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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 ± 233g (n = 79) and 2089 ± 195 (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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PO45
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 egg number/month was 14.5, egg weight mean 61 ± 3g 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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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),
Several hundred single nucleotide polymorphisms in candidate genes: association with six production, carcase, and meat quality traits in Italian Large White pigs

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Italian heavy pig selection programmes include production (average daily gain, ADG; feed gain ratio, FGR), carcass and meat quality traits (weight of LC: lean cuts; HW: ham weight; BFT: backfat thickness; HWLFS: ham weight loss at first salting; and VIF: visible intermuscular fat). In this study, we wanted to evaluate if a selection genotyping approach designed for BFT could identify markers associated with other traits. Italian Large White (ITALW) gilts were chosen according to their extreme estimated breeding values (EBV) for BFT (276 with the most negative and 279 with the most positive EBVs) within a population of about 12,000 sib-tested pigs. A total of 736 single nucleotide polymorphisms (SNPs) within candidate genes were used in this study. Of the genotyped markers, 280 SNPs in 211 genes that had minor allele frequency >5% and call rate >90 were used in association analyses with six traits (ADG, FGR, LC, HW, HWLFS and VIF). To deal with the multiple testing problem in a candidate gene approach, we applied the proportion of false positives (PFP) method, setting a threshold for significance of 0.10. Six SNPs were significant: four for HWLFS and two for LC. The significant SNPs for HWLFS were within genes encoding proteins involved in carbohydrate metabolism (phosphoglucomutase 3, PGM3; and glycogen phosphorylase L, PYGL), transcription regulation and development (mitogen-activated protein kinase 8, MAPK8), and cellular RNA processing and degradation (exosome component 1; EXOS1). The two significant markers for LC were within the TBC1 domain family, member 1 (TBC1D1) gene encoding a protein implicated in regulating the trafficking of glucose transporter 4. These results reveal a possible genetic basis for the relations among BFT, HWLFS and LC, beyond the trivial consideration that fatter hams necessarily lose less weight and complement results obtained in genome-wide association studies.

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Heritability and correlations among milk yield, Body Condition Score and type traits in the Italian Mediterranean Buffaloes (Bubalus bubalis)

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Italian heavy pig selection programmes include production (average daily gain, ADG; feed gain ratio, FGR), carcass and meat quality traits (weight of LC: lean cuts; HW: ham weight; BFT: backfat thickness; HWLFS: ham weight loss at first salting; and VIF: visible intermuscular fat). In this study, we wanted to evaluate if a selection genotyping approach designed for BFT could identify markers associated with other traits. Italian Large White (ITALW) gilts were chosen according to their extreme estimated breeding values (EBV) for BFT (276 with the most negative and 279 with the most positive EBVs) within a population of about 12,000 sib-tested pigs. A total of 736 single nucleotide polymorphisms (SNPs) within candidate genes were used in this study. Of the genotyped markers, 280 SNPs in 211 genes that had minor allele frequency >5% and call rate >90 were used in association analyses with six traits (ADG, FGR, LC, HW, HWLFS and VIF). To deal with the multiple testing problem in a candidate gene approach, we applied the proportion of false positives (PFP) method, setting a threshold for significance of 0.10. Six SNPs were significant: four for HWLFS and two for LC. The significant SNPs for HWLFS were within genes encoding proteins involved in carbohydrate metabolism (phosphoglucomutase 3, PGM3; and glycogen phosphorylase L, PYGL), transcription regulation and development (mitogen-activated protein kinase 8, MAPK8), and cellular RNA processing and degradation (exosome component 1; EXOS1). The two significant markers for LC were within the TBC1 domain family, member 1 (TBC1D1) gene encoding a protein implicated in regulating the trafficking of glucose transporter 4. These results reveal a possible genetic basis for the relations among BFT, HWLFS and LC, beyond the trivial consideration that fatter hams necessarily lose less weight and complement results obtained in genome-wide association studies.

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