

P001

Distribution of functional variants within runs of homozygosity in four Italian cattle breeds

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Several methods have been used to identify genomic regions subjected to selective sweeps. An alternative method can make use of runs of homozygosity (ROH), defined as stretches of homozygous regions in a genome. The aim of the present study was to detect selective sweeps using ROH in four cattle breeds. Individuals of Cinisara (71), Modicana (72), Reggiana (168) and Italian Holstein (96) were genotyped with the Illumina Bovine50SNP v2 BeadChip. To identify genomic regions that were most commonly associated with ROH within each breed, the percentage of occurrences of a single nucleotide polymorphism (SNP) in ROH was calculated across animals. The genomic regions most commonly associated with ROH were identified by selecting the top 1% of the SNPs most commonly observed in ROH in each breed. This approach resulted in the identification of 11 genomic regions in the Cinisara and Italian Holstein, and 8 in Modicana and Reggiana showing increased frequency of ROH. Generally, ROH patterns differed between breeds. There were two commons genomic regions between breed pairs, and in particular one in BTA6 between Modicana and Reggiana and one in BTA10 between Cinisara and Italian Holstein. A highly homozygous region (>45% of individuals with ROH) was found only in Modicana breed in BTA6 (6:37,019,972-39,069,719) within a QTL affecting milk fat and protein concentration. In these genomic regions we identified from 126 to 347 genes for each breed. According to Panther and KEGG database, a majority of the genes was involved in multiple signaling and signal transduction pathways in a wide variety of cellular and biochemical processes. Several of these genes were also comprised in a list of genes related to phenotypes for which cattle breeds have been subjected to strong positive selection. For most genes associated with ROH islands, a biological link to traits such as milk yield and composition, reproduction, immune response, coat colour, genetic disorders and resistance/susceptibility to infectious and diseases, which are known to be under selection, can be hypothesized. These results showed that selective sweeps detected with ROH approach are shared among breeds and that scanning the genome for ROH might be an alternative or complementary strategy to detect selective sweep related with important economically traits.

P002

Litter size traits in Black Slavonian and Nero di Parma pig breeds: effects of farrowing management and sow number *per* herd

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The management of reproduction of local breeds of pigs is the key factor influencing their reproductive efficiency, genetic and biodiversity. The production of offspring and their further raising make the basis of production organization, as well as management strategies in conservation procedure for local pig breeds. The aim of this study was to analyse and evaluate Litter Size (LS) traits in two autochthonous pig breeds according to their similarity in breeding procedure, as Management of Farrowing (MF) and Number of Sows per Herd (NSH), to improve their reproductive performance and self-sustainability. Data analysis included 2026 parities of Black Slavonian (BS) and 906 of Nero di Parma (NP), from the 1st to 10th parity (PAR). The LS traits referred to Total Number of Born (TNB), Number of Born Alive (NBA) and Number of Weaned (NW) piglets. Data analysis was performed using GLM (SAS). Five effects with two double interactions were included in the model of calculation to analyse the possible factors influencing between-breed differences in reproductive efficiency. The following effects were tested: breed (BR), PAR, four season of farrowing (SF) according to calendar year, NSH (three levels: 1-3, 4-10 and 10 reproductive sows per herd) and MF (two levels: controlled farrowing in roofed premises and farrowing at uncontrolled and non-roofed sites) with interaction in the scalar equation as BR*MF and BR*NSH. The results were expressed as Least Squares Means ± SE. Pooled farrowing analysis showed TNB to be lower in BS (6.93 ± 0.08) compared with NP sows (8.31 \pm 0.13), with significant effects (p < .05) of BR, PAR, MF, BR*NSH and BR*MF. The NBA was 6.48 ± 0.09 in BS vs 8.01 ± 0.15 in NP sows, with significant effects (p < .05) of BR, PAR, MF, BR*NSH and SF. The



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analysis of NW with 6.24 ± 0.09 in BS and 6.47 ± 0.15 in NP sows pointed to significant effects (p < .05) of PAR, SF, MF, BR*NSH and BR*MF. Accordingly, differences between the breeds could be ascribed to the higher number of controlled farrowing in population of NP *vs* BS with the best results in LS within a group from 4 to 10 sows per herd.

P003

A methodology for the parentage diagnosis of the Italian Brown breed

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Parentage is a measure of the genetic similarities between two related individuals: it is defined as the possession of genes identical by descent. Since the amount of common genes determines phenotypical similarities, e.g. morphological and production-related features, an accurate parentage test is crucial in the selection process. The advent of genomic analyses has paved the use of SNPs information to accurately investigate parentage. However, the current transition from traditional to genomic selection needs methods able to combine different sources of genetic information. In particular, since genomic information is not available for all animals, there is the practical and economic need to cross-examine parentage of genotyped offspring and parents with microsatellites information only. Two steps are necessary to overcome this issue: firstly, to assign microsatellite information from SNPs data of a genotyped animal and secondly, to use microsatellites for the lineage verification.

The objective of this study was to design a method capable to analyse microsatellites data that validates pedigree information. The data was provided by National Brown Cattle Breeders' Association (ANARB) and was made up of 49,828 cattle with microsatellite information from SNP data, 37,262 cattle with official microsatellite data and a pedigree database with 2,399,305 cattle.

The first stage was to create an algorithm that cross-examined 12 microsatellites per animal along with the microsatellites from the presumed parents, to check the correctness of the pedigree.

The procedure was developed by using the software R, which has permitted to deal with large databases. The conditions used for the parentage diagnosis followed the ISAG protocol and the ICAR guidelines. The accuracy of the method was checked by comparing the results obtained by microsatellite analysis with the official parentage data for the 37,262 animals where official analyses were available. The comparison of the results between the proposed method and the available official verifications led to an accuracy of 96.2%. Consequently, the procedure has allowed more than 12,000 new parentage verifications and the correction of 600 pedigree information.

This procedure is useful for direct verification, without further external laboratory testing, of parentage compatibility when different sources of information are already available: SNPs and microsatellites.

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P004

Biodiversity in tench populations of Sicily

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Previous studies on mtDNA revealed the existence of genetic variability in Italian tench populations. With this study we extended the analysis to tench populations of Sicily, with the aim of verifying if the long geographical isolation affected their genetic differentiation.

A total of 72 fin samples were collected from six wild tench populations living in rivers (Alcantara, ALC; Irminio, IRM; Prainito, PRA; Sant'Elia, SEL) or water basins (Cesarò, CES; Santa Ninfa, NIN) located in different areas of Sicily. The PCR-RFLP technique was used to analyse the variability at the same four mtDNA segments considered in the previous studies (ND1, ND6, cytb and D-loop) to make it possible the comparison of all the Italian populations studied so far. MEGA and Arlequin softwares were used for data analysis.

Three haplotypes (H1, H3, H5, according to the nomenclature used in the previous studies) were found in the Sicilian populations: H1 was present in all the populations (frequency: $0.4 \div 1.0$); H3 was observed in ALC, CES, IRM and PRA, while H5 was found only in PRA. Therefore H1 was confirmed as the most widespread haplotype in tench; H3, exclusive of Italian populations, had been also reported in tench of the Central Italy, suggesting a common phylogenetic history; surprisingly, tench living in Prainito river share the H5 haplotype with fish from Valagola lake (Autonomous Province of Trento, Northern Italy). The more ancestral origin of H3 with respect

