The need for environmental/genetic impact assessments of gene flows. Possible positive and negative effects.

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Introduction

The convention on Biological Diversity (CBD) defines genetic resources as "genetic material of actual or potential value." Whereas, Genetic material is defined as "any material or plant, animals, microbial or other origin containing functional units of heredity." (CBD, 1992, Article 2, Section 10). This definition seeks to target or cove the uses of living organisms (biological materials) when they seek to capture the value of the genes in direct manner (Tvedt, 2006). Thus, genetic resources include both (micro) physical, tangible genetic material and to the genetic information and knowledge.

Animal genetic resources (AnGR) refer the genetic resources of those animal species that are used, or may be used, for the production of food and agriculture, and the populations within each of them. These populations within each species can be classified as wild and feral populations, landraces and primary populations, standardized breeds, selected lines, and any conserved genetic material (FAO, 2000).

Livestock production systems and agricultural practices have changed in ways that have a major impact on the use, exchange and conservation of farm genetic diversity. The loss of genetic diversity is closely associated with a transition of small-scale, often largely subsistence modes of agriculture to large-scale industrialized or semi-industrialized forms. The exchange of animal genetic resources has also raised questions about access to AnGR by livestock keepers and breeders, and the fair and equitable sharing of benefits arising out of the use these resources. There is a latent conflict between unconstrained access to genetic resources with, on one hand, benefit sharing and, on the other hand, the protection of investments in research (Rosendal *et al*., 2005). In this perspective, the need for environmental/genetic impact assessments of gene flows, its positive and negative effects on the livestock production system is quite pertinent.

Gene flow:

It is a complex challenge to understand how genes and environment interact to produce phonotype of the animals. Gene flow gives us a clear picture of the nature and structure of genetic diversity, and helps us to determine how best to apply this knowledge to meet our goals. Gene flow allows us to study the inheritance of a trait, explore the relationship between genetic makeup and observed phenotype, look for genetic components associated with a trait, and identify ancestors that are the likely sources of a gene or trait, and much more, all from a single platform.

Though animal migration and exchange has always taken place the beginning of 20th century development of modern breeding methods, advances in trade, transportation, communication and a trend to uniformity of breeding goals increasingly fostered the exchange of breeding animals and materials (Musavaya *et al*, 2006). Some of the primary components of the gene flow system have been summarized as below:

Pedigree module: This module uses a pedigree-based display and supports the overlay and analysis of genetic and phenotypic data within the context of known family relationship.

Genotype module: This module provides a detailed, chromosome-level view of the genetic content and organization of various individuals. This is helpful to immediate identification of pattern of inheritance and similarity and dissimilarities among the individuals.

Population module: Analysis of structured population, ranking the progeny and producing a detailed report can be effectively done from this module. It is also helpful to quickly decide which progeny to select and markers to track that makes the selection process much more efficient.

Report module: This indispensable component generates a large number of key reports and graphs. Many of the reports integrate genotype and phenotype data, shedding light on the structure of genetic diversity, and the relationship between genes and traits.

Workbench: It serves as a holding area for subsets of accessions, markers and traits, providing powerful filtering capabilities. Analysis can be run using the entire database or just a subset, allowing us to target queries and compare results between different segments of data.

Germplasm security module: This module protects the time and money invested in developing proprietary materials be detecting and displaying patterns of containment of one genotype within another.

Multiplex module: This module automates the complex and time consuming task of determining the most efficient way to multiplex a set of markers. The kits can be customized, edited and displayed graphically.

Global exchange of AnGR has been vital for breed and livestock sector development at all continents. In the 19th century, urbanization and the development of more intensive agriculture led to the stabilization of many breeds as distinct genetic entities through the establishment of breed societies that defined breed characteristics and purity. Breeds very often originated from a regional population that contained diverse genetic origins. Breeds better adapted to modern production systems became more widespread, while other breeds consequently declined and even became extinct in a considerable number of cases. In the middle of late 20th century, modern within-breed genetic improvement programs became widely established. This was coupled with specialization in the livestock sector, extensive use of cross-breeding and the rise of breeding cooperatives and companies. Quantitative data on the exchange of livestock genetic resources between the various regions of the world is still lacking. The advantages and disadvantages of gene flow for stakeholder has not yet been fully assessed, although some stakeholders complained that animal genetic resources were being used without sharing of benefits (Maier *et al.*, 2002).

Research leading to sustainable utilization of livestock germplasm is relatively expensive and requires long term investment and commitment. The cost of such research remains beyond the reach of most Southern countries and national capacities in those countries requires considerable strengthening. Reproductive technologies have revolutionized the animal breeding sector and facilitated gene flow between countries and regions of the world. Two recent studies (Valle Zerate *et al.*, 2006; Mathias and Mundy, 2005) analyzed historical and current AnGR exchange and aimed to quantify and assess trends in the transfer of AnGR. Although these studies provide interest in example of gene flow, the global flow of AnGR remains poorly understood in quantitative terms.

The current gene flow can be characterized using a rather single distinction between North (industrialized countries with predominantly intensive production systems) and South (developing countries with a wide diversity of production systems). It is understood that there are pockets of intensive production in most developing countries. It should also be noted that developed countries in tropical environment such as Australia were grouped together with Northern countries and some countries in the Northern hemisphere such as India and China were grouped together with Southern countries. The gene flows in these countries are seen as below:

1. **North to North flow:** There have been very extensive North to North flows, driven by advances in reproductive technology, which have largely taken place in a relatively free market managed by breeding companies, cooperatives and individual breeders. Such flows have driven the rapid expansion of highly improved livestock adapted to the intensively managed systems.
2. **South to South flow:** Historically, South to South movements of livestock germplasm have been extensive and have had major positive impacts on productivity (Gibson & Pullin, 2005). One relevant example is the introduction of Indian cattle breeds (Kankrej, Gir etc.) into Latin America which were further developed there leading to a significant increase in their productivity; or the spread of the improved Awassi sheep from the Middle East (Galal *et al*., 2006).
3. **North to South flow:** There are striking examples where such movements of germplasm, supported by business, interests and development agencies, proved insufficiently adapted to local conditions. Some of these movements have been successful, especially where they were based on intensification of production systems. An example is the successful cross breeding of pigs in Vietnam. The North to South flow, particularly of cattle, pigs and poultry is mainly driven by commercial breeding companies. 'Exotics' are often promoted by intermediate organizations that aim at poverty reduction and food security.
4. **South to North flow:** Movements of livestock germplasm from South to North have been rare in the past century, and in most cases the economic benefits to both North and South have been relatively small. Return on investments in animal breeding industry to make a profit by selling improved germplasm in the South is currently limited. The potential for profit in North is higher, but there is little or no demand in the North for the traits of indigenous livestock that make them so valuable in the South due to the big differences between Northern and Southern production circumstances. The net result is generally that Northern businesses currently show little interest in Southern livestock genetic resources. An example of a South to North exchange is the Tuli, a Sanga cattle breed in Southern Africa, which was introduced to and commercialized in Australia and the USA.

Gibson & Pullin (2005) argue that movements of germplasm, cross-breeding and within-breed selection in the developing world are all likely to accelerate in the future. Although a clear picture of current and future international exchange of animal genetic material is lacking, it is expected that the flow of animal genetic resources from Northern to the Southern hemisphere and vice versa will increase in the future. Further analysis of this gene flow and the potential impact of access and benefit sharing arrangements are recommended (Lansbergen and Hiemstra, 2003).

The need for impact assessment of gene flow:

Livestock keepers and breeders in all regions of the world utilize genetic resources that originated elsewhere. It reveals little about current patterns of genetic transfer or about the quantity or value of the material involved. Quantitative assessments of international exchange of AnGR are constraints by number of factors as below (Hiemstra *et al*., 2006):

1. Data on international movements of live animals often do not distinguish between breeding animals and those used for production,
2. Transnational breeding companies do not provide data on within-company exchange,
3. Import/export data frequently do not indicate the source or distinction of the material involved, and
4. Unrecorded movements (e.g., transhumant livestock systems that extend across national borders) that take place in some parts of the world.

Study over the patter of gene flow revealed that North to South and North to North flows are substantial over the South to North or South to South flows. More specifically, the exports of genetic materials are dominated by North America and Europe. Gollin *et al.*, 2008 reported that North-North trade was still dominated over all, but its share had declined since the 1990's largely reflecting the collapse of cross-border trade in live animals in North America. Hiemstra *et al.*, 2006 concluded that "movements of livestock germplasm from South to North have been rare in the past century, and in most cases the economic benefits to both North and South have been relatively small."

The need for impact assessment of the gene flow seems pertinent because of the fact that the imported breeds might prove to be unsuited to the conditions in the receiving production systems or they might prove to have characteristics that provide unforeseen economic benefits to the recipient (the former eventually seems to be more common). To these considerations, general pattern of global gene flow can add the possibility of negative impacts on public goods (e.g., loss of biodiversity), and possibility of differences in market power and knowledge between providers and the recipients. However, the global livestock sector is expressing an unpredicted rate of change. It cannot be taken for granted that the current patterns of change will necessarily continue far into the future. Four scenarios are identified that may affect the future management of AnGR:

1. **Globalization**: Livestock production is shifting from being a multipurpose activity with mostly non-tradable outputs, to one focused on food production in the context of globally integrated markets. Retailers and supermarkets are the leading actors in the globalization process. Major increase in the share of total livestock production and consumption in developing countries is leading because of the so called livestock revolution (Delgado *et al*., 1999).
2. **Biotechnology**: Continued and rapid progress in reproductive and cryoconservation technologies, quantitative genetic tools, improved efficiency and safety of transgenic and cloning technologies and prevention and control of animal diseases are expected to accelerate ongoing changes in livestock sector.
3. **Climate change**: Changes to temperature, precipitation, rising sea levels, changing incidence of extreme weather events and increasing atmospheric carbon dioxide and other greenhouse gas content are the five main climate change-related drivers that may bring change in livestock production systems. Climate change affects livestock productivity directly by influencing the balance between heat dissipation and heat production, and indirectly through its effect on the availability of feed, fodder and water, as well as via changes in disease challenge.
4. **Diseases and disasters**: Increased international trade and travel, along with the effects of climate change, are expected to promote the spread of livestock diseases into new geographical areas in the coming years. The potential contribution that the breeds with high levels of genetic resistance or tolerance can make to disease-control strategies.

Pattern of gene flow among the major livestock species:

Livestock species spread gradually from neighbor to neighbor from their centre of domestication. Colonization was an important vehicle of genetic transfer. The Romans, for example, invested in livestock breeding, and there is archeological evidence that their improved, larger-sized breeds were disseminated to the lands that they occupied. Christopher Columbus brought pigs from the Canary Islands to the Caribbean in 1493. Cattle, sheep and goats also were taken on the shores of the American continent in European ships. Australia had no domesticated livestock before the arrival of Europeans. A brief account of the flow and distribution of major livestock species has been presented below:

Cattle:

Breeds of European descent account for eight of the world's top ten most widely distributed cattle breeds. The Holstein-Friesian is reported in at least 128 countries, and in all regions. Jersey is utilized in 82 countries, the Simmental (a dual-purpose breed) is utilized in 70 countries, Brown Swiss (a dual-purpose breed) is utilized in 68 countries and Charolais (beef breed) is utilized in 64 countries. European breeds have been further developed in other regions, particularly in North America, Australia and New Zealand, where production of meat and milk often outstrips the level achieved by the breeds in their areas of origin. New breeds, e.g., Polled

Hereford, Red Aungus and Milking Devon were developed in the USA based on the European stock. The top five European breeds mentioned above are also reported in 11 or more countries in Africa, 16 or more in Latin America and the Caribbean and five or more in Asia. South Asian cattle breeds have also spread over many parts of the world. These breeds are of all *Bos indicus* types. Sahiwal- a dairy breed originating from Pakistan and India has been introduced to 12 African countries. Ongole and Gir cattle are famous in Brazil. Gir cattle, indigenous to Gujrat, India, is the best breed in Brazil now. The Times of India, September 27, 2010 states as, "The Indian 'Holy Cow, Gir' has turned out to be a great money-spinner for Brazil". African breeds account for relatively few of the breeds that have spread outside their home ranges. The N'dama, a trypanotolerant breed, developed in Guinea, is reported in 20 West and Central African countries. The Boran, developed in Ethiopia, improved in Kenya (Homann *et al.*, 2006), is reported in 11 countries (nine in East, Central and Southern Africa, plus Australia and Mexico). These are some of the examples of the patters of cattle exchanges.

Buffaloes:

Buffalo was originated in Indian sub-continent. Out of 170 millions buffalo in the world about 97% are found in Asia. Hence, buffalo is known as 'Asian Animal'. Out of two sub-species, riverine and swamp, riverine is famous for their milk production along with high fat content. Most of the buffaloes are found in India, Pakistan, China, Nepal, the Philippines, Sri Lanka, Thailand, Brazil, Italy, Bulgaria, etc. Buffaloes were brought to Italy, Brazil and Bulgari from India and Pakistan. Most of them are Murrah buffalo types. Buffaloes in Italy are famous for their milk to produce mozzarella cheese. These days, buffaloes can be found in all continents of the world.

Sheep:

The gene flows of the sheep and goat were relatively small in number. European sheep breeds are the most widespread in the world. They account for five out of the top ten most widely distributed breeds. The top three breeds are all European origin, the Suffolk (a meat/wool breed from England) is found in 40 countries, the Texel (a meat breed from the Netherland) is found in 29 countries and the Merino (a wool breed from Spain). Merino would probably rank first, if all its many derivatives were counted together. Very few breeds from Asia and near and Middle East have spread outside their home ranges-despite the fact that Asia is the home to around 36% of the world's sheep population and 25% of sheep breeds. The Awassi sheep of Israel is a good example of gene flow from South to North, North to South and South to South. Today, the majority of improved Awassi sheep are kept in European countries, north of Isreal. While the South to North movement was dominated by the Assaf breed, in the movement to the South (Australia and some developing countries) the improved Awasssi played the major role.

Goats:

Goats are major economic significance for smallholders in the South, particularly in economically marginal areas. Goat breeds are much less widely distributed than either cattle or sheep breeds. Purely European breeds are less dominant in this species, accounting only for 6 out of 25 reported trans-boundary breeds. The Sanen dairy goat is the world's most widely distributed breed, found in more than 81 countries and in all regions of the world. Angora (originated in Turkey), Anglo-Nubian (developed in the UK by crossing British, African and Indian goats), Boer (bred in South Africa from indigenous, European and Indian animals), and Criollo (developed in the Caribbean from European and African breeds) are some of the important goats found in many countries of the world. Pure African breeds with some exceptions are confined to Africa. Breeds from Asia and Near East are also largely confined to their regions of origin. The Damascus has recently been improved in Cyprus and has gained international recognition as an outstanding dairy breed for the tropical and sub-tropical regions (Alandia et al., 2006). Jamunapari, Barberi, Beetle and some local breeds are popular in India, Pakistan, Nepal, and in other Asian countries.

Pigs:

The combination of European and Asian genetic material laid foundation for the creation of modern European pig breeds. After 1945, national and commercial pig breeding programmes in Europe and North America began to develop. Pure breeds, Hampshire, Duroc and Yorkshire, from the USA were exported to Latin America and Southeast Asia; Large white and Swedish Landrace from the UK to Australia, New Zealand, South Africa, Kenya and Zimbabwe. The worldwide distribution of pigs is dominated by breeds from Europe or the USA. The most important are the Large White in 117 countries, Duroc in 93 countries, Landrace in 91 countries, Hampshire in 54 countries and Pietrain in 35 countries. Despite the huge number of pigs in Asia (more than half the world's total population), none of the world's most widespread breeds come from this region except small light-boned pigs from China and Southeast Asia that were brought to Europe and laid the foundation for the creation of modern European pig breeds.

Chicken:

Commercial strains dominate the worldwide distribution of chickens, accounting for 19 of the 67 breeds reported in five or more countries. These strains are controlled by a small number of transnational companies based in Northwestern Europe and the USA. Because the companies involved do not make their breeding information publicly available, there is limited information on the provenance of these strains. However, most appear to be derived from White leghorn, Plymouth Rock, New Hampshire and White Cornish and are thus largely of European and North American ancestry. Chickens were introduced in the USA by the Spanish and other Europeans in the sixteenth century where from Rhode Island Red, Plymouth Rock and New Hampshire are distributed all over the world. The White Leghorn from Italy to the USA and other European countries; Sussex and the Black Orpington from the UK; Brahma, Langshan and Cochin from China are the famous breeds of the chicken distributed worldwide. Several other Asian breeds, e.g., 'ornamental breeds' like Sumatra from Indonesia, Malay Game and Onagadori from Japan are also found in other parts of the world.

Possible positive and negative effects of gene flow:

Human migration, since long back, was one of the most important factors for gene flow. It led to enhanced breed diversity through domestication. Exchange of stock was an important tool in breed formation and development. Advanced mobility, reproduction biotechnology and modern breeding methods enhanced gene flow further in the 20th century. Especially in cattle, gene flow was stimulated by the development of artificial insemination and embryo transfer. The concentration on a few successful breeds in the second half of the 20th century led to their worldwide expansion, often at the expense of local breeds. Although this tend resulted in loss of biodiversity, transfer of breeds that are suitable for respective production systems benefit farmers economically (Katina et al., 2005).

It is important to note that cross-breeding may offer short term benefits, such as improved meat and milk production, but indiscriminate cross-breeding could also cause the disappearance of valuable traits developed over thousands of years of natural selection. According to the United Nations food and agriculture Organization, some 20 percent of the world's 7616 livestock breeds are now viewed as risk (Science Daily, July 21, 2010).

As a case study, we can take the example of local cattle breeds of Southern Mali. These cattle, especially N'dama, have natural resistance to trypanosomosis. Trypanosomosis kills an estimated three to seven millions cattle each year and costs farmers billions dollars each year in Africa. These breeds are being cross-bred with breeds from West Africa's Sahel zone, breeds from Europe and America. The local breeds of West and Central Africa that have evolved in those regions along with their parasites for thousands of years and therefore have evolved ways to survive many diseases, including trypanosomosis, which is spread by Tsetse flies, and also tick-borne disease. Moreover, they have the ability to withstand harsh climates. According to Abdou Fall, leader of ILRI's livestock diversity project for West Africa, the short-horn hump-less breeds native to those regions are indiscriminately crossbred and are indiscriminately slaughtered has put them on a path to extinction. He urged to preserve these breeds either on the farm or in livestock gene banks because their genetic traits could be decisive in the fight against trypanosomosis, while their hardiness could be enormously valuable to farmers trying to adapt to climate change.

Another case study could be presented from Nepal. A native cow of Far-western region of Achham district, known as nine-palm height cow (Achhami cow) which has the characteristic features to survive in a harsh environment, efficient milker, bullock good for plowing even on a steep slope terrains, resistance to disease and parasites are now in a verge of extinction. They are being cross-bred indiscriminately with other exotic breeds, e.g., Hariyana breed of India. The number of these cattle is below 1000 and hence has to give high priority to conserve/preserve them.

Conclusion:

The assessment of gene flows provides information on the nature and structure of genetic diversity that helps us to determine the knowledge to meet the goals. It helps to study the inheritance of a trait and genotypic and environmental interactions. The components of the gene flow systems can be analyzed by using different modules, e.g., pedigree, genotype, population, etc. Current pattern of gene flow is mainly from North to South and North to North. Because of the globalization, biotechnological progress, climate change, and diseases and disasters, future trend of the gene flow may not continue as before.

The need for impact assessment of the gene flow seeks to understand the adaptability of the imported genes based on the positive and/or negative effects on profitability, acceptability and sustainability. The pattern of gene flows for different species differs greatly. However, the European and North American regions dominate the genetic flows to other countries of the world. The current gene flows are useful to provide the milk and meat to the ever growing population of the world but due care has to be given on the possible negative impacts on bio-diversity, differences in market power and knowledge levels between the providers and the recipients.

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