



Globaldiv

GLOBALDIV NEWSLETTER

ISSUE N. 4 – 27TH JULY 2008

Editorial - A breed is a breed if enough people say it is

The quote in the title is not from me, although I wish it were. It is from Keith Hammond, former head of the FAO farm animal genetic diversity unit. It has appeared in various forms in other places, but I first heard it from Mr. Hammond himself. At the time I had just started my PhD work, which for the first two years was embedded in an EU Concerted Action program. Which meant that for the first half of my PhD I was graced with the guidance and supervision of no less than 13 established scientists, of which Keith Hammond was one.

Coming from an animal genetics background, I had always intuitively 'known' that a breed is identifiable as a subset of a species, the members of which are identifiable by shared phenotypic (and hence: genetically encoded) characteristics. When Keith told me what is now the title of this editorial in a discussion on the definition of a breed I was taken aback. But, still being afflicted with the arrogance of youth, I automatically assumed Keith did not know, or had unfounded reservations,

about the latest molecular and population genetics techniques and insights. Over the years, however, I have come to realize that Keith was more right than I was willing to admit at the time.

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Breed formation

The concept of breeds is a Western European invention that came to fruition with the establishment of the first herd books in the second half of the 18th century. It is noteworthy that this happened a good century before Mendel started his famous experiments that formed the basis of modern genetics. The implication is that genetic considerations in breed definition were 'tacked on' after the fact. Before, access to a herd book was granted if an individual was of the right pedigree, but the ultimate decision was based on an animal's phenotype: If it displayed all the traits that were expected of an animal from a specific breed, it was considered to be of that breed. It was only later that herd books became 'closed' so as to maintain the genetic 'purity' of a breed.

This has had the unfortunate effect that gene flow between breeds was limited to the extent of completely isolating breeds from others. Depending on severity of selection within the breed, or the effective size, and the time since isolation this has meant that the genetic variation within a breed was narrowed considerably. Dr. Cunningham, of Trinity College in Dublin, illustrated this rather graphically in British thoroughbred horses, where the contemporary population can trace its lineage back to one stud and seven mares only. The contribution of all other founder animals have vanished, become extinct.

A similar effect can be seen in a great number of European indigenous breeds. Most of these no longer play an economical role of any importance and are often delivered into the hands of a number of volunteers preserving the breed. Of necessity this greatly decreases the effective size of a population, increasing genetic drift and inbreeding. Thus an increasing number of these breeds are faced with problems of a genetic nature to such an extent that survival of the breed in the long-term becomes doubtful.

Breeds outside Europe

The concept of a breed as a subpopulation of a species with clearly defined genetic boundaries defines the thinking of many working in the field of livestock genetic diversity conservation. However, especially in developing countries practical circumstances stubbornly defy such a nice theoretical order. Local populations of a species of livestock are often named after the region where they are found and are not properly defined or managed as a breed in the European sense of the word. Neighbouring populations often experience massive mutual gene flow, creating close relations between populations. So much so, in fact, that it is often difficult, from a genetics point of view, to distinguish between breeds. See for instance Muchadeyi *et al.* (2007) for a good example of this in Zimbabwean chicken populations.

While this fact may seem to be disadvantageous to the study of livestock genetic diversity, this does have the effect that genetic diversity in these populations is high. This is true for basic diversity measures like heterozygosity and F-statistics. But it holds equally for more elaborate genetic diversity assessments like core set calculations or the Weitzman/Simianer diversity function. So what we are seeing in effect is that the absence of a



clear, stringent definition of breeds has prevented the massive loss in genetic diversity we have seen within individual European breeds.

Phenotypic differentiation equals diversity?

Hans Lenstra, genetic diversity researcher at the University of Utrecht, has done considerable work on, amongst others, genetic diversity in sheep and goat. He once shared with me the observation, that while European sheep breeds are readily distinguishable phenotypically they do not possess all that much genetic variation. On the other hand sheep breeds in the Middle East are all of the 'generic type' phenotypically and not easy to tell apart. But paradoxically, they display much more genetic variation than European breeds. If we can generalize this observation, it seems that the degree in which livestock populations are distinguishable is a reflection of their genetic distance.

Genetic distance has long been thought of as positively correlating with genetic diversity. However, this is only true for between breed variation and even then only when within breed diversity is fixed. In reality the genetic distance between populations is mainly determined by isolation of breeds and the effective population size: the smaller the effective size, the larger the distance. But also: the greater the loss in diversity within a population. Large genetic distance increases the importance of between breed variation, but this is a relative increase. It is a function of decreased within breed diversity (due to drift and limited effective size) and hence decreased total diversity.

Breed genetic diversity

Humans have this uncanny ability to make sense of their world by identifying units or entities, even where their actual existence is tenuous at best. In normal day to day conversation we talk of one forest or two flocks of sheep, where in actuality we mean a set of individuals (trees or sheep) that may be very fluid and defies rigid definition. This is also valid for the concept of breeds. We use the word in daily conversations without any problems. Problems arise only when we try to rigorously define what constitutes a breed.

In essence the term 'breed' is descriptive: referring to 'breed X' is describing a group of animals of similar genetic background showing similar phenotypes. What we must remember is that naming a group of animals a breed can not be used as a definition of membership of the group. For that the variation between members of any group of animals, apart from a group of identical clones, is just too large. There will always be animals that are considered of a specific breed, but that, on closer inspection, reveal themselves to be not quite satisfying the terms set in the breed definition. Imposing limits on whether an individual is or is not member of a breed is therefore arbitrary, even if these limits are based on genetic considerations.



Back to basics

And so we are back to dr. Keith Hammond: the bottom line is that a breed is a breed if enough people say it is. This has a number of implications for conservation genetics. Firstly, we should abandon the idea that 'breed' is a genetic concept. It is not, and in reality it never was. The way the term is used in everyday conservation is based on shared characteristics within a group of animals. This also implies that the term 'breed' should be used descriptively only: it is a convenient term to indicate a group of similar animals within a species.

Abandoning the term 'breed' as a genetic concept does not mean that studying genetic diversity within and between breeds using, for instance, molecular genetics, is invalid. Molecular tools will still be needed to characterize relations between populations and/or individuals and identify those that contribute more to genetic diversity. There will be genetic phenomena we can observe that are associated with breed formation and separation. Again: the difference is between using such descriptively or definitively. It is feasible to use molecular genetics to describe a population (which has been done successfully in numerous studies in the past). It is only when we try to use molecular genetics (or any other tool) to define a breed, that one runs into problems.

Secondly, this idea of using the term 'breed' descriptively only should be propagated more forcefully: if an animal looks like it's of a certain breed it most probably is. Breed definitions should be used descriptively, not definitively. Hence herdbooks, especially those of small breeds under threat of extinction, should be encouraged to open up their registration. This would allow some gene flow into the population, with all the benefits for the genetic make up of the population. In short: We should go back to using the term 'breed' in the way when it was first coined, some 250 years ago.

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News

Globaldiv Summer School – Auditor seat available!

GLOBALDIV Summer Schools are training activities, comprising theoretical and practical lectures, organized by the project on 2008 and 2009, to train PhD students and junior researchers on specific topics related to the use of the new technologies and approaches to characterize and conserve genetic diversity in farm animal species.

The 2008 School is dedicated to train students in technologies, statistics and methods for the investigation of animal genomes and the characterization of their diversity.



The 2009 School will be devoted to socio-economic aspects of conservation, to breed prioritization and conservation strategies, integrating genetics, socio-economic, environmental data and geography.

If you are interested to follow one single course or more, some auditor seats are available. Please send the request to summerschool@globaldiv.eu.

For more information: www.globaldiv.eu/Summer%20School/Home.html

The breed of the month

The 'Big Five' African Vintage Cows

We are losing the genetic resources locked up in the world's domesticated livestock at an unprecedented rate. Of the 7,616 breeds of domestic livestock reported to FAO, 1,491, or 20%, are classified as being 'at risk'. What's at stake in this 'livestock meltdown' is nothing less than the animal basis for world food security. If we are to adapt food production systems to radically changing conditions in the coming decades, animal as well as plant genetic diversity will be critical resources for doing so. Traditional breeds offer diversity, which is the only base for future selection and adaptation. The on-going loss of our livestock genetic heritage is tantamount to losing a road map for survival—the key to food security, environmental stability and improving the human condition.

This month another 'vintage cows' of Africa that could be part of that road map.

Kuri

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



Article of the month

North-to-South Livestock Gene Flows Crowd out Local Breeds

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

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

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

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

This breed replacement process has already run its course in North America and Europe, where half of all breeds documented are now extinct or in danger of becoming so. North America has the highest proportion of extinct breeds (25 per cent) among its recorded breeds, a fact due not only to the domination of just a few breeds produced in highly specialized livestock industries but also perhaps to the region's high levels of breed recording.

The South now possesses an estimated 70 per cent of the world's known livestock breeds, partly because in most countries commercial breeding has not yet taken hold, breeding stock is still traded without involvement of breeding organizations or companies, and many areas still lack artificial insemination coverage. In the face of the on-going Livestock Revolution, for example, it's probable that the transfer of pig and cattle breeding genotypes and systems will increase in rapidly developing countries of the South. In Viet Nam, for example, the percentage of indigenous sows declined from 72 per cent of the total population in 1994 to only 26 per cent just



eight years later, in 2002. Of the country's 14 local pig breeds, five are vulnerable, two are in critical state and three are facing extinction. And in some countries, national chicken populations have changed practically overnight from genetically heterogeneous backyard fowl to selected homogeneous stocks raised under intensive conditions. Generally, introduction of Formula One animals continues to be seen by developing countries as a solution to low productivity of local breeds even in areas where the exotic genotypes are ill-adapted and local breeds outperform crossbreds.

It is alarming that of the nearly 3,000 breeds newly reported to FAO between 1999 and 2006 and for which we have population data, 45 per cent are either at risk or already extinct. It is clear that the South, currently rich in its livestock genetic diversity, will be the hotspot of breed losses in the twenty-first century. The crowding out of local breeds is set to accelerate in many developing countries unless special provisions are made for their conservation by providing livestock keepers with appropriate support.

Events calendar

Many events concerning different issues related to GLOBALDIV project will take place in the coming months. Here is a selection of conferences and other events sorted by date:

- 29th World Veterinary Congress
Vancouver, B.C. (Canada)
27-31 July 2008
- International Society for Animal Genetics (ISAG)
20 to 24 July 2008
Amsterdam, Netherlands
Website: <http://www.isag2008.nl>
- Annual workshop of the European Regional Focal Point for Animal Genetic Resources
Vilnius, 21-23 August 2008
- 59th Annual Meeting of the European Association for Animal Production
Vilnius, 24th - 27th August 2008
- World Biodiversity Congress
Chiang Mai, Thailand, 20-22 November 2008
- 10th World Conference on Animal Production
Cape Town International Convention Centre, Cape Town, South Africa
23-28 November 2008



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