

GENETIC CHARACTERIZATION OF CINTA SENESE PIG BREED: ANALYSIS OF POLYMORPHISMS IN FOUR GENES AFFECTING PERFORMANCE AND PHENOTYPIC TRAITS

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Summary

We analysed 66 Cinta Senese pigs for polymorphisms at two coat colour genes (*MC1R* and *KIT*) and showed that, these loci can be useful for the traceability of meat products of this breed. Moreover, in this breed we identified the presence of the *1843T* allele (~0.04) at the *RYRI* locus and observed the presence of the *B* allele (~0.07) at the *ESR* locus. The information can be used in selection plans aimed to improve the performances of this local pig breed.

Keywords

Cinta Senese, Pig, Polymorphisms, Coat colour, Meat quality

Introduction

Cinta Senese (CS) is a white belted pig breed originated in the Montagnola uplands near Siena, in Tuscany, Italy [1]. Its presence is well documented in several old paintings since the 14th century. This breed has suffered a severe bottleneck in the 1980s and passed from 160,000 heads in 1950s [2] to 81 sows and 3 boars in 1986 [3]. During the 1990s the population size increased reaching in 2003 the number of 886 sows and 201 boars spread in 188 herds. In 1996, a genetic management programme started and a reduction of the inbreeding level of the animals (from 0.21 in 1995 to 0.15 in 2003) was obtained [4]. The breed is well known for the production of high quality meat, has a high degree of rusticity and it is well adapted to outdoors rearing with pasture on woods of chestnuts and acorn. In comparison to selected breeds, CS is characterised by a poorer *in vita* performances and fatter carcasses [5,6]. CS breed shows low reproductive performances (7.68 ± 1.98 litter size at birth and 6.71 ± 2.12 litter size at weaning) in comparison to the improved breeds. In 1998, the national herd-book was started on the basis of recordings going back to the 1970s and Tuscany region promoted a five year research programme on the breed. Moreover, a request of Guarantee of Origins Protection (DOP; Regulations CEE 2081/92) has been presented to EU for CS meat products. With the aim to identify molecular markers that could be used for the traceability and valorisation of the products obtained with this breed we investigated polymorphisms in two genes affecting coat colour, *MC1R* and *KIT* that are coded by the extension and dominant white/white belted loci, respectively. Moreover, we analysed mutations in two other genes affecting meat production, quality and stress resistance traits (*RYRI*) and reproductive parameters (*ESR*) with the final objective to use these data in selection plans aimed to improve the performances of this breed.

Material and Methods

Hair or blood was sampled from a total of 66 CS animals. DNA was extracted and PCR amplified for two fragments (one of 196 bp and one of 154 bp) of the *MC1R* gene [7], for two

products (a 175 bp fragment and a diagnostic product for the duplication) of the *KIT* gene [8,9], for a 134 bp fragment of the *RYRI* gene [7,10] and for a 120 bp fragment of the *ESR* gene [7,11]. The PCR products of the *MC1R* gene were digested with *Bsp*HI (for the 196 bp fragment), *Hha*I and *Bst*UI (for the 154 bp fragment) to distinguish the E^+ , E^{D1} , E^{D2}/E^P (the genotyping methods used here cannot distinguish the E^{D2} allele from the E^P allele) and e alleles at the *extension* locus, the 175 bp products of the *KIT* gene were digested with *Nla*III to analyse the splice site mutation of intron 17 (ssm+, ssm-), the PCR fragment of the *RYRI* were digested with *Hha*I or *Cfo*I to analyse the C1843T mutation and the *ESR* amplicons were digested with *Pvu*II to differentiate the *A* and *B* alleles. The second product of the *KIT* gene is amplified only in animals carrying the duplication (d+) reported by [9].

Results and Discussion

At both coat colour loci, the breed was fixed. At the *MC1R* gene, the analysed animals showed only allele E^{D2}/E^P . At the *KIT* locus, the CS pigs did not show the presence of the splice site mutation of intron 17 (ssm-) and did not show the presence of the duplication breakpoint (d-). Considering these data with what was reported for other breeds at these two loci [8,9,12,13] it is possible to distinguish CS pigs from Wild Boar (E^+ , ssm-, d-), Meishan and Large Black (E^{D1} , ssm-, d-), Duroc (e , ssm-, d-), Large White (E^P , ssm+, d+) and Landrace (E^P , ssm+, d+) pigs. However, using these data, it is not possible to distinguish CS animals from Hampshire (E^{D2} , ssm-, d-) and, in some cases, from Pietrain (E^P , ssm-, d+ or d-) pigs. Thus, the information obtained at the two coat colour loci, if confirmed in a larger sample of animals, can be used to implement a first traceability protocol for the CS products.

At the *RYRI* locus, 5 animals were carriers of the *1843T* recessive allele, thus its frequency in the breed was ~0.04 confirming what was reported by [14]. This allele causes halothane sensitivity, porcine stress syndrome and PSE (pale, soft, exudative) meat and it will be important to eradicate it from the breed even if no indication of poor meat quality and stress sensitivity has been reported so far in CS. Genealogical data will be analysed in order, eventually, to identify if a blood line may be responsible for the diffusion of this negative allele. A low level of variability was observed also at the *ESR* locus. Allele *A* was the most frequent (~0.93) and only 9 animals were heterozygous for the *B* allele. This allele, in other breeds [11], has been associated with an increased litter size and it will be interesting to evaluate if the same effects could be confirmed also in CS.

In conclusion, with this first study we obtained information that could be used for the protection and valorisation of CS products as well as for the implementation of selection plans avoiding the spreading of negative alleles. Other studies, including more genes, are needed to have more data on the genetic variability and the genetic potential of this breed.

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