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| **Genome-wide association study of resilience traits in two dairy sheep breeds****Application:** Resilience of dairy sheep to disease and environmental stressors can be improved through selective breeding. Genetic markers highlighted herein could be applied in such breeding programs, but differences among breeds should be considered.**Introduction:** Genetic selection of dairy sheep has been mainly focused on higher milk production. However, over the years, this practice increased susceptibility to diseases and environmental stressors, and adversely affected their health and welfare status and overall production efficiency (Mucha et al., 2022). Improving resilience to such stressors can enhance the ability of dairy sheep to overcome these challenges while maintaining sufficient productivity; local breeds are well-adapted to their natural environment and may have adequate genetic potential for enhanced resilience. The objective was to estimate heritability of three proxy traits for resilience (milk somatic cell count, lactation persistency and body condition score) and perform genome-wide association studies to detect single nucleotide polymorphisms and candidate genes associated with these traits in Chios and Frizarta dairy ewes. **Material and methods:** A total of 317 Chios and 346 Frizarta ewes were randomly selected from two intensive and two semi-intensive farms (one of each per breed) in Greece. Ewes were monitored monthly for two consecutive milking periods; individual records of milk yield and body condition score, and milk samples were collected. Milk samples were analysed to determine somatic cell count. Body condition score was assessed by palpation of the lumbar region based on previously described methodology (Russel et al., 1969). Prior to further analyses, individual repeated records of body condition score were averaged over both milking periods of the study. Regression coefficient of daily milk yield (after peak of lactation) on days from lambing, corresponding to lactation persistency, and mean somatic cell count weighted over daily milk yield were calculated for each ewe per milking period. Individual lactation persistency and mean somatic cell count per milking period were averaged over both periods of the study and used for further analyses. Genomic DNA was extracted from blood samples and genotyped with Illumina OvineSNP50 Genotyping Beadchip. Genotype quality control was performed with PLINK 1.9 software (Chang et al., 2015); thresholds for single nucleotide polymorphism and sample call rate (at 97% and 90%, respectively), minor allele frequency (at 2%) and deviations from Hardy-Weinberg equilibrium (*P*-value=10-6) were set. Breed-specific principal component analyses were performed with GEMMA version 0.98.1 (Zhou and Stevens, 2012) to explore genomic population structure. Single-trait animal linear mixed models with genomic relatedness matrices were used for variance components analyses (performed with ASReml version 4.2) and genome-wide association analyses of studied traits (performed with GEMMA version 0.98.1).**Results:** Moderate to high heritability estimates were observed for all studied traits (body condition score: h2 = 0.54 and 0.55, somatic cell count: h2 = 0.25 and 0.38 and lactation persistency: h2 = 0.43 and 0.45, for Chios and Frizarta ewes, respectively). Unlike all other estimates, heritability of somatic cell count in Chios sheep was not statistically significant (α=0.05). In both breeds, population structure associated with farm of origin of ewes was revealed by principal component analyses. Genome-wide association studies detected seven novel single nucleotide polymorphisms associated with the studied traits. Specifically, one genome-wide (rs403061409 on chromosome 9) and two suggestive (rs424064526 and rs428540973 on chromosomes 1 and 12, respectively) significant associations with somatic cell count of Frizarta ewes were detected; one suggestive significant association with body condition score of Chios ewes (rs424834097 on chromosome 4); three suggestive significant associations with lactation persistency, two of which in Frizarta (rs193632931 and rs412648955 on chromosomes 1 and 6, respectively) and one in Chios analyses (s428128299 on chromosome 3). Single nucleotide polymorphism annotation and previously reported associations revealed a total of nineteen candidate genes: two for body condition score in Chios sheep (*POT1, TMEM229A*), thirteen for somatic cell count in Frizarta sheep (*NTAQ1, ZHX1, ZHX2, LOC101109545, HAS2, DERL1, FAM83A, ATAD2, RBP7, FSTL1, CD80, HCLS1, GSK3B*), three (*GRID2, FAIM, CEP70*) and one (*GRIP1*) for lactation persistency of Frizarta and Chios sheep, respectively. The above genes are involved in regulation of cell apoptosis, telomere length, reproductive hormones excretion, mammary growth and immune response. **Conclusion:** The studied resilience traits were significantly heritable and hence amenable to improvement. They contribute to further unravelling the genetic architecture of somatic cell count, lactation persistency and body condition score. Absence of common single nucleotide polymorphisms or genes among breeds, suggest polygenic inheritance of the studied traits and emphasize the need for within-breed studies. Further studies will focus on the impact that different alleles of significant single nucleotide polymorphisms have on the studied traits and search for possible correlations among the studied and other production traits to allow effective incorporation into breeding programs aiming to improve resilience.**Acknowledgements:** This research was funded by the European Union’s H2020 research and innovation program for the projects SMARTER – “SMAll RuminanTs breeding for Efﬁciency and Resilience” (grant number 772787; https://www.smarterproject.eu/) and iSAGE – “Innovation for Sustainable Sheep and Goat Production in Europe” (grant number 679302; https://www.isage.eu/).**References:** Chang, C.C., Chow, C.C., Tellier, L.C., Vattikuti, S., Purcell, S.M. and Lee, J.J. 2015. 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