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Review

Thai pigs and cattle production, genetic diversity of livestock and strategies for preserving animal genetic resources

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Abstract: This paper reviews the current situation of livestock production in Thailand, genetic diversity and evaluation, as well as management strategies for animal genetic resources focusing on pigs and cattle. Sustainable conservation of indigenous livestock as a genetic resource and vital components within the agricultural biodiversity domain is a great challenge as well as an asset for the future development of livestock production in Thailand.

Keywords: animal genetic resources, genetic diversity, Thai pig and cattle breeds, livestock production

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INTRODUCTION

Indigenous livestock has played an important role in smallholder farms and local populations for a long time. They have been raised using low input but they still generate their products and by-products to meet household needs. Moreover, in relation to biodiversity, indigenous livestock seem to be a reservoir of genes that could be an asset for future use. However, in recent years livestock production in Thailand was switched from backyard systems to industrialised husbandry [1, 2]. In parallel, exotic livestock was imported to improve the production performance and for economically important traits. Indigenous livestock were therefore gradually used for crossbreeding and were finally replaced completely by exotic commercial breeds. These breeding strategies oppose the concepts of sustainability and resource management and their long-term use threatens the loss of the genetic identity and diversity of the indigenous breeds.

CURRENT SITUATION OF LIVESTOCK PRODUCTION IN THAILAND

A major structural change in livestock production occurred in the past 20-25 years in Thailand. Private sector innovations such as improved breeds, feed technology, housing, farm management and contractual arrangements have been the prime drivers of growth and export opportunities, and rapid domestic and regional economic growth during the 1985-1995 period were the essential catalysts [1]. The livestock industries have been clustered in close proximity to Bangkok and the heavy concentration of animals is causing environmental stress. Farm sizes have become significantly large and the expansion is made possible by imported technology and increasing domestic demand. Pig and cattle development have been driven by domestic market demand and significantly affected by governmental regulations of slaughterhouses and by subsidies [1]. In this section, general information on the Thai agricultural sector and livestock production focusing on pig and cattle production is provided.

Economic Values of Agriculture and Livestock Production

According to the National Statistical Office (NSO), the population of Thailand stood at about 67,070,000 inhabitants in 2009 and the gross domestic product (GDP) was US$ 3,939 per capita [3]. Thailand is an agricultural country with around 34% of the households throughout the country working in agriculture and 93% of them located in rural areas. The two major activities in the agriculture area are the cultivation of crops (54%) and integrated crop-livestock farming (35%). Fifty-three per cent of the cultivated areas are being used for rice production [4]. The major forms of livestock in Thailand are pigs, chicken and cattle. Thailand is a major agricultural exporter to countries all over the world. Agriculture's share of the GDP in 2009 was around 9.2%. Within the agricultural sector, crops account for approximately 68% of the total output while the livestock are only a relatively small part of the overall agricultural sector, contributing 17% in 2009 [3, 4].

The agricultural sector in Thailand has undergone a substantial transformation to non-traditional crops since the past few years. It has shifted away from commodities such as rice and cassava towards more highly valued products. Para rubber, frozen chicken and shrimp products have become important, particularly for export markets. According to the Office of Agricultural Economics (OAE), the major export products in 2009 were rice (US$ 4,784 million), Para rubber (US$ 3,595 million), shrimp products (US$ 2,588 million), frozen chicken (US$ 1,304 million) and cassava products (US$ 1,296 million) [5].

For 2010, the Office of Agricultural Economics [5] recorded a decrease of 0.9% in the agricultural share of Thailand's economy. The two major contributing factors were a serious drought and the infestation of crop pests in the early months of the year 2010, which was accentuated by heavy floods later in the year. Consequently, the impact upon most of the major crops was a decline in production as the yearly crop production index fell by 2.1% compared to the year before. However, the overall prices of crops remained favourably high, especially for Para rubber, cassava and palm oil. For rice alone, even though yields were lower than in 2009, they still reached high levels contributing to a 22.8% increase in the farmers' income index. Livestock production is expected to be on the rise by 1.5% per year due to favourable price incentives coupled with the absence of serious livestock epidemic outbreak and bright export trends. Livestock produce such as dairy products and beef is an almost insignificant component of the Thai economy in terms of aggregate output despite a more than fourfold increase in the number of dairy cattle stocks and a 10 per cent increase in beef cattle stocks in 1986 and 1999 [1]. Furthermore, the growth of the fishery sector is expected to reach 1.2% due to its production expansion as a result of the growing demand for raw material supplies used in the processing facilities for export purposes. The fishery sector will therefore continue to grow [5].

Pig and Beef Cattle Husbandry in Thailand

At present, livestock production in Thailand is growing very quickly and plays an important role in food production. It has shifted from backyard animals and integrated crop-livestock farming systems to industrial livestock farming enterprises [1, 2], although the extent of this development differs among livestock species. Rapid growth has occurred in pig and poultry production. Pigs as well as broilers and layers have been produced mainly by large agribusiness companies for the export markets [1, 5, 6]. The principal challenge for pig production in Thailand is to close the wide gap between demand and production by upgrading the current production system towards that with high input and high output. In contrast to the pig production situation, the importance of beef cattle and buffaloes is still low in spite of the fact that they are mostly raised by smallholders in rural areas rather than by companies.

Pig production

The development of pig production started in the 1960s when the first group of exotic pig-breeds was imported by the Department of Livestock Development from the United Kingdom. These were Large White, Tamworth and Berkshire breeds. Later, Landrace and Duroc pigs were imported from the United States [2]. Before these exotic breeds were introduced, farmers relied on the relatively slow growing native pigs that had the desirable quality of not needing much in the way of trade inputs [1]. Since 1981 pig breeding has steadily been industrialised in Thailand. Thus, indigenous native pigs have been increasingly mated with imported breeds to improve their performance in economically important traits. Native pigs have gradually become crossbreeds and are finally replaced by European commercial breeds as the meat delivering end product in the pork industry [7].

Nowadays, like in other major swine-producing areas of the world, there has been a change from small farms to large farming enterprises. This trend will continue and is expected to lead to improved quality pork and to better meet the requirements of overseas importers. Ten large operators account for most of the increase in the current production and the outlook for development is significantly positive. Groups of agribusiness companies such as Charoen Pokphand (CP), Betagro, Laem Thong and Mittraparp are integrated and account for more than 20% of the swine production in Thailand. The operations employed by these companies are fully automated and have increased the efficiency of production, which will make them competitive in the world market.

The total commercial breeding swine population in 2009 was 991,140 animals. The boar population was 85,041 animals and the sow population was estimated at 906,099 animals. These sows wean an average of 17 pigs/sow/year [2]. The primary swine-producing area is the central region with approximately 57% (4,669,535 head) of the country’s pig population (8,537,703 head). The southern part has the lowest number of pigs, possibly reflecting the higher cost of pig fattening because of a shortage of feed in this region, or the fact that the southern part of Thailand has a relatively high Muslim population that do not consume pork meat. Most of the pork produced in Thailand is consumed domestically; export markets are limited to Hong Kong, Vietnam and Singapore. Processed pork products are, however, more widely exported [1, 2].

Native pigs

Contrary to commercial pigs, Thai native pigs are predominantly raised by communities in the northern region, representing almost half of the country's native pig population (Table 1). The average number of pigs per household is 4.3 head. Smallholders in the hill tribe communities traditionally raise a few indigenous pigs following local custom and religion. Animals are sacrificed at special celebrations such as New Year and wedding [7-9]. However, small pig populations without any scrutinised breeding programme are always at risk of losing genetic diversity and identity [10, 11].

Table 1. Regional distribution of pig farming in Thailand

Region	Number		Number		Total	
	Native breeds	Farmers	Commercial breeds [a]	Farmers	Animals	Farmers
Northern	218,406	50,365	1,145,564	47,943	1,363,970	98,308
North-eastern	142,116	26,033	1,340,001	63,022	1,482,117	89,055
Central	36,910	4,671	4,632,625	19,500	4,669,535	24,171
Southern	57,459	7,933	964,622	28,322	1,022,081	36,255
Total	454,891	89,002	8,082,812	158,787	8,537,703	247,789

Source: Modified from the Department of Livestock Development [2]
[a] Breeding and fattening pigs

Thai native pigs are classified as lard-type pigs. They grow slowly and their reproduction rate is low. However, they adapt well to hot and humid climate, tolerate low-quality feed and are probably resistant to foot-and-mouth disease and internal parasites, among others [7]. The characterisation of Thai native pigs has been made by the domestic animal diversity information system of the FAO [12]. Native Thai pigs are classified into four 'breeds', viz. Raad (or Ka Done), Puang, Hailum and Kwai (Table 2 and Figure 1), according to their physical appearance and the region where they are predominant.

As pigs in northern Thailand have also been kept and bred by hill tribes, some researchers have classified them as an independent group [7]. They have a narrower head, a longer snout and a shorter body compared to Thai native pigs from the lowlands. Hill-tribe pigs can be classified into two types: the small black type (similar to Raad or Ka Done pigs) and the black-and-white type (similar to Hailum and Kwai pigs), 70% of them being of the former type. Large-eared pigs found in Thunghuachang district of Lamphun province, which are probably cross-bred from hill-tribe pigs and Chinese Meishan pigs, are more prolific than indigenous hill-tribe pigs. However, nowadays it is difficult to determine any unique characteristics that are specific for each pig breed [7, 10, 11].

Table 2. Phenotypic classification of four Thai native pigs

Name	Weight [a] (kg)	Specific phenotype	Number of teats	Litter size	Predominance in Thailand
Raad	60-70	Black hair-coat colour; short body; small head; small and erect ears; long and straight snout	9-12	5-6	Lower north-eastern
Puang	120-130	Black and wrinkled skin; large thick ears; similar to Chinese Taihu pigs	N/A [b]	6-7	Upper north-eastern
Hailum	110-120	Black-and-white hair-coat colour; black colour at head, back and rump; white at belly and legs; short and straight snout; small and erect ears; similar to Chinese Hainan pigs	10-14	7-8	Central, eastern and southern
Kwai	130-150	Black hair-coat colour; white legs; long and straight snouts; larger ears; white ring around black cornea	10-12	6-7	Northern

Source: Modified from Rattanaronchart [7] and DAD-IS [12]

[a] Average mature weight of female and male pigs

[b] Not applicable

Raad (or Ka Done)

Puang

Hailum

Kwai

Figure 1. Four breeds of Thai native pigs [2, 7]

Beef cattle production

According to the Department of Livestock Development [2], the beef cattle stocks increased from 4,635,741 to 8,595,428 between 2000 and 2009. The increase was due to the policy of the Thai government to encourage farmers to raise beef cattle in an effort to reduce the amount of imported beef [13]. Several activities aimed at increasing beef cattle production initiated by the Thai government were initiated, such as the royal-initiated Cattle-and-Buffalo Bank project in 1978, the Beef Cattle Farm promotion in the north-eastern region in 1989 and the One-Million Beef Cattle Households promotion in 2004 [2].

In 2009 the average number of cattle per household for the whole country was just 6.2 head. This indicates that smallholders own the majority of beef cattle. The main region is the north-east where 54% of Thailand's beef cattle were found (Table 3). The number of pure-bred and cross-bred cattle was 3,153,013 head compared to 5,442,415 head of native cattle, which indicates the genetic potential of the indigenous animals. Beef cattle in Thailand are produced by extensive grazing systems rather than in confined feedlots or under controlled grazing. Village farmers who generally raise few ruminants usually use small areas beside crop fields for grazing in addition to paddy fields after the harvest [2, 14].

Table 3. Regional distribution of cattle farming in Thailand

Region	Number		Number		Total	
	Native breeds	Farmers	Exotic/cross-breeds	Farmers	Animals	Farmers
Northern	1,008,686	108,091	669,246	59,098	1,677,932	165,223
North-eastern	3,083,410	623,931	1,572,034	331,991	4,655,444	898,305
Central	710,758	58,534	785,275	58,097	1,496,033	114,228
Southern	639,561	163,357	126,458	38,936	766,019	191,962
Total	5,442,415	953,913	3,153,013	488,122	8,595,428	1,369,718

Source: Modified from the Department of Livestock Development [2]

Native cattle

Thai native cattle are classified as *Bos indicus* cattle and were predominantly used as draught animals in the past. They have accompanied Thai people for a long period of time and have now adapted well to local environments [15]. The north-eastern part of the country is also the most important area in terms of native cattle production with an average of five head per household. Thai native cattle are mainly kept under extensive grazing. During the dry season the animals graze in the forests or are fed only rice straw. Thai native bulls weigh between 300-450 kg and cows 200-300 kg on average [2]. Although Thai native cattle are small framed and display a low growth rate, they seem to have a good adaptability to low quality feed. They are also heat tolerant and resistant to parasites. The low energy requirement and the efficient utilisation of low quality roughage without protein favour their survival under severe feeding conditions [2, 14, 15].

Thai native cattle are categorised into four ecotypes, viz. the Northern ecotype (White Lamphun), the North-eastern ecotype, the Central ecotype and the Southern ecotype (Figure 2). This classification is confirmed by the study using phenotypic information of cattle kept on government research farms by their original region using a cluster analysis with a 75% coefficient of determination. However, there has been no genetic information with respect to the difference between the ecotypes [15-17].

Figure 2. Four ecotypes of Thai native cattle [2, 17]

In northern Thailand, the White Lamphun and the mountain cattle are the two most widespread native cattle breeds. They show a rather high rate of fertility, are tolerant to a poor quality of natural grasses and are well adapted to internal and external parasites. They are also resistant to diseases such as Anaplasmosis. They adapt well to hot and humid climate [18]. The White Lamphun breed shows an entirely white phenotype and are pink-skinned. They are classified as an endangered-maintained breed (with probably fewer than 1,000 breeding females). Their origin is still unknown but it has been a popular breed among northern Thai populations. The name is derived from Lamphun province where the breed is prevalent [2, 18]. The mountain cattle vary in colour (red brown, white gray or black) and are probably the smallest breed (150-200 kg mature wt.) among the Thai native cattle breeds. They are mainly raised in mountainous areas [18].

The performance advantages of native Thai cattle have been overshadowed by the large body size of imported exotic breeds. Indigenous cattle have therefore been neglected and crossed with zebu cattle (*Bos indicus*) such as Brahman and several *Bos taurus* breeds [2, 19]. These were mostly imported into the native cattle population by means of frozen semen such as that of Charolais, Hereford, Simmental and Shorthorn for the purpose of crossbreeding [1, 15].

GENETIC DIVERSITY AND EVALUATION OF LIVESTOCK

Genetic diversity is generated by either mutations, frequency of different allele changes due to migration, selection, or chance. Genetic diversity of livestock represents the heritable variations within and between populations. Populations may be either the entire species or a specific collection of individuals within a species, such as a breed, a strain, a line, or even a herd/flock [20]. Genetic diversity is required for populations to evolve and to cope with environmental changes. A loss of genetic diversity is often associated with inbreeding and a reduction of reproductive fitness. Genetic diversity and the evaluation of domestic animals have attracted attention worldwide. Consequently, the International Union for Conservation of Nature (IUCN) recognises the need to conserve genetic diversity as one of the three global conservation priorities [21]. Thus, a better understanding of the mechanisms which cause genetic diversity is a necessary priority in managing livestock populations. Worldwide efforts have been undertaken to conserve livestock diversity. Monitoring the number of breeds, their population size and degree of endangerment is coordinated by the FAO on a global level. The FAO report on the state of the world's animal genetic resources shows that roughly one third of all breeds are considered to be at risk of extinction [22].

Assessment of Genetic Diversity and Phylogeny

DNA sequence variants may result in amino acid substitutions within the protein encoding the locus. Such protein variations may result in functional biochemical or morphological dissimilarities that cause differences in the reproductive rate, the survival or the behaviour of individuals. These genetic variations are spread through the population by recombination events due to sexual reproduction [21]. Genetic diversity has been measured for many different traits including continuously varying (quantitative) characters, as well as for deleterious alleles and for proteins, nuclear DNA loci, mitochondrial DNA (mtDNA) and chromosomes. Genetic diversity is typically described using parameters that reflect the amount of polymorphism, the average heterozygosity, the allelic diversity and the genetic distance (Table 4).

The data on genetic diversity has been used to reconstruct phylogenetics on the order of genome rearrangement, the so-called breakpoint phylogeny [23]. Phylogeny is the study of genetic relationships among various groups of organisms (e.g. species, population) that descend from a common ancestor. This approach can be used to compare any two existing organisms, no matter how greatly they may differ in their morphological traits [24].

The classification of the methods used to construct phylogenetic trees from molecular data can be of two types depending on the type of data used. Firstly, classification occurs according to whether the method uses discrete character states or a distance matrix of pairwise dissimilarities. Secondly, classification depends on whether the method clusters include stepwise operational taxonomic units (OTUs), resulting in only one best tree, or all theoretically possible trees are considered. Table 5 lists the state of the phylogenetic tree construction and tree analysis methods, and their classification according to the above-mentioned strategies used. Computer programmes such as PHYLIP [25], MEGA [26] and PAUP [27] can be used to construct phylogenetic trees.

Table 4. Terminology used to describe genetic diversity

Terminology	Description
Genome	The complete genetic material of a species or individual (all of the DNA, all of the chromosomes)
Locus	A segment of DNA or an individual gene
Alleles	Different forms of the same locus that differ in the DNA sequence, e.g. alleles A, a, B and b
Genotypes	The combination of parental alleles present at a locus in an individual, e.g. A/A, A/a or a/a
Haplotypes	Parental alleles at several loci on the same chromosome, e.g. A-b-c
Homozygous	An individual with two copies of the same allele at a locus, e.g. A/A or a/a
Heterozygous	An individual with two different alleles at a locus, e.g. A/a
Allele frequency	The frequency of an allele in a population
Monomorphic	Lacking genetic diversity; a locus in a population is monomorphic if it has only one allele present in the population.
Polymorphic	Having genetic diversity; a locus in a population is polymorphic if it has more than one allele present in the population.
Proportion of polymorphism (*P*)	Number of polymorphic loci / total number of loci sampled
Average heterozygosity (*H*)	Sum of proportions of heterozygotes at all loci / total number of loci sampled. Typically, expected heterozygosity (H_e) is less sensitive than observed heterozygosity (H_o). In random mating population, H_e and H_o are similar
Allelic diversity (*A*)	Average number of alleles per locus
Co-dominance	Situation where all genotypes can be distinguished from the phenotype, i.e. A/A, A/a, a/a can be phenotypically distinguished.
Genetic distance	A measure of the genetic difference between allele frequencies in population; it is based on many loci and can be used to reconstruct phylogenetic trees, e.g. Nei’s genetic distance.

Source: Modified from Frankham et al.. [21]

Table 5. Phylogenetic analysis methods and their strategies

	Exhaustive search	Stepwise clustering	Software
Character state	Maximum parsimony (MP)		PAUP, MEGA, PHYLIP
	Maximum likelihood (ML)		PAUP, PHYLIP
Distance matrix	Fitch-Margoliash	UPGMA[a]	PHYLIP
		Neighbour-joining	PAUP, MEGA, PHYLIP

Source: Modified from Salemi and Vandamme [24]
[a] Unweighted pair group method with arithmetic mean

Molecular Markers of Genetic Characterisation in Livestock

The application of molecular markers to the study of genetic diversity has evolved very rapidly since the mid-1960s. The dominating protein electrophoresis approaches within the field of population genetics and evolutionary biology were replaced by DNA analyses in the late 1970s, primarily through the use of restriction enzymes. In the 1980s DNA fragment approaches and mitochondrial DNA sequence analyses became more popular. More recently, the introduction of PCR-mediated DNA genotyping or sequencing has provided the first rapid and easy access to the ultimate genetic data [20].

At present, several molecular markers have been widely used for genetic diversity and phylogenetic analyses in livestock. These are microsatellite analysis, restriction fragment length polymorphism (RFLP), random amplified polymorphic DNA (RAPD), amplified fragment length polymorphism (AFLP), single nucleotide polymorphism (SNP), direct sequencing, mitochondrial DNA (mtDNA) analysis and Y-chromosome specific markers [28, 29]. In the following section, mtDNA, microsatellite and SNP analyses focusing on pigs and cattle are discussed.

Mitochondrial DNA (mtDNA) markers

MtDNA is maternally inherited without recombination. The number of nucleotide differences between mitochondrial genomes therefore directly reflects the genetic distance that separates them. Moreover, mtDNA mutates 5-10 times more frequently than nuclear DNA, thus allowing the study of the divergence between wild and domestic populations under the short time scale of domestication [28].

In pigs the initial mtDNA studies showed that European and Chinese pigs were domesticated independently from European and Asian subspecies of wild boar [30, 31]. Later studies, however, suggested at least seven domestication events across Eurasia and East Asia [32-34]. These studies also suggested the occurrence of introgression of Asian domestic pigs into some European breeds during the 18th and 19th centuries.

Larson et al. [33] demonstrated that multiple domestication occurred at different locations on the islands of South-east Asia and Oceania. Domestic pigs of Near-Eastern ancestry were introduced to Europe during the Neolithic period. The European wild boar was also domesticated at this time. Once domesticated, European pigs rapidly replaced the introduced domestic pigs of the Near-Eastern origin throughout Europe. A recent study hypothesised five new cryptic domestication events from three geographical locations, namely India (MC1), South-east Asian peninsular (MC2, MC3, MC4) and the coast of Taiwan (MC5) [35]. Charoensook et al. [36]

further resolved porcine phylogeny in South-east Asia by analysing Thai mtDNA haplotypes (Thai native pigs and Thai wild boars). They supported a putative independent domestication event as they incorporated eight of their haplotypes into clade MC3, which represents exclusive samples that are indigenous to the Indo-Burma biodiversity hotspot, a region that includes Thailand to the Kra Isthmus.

In cattle one of the first contributions of DNA research to reconstruct the domestication was a comparison of the mtDNA of taurine and indicine cattle [37]. The divergence of their control regions implied separate domestication events, which most likely started around 8,000 years BC in South-western Asia and the Indus Valley respectively [38]. Zebus were probably imported into Africa after the Arabian invasions in the 7th century [39]. Interestingly, the discovery that African zebus carry taurine mtDNA implies that African zebus were the result of crossing zebu bulls with taurine cows [39].

Furthermore, mtDNA polymorphisms have revealed several other aspects of the early differentiation of taurine cattle. The predominance of one taurine mtDNA haplogroup (T1) in Africa [40] and a new haplogroup in Eastern Asia (T4) suggest two other regions of domestication [41, 42]. However, complete mtDNA sequences show that T1 and T4 are closely related to the major T3 haplogroup, so their predominance probably reflects founder effects in Africa and Eastern Asia respectively [43]. The T3 mtDNA haplogroup is predominant in most European and Northern Asian breeds [42] and is one of the four major haplogroups (T, T1, T2 and T3) in South-western Asia. By contrast, in the African taurine cattle haplogroup T1 is dominant, which is rare in South-western Asia. These observations are in line with the South-west Asian origin of European cattle, confirming the paleontological evidence of a gradual introduction of domestic cattle in Europe from South-western Asia [29, 38].

Microsatellite markers

There are several types of nuclear DNA markers. Microsatellites have been the markers of choice to study genetic variation in recent years. Based upon the sites on which the same short sequence is repeated multiple times, they present a high mutation rate and have a co-dominant nature. This makes them appropriate for the study of both within-breed and between-breed genetic diversity. According to the FAO and the International Society of Animal Genetics, microsatellite panels have been established for the genetic characterisation of pigs and cattle [44]. The porcine panel consists of 27 and the bovine of 30 polymorphic markers.

In a collaborative EU project (PigBioDiv1) [45] 58 European pig populations including local breeds, national varieties of international breeds, privately owned commercial populations and the Chinese Meishan breed as an out-group were genotyped for 50 microsatellite markers. The microsatellite data show that the individual breed contribution to between-breed diversity ranges from 0.04% to 3.94% of the total European between-breed diversity. The local breeds account for 56%, followed by commercial lines and international breeds [45]. The ongoing project PigBioDiv2 covers 50 Chinese breeds and investigates mtDNA and Y-chromosomal regions in addition to the microsatellite data of the European breeds [29]. Trait gene loci and markers are also to be analysed to seek insight into the functional differences between breeds. The first results of the microsatellite-based analysis using pooled DNA samples indicate that Chinese breeds, both within and between breeds, reveal a higher degree of genetic variability than the European breeds, [29, 46].

Bovine microsatellite data [47-49] and AFLP fingerprinting results [50] are in line with the endemic expansion of agriculture and the raising of cattle from South-eastern to North-western

Europe [29]. Cymbron et al. [48] observed that the correlations between genetic and geographical distances are different for the Mediterranean and Northern cattle breeds, suggesting that this reflects the separate Neolithic migrations along the Mediterranean coasts and the Danube respectively. A larger set of microsatellite data [51, 52] indeed indicates a separate position of the Mediterranean cattle, but divides the trans-alpine cattle into two different clusters of breeds: the Central-European (alpine, southern-French) one and Northern European one. Genotypes from 30 microsatellites for 69 European breeds were used to test the formal criteria of conservation [51]. The popular Weitzman method based on genetic distances favours highly inbred populations even if these have been derived recently from other populations. The ranking of conservation priorities on the basis of marker-estimated kinships is less influenced by inbreeding and favours the Mediterranean breeds. These breeds indeed display a relatively high degree of molecular diversity which, next to phenotypic uniqueness, is an obvious argument for conservation [29].

Single nucleotide polymorphism (SNP) markers

SNPs are point mutations in the genome sequence, predominantly bi-allelic and highly abundant throughout the genome. They are widely used in animal genetics and breeding because they have the potential to detect both neutral and functional genetic variations, and although most of them are located in non-coding regions, some correspond to mutation-inducing changes in the expressed genes [28, 53, 54].

Fang et al. [54] investigated genetic variations in the melanocortin receptor-1 (MC1R) gene among 15 wild and 68 domestic pigs from both Europe and Asia to address the genetic determination of coat colour, which is so much more variable in domestic animals than in their wild ancestors. They found that all mutations are silent in wild animals, suggesting a purifying selection. However, nine of ten mutations found in the domestic pigs result in altered protein sequences, suggesting that early farmers intentionally selected for novel coat colour.

Amaral et al. [53] evaluated linkage disequilibrium (LD) and haplotype block structures in 15 to 25 individuals from each of 10 European and 10 Chinese pig breeds genotyped for 1,536 SNPs in three genomic regions. The LD extends up to 2 cM in Europe and up to 0.05 cM in China. The authors suggested two possible explanations: either the European ancestral stock has a higher level of LD or modern breeding programmes have increased the extent of LD in Europe.

The haplotypic diversity using SNPs was also the focus of another study investigating the polymorphism of porcine IGF2 gene [55]. The results show that selection can be observed and analysed in the making by comparing different breeds that represent distinct stages of the selective process. Furthermore, there is no evidence that, overall, domestication reduces genetic variability in the *IGF2* region with respect to current wild ancestors of the pig (although a complete selective sweep is found in some very lean breeds such as Pietrain) [29].

The SNP data [56, 57] would reveal more about the history of European cattle. SNPs emphasise the zebu-taurine divergence and hence also the difference between Podolian and other European cattle [50]. Large-scale SNP analysis shows that in several breeds LD extends further than in humans but is hardly detectable at distances of over 200 kb [57, 58]. These data also suggest a rapid recent decrease of the effective population size of domestic cattle [42, 59].

Large numbers of SNPs, however, are required for precision; as a rule of thumb about six SNPs are equivalent to one microsatellite [28]. In addition, another critical aspect is their discovery, usually through sequencing techniques. Nevertheless, it seems that they are becoming the markers of choice because of increasing automation coupled with low costs. Several large-scale projects are currently carried out to identify SNPs in livestock. According to the National Centre of Biotechnology Information (NCBI) [60], 4,931,454 bovine and 557,135 porcine SNPs have been recorded so far (as of April 8th, 2012). In the near future, new technologies such as high throughput SNP typing or even whole-genome sequencing are likely to revolutionise our knowledge about the diversity and uniqueness of breeds with the ultimate objective of gaining a complete understanding of the molecular basis of functional diversity [29].

MANAGEMENT STRATEGIES FOR PRESERVING ANIMAL GENETIC RESOURCES IN THAILAND

The FAO defines genetic resources as those populations that show the highest genetic differences within a species and/or show unique alleles and allelic combinations [61]. The term animal genetic resources (AnGR) is used to include all animal species, breeds and strains that are of economic, scientific and cultural interest to humankind in terms of food and agricultural production for the present or the future. Another equivalent term increasingly used is livestock genetic resources. Since the past 10-12 thousand years, there have been more than 40 species of animals that are domesticated (or semi-domesticated) that contribute directly (through animal products used for food and fibre) and indirectly (through functions and products such as draft power, manure, transport and store of wealth). Common species include cattle, sheep, goats, pigs, chickens, horses and buffaloes, but many other domesticated animals such as camels, donkeys, elephants, reindeer and rabbits are important to different cultures and regions of the world [20, 22, 61]. The conservation and utilisation of indigenous AnGR has recently become concepts of greater importance. Conservation of animal genetics is now vital for sustainable management of these resources. This can be accomplished by the preservation of endangered and valuable breeds, selection programmes which will restore genetic diversity in industrial breeds, or the cryo-conservation of gametes, embryos and somatic cells of the existing gene pool [62]. The utilisation of indigenous AnGR will be a benefit to breeding programmes of high-production livestock under tropical climates.

Thailand has agreed upon the Agenda 21 of the United Nations Conferences on Environment and Development in 1992 to conserve the biological diversity and global environment. The National Environment Board of Thailand established the action plan for sustainable conservation of biological diversity in 1998. Strategies were outlined to strengthen the capacity for sustainable use of the environment and natural resources and to define and implement standard criteria for the conservation of biological resources that are applicable to the country [2]. The Department of Livestock Development under the Ministry of Agriculture and Cooperatives is responsible for livestock health and production. The activities regarding the conservation of AnGR are described in the national plans for biological diversity. The strategies are as follows: (i) to enhance capacity building, (ii) to increase the ability to conserve effectively, (iii) to create public awareness of conservation of AnGR, (iv) to conserve the diversity of breed, population and genetic resources, (v) to minimise harmful activities against biodiversity, (vi) to encourage the conservation and use of national resources including both the environment and the culture, and (vii) to encourage the cooperation between all agents both nationally and internationally. All activities focus on the indigenous AnGR [2, 63] and adequate approach is important for a management strategy of indigenous AnGR (Figure 3).

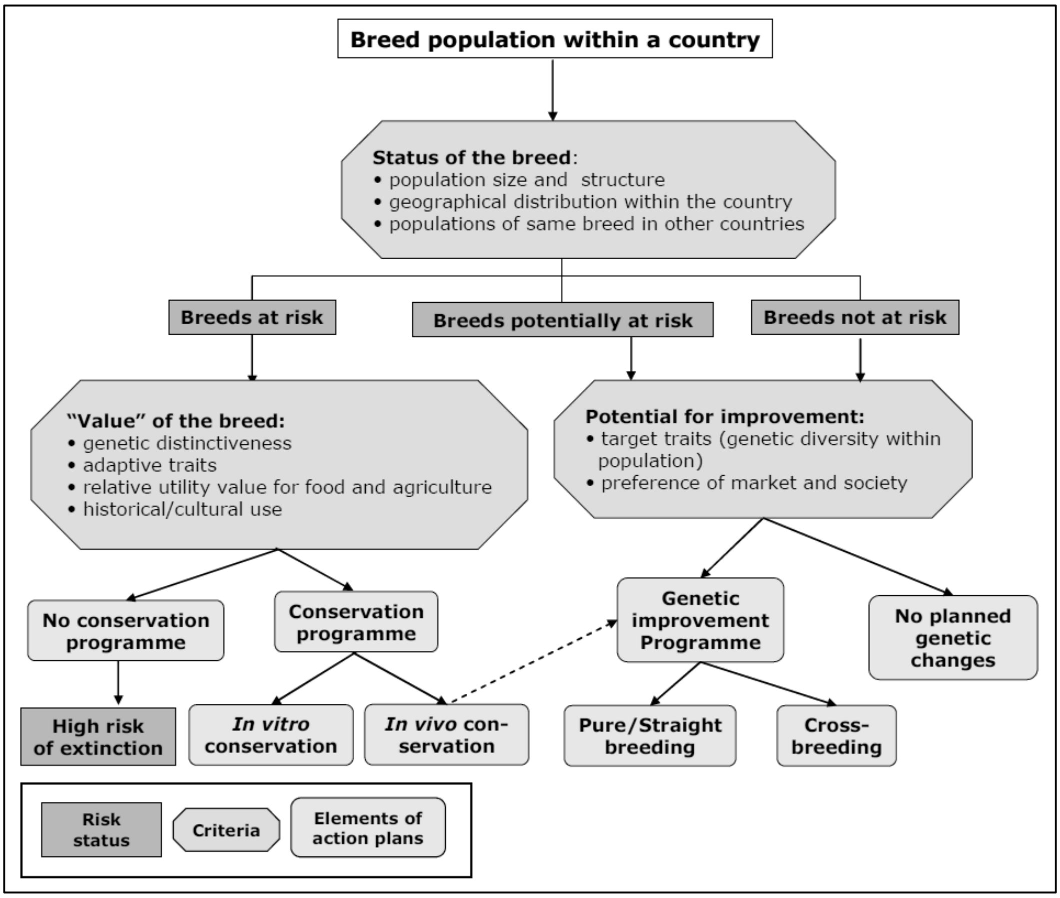

Figure 3. Design of animal genetic resources management strategies [60]

At present, however, the knowledge of indigenous species is still limited and scattered among agencies. A further collaboration among the agencies within the country is required. The livestock sector is a system which combines all the components of biological diversity, economy, social aspect and culture. The research purposes are to develop sustainable livestock in order to produce quality food, as well as to protect the safety of humans and the environment. Thus, research should emphasise the management of AnGR as an integral part of agricultural biodiversity [63, 64]. Breed improvement programmes have been initiated for some livestock species, viz. dairy cattle, beef cattle, buffalo and swine in some limited herds, although a national breeding programme is not available due to the lack of a recording system. In vitro conservation, considered as a sustainable process, has been performed through the cryopreservation of eggs, semen and embryos, and collection of seeds, tissues and cells, which can have a large impact on community participation [22, 61, 65].

CONCLUSIONS AND RECOMMENDATIONS

Livestock production in Thailand has dramatically changed from the ownership of backyard animals to an industrialised husbandry approach. Most of the animals used for food production are imported exotic breeds or their cross-breeds with indigenous animals. Although the indigenous animals have a large genetic diversity, there have been very few efforts to characterise their genetic background. Thus, sufficient information to confirm their original identity is still missing. Breed characterisation based on local names and phenotypic descriptions that have been used for a long time cannot clarify the admixture or gene introgression in populations. Well-characterised populations and appropriate breeding programmes must therefore be established to describe the uniqueness of the resources.

The need to conserve and utilise existing genetic diversity is a process in which all stakeholders should participate for future benefits to mankind. Studies on the development of economic traits, genetics and preservation of indigenous breeds are crucial to the defining and registering of genetic resources. Well-planned breeding programmes and measures for effective communication, especially between the decision-makers, are urgently needed. Sustaining conservation of indigenous livestock genetic resources as a vital component within the agricultural biodiversity domain will be a great challenge as well as a benefit for the development of livestock production in Thailand.

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