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 diSNP v1.47 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.

**P014**

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

Daniela Finizio1, Antonino Di Grigoli2, Carmelisa Valluzzi1, Paola Di Gregorio1, Adriana Di Trani1, Andrea Rando1, Giuseppe Maniaci2, Marco Alamisa2, Adriana Bonanno2

1Scuola di Scienze Agrarie, Forestali, Alimentari ed Ambientali, University of Basilicata, Italy
2Dipartimento Scienze Agrarie e Forestali, University of Palermo, Italy

Contact: paola.digregorio@unibas.it

In bovine milk about 37-40% of total casein is represented by αs₁-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 ref1. This allele is responsible for a reduced mRNA stability. The lower proportion of αs₁-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 Cacciocavare Palermitano, a typical stretched-curd (pasta filata) cheese. This product represents an example of link between breed, breeding environment, and traditional dairy 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 αs₁-casein) and 23 control cows (normal αs₁-casein) were analysed for total nitrogen (TN) and non-casein nitrogen (NCN) according to FID-IDF standard procedures, and for fat by an infrared method (Combi-foss 6900, Foss Electric, Hillerød, Denmark). Coagulation properties were measured using the Formograph. 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 < 0.049), casein (p < 0.046), and casein index (p < 0.059). Moreover the milk of cows with CSN1S1 G allele show a tendency to a lower percentage of fat (p < 0.072). As a consequence, the CSN1S1 G allele is associated with significantly lower coagulation time (r) (p < 0.019), and tendentially lower curd firming time (k90) (p < 0.057), and higher curd firmness (α30) (p < 0.063). 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 Cacciocavare Palermitano cheese.

**Acknowledgements**

The research was funded by Regione Sicilia, Italy, and by University of Basilicata research funds (RIL).

**P015**

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

Mayra M. Gómez Carpio1-2, Vincenzo Landi1-2, Amparo Martínez Martínez1, José Manuel León Jurado3, María Antonia Revidatti4, José Luis Vega-Pla2, Juan Vicente Delgado Bermejo2, BioHorse Consortium

1Department of Genetic, Faculty of Veterinary. University of Cordoba, Spain
2Animal Breeding Consulting, S.L., Cordoba, Spain
3Laboratorio de Investigación Aplicada, Ministerio de Defensa, Cordoba, Spain
4Facultad de Ciencias Veterinarias, National University of the Northeast, Corrientes, Argentina
5BioHorse Consortium: http://biohorse.jimdo.com/
Contact: mayrgomezcari@gmail.com

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.