loci for tick burden and *T. parva parva* infection, respectively. By exploring a region of 25 kbp around the significant loci, two genes were identified as putatively involved into local adaptation for ECF: PRKG1 (Protein kinase, cGMP-dependent, type I) and SLA2 (Src-like-adaptor 2). PRKG1 is an inflammatory response-related gene already described as associated with tick resistance in indigenous South African cattle. SLA2 is involved with lymphocyte proliferation regulatory pathways, which are known to be modified by *T. parva parva* infection. Additionally, a preliminary ancestry analysis of the highlighted candidate regions showed a mixed sanga (African taurine *x* zebu) and zebuine origin for PRKG1 region, and a prevalent sanga origin for SLA2 region.

Acknowledgements

The research was funded by the European project NEXTGEN, which allowed both genotyping and epidemiological data collection. The authors are also grateful to Graeme S. Cumming who kindly provided *R. appendiculatus* occurrence dataset used in species distribution modelling.

*Co-senior authorship

O018

Variation of Madura cattle in Madura Island, Indonesia

Tri Satya Mastuti Widi[1], Nuzul Widyas[2]

[1]*Department of Animal Production, University of Gadjah Mada, Yogyakarta, Indonesia*
[2]*Department of Animal Husbandry, University of Sebelas Maret, Surakarta, Indonesia*
Contact: widi.tsm@ugm.ac.id

Madura cattle are between the most important local cattle in Indonesia: they are probably a crossing of Bali (a domesticated form of the Banteng, *Bos javanicus*), *Bos indicus* and *Bos taurus* breeds. The uniformity of this hybrid was achieved after hundreds years of selection in the island of Madura. Madura cattle are embedded in many cultural aspects of local people. Two famous traditional festivals involving Madura cattle are Karapan (a bull racing) and Sonok (a cow/heifer beauty contest); animals from different areas are bred specifically for each event, and also the management practices are differently focused: as a result, there are visible phenotypic differences between the Karapan and Sonok sub-populations.

The aim of this study was to prove scientifically the existing phenotypic variation between these two sub-populations. Phenotypic traits were collected from 38 and 86 cows used for Karapan and Sonok breeding respectively, obtained data were analyzed using "R" programme. T-test was used to analyze body measurements data and showed that Sonok is significantly larger than Karapan ($p<.05$) in all dimensions. Exterior traits like body color patterns, dewlap, hump or backline were analized using χ^2 which also showed significant differences ($p<.05$) between the two sub-populations. Principal Component Analysis was used to visualize the underlying pattern of body measurements data. We could see separate clusters between the Sonok and the Karapan where the first two PC explained 67% and 16% of the total variance. These results allow discriminating the Sonok from the Karapan by means of body measurements and exterior traits.

Acknowledgements

The research was funded by Directorate General of Higher Education, Ministry of Research, Technology and Higher Education, Republic of Indonesia.

O019

BOVITA: a first overview on genome-wide genetic diversity of Italian autochthonous cattle breeds

Salvatore Mastrangelo[1], Paolo Ajmone-Marsan[2], Alessandro Bagnato[3], Luca M. Battaglini[4], Riccardo Bozzi[5], Antonello Carta[6], Gennaro Catillo[7], Martino Cassandro[8], Sara Casu[6], Roberta Ciampolini[9], Elena Ciani[10], Paola Crepaldi[3], Mariasilvia D'Andrea[11], Rosalia Di Gerlando[1], Luca Fontanesi[12], Maria Longeri[3], Nicolò P. P. Macciotta[13], Roberto Mantovani[8], Donata Marletta[14], Donato Matassino[15], Marcello Mele[16], Giulio Pagnacco[3], Camillo Pieramati[17], Baldassare Portolano[1], Francesca M. Sarti[18], Fabio Pilla[11]

[1]*Dipartimento Scienze Agrarie e Forestali, University of Palermo, Italy*
[2]*Istituto di Zootecnica, Università Cattolica del Sacro Cuore, Piacenza, Italy*
[3]*Dipartimento di Medicina Veterinaria, University of Milano, Italy*
[4]*Dipartimento di Scienze Agrarie Forestali e Alimentari, University of Torino, Italy*
[5]*Dipartimento di Scienze delle Produzioni Agroalimentari e dell'Ambiente, University of Firenze, Italy*
[6]*Unità di Ricerca di Genetica e Biotecnologie, Agris Sardegna, Sassari, Italy*
[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]*Dipartimento di Agronomia Animali Alimenti Risorse Naturali e Ambiente, University of Padova, Italy*

[9]Dipartimento di Scienze Veterinarie, University of Pisa, Italy
[10]Dipartimento di Bioscienze Biotecnologie e Biofarmaceutica, University of Bari, Italy
[11]Dipartimento Agricoltura, Ambiente e Alimenti, University of Molise, Italy
[12]Dipartimento di Scienze e tecnologie Agroalimentari, Alma Mater Studiorum University of Bologna, Italy
[13]Dipartimento di Agraria, University of Sassari, Italy
[14]Dipartimento di Agricoltura, Alimentazione, Ambiente, University of Catania, Italy
[15]Consorzio per la Sperimentazione, Divulgazione e Applicazione di Biotecniche Innovative, Benevento, Italy
[16]Dipartimento di Scienze Agrarie, Alimentari e Agro-ambientali, University of Pisa, Italy
[17]Dipartimento di Medicina Veterinaria, University of Perugia, Italy
[18]Dipartimento di Scienze Agrarie, Alimentari, Ambientali, University of Perugia, Italy
Contact: pilla@unimol.it

Analysis of genomic data is increasingly becoming part of the livestock industry and is an invaluable resource for effective management of breeding programs in small populations. The recent availability of genome-wide SNP panels allows providing background information concerning genome structure in domestic animals, opening new perspectives to livestock genetics. BOVITA was established to join local efforts and resources for the genomic characterization of Italian local cattle breeds. Despite the growing diffusion of some cosmopolite specialized breeds, several autochthonous breeds are still bred in Italy. The main aim of the BOVITA is to investigate the genomic structure of Italian local cattle breeds, to provide information on their genetic status that will be useful for the management of the genetic variability, as a contribution to biodiversity conservation and prioritization actions.

A total of about 800 animals (20-32 per breed) belonging to thirty Italian cattle breeds (Agerolese, Barà-Pustertaler, Burlina, Cabannina, Calvana, Chianina, Cinisara, Garfagnina, Italian Brown, Italian Holstein, Italian Simmental, Marchigiana, Maremmana, Modenese, Modicana, Mucca Pisana, Pezzata Rossa d'Oropa, Piedmontese, Pinzgau, Podolica, Pontremolese, Pustertaler, Reggiana, Rendena, Romagnola, Rossa Siciliana, Sarda, Sardo-Bruna, Sardo-Modicana and Ottonese-Varzese) and two cosmopolitan breeds (Charolaise and Limousine) genotyped with the Illumina BovineSNP50 v2 BeadChip array were collected for the analysis. The genotypes of several breeds were detected in the frame of the project, whereas for some breeds these data are derived by previous studies. The dataset will be analyzed to: study several aspects of population genetic diversity, multidimensional scaling plot, population structure, linkage disequilibrium, and runs of homozygosity. In addition, comparative analysis of conserved haplotypes will be conducted to identify genomic segments under selection pressure. Such information also provides important insights into the mechanisms of evolution and is useful for the annotation of significant functional genomics regions. Data analysis will also be useful to select SNPs suitable for parentage test and breed genetic traceability. The analysis of the data will pinpoint the genetic distinctiveness of Italian breeds. Moreover, the obtained results contribute to a better characterization of history and genetic structure of Italian cattle breeds.