

## Genetic diversity of horses and chickens – a review

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### ABSTRACT

The diversity of farm animals is the result of the domestication of species through a long process of migration, selection, adaptation, and other natural events. This species diversity of farm animals needs to be conserved through demographic characteristics, recording of the production environment, and effective data management. In this process, the data presented based on molecular biology tracing becomes very important because of the discovery of so many breeds livestock found today, especially horses and chickens. Data based on production records or morphological characteristics becomes difficult to use in an effort to determine the species hierarchy of horses and chickens, especially in population studies that are mostly carried out in livestock studies. Through molecular studies, variations in the genetic diversity of horses and chickens will be easier to understand. The domestication of chickens is believed to be the result of several domestication events, most notably the red jungle fowl (*Gallus gallus*) and may also involve *Gallus sonneratii* and possibly *Gallus lafayettii*. Horses were domesticated in broad areas of Eurasia steppe. It is thought that mares underwent the domestication process many times, but few stallions contributed to the genetic formation of domesticated horses.

**Keywords:** Genetic Diversity, Horses, Chickens, Domestication, Livestock genetic database

### ABSTRAK

**KEANEKARAGAMAN GENETIK TERNAK KUDA DAN AYAM- JURNAL REVIEW.** Keanekaragaman hewan ternak merupakan hasil domestikasi spesies melalui proses panjang migrasi, seleksi, adaptasi, dan peristiwa alam lainnya. Keanekaragaman jenis hewan ternak ini perlu dilestarikan melalui karakteristik demografi, pencatatan lingkungan produksi, dan pengelolaan data yang efektif. Dalam proses ini, data yang disajikan berdasarkan penelusuran biologi molekuler menjadi sangat penting karena disadari begitu banyak *breed* ternak yang ditemukan saat ini, terutama kuda dan ayam. Data berdasarkan catatan produksi atau ciri morfologi menjadi sulit digunakan dalam upaya penentuan hirarki spesies kuda dan ayam, terutama pada studi populasi yang banyak dilakukan pada studi peternakan. Melalui studi molekuler, variasi genetik kuda dan ayam akan lebih mudah dipahami. Domestikasi ayam diyakini sebagai hasil dari beberapa peristiwa domestikasi, terutama dari *Gallus gallus* dan mungkin juga melibatkan *Gallus sonneratii* dan *Gallus lafayettii*. Kuda didomestikasi di dataran padang rumput Eurasia. Diperkirakan bahwa kuda betina menjalani proses domestikasi berkali-kali, tetapi hanya sedikit kuda jantan yang berkontribusi pada pembentukan genetik kuda saat ini.

**Kata kunci:** Keanekaragaman genetik, Kuda, Ayam, Domestikasi, Database genetik ternak

## INTRODUCTION

Domestication of animals is an important breakthrough in the development of human demography and culture. Over the course of livestock history, the evolutionary forces of processes of mutation, selective breeding, adaptation, isolation and *genetic drift* have created tremendous diversity of local populations, so that local species are replaced by highly productive breeds. This interesting fact about the productivity of livestock species raises concerns about the erosion of genetic resources (United Nations Food and Agriculture Organization, FAO 2007b). Existing livestock traits, however, derive from the genetic diversity of local breeds. Such conditions should be anticipated through the conservation of germplasm of local breeds. According to FAO, 20% of the approximately 7600 breeds reported worldwide, including 18 species of mammals and 16 species of birds, are at risk of extinction, and there have been 62 breeds that have become completely extinct in the first 6 years of this century (FAO 2007b).

An understanding of breed characteristics, including data on population size and structure, geographic distribution, production environment, and genetic diversity within and between breeds is essential in efforts to manage livestock genetic resources. The importance of a comprehensive and integrated understanding of all the above factors has been one of the four Strategic Priorities of the Global Plan of Action for Animal Genetic Resources adopted by 109 countries at the first International Conference on Animal Genetic Resources held in *Interlaken*, Switzerland in 2007, and endorsed by the FAO Conference (FAO 2007a).

It is recognized that detailed molecular data both between and within breeds are essential for effective management of livestock genetic resources. The mechanisms controlling biodiversity are not yet fully understood. However, data on the environment in which

the breed is raised may provide informative data. Based on the various information previously mentioned, the discussion in this paper will begin with the demographic characterization and production environment, followed by a review of the *breed* description database. The main part is the section on genetic characterization in livestock focuses on the domestication process and genetic diversity of major livestock such as horses and chickens.

Technological advances in the field of molecular genetics have contributed significantly to a detailed understanding of species diversity. Blood grouping, enzyme polymorphisms, transplant antigens, and RFLP have been complemented by molecular observations such as mtDNA haplotypes, Y chromosomes, and autosomal microsatellite. For all domestic species, mtDNA data have allowed explanation of their relationship to their wild ancestral species, and for most species these data have also been informative at the intercontinental level.

## DISCUSSION

### Demographic Features

Assessment of the risk status of a *breed* requires accurate data on demographic characterization. The risk status of a breed depends on several factors, but the main one is population size and structure (FAO 1992; Gandini *et al.*, 2004). The value of  $N_e$  is very important to determine the inbreeding that occurs in livestock populations, which in turn will be able to assess the loss of genetic diversity in the population. Local *breeds* is given to species that are only found in a certain area/country. Conversely, species found in more than one country is referred to as transboundary breeds or cross breed (FAO 2007b). In 2008, there were recorded in the FAO Domestic Animal Diversity Information System (DAD-IS; <http://www.fao.org/dad-is/>) as many as 7040 breeds categorized as local, 500 *breeds* as regional transboundary

breeds, and 551 internationally transboundary breeds (FAO, 2009).

Data on the geographic distribution of breed populations are lacking and limited to a few central databases. However, efforts have been made more intensively to provide more reliable information. Key challenges for the future include developing methods for sampling animal populations, in addition to the lack of measures that cover the negative effects of crossbreeding (FAO, 2007b). Molecular characterization studies are an alternative to help reveal this kind of phenomenon.

### Breed Database

Conservation and utilization of genetic resources is an important basis for basic information to create a good database. Various websites try to provide valid information.

The “Convention on Biological Diversity” adopted at the United Nations Conference on Environment and Development held in Rio de Janeiro in 1992 inspired national-scale sites with complete coverage of breeds. Two examples created after the conference were the German Center of Animal Genetic Resources Documentation (TGRDEU; <http://www.tgrdeugenres.de/>) and the French Bureau des Ressources Genétiques (BGR; <http://www.brg.prd.fr>).

Meanwhile at the international level, the *Breeds of Livestock* website managed by the University of Oklahoma (<http://www.ansi.okstate.edu/breeds/>) provides data on the number of livestock breeds, including horses and poultry, with different levels of detail. Meanwhile, the EAAP (European Association for Animal Production) database which was started in the 1980s is considered to provide factual data on breeds from all over Europe. This database was later redesigned to become FABISnet, a global network consisting of databases that accommodate national and regional data (Groeneveld *et al.*, 2006).

The FABISnet database is considered the most comprehensive dataset, covering

data from 198 countries and territories for more than 14,000 populations of 37 species, including descriptions of morphology, performance, reproduction and demographic data. FABISnet is now better because it provides information on breed descriptions, conservation, and utilization.

### Livestock Genetic Characteristics

#### Horse

More than 100 equine mtDNA haplotypes have been analyzed to focus on horse domestication process. Combined analysis of horse mtDNA revealed an *unrooted* structure (Jansen *et al.*, 2002; Kavar and Dovc, 2008). Involving wild horses from 12,000 to 28,000 years ago, unexpectedly high genetic divergence between horse *clades* was found (Vila *et al.*, 2001). Analysis of DNA taken from 3rd century BC horses in China (China Tombs) (Keyser-Tracqui *et al.*, 2005) and from the Bronze Age (Lei *et al.*, 2009) showed that mtDNA diversity was detected prior to domestication, which is thought to have occurred about 6000 years ago in the vast plains of Eurasia. DNA analysis succeeded in tracing the domestication process of horses which indicated that it was not limited to a certain area but was widespread and very complex. It was further proved by Ludwig *et al.* (2009) who analysed based on fossil remains that the domestication of horses from 5000 years ago onwards was followed by the spread of mutations that produced various coat colours.

Based on AMOVA analysis of 72 horse populations from Europe, Southwest Asia, East Asia and Africa, it is evident that there has been a non-random distribution of diversity between populations. In addition the data show that, although weak, there has been geographic partitioning based on variations in mtDNA (McGahern *et al.*, 2006). The mtDNA data also indicate that the Iberian horse haplotype reproduces with high frequency (Luis *et al.*, 2006), which is in agreement with historical evidence for the origin of the American horse. Meanwhile,

Yang *et al.* (2002) identified the Mongolian haplotype in the Korean Cheju breed.

Analysis of non-coding Y chromosome data by Lindgren *et al.* (2004) along 14.3 kb of 52 stallions from 15 different breeds failed to identify a separate group. These results at least conclude that the stallion's genetic contribution to the domestication process is lacking.

DNA studies on horses so far still has many problems because of the sensitivity of the horse breeding business of each breeder group. However, using microsatellite data, proteins, and various markers, consistently, supports various morphological appearances of different breeds. Aberle *et al.* (2004) using microsatellites succeeded in obtaining three clusters between breeds (1. Riding breeds of Arabian and Hanoverian; 2. primitive breeds [Exmoor and Sorraia]; and 3. German Cold-Blooded). Furthermore, there is a distinct separation by 12 markers to cluster Thoroughbred and Anglo-Arabian breed and of of Haflinger, Italian heavy draught and Bardigiano (Bigi *et al.*, 2007). Another study using 17 proteins and 12 microsatellite markers succeeded in classifying eight breed clusters among 33 breeds, specifically four groups formed a clear cluster, namely:

1. Andalusia with Lusitano ; 2. Friesian with two ponies; 3. Morgan, standardbred, Rocky Mountain and American Saddlebred; 4. Irish Draught, Hanoverian, Holsteiner and Thoroughbred (Luis *et al.*, 2007). The origin of the horse has also been identified by microsatellite analysis, such as that conducted by Kakoi *et al.* (2007) who found evidence of Mongolian ancestry in Japanese breed horses.

### Chicken

The ancestors of today's domesticated chickens are believed to have come from the red jungle fowl (*Gallus gallus*). Distribution of this chicken occurs widely in East Asia, from Pakistan through China, East India, Burma, most of Indo-China, and on the islands of Sumatra, Java and Bali (Crawford, 1990). Variations in mtDNA sequences,

particularly in highly polymorphic regions, have been used to study the domestication process of chickens. From the results of DNA observations using four wild *Gallus* species, local chickens from Indonesia and two commercial breeds, concluded that the domestication of chickens only comes from one species, namely *Gallus gallus*, and a single domestication center is very likely to occur in Thailand and the surrounding areas (Fumihito *et al.*, 1996). Other studies using the entire mtDNA sequence and two core markers revealed that *Gallus sonneratii* and *Gallus lafayettii* may also contribute to the genetic makeup of contemporary domesticated chickens, albeit to a lesser extent (Nishibori *et al.*, 2005). Research conducted by Eriksson *et al.* (2008) using sequence variations of the BCDO2 gene showed that domestic chickens and wild species are quite closely related. The use of BCDO2 (encodes beta-carotene dioxygenase 2 which has the function of breaking down feather-colouring carotenoids into colourless apocaretenoids) is necessary because the yellow skin color, a common feature of many domestic chicken breeds, does not originate from the red jungle fowl (*Gallus gallus*) gene, but most likely derived from the grey jungle fowl (*Gallus sonneratii*), a wild type of chicken related to the domestic chicken in India. Another study involving African domestic chickens revealed that there were two female offspring among the Zimbabwean, Sudanese and Malawian chickens, one from Southeast Asia, and the other possibly from India (Muchadeyi *et al.*, 2008). The mtDNA analysis also proved that the descendants of modern Chilean chickens did not originate from Polynesia (pre-Columbian), but from Indo-Europe and Asia. The study results of ancient mtDNA haplotypes found in chickens in the pre-Columbian archaeological era support the theory of Polynesian/Pacific chicken transportation. This haplotype apparently never arrived in South America, or may have been replaced by new introductions (Gongora *et al.*, 2008).

As one of the main sources of protein for humans, chicken is widely distributed to various countries, continents and cultures. As a result of years of adaptation and breeding, various types of broilers were found today. Various treatments of breeders and hobbyists have changed the original chicken breeds. As a result, more and more local chicken breeds are under threat of extinction (Blackburn, 2006).

Overall, the results of studies using microsatellite markers indicate that the jungle fowl population as the origin of current chickens and unselected traditional breeds is a broadly heterogeneous population, accounting for most of the total genetic diversity. In commercial chickens, *broiler* lines are slightly more polymorphic than *layers*. Meanwhile, between *layers*, the white *layer* is less polymorphic than the brown *layer*. In recent years, there has been concern about reduced genetic variability in commercial egg white *layers* derived from a single *breed*, the *Single Comb White Leghorn*.

A large-scale analysis of 2000 individuals from 65 populations representing different chicken breeds from various geographic areas was carried out by Hillel *et al.* (2007) used 29 microsatellite loci showing that the population was grouped according to geographic origin and cultivation history, namely Asia, Europe and Africa. Using the same dataset, Granevitze *et al.* (2007) showed that the degree of polymorphism varied between groups. Relatively low genetic diversity was observed in indigenous European ancestry. In contrast, indigenous populations from Africa and Asia have high genetic diversity and do not exhibit a distinctive population structure. Differentiation is only observed between populations originating from two locations and countries that are far apart. Furthermore, small-scale studies analyzing only a few Italian or Japanese *fancy breeds* have shown these two breeds might be and generally exhibits low genetic diversity (Tadano *et al.*, 2007; Zanetti *et al.*, 2007).

Research using SNP markers can identify a loss of 50% or more of the genetic diversity of commercial chickens. Only a small part of this loss can be recovered by combining all commercial poultry stocks. However, modern breeding is not the only cause of allele loss in chickens, as many alleles loss were also recorded before that.

An assessment of the level of Linkage disequilibrium (LD) which is an indicator of the consistency of a population has been carried out in nine commercial *broiler* breeding populations based on the analysis of genotype data for 959 and 398 SNPs on chromosomes 1 and 4, respectively (Andreescu *et al.*, 2007). The results of this study indicate that this LD level does not exceed the limit of about 0.5 cM, which is shorter than previously reported for other livestock species. However, this value is likely to be much greater in the case of White *Leghorn* based breeds. If the LD value is within 1 cM, the population tends to be consistent across related populations.

## CONCLUSION

Domestication of livestock, directly or indirectly, affects genetic variation in livestock. The data presented based on molecular biology tracking are very important considering the many discoveries of livestock breeds found today, especially horses and chickens.

The domestication of chickens is thought to be the result of several domestication events, most notably the red jungle fowl (*Gallus gallus*) in Southeast Asia and may also involve *Gallus sonneratii* and possibly *Gallus lafayetii*. Horses were domesticated in broad areas of Eurasia steppe. It is thought that mares underwent the domestication process many times, but few stallions contributed to the genetic formation of domesticated horses.

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