

Title:	Genomic connectedness between flocks – case study on Istrian sheep breed
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Abstract:	The genetic connectedness between flocks is crucial for unbiased ranking of estimated breeding values obtained under the framework of across-flocks BLUP genetic evaluation system. Connectedness between flock is weak in many sheep populations worldwide, thus significantly limiting the accuracy of genetic evaluation and often leading to sub-optimal usage of the available genetic variation. Until recently, due to very complex and exhaustive calculations, estimation of connectedness was limited to researchers with advanced experience in both quantitative genetics and programming. Fortunately, now there is an R package, GCA, which utilizes both pedigree and genomic data to measure the connectedness between individuals across management units. This “tool” can be used with much less efforts to manage risks associated with biased comparison of estimated breeding values of animals belonging to different flocks. The issue of disconnectedness has been neglected in many animal breeding programs, usually wrongfully relying on the unconditional power of BLUP. This has been especially pronounced in the era of genomic selection which is supposed to alleviate this issue by detecting relationships between animals that cannot be determined through the pedigree. Therefore, the main aim of this study was to estimate the level of connectedness between flocks of Istrian sheep with both pedigree and genomic data (SNP array with 54K markers) to determine if usage of genomic data can unravel the true connectedness between flocks under the BLUP framework. Two PEV-derived statistics were analyzed: the prediction error variance of difference ($PEVD$) and coefficient of determination (CD). The estimated $PEVD_{ped}$, $PEVD_{gen}$, CD_{ped} and CD_{gen} were 0.78, 0.071, 0.61, and 0.69, respectively. The determined change $\Delta PEVD_{ped \rightarrow gen} = -10\%$, and $\Delta CD_{ped \rightarrow gen} = +13\%$, consistently showed the contribution of genomic information in unraveling connectedness between flocks under the BLUP framework, which will translate in more accurate estimates of breeding values for genomic selection versus traditional pedigree-based selection.