animals' life. A strategy to identify causal mutations and LD markers in the selected genomic regions has been set up for the most significant locations. For each trait, it consists in the whole genome re-sequencing of 2 animals with high probability to be homozygous at the favourable and unfavourable variants. A further animal with high probability to be heterozygous was re-sequenced as control. This approach was applied to investigate 4 regions associated with FEC, SCC and PTB. In this paper we present the strategy focusing on the position associated ($p<.10E-13$) with susceptibility to paratuberculosis on OAR 20 (24875590 bp). Genomic re-sequencing with 12X coverage was performed with an Illumina HiSeq sequencer. The quality controls were performed with fastQC, and sequences were mapped to the reference genome (Ovis aries v3.1, Archibald 2010), with BWA (Li, 2009). Variant call was performed with GATK (McKenna, 2010) with a base quality cut off >30 bases for calling. The segment to focus on was defined basing on IBD coefficients between the two analysed haplotypes (H+ and H-). The hypothesis was that causal mutations were alternatively homozygous in the two animals and included in the genome portion where the segment showing IBD = 1 between the 3 H+ overlapped with the segment showing IBD = 1 between the 3 H- ones. This explored region spanned from 24389525 to 25565801 bp, overlapping part of the MHC region. Identified polymorphisms were filtered for concordance with the expected genotypes (alternative homozygous). Functional annotation of filtered SNPs (n = 3535) and INDELs (n = 239) was performed by Variant Effect Predictor (McLaren et al. 2010) using the gene annotation database from Ensembl release 87 (2016). In the explored region, 1125 variants were identified on 21 annotated genes. Three non-synonymous SNP were identified in 2 protein coding regions (ENSOARG014759, and ENSOARG015866). A further Stop_gained variant was detected on ENSOARG015660.

Acknowledgements

The research is funded by MIPAAF through the project "BIODIVSEL".

O074

Drawing up worldwide goat diversity and post-domestication history: update from ADAPTmap project

Licia Colli[1,2], Marco Milanesi[1,3], Marcello Del Corvo[1], Andrea Talenti[4], Francesca Bertolini[5], Minhui Chen[6], Alessandra Crisà[7], Kevin Daly[8], Bernt Guldbrandtsen[6], Stéphane Joost[9], Johannes A. Lenstra[10], Ezequiel L. Nicolazzi[11], Estelle Rochat[9], Benjamin D. Rosen[12], Max F. Rothschild[5], Bertrand Servin[13], Tad S. Sonstegard[14], Roberto Steri[7], Elia Vajana[1], Curtis P. Van Tassell[12], Paolo Ajmone-Marsan[1,2], Paola Crepaldi[4], Alessandra Stella[11], the ADAPTmap Consortium

[1]*Istituto di Zootecnica, Università Cattolica del Sacro Cuore, Piacenza, Italy*
[2]*BioDNA Centro di Ricerca sulla Biodiversità e sul DNA Antico, Università Cattolica del Sacro Cuore, Piacenza, Italy*
[3]*Department of Support, Animal Production and Health, São Paulo State University, Brazil*
[4]*Dipartimento di Medicina Veterinaria, University of Milano, Italy*
[5]*Department of Animal Science, Iowa State University, United States of America*
[6]*Center for Quantitative Genetics and Genomics, Aarhus University, Denmark*
[7]*Centro di Ricerca per la Produzione delle Carni e il Miglioramento Genetico, Consiglio per la Ricerca in Agricoltura e l'Economia Agraria, Monterotondo (RM), Italy*
[8]*Population Genetics Lab, Trinity College of Dublin, Ireland*
[9]*Laboratory of Geographic Information Systems, École Polytechnique Fédérale de Lausanne, Switzerland*
[10]*Faculty of Veterinary Medicine, Utrecht University, Netherlands*
[11]*Fondazione Parco Tecnologico Padano, Lodi, Italy*
[12]*Animal Genomics and Improvement Laboratory, Beltsville, Maryland, United States of America*
[13]*Génétique, Physiologie, Systèmes d'Élevage, French National Institute for Agricultural Research, Toulouse, France*
[14]*Recombinetics Inc., Saint Paul, Minnesota, United States of America*
Contact: licia.colli@unicatt.it

The study of goat adaptation to different environments is a major aim of the international ADAPTmap project, which joins the genotyping and re-sequencing efforts of the International Goat Genome Consortium (IGGC), the African Goat Improvement Network (AGIN), Feed the Future program of United States Agency for International Development and NEXTGEN EU project.
Having a worldwide distribution, and thriving across a variety of contrasting habitats, goats offer an attractive opportunity to address the genetics of adaptation. This has to start with extensive analyses of the patterns of diversity, thus, a set of 144 breeds, representing 36 countries from 5 continents, has been genotyped with the Illumina GoatSNP50 BeadChip. Several analytical approaches have been adopted to describe the patterns of molecular variation across Africa, Europe and western Asia. The results obtained so far reveal a strong partitioning among continents. Three major gene pools correspond to goats from Europe, Africa and western Asia, while

further sub-structuring reflects the main post-domestication migration routes. The reconstruction of past migration events highlighted several exchanges mainly between African populations, which often involve admixed and cosmopolitan breeds. In addition, extensive gene flow was revealed within specific areas (e.g., southern Europe, Morocco and Mali-Burkina Faso-Nigeria), while isolation due to geographical causes (e.g. insularity) or human management has brought a decrease in local gene flow. Taken together, these results confirm that after domestication in the Fertile Crescent in the early Neolithic era (approx. 15,000 BP), domestic goats spread to Europe, Africa and Asia through divergent migration routes, which determined the major genomic background of the continental populations. During the following centuries, due to geographical and reproductive isolation, further sub-structuring of diversity occurred at the local level. This has been accompanied by additional migrations and/or importations, the traces of which are still detectable, such as the clear African signatures in the goat populations of the Canary Islands and Southern America.

O075

Italian Goat Consortium: a collaborative project to study the Italian caprine biodiversity

Andrea Talenti[1], Stefano Frattini[1], Salvatore Mastrangelo[2], Rosalia Di Gerlando[2], Baldassare Portolano[2], Emiliano Lasagna[3], Francesca M. Sarti[3], Simone Ceccobelli[3], Marco Milanesi[4], Licia Colli[4], Elena Ciani[5], Dominga Soglia[6], Stefano Sartore[6], Roberta Ciampolini[7], Alessandra Crisà[8], Roberto Steri[8], Gennaro Catillo[8], Donata Marletta[9], Salvatore Bordonaro[9], Mariasilvia D'Andrea[10], Stefania Chessa[11], Bianca Castiglioni[11], Pasqualino Loi[12], Tiziana Sechi[13], Antonello Carta[13], Riccardo Negrini[4,16], Alessandra Stella[11], Alessio Valentini[15], Francesco Panella[3], Giulio Pagnacco[1], Fabio Pilla[10], Paolo Ajmone-Marsan[4], Paola Crepaldi[1], the Italian Goat Consortium

[1]Dipartimento di Medicina Veterinaria, University of Milano, Italy
[2]Dipartimento Scienze Agrarie e Forestali, University of Palermo, Italy
[3]Dipartimento di Scienze Agrarie, Alimentari ed Ambientali, University of Perugia, Italy
[4]Centro di Ricerca sulla Biodiversità e sul DNA Antico, Università Cattolica del Sacro Cuore, Piacenza, Italy
[5]Dipartimento di Bioscienze, Biotecnologie e Biofarmaceutica, University of Bari "Aldo Moro", Italy
[6]Dipartimento di Scienze Veterinarie, University of Torino, Italy
[7]Dipartimento di Scienze Veterinarie, University of Pisa, Italy
[8]Centro di Ricerca per la Produzione delle Carni e il Miglioramento Genetico, Consiglio per la Ricerca in Agricoltura e l'Economia Agraria, Monterotondo (RM), Italy
[9]Dipartimento di Agricoltura, Alimentazione e Ambiente, University of Catania, Italy
[10]Dipartimento Agricoltura, Ambiente e Alimenti, University of Molise, Campobasso, Italy
[11]Istituto di Biologia e Biotecnologia Agraria, Consiglio Nazionale delle Ricerche, Italy
[12]Dipartimento di Scienze Biomediche Comparate, University of Teramo, Italy
[13]Dipartimento per la Ricerca nelle Produzioni Animali, AGRIS Sardegna, Olmedo (SS), Italy
[14]Associazione Italiana Allevatori, Laboratorio di Genetica e Servizi, Italy
[15]Dipartimento per l'Innovazione dei Sistemi Biologici, Agroalimentari e Forestali, University of Viterbo, Italy
[16]Associazione Nazionale della Pastorizia, Italy
Contact: paola.crepaldi@unimi.it

The Italian Goat Consortium (IGC), joined the effort of many Universities and Research Institutes, in a comprehensive study of the Italian goat population genetic makeup using a medium density (54K) SNPs chip. Currently IGC has genotyped more than 1,000 animals from more than 30 goat breeds and populations from all Italian geographical and agro-ecological areas of goat rearing.

The aim of this work is to obtain a clear picture of the Italian caprine biodiversity, to reconstruct the ancestry, to disentangle the genetic background and to assess the relationships among and within the investigated breeds. To date, the IGC dataset includes about 50 million genotypes. The data were quality checked by excluding markers and individuals on the basis of missing genotypes, minor allele frequency and close individual relatedness. Genetic relationships among and within breeds was investigated by Multi-Dimensional Scaling and Principal Component Analysis. Population structure, ancestry models and admixture were estimated by ADMIXTURE and fastSTRUCTURE software. Finally, phylogenic trees were reconstructed with PHYLIP software suite starting from shared-allele identity by state, and Reynolds distance matrices, while past migration events were modeled with TreeMix software.

The results confirmed high levels of genetic polymorphism and confirmed the North-South geographical pattern of diversity, previously reported on a smaller sample of Italian goat breeds. The analysis also revealed a pivotal role of Central Italy in connecting the genetic resources of the northern and southern areas of the country, and confirms the genetic isolation of insular breeds. Moreover, some breeds show clearly distinctive and homogeneous gene pools, whereas other breeds present complex and, in some cases, dishomogeneous genetic background.