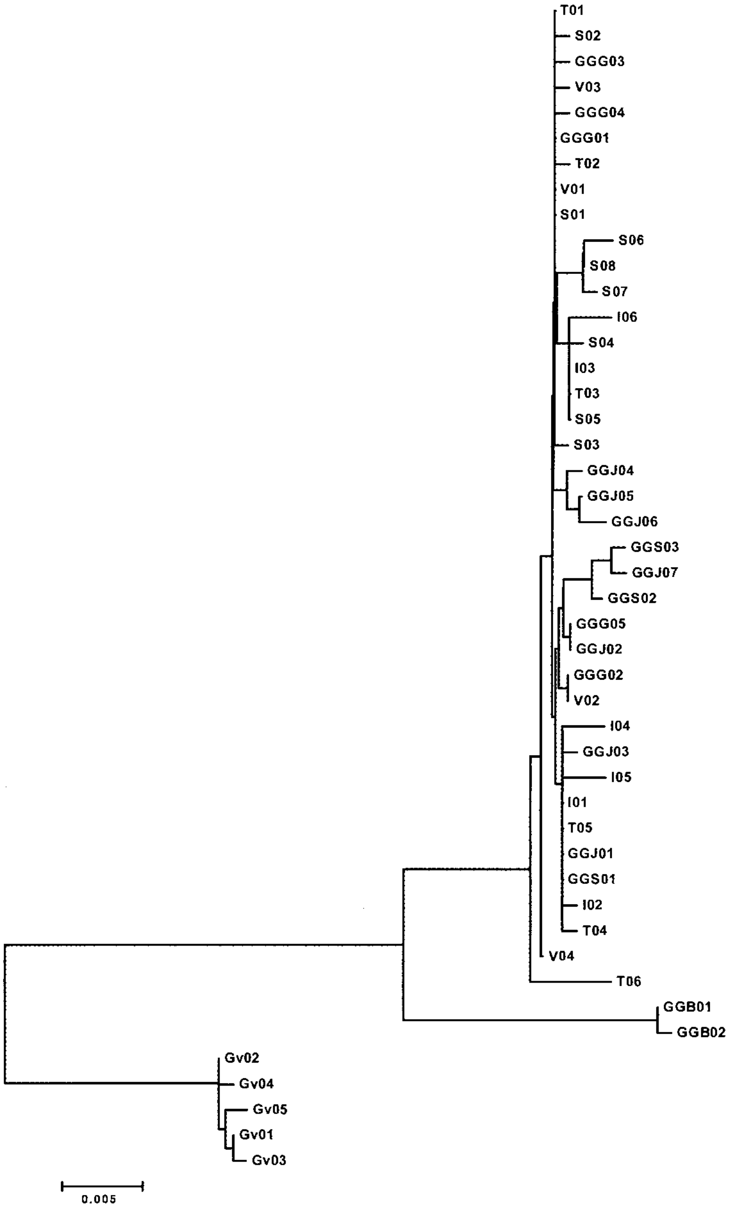

Figure 2. Haplotypic neighbor-joining tree of cyt b sequences. Haplotype names are as follows: G.g.gallus, GGG01-05; G.g.spadiceus, GGS01-03; G.g.jabouillei, GGJ01-07; G.g.bankiva, GGB01-02; G.varius, GV01-05; Indonesian native fowl, I01-06; Sri Lanka native fowl, S01-08; Thailand native fowl, T01-06; Vietnam native fowl, V01-04.

Table 6 shows a summary of matrix of Slatkin linearized FSTs and exact test of sample differentiation based on haplotype frequencies. Some indication of clustering of variation was detected from pairwise FST genetic distances between populations.

Table 6. Population pairwise Fst genetic distances among populations.

	G.g.g	*G.g.s*	*G.g.j*	Thailand	Vietnam	Sri Lanka	Indonesia
G.g.gallus		0.00055	0.00000	0.05545	1.00000	0.05470	0.05470
G.g.spadiceus	0.59167		1.00000	0.14975	0.00040	0.00615	0.30675
G.g.jabouillei	0.26002	0.01537		0.13775	0.00040	0.02280	0.63465
Thailand	0.07628	0.13115	0.02435		0.03880	0.18240	0.27585
Vietnam	0.00000	0.88988	0.42857	0.14669		0.04120	0.00300
Sri Lanka	0.07237	0.31992	0.09756	0.02480	0.15522		0.30505
Indonesia	0.21988	0.07834	0.00000	0.00000	0.38051	0.03319	

Above diagonal: Non-differentiation exact P values; below diagonal: Slatkin linearized FSTs.

In order to focus on the relationship among three red jungle fowl subspecies (G.g.gallus, *G.g.spadiceus*, and *G.g.jabouillei*), a minimum spanning tree was constructed from two components (figure 3). The first one includes haplotypes from *G.g.gallus*. The second group contains the other two subspecies. Native fowl populations were included each.

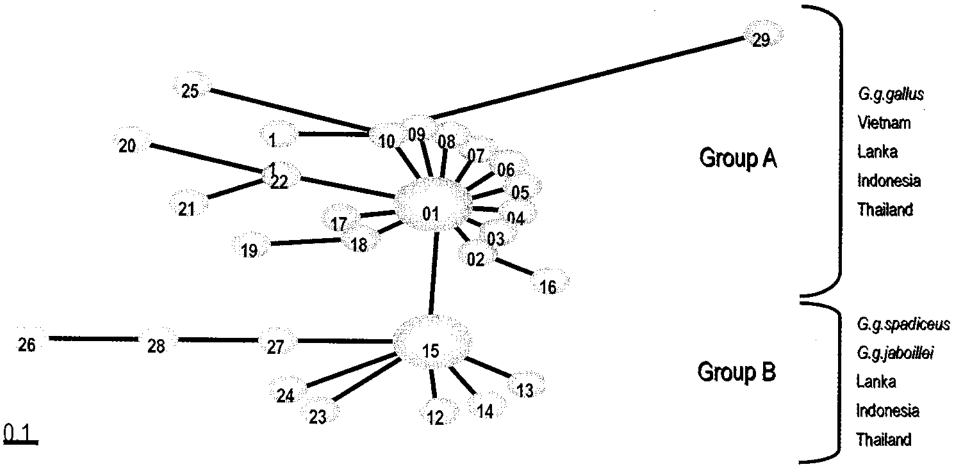

Figure 3. Minimum spanning tree constructed from fowl 1143bp cyt b sequences.

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Ito: How about the morphology of the third chromosome in phasianidae other than Gallus sp., such as pheasants and quails?

Okamoto: The third chromosome of the quail is acrocentric. Unfortunately, we did not study the other species of the phasianidae family.

3. General Discussion

Chairpersons NAMIKAWA, T
AMANO, T

Comments

Chinese Animal Resources

CHANG, Hong

Yangzhou University, China

Chinese native cattle have differentiated into three types: the south yellow cattle in the Yangtze River valley and to the South of it, the north pastureland yellow cattle and the central plains yellow cattle distributed in the middle and lower reaches of the Yellow River.

Chinese cattle were regarded as a mixed blood race between common cattle and the zebu. In the 1980s, Namikawa suggested that the Banteng (viz.. *Bos sondaicus*) is one of the sources of domestic cattle in Southeast Asia. This inference concurs with accounts on wild bovine in Chinese ancient books.

The Chinese south yellow cattle, especially mini-cattle in the mountain area of Hunan province and the Guangxi region are thought to be mixed blood descendants of some extinct land subspecies of Banteng. This subspecies have been widely distributed in the southern part of China.

From the point of view of use as meat, yellow cattle, in the middle and lower reaches of the Yellow River, are better than those either in the pastureland areas or in the southern areas. On the other hand, this breed is also thought to be more advantageous than modern beef breeds originating from Western Europe from the following three aspects: firstly, the muscle fiber is thin, the meat tastes good; secondly, it can be digested as a byproduct of commodity production, which reduces the raising costs; thirdly, it has adapted to tropic climates. The past bad impression as to its meat properties seems to be the result of the use of cattle that were too old for meat production. During the 1980s, the late professor Qiu Huai revealed that the meat qualities of Qinchuan cattle, such as the average daily weight increase, dressing percentage, lean meat percentage and rib eye area during the fatting period, were not inferior to those of the Shorthorn, Charolais or other beef breeds. These findings indicate that middle land yellow cattle had the potential to show good meat properties, but this conclusion was ignored.

Presently there are seven subspecies of Wild Boar in China. The origin of Chinese swine is multiplex at the subspecies level. China is a broad region with a varied range of ecosystems, socioeconomic and cultural backgrounds. Over a long period of historical development, various local swine breeds have formed. Chinese swine has many excellent properties. Besides the outstanding reproductivity of the populations in the Taihu basin, the other advantages of various local breeds are becoming increasingly recognized. North China breeds have better meat qualities, such as thin muscle fiber, high density of muscle fiber in the muscle cross section, much intermuscular fat, less connective tissue, more defined test values for muscle hydroaffinity, total pigment, tenderness and cooked meat proportion, than for European breeds. The nearly 20 years of emphasis on average daily weight gain and lean meat rate has had a great impact on the conservation of local swine breeds. For most people, however, meat from traditional breeds has a better taste. The price trend among various local breeds has been the main force influencing farmers to contend with hybridization pressure.

Chinese native sheep breeds include thin-tailed, short-fat-tailed, large-fat-tailed and fat-hipped breeds. They have the potential for various uses such as for carpet wool, lambskin, pelts and meat. Recent studies reveal that they are the paramount genetic resources for high reproductive rates, large body size, and adaptability to high elevations.

According to Nozawa's classification, Chinese goat populations belong to the Bezoar-type, Savanna-type or cross types of these. They have varied ecological characteristics and economic uses. It is evident that the high reproductivity of goats from the Huang-Huai river basin and the productivity of Cashmere goats from North China and Tibet are valuable genetic resources.

In a word, the native domestic animal breeds should be preserved, because:

1) They contain various valuable genetic resources for the further improvement of the Cashmere breeds;

2) Human beings have varying needs at different times and in different areas. Breeding practice depending on a poor gene pool will never be able to meet the long-term needs of social development;

3) Genetic resources adapted to harsh environments should be preserved to allow adaption to varied ecological conditions;

4) Some ancient local breeds such as the long-tailed chicken from Japan and Huacaya from Peruvian plateau are of vital cultural and scientific value.

Characterization and AnGR Inventory in Myanmar

U Maung Maung Nyunt

Livestock Breeding and Veterinary Department, Myanmar

Myanmar has become one of the twelve participating countries in the Regional FAO project entitled "Conservation and Use of Animal Genetic Resources in Asia and the Pacific." With the assistance of this project it has initiated some activities in breeding surveys. The first stage of the survey is to identify breeds and their estimated population structure. Identification of distinct livestock breeds in many cases is a difficult task. Judgment may vary depending on the person who prepares the inventory. In poultry, there are so many phenotypic variations that grouping them into distinct breeds is a complicated task.

In Myanmar, there are still no breeding associations or similar groups dedicated to maintaining breeds in a relatively distinct form. Factors to be considered are regional isolation, use patterns, differences in morphological and physiological characteristics, breeding patterns, historical background as to the origin of the breed, and finally, the most important factor is the degree of genetic isolation.

Myanmar has attempted a listing of livestock breeds during the project period. More thorough and comprehensive study and the detailed characterization of breeds is yet to be undertaken.

Present level of technology relevant to AnGR

In Myanmar artificial insemination technology has been established for cattle. It is used to some extent for pigs. It was also tried on buffalo, mithan and poultry. On military farms, it is used to breed mares with donkeys to produce mules. The technique has never been applied to sheep and goats. AI is extensively used in only one species, cattle AI, which was started in 1967 with fresh semen and this was replaced by frozen semen in the early eighties. The frozen semen technique has never been attempted for pigs.

Research Collaboration

Information on the genetic resources of native livestock and closely related wild animals in Myanmar has been summarized by LBVD. Due to the ongoing crossbreeding between native livestock and exotic breeds, the number of pure native livestock has been declining. In this context, studies on the genetic constitution of native livestock in Myanmar is a critical requirement. Research collaboration has been initiated between LBVD and Japanese scientists to study the genetic properties of the animal resources of native livestock in Myanmar.

Under the research collaboration program

Fourteen Professors, Assistant Professors and PhD students led by Dr. Y. Maeda visited Myanmar twice in the year 2000 and 2001. This was to evaluate the genetic properties of cattle, water buffalo, mithan, horses, sheep, goats, pigs, chickens, ducks, jungle fowl and mice by means of genetic analysis such as the study of body size, external characteristics, protein polymorphism, blood type and DNA polymorphism. The evaluation of livestock genetic resources in Myanmar by means of biochemical and molecular techniques, a workshop on electrophoresis techniques, a seminar on Genetic Studies of Native Livestock in Myanmar and Asia have been conducted. Papers on the principles of livestock breeding by Dr. Y. Maeda and papers on genetic studies on native chickens in Asia by Dr. Y. Yamamoto in the MVC annual meeting were presented.

Future requirements

At present, there are a few qualified trained personnel in genetic resources issues in Myanmar. Most of the graduates are trained in population genetics and molecular genetics is a new subject for the country. For this reason, training in these subjects should be given both locally and abroad. Higher academic courses such as at the M.Sc and Ph.D level are also required for the development of competent personnel. In addition, the dissemination of knowledge on genetics should be conducted at the level of livestock farmers to enable them to participate actively in the project. Due to this project, Myanmar has just initiated genetics activities in the country. With the cooperation of the Japanese Government, Myanmar will be able to extend its ongoing activities in the near future.

Indigenous animal breeds in Myanmar

Annex Table (A)

Sr. No	Species	Name of Species	Breed available	Agro-Eco zone	Used
1	Cattle	*Bos taurus indicus*	Pya Sein, Shwe Ni Gyi, Shan, Kyauk phu, Yanbye, Kadarta	Central Myanmar	Draught & meat
		Bibos frontalis	Mythun (Mithun)	Chin hill	Meat
2	Buffalo	*Bubalus bubalus*	Myanmar Kywe (Shuntlu Kywe)	Northem and lower Myanmar	Draught & Meat
			Shan Kywe	Shan plateau	Draught
3	Horse	*Equus caballus*	Myanmar Myin	Centfal Myanmar	Draught
			Shan Myin	Shan Plateau	Draught
4	Ass	*Equus asinus*	Myanmar Mye	Shan state	Draught
5	Pig	*Sus domesticus*	Bocake, Wet taung	Central Myanmar	Meat
			Badaung	Srtan plaieau	Meat
			Ah Kha	Northern Shan	Meat
			Chin wet	Chin Hill	Meat
6	Goat	*Capra hircus*	Nyaung Oo (Htain San, Waithali)	Central Myanmar	Meat
			Jade Ni (Seik Ni)	Central Myanmar	Meat
			Kway Seik	Rakhine	Meat
7	Sheep	*Ovis aries*	Myanmar Thoe, Kalar Thoe	Central Myanmar	Meat & carpet wool
8	Chicken	*Gallus gallus*	Taik kyet, Hinsar Kyet	Wide spread	Meat & egg
			Inbinwa Kyet	Wide spread	Meat & egg
			Tannyin Kyet, Kyet Lada	Wide spread	Meat & egg
9	Turkey	*Meleagris gallopavo*	Kyetsin	Central Myanmar	Meat
10	Duck	*Anas platyrhynchos*	Khayan	Wide spread	Egg
			Tawbe	Wide spread	Egg
	Muskovy Duck	*Cairina moschata*	Mandarllie	Wide spread	Egg
11	Goose	*Anser cygnoides*	Ngan	Wide spread	Egg
12	Quail	*Coturnix spp*	Ngown	Wide spread	Meat& egg

Survey of 12 Species of domestic animal and there are about 33 breeds of livestock in Myanmar
Population size and date pertaining to these breeds is still yet to be thoroughly surveyed

Exotic livestock. breeds available in Myanmar

Annex Tabl (B)

Sr. No	Species	Name of Species	Breed available	Used
1	Cattle	*Bos taurus*	Friesian, Jersey	Dairy. Purpose
2	Buffalo	*Bubalus bubalis*	Murrah	"
3	Sheep	*Ovis aries*	Corridale (Australia), Awassi (Middle East)	Wool & Meat, Meat
4	Pig	*Sus domesticus*	Large White, Duroc., Landrace, Berkshire	Meat
5	Chicken	*Gallus gallus*	White Cornish, Ross, Barred Rock, Rode Island Red, Hampshire, White Leghorn	Meat, Meat & Egg
6	Duck	*Anas platyrhynchos*	Cherry vally	Meat & Feather
			Khaki campbell	Egg

Animal Genetic Resources in Korea

CHO, Chang Yeon

National Livestock Research Institute, Korea

Many wall paintings excavated from graves or caves of 1,500 years ago show horses and cattle, but there are no pictures of goats.

We have native cattle, goats, horses, pigs and chickens in Korea. The situation of Korean native domestic animal breeds is similar to Japan in that they are at risk of extinction.

Most of Korean cattle are yellow, and occasionally other colors, tiger-striped or black are found. Korean cattle have been utilized from around 2,000 years ago in Korean Peninsula and are temperate and were fed on coarse feedstuff. The meat quality of the cattle is good. Korean cattle have been used in agricultural farming in general, but presently most cattle are being improved for meat production. The number of cattle increased from 400,000 in 1950 to 2.45 million in 1995. However, due to economic circumstances, the number decreased to 1.45 million by June 2002.

Records related to Korean goats have been found from 600 years ago. Most native Korean goats are black with horns and some individuals have a white muzzle. Brown goats are also occasionally found in Korea. The number of native goats in Korea was 440,000 in 2002. Four hundred Korean native goats are conserved as AnGR at the National Livestock Research Institute (NLRI).

Korean native pigs are endangered due to their small size and the native pig had practically disappeared from Korea by 1970. NLRI introduced nine native pigs, four males and five females, in 1988. The numbers had recovered to 10,000 by 1996. Seven national and local research institutions conserved 533 native pigs in 2002.

Korean native chickens became endangered in the late 1970s. NLRI introduced five native chicken lines characterized by their plumage colors of dark red, black, gray, white, and silky from the late 1970s to the early 1980s. The number of native chickens conserved in nine institutions of the national and local governments totalled 12,000. Five million native chickens are being reared by ordinary farmers.

In Cheju Island, the Cheju horse and other native horses are being conserved. The Cheju horse was designated a natural treasure. There are 31 males and 93 females being conserved in a local research institute. The distribution of 559 horses took place to 63 general farms from 1987 to 2001.

The productivity of Korean native livestock has been thought to be unfavorable for farmers, and farmers did not want to keep native livestock. The Korean government implemented legislative action for their conservation and utilization this year. These actions include stipulation of the conservation and management of AnGRs in animal production law and the designation of an implementing organization through the organization of the NCC.

Comprehensive Comment on Asian Native Domestic Animals

NOZAWA, Ken

Prof. Emeritus, Kyoto University, Japan

The most ancient type of domestic goat was indistinguishable from the wild Besoar goat. All the individuals dug up from archeological sites of the period 8000 B.C. to 7000 B.C. were of this type.

After 2000 years of the Besoar, a Savannah type with a screw-shaped horn emerged in Western Asia and spread throughout the world in accordance with the distribution of the Besoar.

Then after 2,000 years of Savannah type dispersal, the Jamnapari type with very long ears emerged in India and dispersed from India into South Asia to the South-East Asian islands. The Jamnapari type easily crossed with other types. The cashmere goat originated in Savanna type. In Northeast Asia, the Besoar and Savanna type became mixed and the extent of hybridization varied depending on the breed. In the Southern part of Asia, the Jamnapari type was mixed further as another genetic factor.

Mannen's report basically concurs with these facts, however, some results were inconsistent with Mannen's results. The inconsistency with Mannen's results might be considered to be due to the fact that his results came from mitochondrial DNA analysis, which is known to be based on maternal inheritance.

In case of the Asian native horse, the genetic factors from Southeast Asia are few and Mongolian horse factors have an overwhelming genetic influence. The genetic constitution of the Cheju horse is almost the same as that of the Mongolian horse. The Japanese horse has come from and passed through Korea to the Hokkaido in the north and to the Yonaguni and Tokara Isles to the south of Japan. Mongolia invaded Vietnam and the Vietnamese horse was also affected by the Mongolian horse. The Bengalese horse was also largely affected by the Mongolian horse and is thought to be minimally affected by the Occidental horse.

The Asian cat was analysed genetically by using morphological phenotypes. The orange color gene (O) frequency showed clinal changes, from high Asia to low Europe. In the Tabby locus, the Abyssinian (Ta) type found frequently in South Asia and the Blotched tabby (tb) type predominates in Europe. A kinky tail was frequently found in Southeast Asia and Japan and in coastal regions around the Chinese trade ports. However, few if any kinky-tailed cats are found in inland China and Europe.

As presented here, the geographical genetic trend differed according to the species. It should be considered that Southeast Asian genetic factors strongly affected the present distribution of native domestic animals in Asia.

General Discussion

Ito: How is the kinky tail of the cat genetically controlled?

Nozawa: The genes involved are not clear and are considered to be of a polygenic character. The frequency data shown was a phenotype of the tail.

Sasaki: From the global point of view, what is the extent of variation of the wild boar or how many species or subspecies of wild pig exist in the world?

Kurosawa: In the Eurasian wild boar, *Sus scrofa*, which is considered to be the ancestor of the pig has altogether 30 subspecies. They are found in Europe, China and Southeast Asia and we do not know exactly where the ancestors come from. As I indicated in the report, the other species, such as the warty pig and bearded pig can be assumed to be among the origins of the pig gene pool. The genes found in the domesticated pig population are also found in the wild pig and vice versa. I think the difference between domesticated pigs and wild pigs is not so great.

Kobayashi: I studied the genetic relationship between pigs and the Japanese wild boar of three regions; Gunma, Shimane and Miyazaki using DNA polymorphism. The wild boars of Miyazaki and Gunma possessed common alleles in one gene locus, 30-40% and less than 10%, respectively, with the domesticated pig. However, no common allele was found in Shimane. It seems the differences found between the regions comes from the difference in the habit of eating wild boar meat. In Miyazaki, eating wild boar meat is popular. In contrast, boar meat is not consumed in the other regions. Wild boar is thought as a pest animal in Shimane but is treated as a marketable product in Gunma. I presume that this result came from pigs being hybridized to increase the productivity of wild boar in the regions where wild boar meat is consumed.

Oda: When were the various morphologies of domestic pigs acquired? I think most of the variation was acquired during and after domestication.

Kurosawa: I agree with you that the variation in pigs occurred after domestication. Clay figures of long-eared pigs of the period before Christ were uncovered in China. So China has a long history of pig domestication.

Faruque: Three questions to Dr. Taneja; 1. With regard to the cattle breeds of India close to Bangladesh, I would like to know the distribution and frequency of Chittagong Red cattle in the eastern part of India; 2. The white Bengal goat is distributed widely in Bangladesh, however, the frequency of occurrence of the white goat is low. I have an interest in getting information on the distribution and frequency of the white Bengal goat in the eastern part of India; 3. Mithan, which is called gayal in Bangladesh, constitutes a small population of gayal and the peripheral population migrates between Bangladesh and India. I would like to know whether the data on mithan were taken from the mithan husbanded by farmers or from governmental institutions.

Taneja: There is a national center for mithan and the focus of the center is basically to look at the mithan population in their native environment, to look at their management system and to look at their utility. We have another institute on the yak. Extensive studies on mithan and yak, which are lesser known species, are undertaken with the focus on optimizing their utility in the regions where they are basically indigenous. There is great scope for improvement both with regards to processing activity both for meat and milk from the yak and so forth. The intention is to increase their acceptability and utility in their production environment. The frequency of the white Bengal is very low. I would like to indicate that some hill goats are small in size but the quality is high. At the moment, by increasing the size, the quality declines. The genetic characterization of these breeds is very difficult since they are in one cluster and there is not a wide variation among them. Regarding the Chittagong Red cattle, India is a large country and has a very high degree of agricultural diversity. This diversity relates to addressing the problem of their resources in their region. What we do if a project comes up on city cattle or Chittagong cattle is that we try to give the farmer the money and ask them that as far as they can they should gather basic information on this. We have already published monographs on Chittagong cattle and Black Bengal cattle.

Wagner: As a member of FAO, our main worry is hunger throughout the world. We are strongly convinced that livestock production is, for many people in the poor and rural areas, a way out of poverty. Now I would like to ask those who did all the research today, whether can we find any positive linkages of this research to improving livestock productivity or perhaps to more economic conservation efforts? That is our view; how can we improve productivity and how can we feed more people in the world. I admit the question is a little bit provocative, but my worry is that many developing countries who want also to engage in this kind of research are going to invest a lot of money in this kind of research. And the question is, would I devote sufficient resources on the other hand for research that will really improve productivity and improve livelihoods in their countries.

Taneja: Research in science should have its ultimate focus on improvement. Ensuring this ultimate focus as we said at the beginning has to be on the sustainable utilization of AnGRs. We started with physical characterization, we went on to cytogenetic characterization, biochemical polymorphism and then today we have come to the stage of using molecular markers for characterization. These polymorphisms will help us greatly as parameters that could be economically linked to improvements. However, a major difficulty arises in terms of the total resource requirement and total resources available. The extent of data and the focus of FAO with regard to the matter of the state of world's animal genetic resources is to identify those breeds that are available for use today and possibly partly due to either industrialization or innovative technologies use on at finding them to be sustainable. Should we conserve those populations, or how long should we conserve these populations and what is the total cost of all this. And I would like to make a request to all those working together in partnership. If we look at these parameters it will greatly help us in looking at the genetic strength of these populations. And after we have looked at the genetic strength in terms of either gene polymorphism or related economic parameters, these should form a significant part of the determination of such priorities. This will greatly help us to identify these populations, which would have value. Secondly, we will need capacity and capability to deal with this issue. Many of these countries may not have the capability or may not have the resources, so it is against this background that the linkages between institutions, linkages between countries will have to be developed. The last speaker indicated the Mongolian lineage with regards to horses and explained that the Jamnapari have moved from India to Asian countries, which clearly indicated the kinds of changes that have gone on. History is able to explain exactly how gene flows occurred and with that background we should try to physically look into populations and conduct analyses.

Obata: Thank you for indicating your valuable opinions and I think the value of having this kind of workshop is to get this kind of opinion. As to animal genetic resources, their importance is well accepted by everyone. As the size of the human population increases, the importance of AnGRs increases even further. I think this is the common awareness of all the participants. In Japan, we have the Society for Research on Native Livestock and we have conducted various basic studies that have been reported on today. The content of the research starts from proteins to DNA and chromosomes, so it is developing in terms of technology and in terms of areas of research. Through the accumulation of data, we can share information with regard to the AnGRs and by accumulating the data, it is possible to have a deeper understanding of the present situation and the challenges ahead. We have the opportunity to prepare a country report for FAO and we have had valuable presentations and exchanges of opinion in the workshop today and yesterday. We will summarize and publish the proceedings of this workshop as reference material that can be distributed to the stakeholders. It can be utilized in many ways as a data source. I think this is one way of contributing to the improvement of the food situation throughout the world.

Closing Remarks

KURISAKI, Junichi

Director of Genetic Diversity Department,
National Institute of Agrobiological Sciences

It is my great pleasure to make these remarks at the end of workshop on behalf of the organizing committee. In the past 5 years, 35% of the mammalian and 63% of avian breeds have been reported to be endangered in terms of agricultural animal genetic resources. Such a critical situation in terms of animal genetic resources is not exceptional for countries in the Asian region. Since the Convention on Biological Diversity came into force in 1993, the importance of the utilization and conservation of animal genetic resources has been much better recognized world wide. In 1999, FAO started developing a global strategy for the management of animal genetic resources. Under this global strategy, the preparation of a report on the state of the world's animal genetic resources is now in progress and nearly 140 countries are preparing country reports and in accordance with such worldwide efforts on animal genetic resources, we planned to hold this international workshop inviting guest speakers from the FAO and Asian countries, including Japan. Yesterday after the introduction by Dr. Wagner on the progress of the preparation of these reports, the present situation of animal genetic resources was comprehensively reported on by the guest speakers from the China, India, Vietnam and Japan. Today, research reviews on the genetic diversity of Asian livestock were presented by the distinguished researchers. In addition, valuable country reports on domestic animals were presented by the commentators from China, Myanmar and Korea, and in addition Dr. Nozawa provided additional information. During this workshop, the importance of international regional cooperation was suggested for survey research on animal genetic resources and also for the achievement of the sustainable use and conservation of AnGRs. All these efforts made this workshop fruitful. We sincerely hope that this workshop will be helpful and encouraging for the preparation of the report on the State of the World's Animal Genetic Resources and also stimulate international collaboration in the utilization and conservation of animal genetic resources as well as in research on the genetic diversity of livestock. Finally, we greatly appreciate all the honorable guests, chairpersons and participants from abroad and Japan for the valuable information, discussions and cooperation they have contributed. Thank you very much.

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