are identified using mpileup command of SAMtools software. The resulting BCF file is passed to "bcftools view" tool to be filtered and converted into VCF format. Finally, for variants annotation the SNPSift software was used. A total of 6,357,170 variations, of which 5,265,739 SNPs and 1,091,431 indels, were discovered. About 77% of the SNPs were present in the *Ovis aries* dbSNP v147 while the remaining were novel SNPs. The discovered SNPs must be validated and then could be used to several applications as phylogenic analysis, genome-wide association studies or genomic selection.

PO14

Effect of *CSN1S1* G allele on some characteristics of milk produced by Cinisara cows

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In bovine milk about 37-40% of total casein is represented by αs_1-casein. The *CSN1S1* G allele is characterised by a less efficient protein synthesis (about 40%) compared with the other known alleles because of the insertion, in the 19th exon, of a Long Interspersed Nuclear Element relict. This allele is responsible for a reduced mRNA stability. The lower proportion of αs_1-casein in milk is associated with faster formation, higher firmness and greater resistance to compression of the curd.

The purpose of this study was to analyse the G allele distribution at the *CSN1S1* locus in Cinisara breed and its influence on some milk traits. The Cinisara is a small Sicilian breed for which, recently, recovery and safeguard actions were accomplished. Milk obtained from this breed is mainly used to produce the *Caciocavallo Palermitano*, a typical stretched-curd (pasta filata) cheese. This product represents an example of link between breed, breeding environment, and traditional dairy technology, factors highly appreciated by consumers today. We typed 192 lactating cows, by means of PCR-RFLP analyses, in order to identify *CSN1S1* G carriers. Individual milk samples of 14 cows (low αs_1-casein) and 23 control cows (normal αs_1-casein) were analysed for total nitrogen (TN) and non-casein nitrogen (NCN) according to FIL-IDF standard procedures, and for fat by an infrared method (Combi-foss 6000, Foss Electric, Hillerød, Denmark). Coagulation properties were measured using the Formagraph. Control cows were chosen in the same herds of G carrier cows and had comparable lactation stage and number. Data were analysed using ANOVA procedure in which the fixed factor of *CSN1S1* was evaluated. The frequency of the *CSN1S1* G allele in the 192 analyzed cows was 0.039 (1 homozygous and 13 heterozygous cows). The analyses of milk traits and clotting parameters show that also in Cinisara the *CSN1S1* G allele is associated with significantly lower protein ($p < .049$), casein ($p < .046$), and casein index ($p < .039$). Moreover the milk of cows with *CSN1S1* G allele show a tendency to a lower percentage of fat ($p < .072$). As a consequence, the *CSN1S1* G allele is associated with significantly lower coagulation time (r) ($p < .019$), and tendentially lower curd firming time (k_{20}) ($p < .057$), and higher curd firmness (a_{30}) ($p < .063$). These results confirm that *CSN1S1* G allele considerably affects milk traits. Further analyses are necessary to evaluate the influence of this allele on yield and composition of *Caciocavallo Palermitano* cheese.

PO15

The genetic structure of Hispano-Arabe horse in the Spanish context

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The Hispano-Arabe horse is the result of the crossed between two breed, the Spanish Pure Breed and Arab Breed and for this particularity to analyze the genetic variability within the Spanish context is necessary. Twenty-five molecular markers were analyzed in 40 random samples from the Hispano-Arabe equine breed, along with 20 other equine races from the Iberian Peninsula. The parameters of genetic diversity estimated in the Hispano-Arabe breed are at the highest compared to the levels obtained in the set of breed analyzed.