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## Book of Abstracts

**Guest Editors: Fulvia Bovera (Coordinator), Marzia Albenzio, Mariangela Caroprese, Rosaria Marino, Gianluca Neglia, Giovanni Piccolo, Angela Salzano.**

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the high-density Affymetrix 600K SNP turkey array were obtained for a total of: 116 individuals from 6 Italian breeds (Colle Euganei, Bronzato Comune Italiano, Parma e Piacenza, Brianzolo, Nero d'Italia and Ermellinato di Rovigo); 7 Narragansett turkeys; 38 turkey from a Commercial Hybrid; 31 Mexican turkeys. A total of 604,196 loci on autosomes were used to identify ROH that were defined setting a minimum of 1000 kb in size and 50 homozygous SNPs; additionally, a maximum gap between SNPs of 100 kb was predefined in order to assure that the SNP density did not affect the ROH. The ROH were obtained with the SVS 8.4 software of Golden Helix®. The proportion of the total genome length affected by ROH was calculated and represent an estimate of the genomic inbreeding F(ROH). The total number of ROH in the overall populations was 3782 with an average number per individual of 42. The breed with the largest average number of ROH (within breed) for individual was the Colli Euganei with 75 (min =11; max =157) while the Mexican (min =1; max =47) and the Hybrid (min =5; max =21) population showed an average number of ROH of 11 and 12 respectively. The Commercial Hybrid was the population with lower number and less variation among individuals of ROH comparable to the Mexican population. According to these results, the Mexican population appears to be under an outbreeding reproductive scheme: in fact, it is farmed as a free-range backyard population where animals are free to mate and migrate across family groups and villages. The two Italian populations with the largest average number of ROH are the Colli Euganei and the Brianzolo with 75 and 64 ROH respectively. The ROH varied in length from 1.4 Mb to 8.37 Mb. Gene Ontology (GO) and KEGG pathways terms for the genes contained in the ROH were identified. The average $F_{IS}$ among all populations in this data set resulted 0.28. The average F(ROH) calculated on the autosome genome length of the Turkey_5.0 assembly resulted 0.031.

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## O024

## Genetic diversity assessment of Kwa-zulu natal native chickens using SSR markers

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Commercialization of breeding in domestic animals has gradually favoured the use of high productive exotic breeds and consequently led to lower population sizes of indigenous, low performing native breeds and South African local chicken populations are no exception to that. Indigenous chickens are recognised as an important component of the rural household livelihood by providing a source of income, and as gifts to strengthen social relationships at a cheaper cost. Characterisation of these important genetic resources can be the first step for their effective management and utilisation, which will facilitate their conservation. The aim of this study was to investigate genetic variation within and between four Kwa-Zulu Natal indigenous chicken populations using 19 microsatellites loci recommended by FAO 2004. Blood was collected from 199 animals of four different regions of Kwa-Zulu Natal: Jozini, Pietermaritzburg, Newcastle, and Port Shepstone. Pure breeds of some South African indigenous chicken breeds (Potchefstroom Koekoek, Ovambo and Venda) were included. One exotic breed (White Sussex) was also sampled to trace any cross breeding. The following parameters were analysed: genetic variation, genetic differentiation, genetic distance, genetic structure and admixture. A total of 161 alleles were observed with an average of 8.47 allele per locus across the 19 microsatellites loci in the eight studied populations. All studied markers were found to be polymorphic. The mean number of observed alleles ranged from 4.63 (Pietermaritzburg) to 5.32 (Port Shepstone). The highest observed heterozygosity (0.70) was detected in Jozini, whereas the lowest (0.61) in Pietermaritzburg. The inbreeding coefficient estimated ranged from −0.0382 in Newcastle to 0.0737 in Pietermaritzburg. The Reynolds weighted genetic distance revealed three distinct clusters; the first cluster included Port Shepstone, Newcastle, Pietermaritzburg and Jozini, the second had Ovambo and Venda, while the last was made of Koekoek and White Sussex. The structure analysis results ascertained that Kwa-Zulu Natal indigenous chickens have distinct gene pools with some level of genetic admixture. The analysed populations are characterised by a noticeable genetic variation; nevertheless, suitable conservation strategies must be planned out before their gene pool could be diluted by uncontrolled breeding with other exotic chickens.

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## O025

## Mating strategy based on DNA parentage information in Italian chicken breeds

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Bionda Piemontese is a slow growing chicken breed, mainly reared for egg and meat production. In this study, we assessed the effect on growth traits of a mating scheme base on genomic parentage information aimed to minimise progeny inbreeding. One hundred and twenty birds (63 males and 57 females) of Bionda Piemontese, were genotyped by a set of 14 microsatellite markers. For each subject, the genetic distances were calculated. Six family lines were identified and hens for each line were grouped in a single box; in every generation for each line the cock with highest genetic variability was identified and mated with the most distant female genetic line. Four hundred and forty individuals of three generations (G0, G1 and G2) were weighed every 15 days from hatch to 180 days of age. Gompertz linear model was used to describe the growth index over the three generations. Daily growth rate significantly increased ($p<.001$) over successive generations in males (G0 = 16 g/d; G1 = 20 g/d; G2 = 23 g/d) and in females (G0 = 12 g/d; G1 = 14 g/d; G2 = 18 g/d). Inflection point age significantly decreased in the last generation ($p<.001$) in males (G0 = 82 d; G2 = 64 d) and in females (G0 = 76 d; G2 = 61 d). Live weight in correspondence of the inflection point increase the last generations in males (G0 = 1035 g; G2 = 1067 g) and in females (G0 = 786 g; G2 = 795 g). Estimated weight at 180 days of age increased over the generations: +20% in cocks (G0 = 2212 g; G1 = 2453 d; G2 = 2657 g) and +17% in hens (G0 = 1713 g; G1 = 1752 g; G2 = 2000 g).

The results showed an improvement of growth performance as rate of growth and final body weight; this can be related to offspring heterozygosity increasing (G0 = 0.66%; G1 = 69%; G2 = 70%) and consequently to inbreeding depression reduction. The use of molecular parentage in mating schemes could be a reliable tool for the management of small size chicken populations and the improvement of their production.

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## O026

## Exploring polymorphisms in genes affecting energy metabolism and skeletal muscle in broiler chickens

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Chicken meat is one of the most popular sources of animal protein for human consumption worldwide. Through advances in genetic selection, farming practices and nutrition, the production of broiler chickens has become more efficient. Genetic selection has contributed significantly to the improvement in growth rate, biological efficiency, breast yield, longevity and leg health. Besides, any condition which impacts the quality of breast meat is of great importance to breeding companies and broiler producers. Carcases affected by breast muscle myopathies (BMM) can be downgraded or in some cases condemned, resulting in economic losses for poultry meat producers. In the present work, we investigated three genes, Peroxisome proliferator-activated receptor gamma coactivator 1-alpha (*PPARGC1A*), that plays a role in glucose and fatty acid metabolism, Growth differentiation factor-8 (*GDF8*) and E3 ubiquitin-protein ligase (*WWP1*), involved in skeletal muscle growth. For the experiment, 90 chickens of six different genetic lines were recruited. *Post mortem* breast fillets were scored for different degrees of white stripping and fatty acids were measured both in breasts and legs; DNA was extracted from breast meat. The III and VIII exons for *PPARGC1A*, I and III exons for *GDF8*, X exon for *WWP1* were amplified by polymerase chain reaction (PCR) by using primers designed in the flanking introns and then sequenced. For *PPARGC1A* four single nucleotide polymorphisms (SNPs), were identified, three in the flanking region of III exons, that did not influence splicing sites and one in VIII exon, that caused a missense mutation (C348W). Four SNPs, that caused synonymous mutation, were detected in *GDF8*. Fifteen SNPs were identified in the intron region of *WWP1*. Allelic, genotypic and haplotypic frequencies were calculated for all SNPs. The effect of the non-synonymous variant C384W on PPARGC1A protein function was evaluated by using the SIFT (**S**orting **I**ntolerant **F**rom **T**olerant) algorithm and the substitution of cysteine with tryptophan in the C-terminal region of protein was predicted not tolerated. Because proteins encoded by the three investigated genes are in the same metabolic network and have been shown to interact, the identified mutation could have an effect on skeletal muscle structure and growth.

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LIVESTOCK SYSTEMS – GHG EMISSIONS IN LIVESTOCK

## O027

## Gas and methane production from two rumen inoculums, used warm, refrigerated, chilled or freeze-dried

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