Population Subdivision and Migration Intensity Assessment of Mangalica Pig Breeds Based on Pedigree Analysis

Thi Anh Nguyen , György Köver , Peter Tóth , Ino Curik , Arpad Bokor , Nagy István *

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Article

Population Subdivision and Migration Intensity Assessment of Mangalica Pig Breeds Based on Pedigree Analysis

Thi A. Nguyen [1], György Kövér [1], Péter Tóth [2], Ino Curik [3], Árpád Bokor [1] and István Nagy [1,*]

[1] Institute of Animal Sciences, Hungarian University of Agriculture and Life Sciences (MATE) 7400 Kaposvár, Guba Sándor u.40, Hungary; anhthi379.cpp@gmail.com; kover.gyorgy@uni-mate.hu; bokor.arpad@uni-mate.hu.

[2] Hungarian National Association of Mangalica Breeders, 4025 Debrecen, Piac u. 77, Hungary; toth.peter@moe.org.hu

[3] Department of Animal Science, Faculty of Agriculture, University of Zagreb, Svetošimunska cesta 25, 10000 Zagreb, Croatia; icurik@agr.hr

* Correspondence: Nagy.Istvan.prof@uni-mate.hu (I. Nagy)

Simple Summary: Existence of substructure within isolated subpopulations can increase the risk of inbreeding. Eventually, this leads to a decrease in overall genetic diversity and to an increased susceptibility to diseases or other environmental stressors. Small subpopulations are more prone to genetic drift, where random events may lead to significant changes in the genetic composition. This can be problematic for conservation efforts aiming to maintain specific genetic characteristics. The Hungarian Mangalica with three different colour variations (Blonde, Red, Swallow Belly) representing three different breeds have been preserving the genetic and phenotypic appearance unchanged since 1976. Since all the breeds have been being kept in multiple herds for a long period, the evaluation of the population subdivision based on these herds could help to investigate the dynamic change of population structure under conservation. In our study the population sub-structure of every breed was evaluated with Wright F-statistics and the visualisation of results were accomplished using graphical methods (heat maps and chord diagrams). Based on the results it could be concluded that none of the analysed breeds showed any sign of sub-structure. This favourable phenomenon is the result of the adequate migration rate among the herds showing the adequacy of the applied breeding program.

Abstract: In preserving genetic diversity among domestic animal breeds, the strategies emphasizing between-breed diversity may be not optimal by neglecting within-breed variation. The present study aimed to assess the extent of the population subdivision of Mangalica pigs and the contribution of migration intensity to their substructure. Genealogy analysis was performed for breeding animals born between 1981 and 2023 examining three colour variations (Blonde, Swallow-Belly, and Red). The fixation index (F_{ST}) was calculated and evaluated by Multidimensional Scaling and Clustering to expose the population substructure. The average F_{ST} is 0.04 for the Blonde and 0.05 for the Swallow-Belly and the Red while in the active herds, these parameters are smaller being 0.03 and 0.04, respectively. The migration of individuals affected 61.63% of the Blonde, 75.53% of the Swallow-Belly, and 63.64% of the Red breed herds. No population substructure was found in any Mangalica breed which can be explained by the extensive within breed migration among the herds.

Keywords: Mangalica pigs; population subdivision; fixation index; pedigree analysis; migration

1. Introduction

In the 1830s the Serbian Sumadia pig breed was crossed with the local Hungarian stock and applying an intensive selection, a rustic curly-haired pig was created called Blonde Mangalica [1]. The Swallow Belly Mangalica breed was established later by crossbreeding Mangalica pigs and Szerémségi pigs. The latest breed is the Red Mangalica one, which is the result of the crossbreeding of Mangalica pigs with Szalontai type pigs as well as by using Újszalontai type pigs cross-bred with Mangalica pigs at the beginning of the 19th century [2]. The Mangalica pigs could be characterized by excellent fat production strong motherliness and good adaptability to extensive housing conditions nevertheless, their prolificacy is low [1]. The Mangalica was the main Hungarian pig breed until the 1950s. After World War II due to the changing dietary habits, Mangalica lost its former popularity [3]. Although in 1976, a national program was established to preserve its gene pool the Mangalica almost went to extinction by early 1990 [4]. Fortunately, in 1994 the National Association of Mangalica Breeders was founded to preserve the genetic and phenotypic appearance of the Mangalica pig in an unchanged form [2]. Due to their efficient activity in 2019, the number of registered sows and boars (combining the three breeds) was 6723 and 354, respectively [5]. At present, the Mangalica has three different colour variations (Blonde, Red, Swallow Belly), and based on the molecular genetic analysis Zsolnai et al. [6] it could be stated that these colour variants represent different breeds. Concerning gene conservation, the Mangalica pig breeds are among the most recognized ones in Hungary therefore the maintenance of these breeds has high importance. However, from the aspect of breed loss, to establish an appropriate management assessment and conservation of genetic variability, examining population structure and gene flow is necessary [7]. Recently all the Mangalica breeds were evaluated employing pedigree analysis where the demography parameters, inbreeding level, and the proportion of the maintained genetic diversity were presented [8]. However, since all the breeds are kept in multiple herds these herds can be interpreted as subpopulations. Evaluating the population subdivision based on these herds and the contribution of migration intensity to the population subdivision was the objective of the present study.

2. Materials and Methods

Because the current study exclusively involved the analysis of genealogical data stored in datasets, approval from the Animal Care and Use Committee was not obtained.

2.1. Genealogical data

The data utilized for examination in this study were supported by the Hungarian National Association of Mangalica Breeders. The organization documented information on registered Mangalica pigs listed in the Herdbook, consisting of pigs born from 1981 to 2023. The genealogy analysis was limited to Blonde, Swallow-Belly, and Red Mangalica breeding animals (i.e. that had produced offspring). Among the Mangalica pig breeds under examination, the genealogical record of the Blonde Mangalica breed was the largest, including 14,550 individuals born across 258 herds and originating from 748 boars and 6393 sows. Among these herds, there are 78 still active herds (while the other herds abandoned their breeding activity before 2023) with 427 boars and 3944 sows at the investigating time. In contrast, the genealogical records for the Swallow Belly and Red Mangalica breeds were characterized by a more limited scope. These pedigrees consisted of 2638 pigs originating from 94 herds, with parentage traced back to 237 boars and 1094 sows for the Swallow Belly breed, and 4566 pigs from 154 herds, with lineage attributed to 305 boars and 1779 sows for the Red Mangalica breed. The active herds of the Swallow-Belly Mangalica are 31 with 129 active sires and 669 active sows while the numbers of the Red are 55, 305, and 1779, respectively. Due to the presence of numerous inactive herds during the investigation, the research was conducted both on the total herds and on the currently active herds, respectively.

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2.2. Population subdivision

Genealogical data was utilized to analyse the subpopulation's structure, employing F statistics [9] which were computed according to Caballero and Toro [10] for each specified subpopulation. This method commences with the computation of the average pairwise coancestry coefficient (f_{ij}) between individuals from two distinct subpopulations referred to as i and j. This analysis covers all possible pairs of individuals within the entire metapopulation, considering the sizes of these subpopulations, which results in a total of $N_i x N_j$ pairs being accounted for. Within a specific subpopulation denoted as i, the following metrics can be calculated: the average coancestry, represented as f_{ii}, the average self-coancestry among the N_i individuals as s_i, and the average coefficient of inbreeding as $F_i = 2s_i - 1$.

The Wright [9] F-statistics are computed as follows:

$F_{IS} = \frac{\bar{F}-\overline{f}}{1-\overline{f}}$ (is the inbreeding coefficient of an individual relative to the subpopulations);

$F_{ST} = \frac{\bar{f}-\tilde{f}}{1-\tilde{f}}$ (is the mean inbreeding coefficient of subpopulation relative to the entire population);

and $F_{IT} = \frac{\bar{F}-\tilde{f}}{1-\tilde{f}}$ (is the inbreeding coefficient of an individual relative to the whole set of populations), where $\tilde{f}$, $\tilde{F}$ are, respectively, the mean coancestry and the inbreeding coefficient for the entire metapopulation, and $\overline{f}$ is the average coancestry for the subpopulation. The relationship $(1 - F_{IT}) = (1 - F_{IS})(1 - F_{ST})$ holds for these parameters. The pairwise F_{ST} matrix and its clustering were visualized by heatmap and UPGMA dendrogram. For a comprehensive examination of the relationships and distances between herds, the multidimensional scaling analysis (MDS) [11] based on pairwise interpopulation F_{ST} values was conducted.

2.3. Migration density

The actual migration intensity of pigs among herds derived from the stud book was visualized by the chord diagram.

2.4. Program used.

ENDOG software programs version 4.8 [12] was utilized to calculate pairwise genetic distances (F_{ST}) between pairs of herds. The heatmap.2 function in the R package "gplots" was used to generate a heatmap with an accompanying UPGMA dendrogram, visualizing the pairwise F_{ST} matrix. The chordDiagram function from the R package "circlize" [13] was employed to construct the chord chart. In addition, the Cmdscale function in R was applied for the execution of multidimensional scaling analysis.

3. Results

3.1. Population subdivision

Population differentiation of the Blonde, Swallow-Belly, and Red breeds is presented through the pairwise F_{ST} coefficients, illustrated in heatmaps (Figures S1a, S1b; Figure S4a, S4b and Figures S7a, S7b, respectively). The average F_{ST} is 0.04 for the Blonde and 0.05 for the Swallow-Belly and the Red while in the active herds, these parameters are 0.03 and 0.04, respectively. The heatmaps reveal that the Blonde breed exhibited the highest prevalence of stratification herds ($F_{ST} > 0.15$), followed by Swallow-Belly and Red breeds (Figures S1a, S4a, S7a, respectively). In the current active herds, large-distance herds ($F_{ST} > 0.15$) are observed only in the Blonde and Red breeds, showing a significant reduction compared to the entire herds (Figures S1b and S7b).

Within the Blonde Mangalica, three active herds (1645, 1630, and 1358) display substantial distances from each other (Figure S1b). Despite the presence of some distanced herds, no clusters were identified neither in the total herds (Figures S2a, S2b) nor in the active herds (Figures S2c, S2d).

Concerning the Swallow-Belly breed, large distances were calculated in herds 800, 1336, and 1159 (Figures S4a, S5a, S5b). However, all active herds in this population showed $F_{ST} < 0.15$, indicating the absence of substantial genetic differentiation among the herds (Figure S4b). The active herds are scattered in Figures S5c and S5d, but clusters are not sufficiently formed.

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In the Red breed, large distances are observed among herds 198, 1436, 1646, 1385, 1325, and 1493 (Figures S7a, S8a, S8b). The active herds in this breed exhibit one significant distance between herds 1436 and 1646 (Figures S7b, S8c, S8d). The F_{ST}s remain consistent within the breed, and no clusters are formed (Figures S8a, S8b, S8c, S8d).

The three Mangalica breeds exhibit a consistent F_{ST} pattern between herds. The small F_{ST} group (F_{ST}<0.05) constitutes the largest proportion of more than 58% of the total, specifically accounting for 71.26%, 61.29%, and 58.83% in the Blonde, Swallow-Belly, and Red breeds, respectively. Conversely, the large F_{ST} set (F_{ST}>0.15) represents a consistently minimal percentage of around 1.00%. In terms of moderate distances between herds (0.05<F_{ST}<0.15), the Red breed stands out with the highest proportion at 40.33%, followed by Swallow-Belly at 37.27%, and Blonde at 27.55%. Notably, the Red breed displays a tendency toward herd separation, with the majority of moderate-distance herds. However, the large stratification between herds is found in a very small proportion, accounting for only 0.84%.

While the proportion of the large-distance group in the three breeds is below 2.00%, the Blonde breed stands out with the highest average distance value (average F_{ST}) within this group, measuring 0.24 (ranging from 0.15 to 0.35). In comparison, the Swallow-Belly and Red breeds have got smaller an average F_{ST} of 0.20 (ranging from 0.15 to 0.35) and 0.21 (ranging from 0.15 to 0.34), respectively. Conversely, the average F_{ST} values for the small and moderate groups are approximately 0.03 and 0.07, respectively, across all three breeds (Table 1).

From the total herds, approximately 30% were active, with proportions of 30.23%, 32.98%, and 35.71% for the Blonde, Swallow-Belly, and Red breeds, respectively. When examining the genetic distances between active herds, over 99.70% fall into the small and medium F_{ST} groups. This results in a notable decrease in the proportion of large F_{ST} groups, accounting for less than 0.30% across the three breeds, except for Swallow-Belly, where it is 0% (Table 1).

Table 1. Average pairwise F_{ST} among herds sorted to F_{ST} groups.

Breed	F_{ST}_group	Total herds			Active herds		
		N	Mean	Percent	N	Mean	Percent
Blonde	S	23,625	0.02 ± 0.014	71.26	2,368	0.02 ± 0.014	78.85
	M	9,133	0.07 ± 0.019	27.55	627	0.07 ± 0.017	20.88
	L	395	0.24 ± 0.077	1.19	8	0.18 ± 0.062	0.27
Swallow	S	2,679	0.03 ± 0.013	61.29	310	0.03 ± 0.012	66.67
Belly	M	1,629	0.07 ± 0.020	37.27	155	0.07 ± 0.014	33.33
	L	63	0.20 ± 0.052	1.44	0	0	0
Red	S	6,142	0.03 ± 0.013	58.83	972	0.03 ± 0.013	65.45
	M	4,210	0.07 ± 0.018	40.33	512	0.06 ± 0.013	34.48
	L	88	0.21 ± 0.058	0.84	1	0.30	0.07

F_{ST}: fixation index, S: F_{ST}<=0.05, M: 0.05<F_{ST}<=0.15, L: F_{ST}>0.15, N: number of observations.

3.2. The migration intensity

The migration of individuals within herds was observed to be substantial, involving more than 60% of the total current herds. Specifically, it affected for 61.63% of the Blonde breed, 75.53% of the Swallow-Belly breed, and 63.64% of the Red breed. Across all three breeds, a consistent pattern emerged, indicating that a substantial number of females were transferred between herds, while the movement of males remained relatively minimal in comparison (Figures S3a-d, S6a-d, S9a-d). Within three breeds, the 872 herd is the most active and dominant in providing sires to neighbouring herds (Figures S3a, S3c, S6a, S6c, S9a & S9c).

In the Blonde population, the maximum number of migrating male pigs originating from a specific farm to a given herd is 10, which surpasses the figures for the Swallow-Belly and Red breeds

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at 6 and 4, respectively. Conversely, the range for female pigs is significantly wider, reaching up to approximately 270 individuals. This contrasts with the smaller numbers for the Swallow-Belly and Red breeds, with 86 and 78 individuals, respectively.

The connectivity among migrating herds reveals that more than 80% are linked by a single sire. To be specific, this percentage stands at 80.72% in the current Blonde herds, 87.00% in the current Swallow-Belly, and 90.34% in the current Red. Simultaneously, 90% of these herds establish connections that involve more than two sows, and this holds across all three breeds.

Within the Blonde breed, herd 872 stands out as the primary source of sires for neighbouring herds, while herd 954 attracts the highest number of migrating sires, as detailed in Figures S3a and S3c. Additionally, herds 1509 and 1466 play a significant role in the migration of approximately 270 sows, as highlighted in Figures S3b and S3d.

Figures S6a and S6b indicate that herd 872 experiences the most significant movements, both in terms of departing and arriving sires in the Swallow-Belly breed. In terms of female migration, there is substantial movement from herd 721 to herd 1322, but the most significant influx was observed in herd 1460, as shown in Figures S6b and S6d.

In the Red breed, Figures S9a and S9c reveal that herd 872 contributes the largest number of sires to nearby herds as a common share with other breeds, while herd 751 emerges as the primary sire recipient. Regarding female pigs, herd 675 is the major contributor, and herd 657 is the primary receiver, as demonstrated in Figures S9b and S9d.

4. Discussion

Some research about genetic variability between breeds has been done in Mangalica pigs [6,14]. An examination of the Hungarian population of Mangalica pigs, genotyped at 10 microsatellite loci, revealed the presence of three clusters, being representative of three different breeds, namely Swallow-Belly, Red, and Blond [6]. However, analyses utilizing mtDNA markers were unable to distinguish subpopulations within this Mangalica population [14]. Although studies employing various methods do not consistently delineate the three distinct breeds, in Hungary, breed management and conservation treat the three different fur colour variations of Mangalica as if they were three separate breeds. There is no interbreeding among these distinct variations. Examining the genetic variability within populations and the structure of these breeds could unveil their evolutionary patterns during more than four decades of conservation efforts across numerous herds in Hungary.

Traditionally, conservation priorities have given significant weight to between-breed diversity, as indicated by Barker [15] that the foremost objective in safeguarding domestic animal diversity is the preservation of specific breeds. However, there is a contention that approaches emphasizing the between-breed component of genetic diversity may not be the most effective, as they neglect the within-breed component of variation [16–18]. According to Cervantes et al. [7] accessing genetic variability within populations, understanding population structures, and analysing gene flow are crucial stages in the execution of selection programs. This assessment plays a pivotal role in formulating efficient management strategies for genetic stock, aiming to enhance the genetic basis for selection purposes. According to Molnár et al. [14], populations within a breed that are geographically and/or ecologically isolated may acquire distinct physiological characteristics due to specific selection criteria employed in the breeding process. Consequently, these isolated populations can diverge genetically from other populations of the same breed that share similar phenotypes, potentially leading them to be recognized as distinct breeds [14]. According to Wilkinson et al. [19] the genetic substructure within a breed, as revealed by individual clustering methods, is likely rare in domestic species, with the presence of limited genetic substructure typically observed in only one or two exceptional breeds. However, the intra-breed stratification has been reported in various farm animals, such as chickens [19], horses [20], castles [21], goats [22,23], rabbits [24,25], dogs [26,27], and pigs [28,29].

Estimating the Fixation Index (F_{ST}) provides insights into the degree of differentiation among a group of populations, as applied in the present study to assess the differentiation among herds

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belonging to three Mangalica breeds. The F_{ST} values, ranging from 0 to 1, convey the extent of genetic differentiation. A value of 0 signifies complete sharing of genetic material, allowing for free interbreeding. On the other hand, a value of 1 indicates that all genetic variation is accounted for population structure, indicating no shared genetic diversity, and the populations are considered fixed or distinct [30]. The interpretation guidelines for the fixation index (F_{ST}) were presented by Hartl and Clark [30] as follows: $F_{ST} < 0.05$ _little genetic difference; $F_{ST} = 0.05–0.15$ _moderate genetic difference; $F_{ST} = 0.15–0.25$ _ great genetic difference; $F_{ST} > 0.25$ _ very great genetic differentiation. In addition, Frankham et al. [31] reported that FST values greater than 0.15 indicate significant differentiation, while FST values below 0.05 suggest insignificant differentiation. In the current study, the F_{ST} among herds ranged from 0.00 to 0.35, being representative of the heatmap colours (Figures S1a, S4a, S7a). Most of the examined herds, surpassing 58% entire population (Table 1), exhibited insignificant genetic differentiation by Frankham et al. (2002) guidelines. This group is even more dominant in active herds with more than 65%. Moreover, multidimensional scaling showed that the analysed populations are not sufficient to form clusters for both dimensions 1-2 and dimensions 1-3 (Figures S2a-d, S5a-d, S8a-d), although there are some visual divergence herds. Among active herds, the Swallow-Belly showed quite a big distance from each other, but the substructures also are not formed in this breed (Figures S5c, S5d). This could be because of the smallest population size of this breed. In pigs, by using Bayesian Analysis of Population Structure on genotypic data, Wilkinson et al. [29] detected the substructure within British Meishan but it was not present in other methods. Snegin et al. [28] found the high variability between individual herds within the four commercial pig breeds, contributing to the significant difference between breeds of studied populations.

The Swallow-Belly and Red breeds exhibited a higher inclination towards intra-breed differentiation, with a larger percentage of herds displaying moderate genetic differences compared to the Blonde breed. Nevertheless, the average F_{ST} values between herds remained similar across all three breeds (0.07). This phenomenon may be clarified by the smaller population sizes of the Swallow-Belly and Red breeds.

Significant genetic differentiation was observed in certain herds across the entire studied populations (Figures S1a, S4a, S7a), but they could not establish a substructure (Figures S2a, S2b, S5a, S5b, S8a, S8b). The studied herds, present in pedigrees since 1981, include both active and inactive ones so far. Analysing entire populations provides a comprehensive overview, but accurate information on genetic subdivision relies on active herds. Among active herds, these differentiated herds constituted a minute fraction, amounting to less than 0.30% (Table 1). Examining these herds, such as 1645 and 1630 in the Blonde breed (Figure S1b) and 1436 and 1646 in the Red breed (Figure S7b), each herd featured only one selected sire. When calculating the average coancestry of the herd, the predominant self-coancestry contributes to high F_{ST} values. Consequently, this results in a distinct separation from other groups, as depicted in Figures S2c, S2d, S5c, S5d, S8c, and S8d. However, despite this observed differentiation, the details of the substructure within the herds remain indistinct in the whole view.

The results showed strong migration intensity among herds across three breeds as approximately 60% of herds have some connections with other herds. In addition, more than 90% of the migration involves one sire and more than 2 sows. The extensive exchange of animals between individual herds could be the reason for genetic similarity among herds in this study. Achmann et al. [32] in research on Lipizzan horses found out that the interchange of horses among studs plays a crucial role in mitigating the genetic divergence among the subpopulations. Dumasy et al. [33] determined that an increase in genetic distance is attributed to reduced connectivity among herds. This conclusion was drawn by examining the correlation between Reynolds' genetic distances and the shortest path lengths calculated by the exchange network method. In addition, the Blonde breed exhibits a smaller average F_{ST} (0.04) compared to the Swallow-Belly and the Red breeds (0.05), corresponding to a higher number of exchanged animals between herds within the Blonde breed. Dumasy et al. [33] highlighted the importance of considering the number of exchanged animals in explaining genetic differentiation, and the increase in exchanged animals within the Blonde breed aligns with its lower F_{ST} value. While both male and female individuals play crucial roles in

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establishing robust connections between herds within breeds, females would have a greater impact on genetic similarity in the current study. This could be attributed to the significantly larger number of exchanged animals involving females in the studied breeds.

According to Snegin et al. [28] the intrabreed differentiation was attributed to many factors, including gene flow, geographic isolation, breeding preferences, and the distinctive genetic backgrounds found in the genealogical groups (sire/dam lines) of the breed's founders. The geographic isolation contributed to the formation of intrabreed divergence of local goats in Spain and Portugal [22]. The divergence in dog breeds, as evidenced by Wiener et al. [27] was driven by the direction of breeding or artificial selection [27]. This is primarily not happening in the current study because all registered herds adhere to the same breeding strategy mandated by the Hungarian National Association of Mangalica Breeders. Additionally, there are no notable barriers to gene exchange discovered during the investigation.

5. Conclusions

Utilizing multidimensional scaling and clustering of Wright's F_{ST} does not delineate the substructure within the Blonde, Swallow-Belly, and Red breeds. Additionally, the prevalence of extensive animal exchange between individual herds, the uniformity in mating strategies, and the absence of noteworthy barriers to gene exchange collectively affirm the genetic homogeneity within these breeds. The observed patterns suggest that intending to preserve genetic diversity and mitigate the risk of inbreeding, the studied breeds exhibit positive indications aligning with conservation goals.

Supplementary Materials: The following supporting information can be downloaded at the website of this paper posted on Preprints.org, Figure S1a: Heatmap and dendrogram based on pairwise F_{ST} values among the herds of Blonde Mangalica breed. The heatmap color key and histogram represents the F_{ST} matrix considering different discrete F_{ST} scales, Figure S1b: Heatmap and dendrogram based on pairwise F_{ST} values among the active herds of Blonde Mangalica breed. The heatmap color key and histogram represents the F_{ST} matrix considering different discrete F_{ST} scales, Figure S2a: Multidimensional scaling (MDS) clusters (MDS1&MDS2) of the Blonde Mangalica, Figure S2b: Multidimensional scaling (MDS) clusters (MDS1&MDS3) of the Blonde Mangalica, Figure S2c: Multidimensional scaling (MDS) clusters (MDS1&MDS2) of active herds in the Blonde Mangalica, Figure S2d: Multidimensional scaling (MDS) clusterst (MDS1&MDS3) of active herds in the Blonde Mangalica, Figure S3a: Male migration intensity of the Blonde's total herds, Figure S3b: Female migration intensity of the Blonde's total herds, Figure S3c: Male migration intensity of the Blonde's active herds, Figure S3d: Female migration intensity of the Blonde's current active farms, Figure S4a: Heatmap and dendrogram based on pairwise FST values among the herds of Swal-low-Belly Mangalica breed. The heatmap color key and histogram represents the FST matrix consid-ering different discrete FST scales, Figure S4b: Heatmap and dendrogram based on pairwise FST values among the active herds of Swallow-Belly Mangalica breed. The heatmap color key and histogram represents the FST matrix considering different discrete FST scales, Figure S5a: Multidimensional scaling (MDS) clusters (MDS1&MDS2) of the Swallow_Belly Mangalica, Figure S5b: Multidimensional scaling (MDS) clusters (MDS1&MDS3) of the Swallow_Belly Mangalica, Figure S5c: Multidimensional scaling (MDS) clusters (MDS1&MDS2) of active herds the Swallow_Belly Mangalica, Figure S5d: Multidimensional scaling (MDS) clusters (MDS1&MDS3) of active herds the Swallow_Belly Mangalica, Figure S6a: Male migration intensity of the Swallow_Belly's total herds, Figure S6b: Female migration intensity of the Swallow_Belly's total herds, Figure S6c: Male migration intensity of the Swallow_Belly's active herds, Figure S6d: Female migration intensity of the Swallow_Belly's active herds, Figure S7a: Heatmap and dendrogram based on pairwise FST values among the herds of Red Man-galica breed. The heatmap color key and histogram represents the FST matrix considering different discrete FST scales, Figure S7b: Heatmap and dendrogram based on pairwise FST values among the active herds of Red Mangalica breed. The heatmap color key and histogram represents the FST matrix considering dif-ferent discrete FST scales, Figure S8a: Multidimensional scaling (MDS) clusters (MDS1&MDS2) of the Red Mangalica, Figure S8b: Multidimensional scaling (MDS) clusters (MDS1&MDS3) of the Red Mangalica, Figure S8c: Multidimensional scaling (MDS) clusters (MDS1&MDS2) of active herds in the Red Mangalica, Figure S8d: Multidimensional scaling (MDS) clusters (MDS1&MDS3) of active herds in the Red Mangalica, Figure S9a: Male migration intensity among the Red's total herds, Figure S9b: Female migration intensity among the Red's total herds, Figure S9c: Male migration intensity among the Red's active herds, Figure S9d: Female migration intensity of the Red's active herds.

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