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Mangalitsa: the recovery of a rustic genetic heritage

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Abstract. Nowadays once with the “slow food” trend the old local genetic resources stand out, offering quality instead quantity and not at least with a low carbon footprint. In this context the Mangalitsa swine with a very long history in the Carpathian Basin, comes into researchers and breeders attention with a very promising market, which so far cannot be satisfied by organic products. The main advantages of the breed is the climatic stress and disease resistance, specific quality of fat (higher rate of unsaturated fatty acids against saturated fatty acids) and appreciated taste of meat, but not very prolific and with lower weight gain per time unit toward his commercial conspecifics.

Key Words: Rustic gene, *Sus scrofa ferus*, *Sus scrofa domesticus*, Mangalica, Mangalita.

Introduction. There are a high number of swine breeds reared in conventional farming so called “high maintenance” breeds which require regular, prophylactic measures and concentrated feeds with high carbon footprint to exteriorize their genetic potential. These kinds of breeds are unable to fulfill their potential performance in organic agriculture system. But there is some breeds adapt well to these systems; especially local/native ones since they utilize lower quality feed (low cost, unprocessed), they are more resilient to climatic amplitude, and are more resistant to local parasites and diseases (rustic character). Although the breeding process has to focus on the market demands (mass or niche production) (Ichim 2012; Van Diepen et al 2007).

“The choice of breeds/breeding used in the organic livestock sector needs to ensure the profitability of the farm, safeguard animal health and welfare, focus on conserving genetic diversity, and promote human health. ‘Genotype x environment’ interactions are important, especially when animals are reared under specific environmental conditions (such as organic production or conservation use). When animals are genetically adapted to specific/extreme conditions, they will be more productive and production costs will be lower. It is important to conserve, develop and utilize local breeds that are genetically adapted to their environment” (Ichim 2012).

In this context come into the Mangalitsa breed which is experiencing his new age renaissance do to the “slow food” trend (Petrescu-Mag 2009).

The Hungarian Blonde Mangalitsa (Figure 1) was created in the 1830's using that time local stock and the Sumadia swine from Serbia, applying a rigorous mating scheme and rational feeding. The result was a rustic and good fat yield producer swine, which morpho-productive characteristics is much improved compared to their balkan relatives. The characteristic fur robe color is from light grey or blonde to red-blonde. The Swallow Bellied Mangalitsa (Figure 1) results as a cross between the Blonde Mangalitsa and Black Mangalitsa, the last one extinct in 1970's. The color is black on the back and white or silver-grey on the lower body regions, on the abdomen, on the dewlap up to the mouth commissure. As size it is slightly under the Blonde Mangalitsa but with higher prolificacy and higher resistance to climate and disease (Gajdócsi 2014). The Red Mangalitsa (Figure

1) was bred in 1910's using the Blonde Mangalitsa and the Salonta swine (red colored) (Gajdócsi 2014; Ciobanu et al 2001). In the 1990's the breed almost extinct, counting a stock of 31 sows (with pedigree), but nowadays there is a few 100 sows and they number is raising (Gajdócsi 2014). According to the president of the Hungarian Mangalitsa Breeders Association, the Red Mangalitsa is the most popular due to its fortunate combinability with the Duroc breed without losing the rustic breed characteristics in term of carcass quality.



Blonde Mangalitsa boar



Blonde Mangalitsa sow



Swallow Bellied Mangalitsa boar



Swallow Bellied Mangalitsa sow



Red Mangalitsa boar



Red Mangalitsa sow

Figure 1. The three officially recognized Mangalitsa breeds: Blonde, Swallow Bellied, Red (source: <http://www.mangalicatenyesztok.hu/fajtak.html>).

Renaissance of the Mangalitsa swine. First of all there was a doubt regarding the origin of the three Mangalitsa breed existing today, if the swine's of different colors really belongs to different breeds. Therefore Zsolnai et al (2006) using ten microsatellite markers (S0005, S0090, S0101, S0155, S0355, S0386, SW24, SW240, SW857, SW951) conducted a study to elucidate the genetic relationships among the indigenous Hungarian Mangalitsa swine breeds, using samples from different geographical locations. The results showed estimated distances (D_s , D_a , F_{st}) which were smallest between Swallow-Bellied and Blonde Mangalitsa, and a highest genetic distance of the Red Mangalitsa from the previous two breeds. These results prove the existence of distinct populations and can be used for assignment of individuals with high probability value (in the range from 0.83 to 0.91) to the different Mangalitsa breeds (Table 1).

Table 1
Distances of Swallow-Bellied (SB), Blond (B) and Red (R) Mangalitsa. In each box the first row is for standard genetic distances - D_s - and errors of D_s ; second row: D_a ; third row: F_{st} (Zsolnai et al 2006)

	SB	B
B	0.1138 (0.0426)	-
	0.0845	-
	0.0641	-
R	0.2002 (0.0775)	0.1992 (0.0726)
	0.1883	0.1618
	0.0994	0.0945

If the Mangalitsa breed almost extinct after the Second World War, do to changing the consumer's habits more oriented for white commercial swine's, nowadays fortunately the Mangalitsa was rediscovered due to its adaptability to stress and disease resistance, motherliness and taste of its meat (Zsolnai et al 2006). Figure 2 shows the evolution of the Hungarian Mangalitsa breeding stock evolution until 2007. The graphic also underline the new age renaissance start (end of the 90's) for this promising breed.

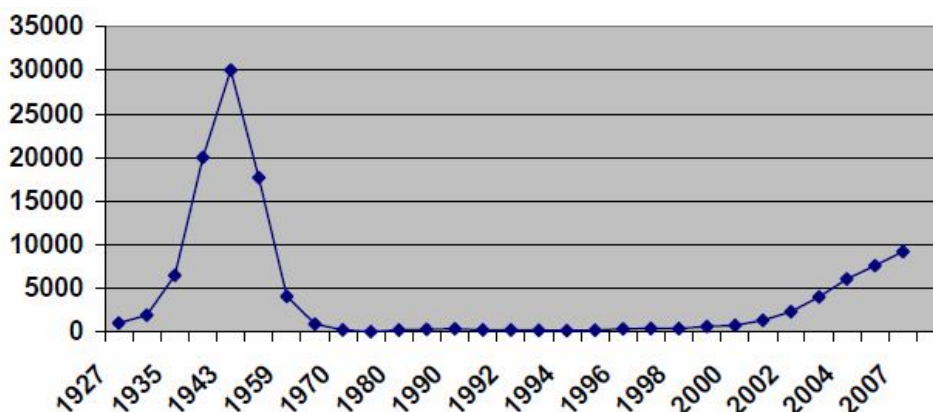


Figure 2. The evolution of the Hungarian Managalitsa stock 1927-2007 (Gajdócsi 2014).

Do to a national Hungarian programme meant to save the breed and ensure breeding stock raising, the number of farms and thus individuals are in a continuous growth (Table 2).

Mentionable populations of Mangalitsa beside Hungary and Romania can be recorded in Germany, Switzerland, Austria and in the area of the formed Yugoslavia (Egerszegi et al 2003; Zăhan et al 2010) (Table 3).

Table 2

Statistics of Mangalitsa farms and breeding stock in 2012, Hungary (Gajdócsi 2014)

<i>Breed</i>	<i>Sow</i>	<i>Boar</i>	<i>Farms</i>
Blonde Mangalitsa	4443	128	75
Swallow Bellied Mangalitsa	1171	55	37
Red Mangalitsa	1877	68	58
Total	7492	251	170

Table 3

The Mangalitsa stock in Europe (Egerszegi et al 2003)

<i>Year</i>	<i>Red</i>		<i>Swallow-Bellied</i>		<i>Blonde</i>	<i>Mangalitsa</i>	<i>Mangalitsa</i>
	<i>Germany</i>	<i>Switzerland</i>	<i>Austria</i>	<i>Germany</i>	<i>Germany</i>	<i>Yugoslavia</i>	<i>Romania</i>
1983	*	*	*	*	*	*	500
1992	*	80	*	*	*	*	*
1994	*	125	*	*	*	*	30
1996	*	105	*	*	*	*	34
1997	50	105	*	45	60	*	*
1998	32	*	*	63	48	*	*
1999	29	*	70	55	43	19	*
2000	45	*	*	80	45	*	*
2001	*	182	*	*	*	*	*
Reference	EAAP	EAAP	GEH	EAAP	EAAP	DAD-IS	EAAP

* No data available; EAAP – European Association of Animal Production; GEH – German Safeguard Society of Ancient and Endangered Domestic Animal Breeds; DAD-IS – Domestic Animal Diversity Information System.

The modern Hungarian Mangalitsa population function of age and gender are characterized by the below presented morphologic indices (Table 4).

Table 4

The characteristic body indices for adult individuals
(source: <http://www.mangalicatenyesztok.hu/fajtak.html>)

<i>Gender</i>	<i>Age</i>	<i>Height (cm)</i>	<i>Weight (kg)</i>
Sow	1	64-67	90-100
	2	72-73	120-140
	3	74-77	140-160
Boar	1	65-70	100-120
	2	75-80	130-150
	3	80-85	150-170

Food and Agriculture Organization (FAO) and International Society of Animal Genetics (ISAG) recommend the use of microsatellite markers for genetic distance characterization of animal breed. Therefore molecular markers became an indispensable tool to understand the genetic structure of populations. A lot of swine breeds were genetically characterized using microsatellite markers. Another important application of microsatellite markers is the identification of individuals and parentage control (Zăhan et al 2009). In order to establish the genetic distance for the Romanian Mangalitsa populations Zăhan et al (2009) conducted studies using 4 microsatellites on samples of 107 Red Mangalitsa individuals from two geographically different locations (Table 5).

Table 5

Characteristics of microsatellite marker (Zăhan et al 2009)

<i>Locus</i>	<i>Chromosome arm</i>	<i>Size (bp)</i>	<i>Sequence of primers (5' → 3')*</i>
SO228	6q	20 24	F: GGC ATA GGC TGG CAG CAA CA R: AGC CCA CCT CAT CTT ATC TAC ACT
SW72	3p	18 20	F: ATC AGA ACA GTG CGC CGT R: TTT GAA AAT GGG GTG TTT CC
SW911	9p	22 21	F: CTC AGT TCT TTG GGA CTG AAC C R: CAT CTG TGG AAA AAA AAA GCC
SW936	15q	21 20	F: TCT GGA GCT AGC ATA AGT GCC R: GTG CAA GTA CAC ATG CAG GG

* F – forward; R – reverse.

Microsatellite markers generated a number between 3 (SW72) and 6 (SW911) alleles per locus, with a total number of 19 alleles. Concerning the size of alleles, these are very much alike with the data's from bibliography (Zăhan et al 2009) (Table 6).

Table 6

The number and size of alleles (Zăhan et al 2009)

<i>Locus</i>	<i>No. of alleles</i>		<i>Size of alleles (pb)</i>	
	<i>References*</i>	<i>Observed</i>	<i>References**</i>	<i>Observed</i>
SO228	12	5	222-266	250-272
SW72	9	3	90-120	97-107
SW911	9	6	149-179	151-165
SW936	13	5	80-124	93-109

* - Laval et al (2000)

** - FAO (MoDAD); Li et al (2004).

The average values of the observed heterozygosity in both populations were higher than the expected one (0.591 – Roman and 0.583 – Turda). But this level of polymorphism is in accordance with the values so far reported for microsatellites in European pig breeds, with an average observed heterozygosity of 0.5. This data indicates that both populations are in genetic imbalance, due to the higher observed heterozygote than the expected one. In the case of the Roman population this situation is due to the imports from Hungary and Austria (Zăhan et al 2009) (Table 7).

Table 7

Frequency of heterozygosity and inbreeding coefficient (FIS) in Mangalitsa population (Zăhan et al 2009)

<i>Locus</i>	<i>Heterozygote</i>		<i>F_{IS} (total)</i>		
	<i>Expected</i>	<i>Observed</i>	<i>W&C</i>	<i>R&H</i>	<i>Individuals</i>
Population of Roman					
SO228	37.9548	44	-0.1602	-0.0715	100
SW72	65.3645	77	-0.1790	-0.1673	102
SW911	69.5222	84	-0.2095	-0.0963	102
SW936	68.6847	76	-0.1071	+0.0405	102
Population of Turda					
SO228	3.0000	4	-0.3913	-0.2500	5
SW72	3.4444	4	-0.1852	-0.2125	5
SW911	2.5556	3	-0.2000	-0.1161	5
SW936	2.6667	4	-0.6000	-0.6250	5

Data's revealed a high population variability that there is no the risk of genetic drift due to the inbreeding coefficients which are almost "zero". Because for the Turda population, even if the number of individuals is low, the results show a similar situation to that from Roman, that's way authors suppose that it is possible that certain individuals from this population to have in their pedigree crosses with another breeds (Zăhan et al 2009).

Another studies conducted by Zăhan et al (2010) in order to perform a genetic characterization of Romanian Red Mangalitsa population by individual fingerprinting 14 microsatellite markers were used (SO005, SO090, SO101, SO155, SO227, SO228, SO386, SW24, SW72, SW240, SW857, SW911, SW936 and SW951). According to the Principal Coordinates Analysis (PCA) there were found a homogeneous population. Although, the excess of observed heterozygosity based on calculated fixation index (FIS) is characteristic to gene immigration into the analyzed population (-0.053 ± 0.017). Just like in the previous studies the incoming individuals from foreign population could be explained by the livestock import from Hungary and Austria in the last years in order to avoid the genetic drift (Figure 3).

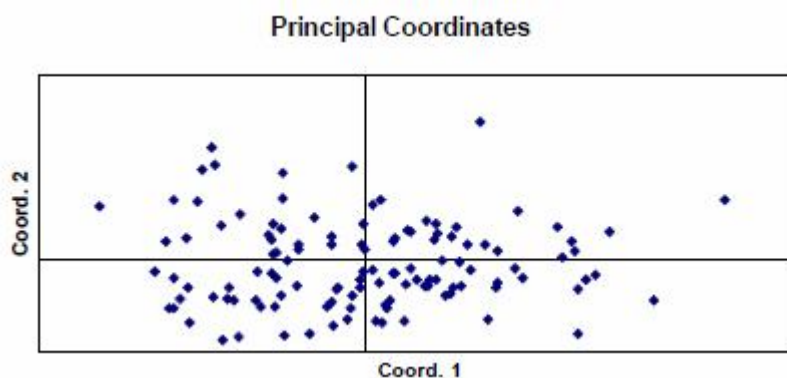


Figure 3. Principal Coordinates Analysis of Mangalitsa (Zăhan et al 2010).

In order to ensure the genetic conservation and genetic variability of a breed threatened by extinction (low breeding stock) the safest method is a gene bank creation (Hettig et al 2012, 2011; Varo-Ghiuru et al 2011a,b; Zăhan et al 2014, 2011).

Conclusions. The rescue of the Mangalitsa breed from extinction is an important task so that is why there is a need of continuous monitoring of the existing populations for a rigorous genetic selection. Using 14 microsatellite markers it was possible to view a homogenate population, with highest level of observed heterozygosity than expected one, as a result of some gene immigration (Mangalitsa import from other population). So far, there is no danger by inbreeding depression. Knowing that the Mangalitsa breed is characterized by a lower prolificacy (Oroian & Petrescu-Mag 2014) than industrial (commercial) breeds and hybrids, researches on reproduction biology and reproductive trait improvement is further needed to make breeding more effective with minimal gene diversity loss per generation.

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