Zootec Vol. 42 No. 2 : 278 – 284 (Juli 2022) pISSN 0852 – 2626 eISSN 2615 – 8698

Domestication and genetic characteristics of pig – a review

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ABSTRACT

Pigs are one of the main types of livestock kept by humans because of their high reproductive system and the ability to survive in all kinds of conditions. Modern pigs have gone through a long history of domestication processes, ranging from migration, selection, adaptation, and other natural events. Important records of pig origins have divided the domestic pig population into two main groups namely Asian and European breeds. These two groups clearly separated about 58,000 years ago. In particular it is recorded that the European wild boar was domesticated around the 4th century BC. European pigs then got new genes since the introduction of the Asian pig which is thought to have occurred at the end of the 18th century. Domestication of pigs affects the genetic diversity of these animals which in turn will disrupt the availability of pig germplasm. However, the need for superior breeds with high productivity values will be indispensable given the increasing food supply for the community both in terms of food quality and quantity. This fulfilment is actually not just for a moment but in a very long and sustainable period, and the latter can only be fulfilled if the genetic resources of pigs are maintained through good gene conservation programs.

Keywords: Pig, genetic diversity, domestication, livestock genetic conservation

ABSTRAK

DOMESTIKASI DAN KARAKTERISTIK GENETIK BABI. Babi merupakan salah satu jenis hewan ternak utama yang dipelihara manusia karena sifat reproduksinya yang tinggi dan kemmpuan bertahan dalam segala macam kondisi. Babi modern telah melewati sejarah panjang proses domestikasi, mulai dari migrasi, seleksi, adaptasi, dan peristiwa alam lainnya. Catatan yang ada memperlihatkan bahwa babi saat ini terbagi dalam dua kelompok utama yaitu babi Asia dan Eropa. Kedua kelompok ini melewati dua jalur domestikasi terpisah dimulai dari 58.000 tahun yang lalu. Domestikasi ternak babi berpengaruh terhadap keanekaragaman genetik hewan ini yang pada akhirnya akan mengganggu ketersediaan plasma nutfah babi. Bagaimanapun, kebutuhan akan breed yang unggul dengan nilai-nilai produktivitas yang tinggi akan sangat diperlukan mengingat pemenuhan pangan masyarakat yang terus meningkat baik dalam hal kualitas dan kuantitas pangan. Pemenuhan ini sejatinya tidak hanya sesaat tetapi dalam jangka waktu yang sangat lama dan berkelanjutan, dan yang terakhir ini hanya dapat dipenuhi apabila sumber daya genetik ternak babi dipertahankan melalui program-program konservasi gen yang baik.

Kata kunci: Babi, domestikasi, keanekaragaman genetis, konservasi genetis ternak

INTRODUCTION

The focus on genetic diversity is starting to get more attention. One important reason for the focus on livestock diversity is the conservation of livestock germplasm because indigenous breeds have been shown to contribute to the genetic and ecological components of species diversity ((United Nations Food and Agriculture Organization, FAO 2007; Bruford *et al*., 2015). One of the important domesticated animals is the pig which actually requires a comprehensive understanding in an effort to maintain its genetic resources. Like other livestock, modern pigs are believed to be the result of domestication of wild boars (Verrier *et al*., 2005; Biscarini *et al*., 2015).

Important records of pig origins have divided the domestic pig population into two main groups namely Asian and European breeds. These two groups clearly separated about 58,000 years ago. In particular it is recorded that the European wild boar was domesticated around the 4th century BC. European pigs then got new genes since the introduction of the Asian pig which is thought to have occurred at the end of the 18th century.

Wild boars and domesticated pigs are animals that belong to the genus *Sus*. Domesticated pig are one of the main livestock because they provide the main source of protein for humans, both as a source of meat and other livestock products. Pigs are chosen by most of the breeders as domesticated species for various reasons such as high adaptability to various livestock management systems and because of their high reproduction rate. The latter makes it easier for farmers to increase livestock populations and of course provides opportunities for economic improvement.

The wild boar has undergone a very long and complicated journey of domestication, involving various cultures, livestock production systems, and modern technological practices. The development of many modern pig breeds according to phenotypes and genotypes that lead to very distinctive production capabilities is believed to be a continuous effort by practitioners and scientists in the field of animal husbandry. This paper focuses on the domestication process of pigs and the diversity of pig genetic resources.

Review of pig domestication

Tracking the domestication process of pigs can be done relatively easily because of the help of molecular analysis (Čandek-Potokar, 2019; Salamon *et al*., 2019). Molecular data through mtDNA tracking is able to explain the process of pig domestication. *Sus scrofa* is believed to be the main ancestor of today's modern pigs. Preliminary mtDNA studies suggest that European and Asian pigs were reared independently although there is evidence of possible introgression of Asian domestic pigs into several European breeds. Larson *et al*. (2007) put forward the theory that domestic pigs of East Asian descent were introduced to Europe during the Neolithic era, at the same time that European wild pigs were domesticated. After being domesticated, European pigs quickly spread throughout Europe replacing pigs introduced from East Asia. Using mitochondrial DNA from 323 modern pig specimens and 221 ancient pig samples, it is known that domestic pigs of Middle Eastern descent were introduced to Europe during the Neolithic era at least as early as the 4th millennium BC. At the same time, it was also noted the possibility of local European wild boars starting to be domesticated. The Neolithic Revolution and detailed genetic records of the origins of domesticated pig populations reveal a complex set of interactions and processes during the early livestock dispersal to continental Europe.

Ramirez *et al*. (2009) and Gvozdanović (2019) analysed the origin of pig breeds through co-analysis of mitochondrial DNA polymorphisms, microsatellite and Y chromosomes in samples of modern and wild pigs distributed worldwide. The results of this study indicate weak genetic differentiation between modern and wild pigs. The explanation for this result is that there is likely to be a continuous gene flow between the two populations. Analysis of mtDNA markers proved that there is a close genetic relationship between the Middle Eastern wild pig and similar pigs in Europe. The same intensity of data between genetic markers was detected in East African breed pigs. It can be concluded from these data that East Africa appears to be the main entry point for pigs on the African continent following the Indian Ocean trade route. It is also noted that some South American pig breeds are closely related to pigs of European descent. The introduction and spread of pigs between continents is very likely as a result of the Spanish and Portuguese commercial routes connecting Asia with the Americas, in this context the introduction of the Far Eastern breed to the European and American continents. Y-chromosome variations provide evidence that Anglosaxone pigs, local African pigs and especially international breeds (eg Large White, Landrace and Pietrain) are the result of European-Asian mixed pigs. Based on the analysis of the Y chromosome, it was found that there was a possibility of intorsion of Asian pigs to mainland England that came from the female parent lineage.

Research conducted by Fang *et al*. (2009) used 15 wild pigs and 68 domesticated pigs from both Europe and Asia through analysis of genetic variation of the melanocortin 1 receptor gene (MC1R) showed that the gene for coat coloration in domestic pigs was more varied than that of wild ancestors. This study found that all mutations occurred silently (silent mutations) in their relatives wild pigs, but nine out of ten mutations found in domesticated pigs resulted in altered protein sequences (gene expression results). The results of this study indicate that the early breeders deliberately selected the coat color of wild pigs.

Pig genetic characteristics

It has been noted that about 400 breeds of pigs are kept and live in this world. Asia and Europe are known to have the highest number of breeds. A collaborative study was conducted to analyze the genetic diversity of pigs based on the genotyping of 50 microsatellite and 148 AFLP markers (Ollivier *et al*., 2005). In this study, various populations of both local breeds, national varieties, international breeds and commercial populations were used. Chinese Meishan breeds and European wild boars were used as outgroups. The results show that there is considerable variability between breeds. Based on the analysis of microsatellite markers it is seen that local breeds make use of 56% of the total intra-breed diversity followed by commercial and international breeds. In contrast, international breed groups make the largest contribution to diversity within breeds, followed by commercial breeds and local breeds. This study also surmises that there is a degree of individual contribution to inter-breed diversity, while diversity within breeds is contributed by international breeds.

Zhang and Plastow (2011) conducted an analysis of the genomic diversity of pigs in a population by testing 17 autosomal chromosomes in 11 European pig breeds. The results show that the average observed heterozygosity is 0.5. Some reports suggest that the expected heterozygosity is much higher than the observed heterozygosity of about 0.53-0.80 among 13 populations from Asia and Europe, including domestic pigs and wild boars. Meanwhile, a higher diversity of 0.700 to 0.876 was found in the pig population in China. Variations were also seen in the inter-chromosomal analysis which could mean that there may have been a long selection in pig breeding practices.

Based on the FST analysis it was seen that the genetic variation between Asian and European populations was much higher than within populations. When compared in two different regions, the genetic differentiation of the Asian population is much higher than that of the European population. The same conclusion was also shown between the domestic wild boar population and the Asian wild boar compared to the European wild boar. These results mean that the Asian pig population is more diverse than that of European population.

Based on mtDNA analysis, Asian domestic populations have much greater variability than that of European breeds. This difference in genetic diversity is consistent with the history of human populations and the domestication of animals. Meanwhile, in another study concluded that the frequency of Asian haplotypes is very small or even absent in the Duroc and Hampshire lines. The Asian pig's introgression looks more towards the Large White line than the Landrace line. Among European pigs, the Pie train haplotype originally developed in Belgium was completely absent in German pigs and some commercial strains. The influence of Asian pigs on the Large White, Landrace, and Duroc breeds was also noted.

In addition to the domestication process, artificial selection is a contributor to the diversity of pigs. Artificial selection will promote DNA variability and thus is responsible for the phenotypic plasticity. Artificial selection has a strong pressure on the level of nucleotide diversity. It has been widely reported how artificial selection reduces the genetic diversity of pigs. The loci responsible for quantitative traits (QTL) were noted to reduce the number of haplotypes because variability was lost by artificial selection (Ojeda *et al.*, 2008). Various studies have demonstrated the combined strength of the domestication process and artificial selection in influencing the genetic variability of pigs. This complex interaction is believed to be the result of economic interests by farmers who only want to benefit from certain genes rather than conservation of livestock genetic resources.

Pig genetic diversity could be revealed by analysis of SNP markers (Škorput *et al.*, 2018). Reports on this analysis began to be widely published. It is noted that the greatest genetic distance lies between the Far Eastern and European pig populations, *Sus scrofa*, while the Mediterranean local pig appears to be closely related to the European wild boar. Data on pig populations in South America show proximity to European pigs compared to Far Eastern populations.

Some exploratory data indicate that South America has no local pigs. Pigs in South America are currently the introduction of European pigs following the era of Spanish and Portuguese colonization. Consistently, European alleles are dominant in South American creole breeds. Iberian (European) pigs are increasingly entering this continent during the Columbus expedition. Gene tracing of European pigs in South American creole breeds has been widely carried out and demonstrated (Ramirez *et al.*, 2009; Souza *et al.*, 2009).

Pig genetic diversity is under selection pressure because farmers prefer high production traits, intensification of livestock production systems, and economic pressures for farmers especially in developing countries. Local breeds that have many important alleles as a source of germplasm are becoming increasingly marginalized in modern livestock production systems. It has been widely noted that when local pigs are crossed with international breeds, it suppresses the development of important genes possessed by local breeds. In the United States, for example, few local pig breeds have survived. As one of the main pig breeders in Europe, Spain has a record of high local pig extinction rates. Several breeds have become extinct and the remaining local pig breeds are also showing a declining trend in population size. More or less the same events was seen in several European countries. The risk of extinction of some local pig breeds must be minimized by various based gene diversity conservation efforts.

Lukic *et al.* (2020) revealed the pressure on local pigs due to intensification of livestock production systems. The high demand for pig production has spurred the rapid decline of many local pig breeds. Based on data on genetic diversity and inbreeding levels, and then compared with data on other local breeds from various countries, modern breeds and wild populations, it was found that Croatian local breeds underwent selective selection in certain genomic regions. Reinforced by the very high inbreeding rate observed in Croatian local pigs, a sustainable genetic diversity-oriented conservation program should be implemented immediately. The same conditions may be experienced by various local breeds scattered in various countries and other geographical areas (Zorc *et al*., 2022).

Apart from small-scale farming, industrialization of large-scale livestock using international breeds also shows a strong tendency for genetic erosion. Welsh *et al.* (2010) analysed the estimated inbreeding coefficients of five US pig breeds (Berkshire, Duroc, Hampshire, Landrace and Yorkshire). The results show surprising numbers because the genetic variation of populations with huge numbers of individuals has been greatly reduced by increasing rates of inbreeding and artificial selection. Based on these figures, it is very necessary to have a good breeding design to prevent the negative impact of inbreeding and artificial selection.

However, the need for superior breeds with high productivity values will be indispensable given the increasing food supply for the community both in terms of food quality and quantity. This fulfilment is actually not just for a moment but in a very long and sustainable period, and the latter can only be fulfilled if the genetic resources of pigs are maintained through good gene conservation programs.

CONCLUSION

Important records of pig origins have divided the domestic pig population into two main groups namely Asian and European breeds. These two groups clearly separated about 58,000 years ago. *Sus scrofa* is believed to be the main ancestor of today's modern pigs. Preliminary mtDNA studies suggest that European and Asian pigs were reared independently although there is evidence of possible introgression of Asian domestic pigs into several European breeds. The need for superior breeds with high productivity values will be indispensable given the increasing food supply for the community. Many practices of artificial selection and inbreeding are carried out in an effort to fulfil this quality feed. This practices negatively affect the genetic variation of pig population. Based on these figures, it is very necessary to have a good breeding design to prevent the negative impact of inbreeding and artificial selection. Sustainable conservation programs are very much needed to maintain pig germplasm.

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