

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 pre-defined 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 $F(\text{ROH})$. 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 $F(\text{ROH})$ 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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particular, the CAN1 (60% of variability) discriminated the strong alleles, CAN2 (22% of variability) discriminated the weak alleles and CAN3 separated the animals carrying the null alleles. The most discriminant SNPs for the three CANs have been found to be located in the casein cluster. In particular two SNPs mapped in the *CSN1S1* chromosomal position and the breeds carrying the null alleles shown opposite allelic frequencies in relation to the other breeds as results of selective selection pressure. Mahalanobis distance, based on the group centroid position in the three-dimensional space, returns a trend of variation from the strong to null alleles classes. Moreover, the CDA analysis allowed to identify associations of *CSN1S1* alleles with other clustered casein genes. This result could help in the developing of a panel of SNPs useful for selection plans aimed to improve milk technological properties for cheese making or, conversely, to modify milk nutraceutical characteristics for goat's milk intolerance.

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P043

Re-sequencing of genes related to mastitis resistance in dairy cows

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Selection for mastitis resistance should be one of the first aims in dairy farms, since mastitis is a major cause of economic loss. Resistance to mastitis is a complex trait and expression profiles of mammary gland infected with different pathogens were conducted for a better understanding of the mechanism underlying this disease. Many different genes were found to be involved with mastitis, but only the identification of causative mutations could be useful for selection of resistant cows. Wide regions of six genes involved in immune response were re-sequenced to look for causative mutation of mastitis resistance: the pentraxin3 (*PTX3*), the chemokine C-X-C motif receptors (*CXCR1* and *CXCR2*), the toll-like receptor 4 (*TLR4*), the mannose-binding lectin 1 (*MBL1*), and serum amyloid A3 (*SAA3*) genes, respectively on BTA1, BTA2, BTA8, BTA28 and BTA29. DNA was extracted from semen of bulls in the positive (58 bulls) and negative (37 bulls) tails of the distributions of estimated breeding values for somatic cell score. Using a target re-sequencing approach by NGS technique on the MiSeq Illumina platform, we identified a total of 1535

polymorphisms (including SNPs and small indels). Excluding mutations, with a minor allele frequency lower than 0.05 only 384 polymorphisms remained. The original phenotypes were adjusted for population structure using the genomic relationship matrix calculated using this dataset and 4 individuals having an identity by state (IBS) > 0.95 were excluded from the following analysis. To test for associations, mutations with a correlation higher than 0.80 with any others were further excluded, together with polymorphisms deviating from Hardy-Weinberg equilibrium. Finally, 101 polymorphisms were tested for associations. A total of 7 SNPs resulted significantly associated with SCS ($p < .05$): one on *PTX3* (rs208223246, missense variant responsible for the amino acid exchange Glu347Lys), one on *CXCR1* (rs109694601, intron variant), one on *TLR4* (rs134052737, intergenic variant), one on *MBL1* (rs208247354 and rs208491630, respectively intron and upstream gene variant), and two on *SAA3* (rs137746604 and rs210417381, both upstream gene variants). These findings represent the first step toward the use of causative mutations in genetic selection for mastitis resistance in dairy cows.

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P044

Genetic diversity, productive and reproductive performance in Italian chicken breed Bianca di Saluzzo

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Bianca di Saluzzo (BS) is a chicken breed reared in Piedmont region and its substitution with commercial lines caused a reduction in size, associated with a progressive decline due to inbreeding. In this study, genetic diversity, productive and reproductive performance were examined. Birds were kept in standard environmental conditions. At hatching, 177 chicks were weighed and at six weeks of age were separated by sex and transferred to growing pens with free-access to water and were fed with a standard commercial starter diet *ad libitum* followed by a growing diet. All birds were genotyped by a set of 14 microsatellite markers chosen by their high polymorphism. Body weight (BW) was

recorded every two weeks from hatching to the age of 27 weeks. Gompertz model was used to define the growth rate. The performance of laying hens was monitored over a period of 6 months. To evaluate fertility and hatchability, all eggs laid in 2 consecutive weeks were hatched for 12 weeks. Data analysis was carried out with the Excel software. Allelic richness was 3.6 and observed and expected heterozygosity were 0.68. Mean live weights for cocks and hens were 2779 ± 233 g ($n = 79$) and 2089 ± 195 g ($n = 98$). Growth rates in the linear phase were 26.95 ± 3.19 g/day and 16.63 ± 1.90 g/day for male and female birds. In egg collection period for hatch mean 179.5 eggs were taken. Fertility and hatchability were 87.2% and 92.3%. The overall mean chick survival rate to six months of age was 4.6%. The age at first lay ranged between 5 and 6 months, and egg number/month was 14.5, mean egg weight was 60 ± 3 g and laying percentage resulted in 51.6% (max: 76.2%). These results provide an important insight on the genetic and productive characteristic of this local poultry breed that can be used for managing new mating schemes aimed to preserve variability and increase productivity.

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P045

Genetic diversity, productive and reproductive performance in Italian chicken breed Bionda Piemontese

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Bionda Piemontese (BP) is a local slow-growing poultry breed that is mainly reared for meat; hens are also bred for egg production. In this study, the genetic diversity, productive and reproductive performance were examined. The birds were kept in standard environmental conditions at the Poultry Conservation Centre of the University of Turin (Italy). At hatching, 218 chicks were weighed, labelled with a wing metal tag. At six weeks of age, birds were separated by sex and transferred to growing pens with access to an external paddock (20 birds/pen). The birds always had free access to water and were fed with standard commercial starter diet *ad libitum* (0–6 weeks) followed by a growing diet. All birds were genotyped by a set of 14 microsatellite markers

selected for their variability. The body weight (BW) was recorded individually every two weeks from hatching to the age of 27 weeks, for a total of 14 weightings. Gompertz model was used to define the growth rate. The performance of laying hens was monitored over a period of 6 months. To evaluate fertility and hatchability, all eggs laid in 2 consecutive weeks were hatched for 12 weeks. Data analyses were carried out with the Excel software.

The results showed a low genetic variability with an allelic richness of 3.3 but a good individual variability: the observed and expected heterozygosity were 0.675 ± 0.040 and 0.680 ± 0.015 , respectively, Fis index was 0.016. The growth performance was good: the mean live weights for cocks was 2797 ± 253 g ($n = 102$) and for hens 2226 ± 249 g ($n = 116$). The growth rates in the linear phase resulted 26.47 ± 3.19 g/day and 18.42 ± 2.63 g/day for male and female. The fertility and hatchability were 86.5% and 94.2%, respectively showing a good reproductive performance. The mean chick survival rate to six months of age was 4.6%. In egg collection period for hatch mean 184.5 eggs were taken; in total 1107 eggs were collected (6 repetitions). The egg production was lower than commercial layer but consistent with local breed: the age at first lay ranged between 5 and 6 months and Iegg number/month was 14.5, egg weight mean 61 ± 3 g and laying percentage 51.6% (max: 70.7%). In conclusion, the results highlight that BS is local slow-growing and dual-purpose breed with good productive performance.

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P046

Dynamic profile of active metabolic pathways in the subcutaneous fat tissue of Holstein cows during early lactation

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Early lactation is a challenging time for dairy cows, which have to simultaneously cope with milk production and body maintenance. The rapid increase in energy requirements is only partially met by feed and cows enter in a state of negative energy balance (NEB),