Genomic PCA – a proxy for monitoring genetic connectedness between flocks (case study on sheep)

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Fair comparison of predicted breeding values of animals belonging to different flocks is crucial for exploiting available genetic pool of breed. Low connectedness between flocks, as commonly present in many sheep breeds, represents unfavourable population structure for joint, i.e. across-flock, genetic evaluation. The issue is mainly present in populations with no or limited: (1) usage of artificial insemination; and (2) exchange of sires between flocks. Genomic selection (GS) is supposed to alleviate this issue in many animal breeding programs. In addition to its benefit in term of accuracy and earlier provision of breeding values for some animals, genomic information can be also beneficial in monitoring connectedness between flocks. The main idea of the study was to examine if results of principal component analysis (PCA) conducted on whole genome SNP markers (Illumina ovine 54K SNP chip) can be used as an easy-to-implement method to examine connectedness. The PCA was conducted on 719 genotyped Istrian sheep coming from 14 flocks. Cleaning of the SNP marker file and PCA were conducted with PreGSF90 program. Genetic variance explained by PC1 and PC2 were 5.8 and 3.5%, respectively. Pedigree based connectedness was estimated by Gene flow method (GF) and Genetic drift variance (GDV) on 5,090 phenotyped ewes and their known ancestors (a total of 6,477 animals in the pedigree). Comparison of PCA, GF, and GDV results revealed substantial matching, implicating that genomic PCA can be used as fast and effective method for this purpose. The genomic PCA has not yet been proposed in this context, despite its simplicity in contrast to other computationally very complex methods, so we hereby advocate its widespread usage.