

(CSN1S2 D) caseins in milk. The genotyping data obtained provide useful information regarding the productive aptitudes of the four AGTs studied. In fact, the high frequency of CSN1S1 N allele in Neapolitan goat, predisposes this breed to produce low-protein milk for fresh consumption while the high frequency of the allele CSN1S1 F in the Lazio AGTs goat addresses their milk to processing for the production of typical cheese with unique organoleptic and flavor characteristics. Developing safeguard plans that take these results into account will have a higher chance of success, with a consequent increase in the number of animals raised.

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Breeders' management in a heritage breeds' rabbitry

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Population size reduction and genetic erosion are two critical events in domestic animals' productions. The aim of the present research is to analyze breeders' management data recorded in a heritage breeds' rabbitry to determine breeders' husbandry strategies and their effects on some reproductive parameters. Litters' registrations including buck id, doe id, day of birth, litter size (born alive) and weaned kitten were analyzed. Three breeds' litters were studied in a 11 years time lapse: Belgian Hare (BEHA; $N = 151$), Burgundy Fawn (BUFU; $N = 105$), Californian (CALI; $N = 212$). Inclusion of external breeders was considered too (buck origin 0, 1; doe origin 0, 1; litter origin 0, 1, 2). Data analysis was performed by ANOVA using the General Linear Model procedure of SPSS. In our model dependent variables were litter size (born alive) and percentage of weaned kitten, and sources of variation were breed, year of birth and litters' origin (three levels: both parents internal, one parent internal and one parent external, both parents external). The post hoc Bonferroni test was used to investigate the significant differences ($p \leq .05$). The dependent variables number of litters per buck and number of litters per doe were analysed with breed as source of variation. Frequencies distribution of buck origin, doe origin and litter origin were analysed using SAS PROC FREQ procedure and the Chi Square test was used to investigate significant differences. Breed had no effects on litter size (means \pm SE; BUFU 5.75 ± 0.25 , CALI 5.77 ± 0.18 , BEHA 6.06 ± 0.20) and percentage of weaned kitten on born alive ones (mean \pm SE; BUFU 87.18 ± 2.45 , CALI 88.89 ± 1.74 , BEHA 89.86 ± 1.97). Year of birth affected significantly the litter size and percentage of weaned kittens in all the considered breeds: in the last years, the percentage of weaned kittens was higher than in the first years of recording. The inclusion of external breeders did not significantly influence recorded

reproductive data. The number of litters per buck (mean \pm SE; BUFU 1.91 ± 0.21 , CALI 2.34 ± 0.16 , BEHA 1.94 ± 0.12) and per doe (mean \pm SE; BUFU 1.61 ± 0.17 , CALI 1.77 ± 0.13 , BEHA 2.10 ± 0.16) were not influenced by breed. The frequency of use of external breeders is breed specific. Data recording is a basic step in conservation plans; our results supply some information about breeder's management strategies in a heritage breed rabbitry aimed to produce morphologically typical rabbits limiting genetic variability reduction.

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A machine learning approach for the identification of population-informative markers from trout genotyping data

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Cost-effective commercial SNP arrays are now available for several species and this has had a substantial impact on livestock as well as on fields of natural ecology, evolution and conservation biology. Nowadays, genome-wide SNP analysis is the method of choice for the characterization of natural populations. In this context, the identification of a minimum number of SNP with the maximum information to differentiate populations is becoming important but challenging. This may have interesting implications for several downstream applications such as allocation of individuals and comparative analyses of selection signatures. Recently, the use of machine learning approaches and notably of random forest classifier (RF) has been proposed for the identification of the most discriminating genetic markers among thousands of SNP. Here we used the RF algorithm to analyse genotyping data obtained with 57K Trout BeadChip array (Affymetrix) from autochthonous and allochthonous trout populations of Molise rivers and their tributaries. The 48 highest ranked SNP were obtained and compared with the list of the most informative SNP estimated using traditional statistical approaches: Delta, F_{ST} and principal component analyses. In total, 103 specimens were enrolled in the study, from a larger cohort of ~300 fishes caught in 30 different sites of Volturino and Biferno basins. The samples were chosen based on results obtained by PCR-RFLP and preliminary fine-scale population structure outcomes. Trout considered in this study were representative of four different native trout subpopulations and one Atlantic species. Four reduced informative panels were obtained and their performances estimated using correct prediction proportions from RF classification. The correct assignment of the

specimens to their subpopulations had an average of ~92% for all tested approaches. RF shared the highest number of SNP with FST method (19 SNP). Chromosome 3 harboured the largest number of selected SNP across all panels. Six SNP resulted in common among the tested approaches resulting in a correct assignment performance of ~69%. For the first time SNP-array technology and machine learning were combined to identify population informative markers in trout species. Further studies with larger populations and samples size are required to evaluate the validity of the approach.

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Genetic biodiversity study in Mediterranean trout population using SNP array: a case study in Molise region

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Mediterranean trout (*Salmo cettii*) is a freshwater fish with economic significance for fisheries management, aquaculture, and conservation biology. Unfortunately, native trout populations' abundance is significantly threatened by anthropogenic disturbance and the introduction of commercial hatchery strains of *Salmo trutta* for recreation activities has compromised the genetic integrity of native trout. This work assesses the genetic structure of Mediterranean trout of the main streams of Molise region (Biferno and Volturno rivers), considering that no previous genetic population structure data are available. Ultimately, this research aims to provide useful information to be considered in conservation management. In total, 288 specimens were caught in 30 different sites (15 per basins). Adipose fin tissues were collected and DNA isolated. Samples were genotyped using the Affymetrix 57K SNP-array. Sample and SNP quality control were applied considering no-call threshold of 0.05 and missing data cut-off of 0.90. SNP with a minor allele frequency below 0.05 were discarded. Since no animals were discarded the final dataset consisted of 288 specimens and 920 polymorphic SNP. Population differentiation was analyzed using global weighted average F-statistic over loci and pairwise FST among sampling sites. All tests were implemented in Arlequin software. The SNP data set was also processed through principal component analysis and Bayesian clustering analysis using Plink and ADMIXTURE

software, respectively. Our data provided a good representation of the population structure of Molise Mediterranean trout at fine-scale and results indicate a high degree of introgression and genetic admixture among introduced Atlantic lineage and native trout, particularly on Biferno river, where the population seems to be exposed to a high risk of genetic integrity loss. In Volturno basin, a high proportion of genetically low-introgressed trout was found strictly connected with the role of artificial and natural barriers. Subpopulations within each river and their related habitats were identified. These outcomes provide useful information to preserve native species in conservation and management programs. In conclusion, this work provided an insight into the genetic relationships and spatial distribution of populations in Molise rivers and the first use of SNP-array technology in research of Italian trout population.

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Relationship between somatic cell score and milk production in Spanish Florida goats

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Genetic improvement of Spanish dairy goats is basically based on milk production traits. Selection for high milk production and ignoring its relationship with other traits in selection programs could lead to undesirable outcomes in the correlated response of certain traits such as fertility and health. During the last years, there has been a growing interest in estimating genetic parameters of other important traits for farm profitability, such as female fertility and mastitis resistance. Mastitis is one of the major diseases in dairy species causing substantial economic losses for dairy farms. Selection for improved resistance to mastitis is commonly done by selecting against somatic cell count (SCC), a trait strongly correlated with mastitis. Herein, the aim of this study was to estimate the genetic parameters of somatic cell score (SCS) and to determine its genetic relationship with milk yield (MY) in Spanish Florida dairy goats. Pedigree and