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Book of Abstracts

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6W

Demographic and genetic parameters in Miniature Pinscher (*Canis familiaris*) Italian populationStefano Paolo Marelli¹, Elena Colombo¹, Rita Rizzi², Michele Polli¹, Emanuela Tullo²¹Dipartimento di Scienze Animali; ²Dipartimento di Scienze Veterinarie per la Sicurezza Alimentare, Università di Milano, Italy

Corresponding author: emanuela.tullo@unimi.it

The aim of this work was to investigate the genetic and demographic parameters of the Italian population of Miniature Pinscher (MP) and its evolution across generations to supply effective and objective tools for breed conservation and selection strategies. MP is a worldwide known toy breed of German origin, part of FCI group 2: Pinscher and Schnauzer - Molossoid Breeds - Swiss Mountain and Cattle Dogs. Height at withers ranges for dogs and bitches between 25 to 30 cm and the weight between 4 and 6 kg. The coat is short, dense and smooth, the colour is black and tan or red-reddish- dark red brown; MP are wonderful companion and guard dogs particularly adapted to apartment life style. Italian Kennel Club (ENCI) Stud Book official data of 25,065 subjects were analysed (12,880 females, 12,185 males); dates of birth ranged from 1965 to 2009. All the calculations were performed using ENDOG V 4.6 software. Mean maximum number of traced generations was 6.84, mean complete generations were 2.85 and mean equivalent generations 4.14. Average inbreeding coefficient (F) was 0.08 and average relatedness coefficient (AR) was 0.02. The maximum number of puppies entered was recorded in 2003 with 1111 new born MP. Alternating F values were calculated with a constant increasing between the end of the seventies and the first years of nineties (0.11, 1989), maximum calculated individual F value was 0.55. MP are characterized by a significant number of entries per year with low average inbreeding values, the coexistence of two subpopulation: 'show' and 'pet' could be supposed. Further investigation are needed to better understand the genetic asset of MP breed.

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Optimisation of bull epididymal spermatozoa extraction techniques: a tool for improving gene bankingFederica Turri^{1,2}, Manuela Madeddu¹, Teresa Maria Gliozzi¹, Gustavo Gandini², Flavia Pizzi¹¹CNR, Istituto di Biologia e Biotecnologia Agraria, Milano, Italy²Dipartimento di Scienze e Tecnologie Veterinarie per la Sicurezza Alimentare, Università di Milano, Italy

Corresponding author: turri@ibba.cnr.it

Animal gene banks development is limited by high costs of creation. The recovery and freezing of viable sperm from the epi-

didymes of slaughtered animals can be a cheap alternative for preserving male gametes. The aim of this study was to optimize the recovery of bull epididymal spermatozoa comparing the effects of two methods of extraction in combination with egg yolk extender. Testis from 23 Limousine bulls, ranging in age from 13 to 20 months, were collected at the abattoir. Spermatozoa were extracted from the epididymes using two methods: the float-up and the retrograde flushing. The average time for extraction was 16 minutes in both methods. Within each methods half of testis were processed with an egg yolk extender and the second half with an egg-yolk free extender. Sperm concentration, motility, viability and morphology were evaluated. Statistical analyses were carried out using the GLM procedure (SAS package v9.1). Methods of extraction, in combination with the presence of egg yolk in the extender, were considered as fixed effects; age of the bull and time for extraction as covariates. Sperm concentration was not significantly different using either the float-up method or the retrograde flushing (283.5 ± 24.7 and $301.5 \pm 30.3 \times 10^6$ cells/mL, respectively). Flushing technique was better than the float-up method in terms of sperm quality, considering total motility ($78.4 \pm 3.1\%$ vs $61.8 \pm 2.6\%$, $P=0.0003$; respectively) and viability ($88.7 \pm 2.1\%$ vs $77.6 \pm 1.7\%$, $P=0.0003$; respectively). Egg yolk influenced positively motility and morphology in the float-up method, whereas decreased viability in flushed samples. In conclusion, samples extracted by flushing method, with egg yolk, showed a better sperm quality. These data suggest the possible use of epididymal sperm collected by the flushing technique for the creation of cattle semen cryobanks.

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Genetic diversity and structure of Italian sheep breeds inferred by genome-wide SNP analysis: overview of the "Italian Project for Sheep Biodiversity"Fabio Pilla¹, Elena Ciani², Francesca Maria Sarti³, Bianca Moioli⁴, Antonello Carta⁵, Donato Matassino⁶, Paola Crepaldi⁷, Roberta Ciampolini⁸, Donata Marletta⁹, Pier Luigi Acutis¹⁰, Nicolò P.P. Macciotta¹¹, Paolo Ajmone Marsan¹², Baldassarre Portolano¹³¹Dipartimento di Scienze Animali Vegetali e dell'Ambiente, Università del Molise, Italy²Dipartimento di Fisiologia generale ed Ambientale, Università di Bari, Italy³Dipartimento di Biologia applicata, Università di Perugia, Italy⁴CRA, Centro di Ricerca per la Produzione delle Carni e il Miglioramento Genetico, Monterotondo, Italy⁵Agris Sardegna, Olmedo, Italy⁶Consorzio per la Sperimentazione Divulgazione e Applicazione di Biotecnologie Innovative, Benevento, Italy⁷Dipartimento di Scienze Animali, Università di Milano, Italy⁸Dipartimento di Patologia Animale, Profilassi e Igiene degli

Alimenti, Università di Pisa, Italy

⁹Dipartimento di Scienze delle Produzioni Agrarie, Università di Catania, Italy

¹¹Dipartimento di Scienze Zootecniche, Università di Sassari, Italy

¹²Istituto di Zootecnica, Università Cattolica del Sacro Cuore, Piacenza, Italy

¹³Dipartimento Demetra, Università di Palermo, Italy

Corresponding author: pilla@unimol.it

So far, genetic diversity within and among Italian sheep breeds has been investigated almost exclusively by microsatellite markers and never at national scale. Recently, high density Single Nucleotide Polymorphism (SNP) arrays have been developed for the major livestock species, including sheep. In the second half of 2010, a large national collaborative project was launched, within the context of the International Sheep Genome Consortium (ISGC), aiming at characterizing at the genomic level the main Italian sheep breeds, together with some endangered local breeds. Around 500 animals evenly distributed among 19 Italian breeds (Alpagota, Altamura, Appenninica, Bagnolese, Bergamasca, Biellese, Comisana, Delle Langhe, Fabrianese, Gentile di Puglia, Laticauda, Leccese, Massese, Pecora Nera di Arbus, Pinzirita, Sambucana, Sarda, Sopravissana, Valle del Belice) have been genotyped using a 50K SNP array. Molecular data have been pruned according to SNP minor allele frequency (MAF<0.01), frequency of missing genotypes (Geno>0.1) and linkage disequilibrium ($r^2 > 0.5$) using the PLINK software package. The subsequent analysis of the massive data generated by genome-wide SNP genotyping will pinpoint the genetic distinctiveness and levels of admixture of Italian breeds, thus unraveling new aspects of the breed formation process. In addition, comparative analysis of conserved haplotypes will identify genomic segments under selection pressure, highlighting interesting genomic regions. Data analysis will also be useful to select SNP loci suitable for parentage and identity DNA test in Italian breeds.

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Differential expression of sarcoplasmic proteins in meat of lambs reared in Continental Southern Italy

Donato Matassino¹, Marzia Albenzio², Mariangela Caroprese², Elisabetta Castellana³, Francesca Cecchi⁴, Roberta Ciampolini⁴, Dario Cianci³, Elena Ciani³, Mariasilvia D'Andrea⁵, Carmen Di Prisco¹, Filomena Inglese¹, Rosaria Marino², Antonio Muscio², Fabio Pilla⁵, Francesco Romagnuolo¹, Antonella Santillo², Agostino Sevi², Aldo Di Luccia^{1,6}

¹Consorzio per la Sperimentazione, Divulgazione e Applicazione di Biotecnologie Innovative – Sub NFPI.-FAO (Biodiversità Mediterranea), Benevento, Italy

²Dipartimento Scienze delle Produzioni e dell'Innovazione nei Sistemi Agro-alimentari Mediterranei; ⁶Dipartimento di Scienze degli Alimenti, Università di Foggia, Italy

³Dipartimento Fisiologia Generale ed Ambientale, Università di

Bari, Italy

⁴Dipartimento Patologia Animale, Profilassi ed Igiene degli Alimenti, Università di Pisa, Italy

⁵Dipartimento Scienze Animali, Vegetali e dell'Ambiente, Università del Molise, Campobasso, Italy

Corresponding author: matassinod@consdabi.org

The proteomic analysis defines the identity, the structure and the relative abundance of proteins in a given type of cell and in a specific set of conditions.

The analysis of protein profile was carried out to identify possible expression differences of muscular proteins between sheep breeds and use these peculiar profiles as trace back biomarkers. The analyses were carried out on a total of 98 samples of *longissimus dorsi* and of leg muscles pools from 49 ovine belonging to five breeds: Altamura (N=9), Bagnolese (N=10), Gentile di Puglia (N=10), Laticauda (N=10) and Leccese (N=10). The protein profile was investigated using analytical proteomic procedures: 2DGE and MALDI-TOF/MS. The two-dimensional maps were compared by image analysis using Image Master 2D-Platinum to define the position and relative intensity (volume %) of every single spot. In the range of our observation, image analysis highlighted 15 spots common to all samples, identified as: Adenilate kinase, DJ-1, Enolase (2 spot), Hemoglobin (Hb), Myoglobin (Myb) (2 spot), Phosphatidylethanolamine binding protein (PEBP), Superoxide dismutase, Triosephosphate isomerase (TPI) (5 spot) and Ubiquitin. With the exception of Enolase, the expression (volume %) of common spots differed between breeds, within the muscle. There were significant ($P < 0.05$) differences of expression between breeds for 5 spots: Enolase, Myb and TPI (2 spots) for the 'Altamura'; Ubiquitin for the 'Gentile di Puglia' and 'Leccese'. It was furthermore detected a different expression of some proteins between two breeding 'bioterritories': (i) higher expression of Myb and of some TPI spots in the breeds reared in the 'Pugliese' 'bioterritory'; (ii) higher expression of DJ-1, Hb, PEBP and Ubiquitin proteins in the breeds reared in the 'Sannita' 'bioterritory'. These differences might probably be ascribed to environmental effects. Thus obtained results suggest a possible use of the proteomic approach to define physiological peculiarity in specific bioterritories; this may allow to establish a link between ovine meat and the territory that can be used to safeguard local productions.

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Ancient autochthonous genetic type Casertana pig: influence of slaughter age on fatty acid composition of subcutaneous adipose tissue

Donato Matassino¹, Carmela Maria Assunta Barone², Carmen Di Prisco¹, Caterina Incoronato¹, Luigina Rillo¹, Giovanna Varricchio¹, Antonio Zullo², Aldo Di Luccia³

¹Consorzio per la Sperimentazione, Divulgazione e Applicazione di Biotecnologie Innovative – Sub NFPI.-FAO (Biodiversità