



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

Journal:	<i>Italian Journal of Animal Science</i>
Manuscript ID	TJAS-2017-0180.R1
Manuscript Type:	Abstract Submission
Date Submitted by the Author:	n/a
Complete List of Authors:	<p>MASTRANGELO, Salvatore; Università degli Studi di Palermo, Scienze Agrarie e Forestali Ajmone-Marsan, Paolo; Università Cattolica del Sacro Cuore, Istituto di Zootecnia Bagnato, Alessandro; Università degli Studi di Milano, Dipartimento di Medicina Veterinaria Battaglini, Luca; University of Torino, Dept. of Agricultural, Forest and Food Sciences; Bozzi, Riccardo; Università degli Studi di Firenze, Scienze delle Produzioni Agroalimentari e dell'Ambiente Carta, Antonello; Agris Sardegna, Unità di Ricerca di Genetica e Biotecnologie, Catillo, Gennaro; CREA-PCM - Consiglio per la ricerca in agricoltura e l'analisi dell'economia agraria, Centro per la Produzione delle Carni e il Miglioramento Genetico, Cassandro, Martino; University of Padova, DAFNAE Casu, Sara; Agris Sardegna, Unità di Ricerca di Genetica e Biotecnologie, Ciampolini, Roberta; Università degli Studi di Pisa, Dipartimento di Scienze Veterinarie ciani, elena; University of Bari Crepaldi, Paola; Università degli Studi di Milano, Dipartimento di Medicina</p>

	<p>Veterinaria D'ANDREA, Mariasilvia; Università degli Studi del Molise, Dipartimento Agricoltura, Ambiente e Alimenti Di Gerlando, Rosalia; Università degli Studi di Palermo, Scienze Agrarie e Forestali Fontanesi, Luca; University of Bologna, Dept. of Agricultural and Food Sciences - Division of Animal Sciences Longeri, Maria; Università degli Studi di Milano Macciotta, Nicolo; University of Sassari, Dept. of Agricultural Sciences Mantovani, Roberto; University of Padua, Department of Agronomy Food Natural resources Animals and Environment (DAFNAE) Marletta, Donata; University of Catania, Di3A Matassino, Donato; Consdabi Mele, Marcello; University of Pisa, Dept. of Agriculture, Food and Environment Pagnacco, Giulio; Università degli Studi di Milano, Dipartimento di Medicina Veterinaria Pieramati, Camillo; Università degli Studi di Perugia, Dipartimento di Medicina Veterinaria Portolano, Baldassare; Università degli Studi di Palermo, Scienze Agrarie e Forestali Sarti, Francesca Maria; Università degli Studi di Perugia, Scienze Agrarie, Alimentari e Ambientali Pilla, Fabio; Università degli Studi del Molise, Dipartimento Agricoltura, Ambiente e Alimenti</p>
<p>Abstract:</p>	<p>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.</p> <p>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, Piemontese, 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, multi-dimensional 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.</p>

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60



SCHOLARONE™
Manuscripts

For Peer Review Only

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

Salvatore Mastrangelo¹, Paolo Ajmone Marsan², Alessandro Bagnato³, Luca Battaglini⁴, Riccardo Bozzi⁵, Antonello Carta⁶, Gennaro Catillo⁷, Martino Cassandro⁸, Sara Casu⁶, Roberta Ciampolini⁹, Elena Ciani¹⁰, Paola Crepaldi³, Mariasilvia D'Andrea¹¹, Rosalia Di Gerlando¹, Luca Fontanesi¹², Maria Longeri³, Nicolò P.P. Macciotta¹³, Roberto Mantovani⁸, Donata Marletta¹⁴, Donato Matassino¹⁵, Marcello Mele¹⁶, Giulio Pagnacco³, Camillo Pieramati¹⁷, Baldassare Portolano¹, Francesca Maria Sarti¹⁸, Fabio Pilla¹¹

¹ University of Palermo, Dipartimento Scienze Agrarie e Forestali, 90128 Palermo, Italy

² University of Sacred Heart, Istituto di Zootecnia, 20122 Piacenza, Italy

³ Università di Milano, Dipartimento di Medicina Veterinaria, 20133 Milano, Italy

⁴ University of Torino, Dipartimento di Scienze Agrarie Forestali e Alimentari, 10095 Grugliasco (TO), Italy

⁵ University of Firenze, Dipartimento di Scienze delle Produzioni Agroalimentari e dell'Ambiente, 50144 Firenze, Italy

⁶ Agris Sardegna, Unità di Ricerca di Genetica e Biotecnologie, 07100 Sassari, Italy

⁷ CREA, Centro per la Produzione delle Carni e il Miglioramento Genetico, 00015 Monterotondo (RM), Italy

⁸ University of Padova, Dipartimento DAFNAE, 35020 Legnaro (PD), Italy

⁹ University of Pisa, Dipartimento di Scienze Veterinarie, 56100 Pisa, Italy

¹⁰ University of Bari, Dipartimento di Bioscienze Biotecnologie e Biofarmaceutica, 70124 Bari, Italy

¹¹ University of Molise, Dipartimento Agricoltura, Ambiente e Alimenti, 86100 Campobasso, Italy

¹² University of Bologna, Dipartimento di Scienze e tecnologie Agroalimentari, 40127 Bologna, Italy

¹³ University of Sassari, Dipartimento di Agraria, 07100 Sassari, Italy

¹⁴ University of Catania, Dipartimento di Agricoltura, Alimentazione, Ambiente, 95125 Catania, Italy

¹⁵ Consorzio per la Sperimentazione, Divulgazione e Applicazione di Biotecnologie Innovative, 82100 Benevento, Italy

¹⁶ University of Pisa, Dipartimento di Scienze Agrarie, Alimentari e Agro-ambientali, 56124 Pisa, Italy

¹⁷ University of Perugia, Dipartimento di Medicina Veterinaria, 06126 Perugia, Italy

¹⁸ University of Perugia, Dipartimento di Scienze Agrarie, Alimentari, Ambientali, 06121 Perugia, Italy

Corresponding author: 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.

1
2
3 51 A total of about 800 animals (20-32 per breed) belonging to thirty Italian cattle breeds (Agerolese,
4 52 Barà-Pustertaler, Burlina, Cabannina, Calvana, Chianina, Cinisara, Garfagnina, Italian Brown,
5 53 Italian Holstein, Italian Simmental, Marchigiana, Maremmana, Modenese, Modicana, Mucca
6 54 Pisana, Pezzata Rossa d'Oropa, Piemontese, Pinzgau, Podolica, Pontremolese, Pustertaler,
7 55 Reggiana, Rendena, Romagnola, Rossa Siciliana, Sarda, Sardo-Bruna, Sardo-Modicana and
8 56 Ottonese-Varzese) and two cosmopolitan breeds (Charolaise and Limousine) genotyped with the
9 57 Illumina BovineSNP50 v2 BeadChip array were collected for the analysis. The genotypes of several
10 58 breeds were detected in the frame of the project, whereas for some breeds these data are derived by
11 59 previous studies. The dataset will be analyzed to: study several aspects of population genetic
12 60 diversity, multi-dimensional scaling plot, population structure, linkage disequilibrium, and runs of
13 61 homozygosity. In addition, comparative analysis of conserved haplotypes will be conducted to
14 62 identify genomic segments under selection pressure. Such information also provides important
15 63 insights into the mechanisms of evolution and is useful for the annotation of significant functional
16 64 genomic regions. Data analysis will also be useful to select SNPs suitable for parentage test and
17 65 breed genetic traceability. The analysis of the data will pinpoint the genetic distinctiveness of Italian
18 66 breeds. Moreover, the obtained results contribute to a better characterization of history and genetic
19 67 structure of Italian cattle breeds.
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60