

A comparison between pedigree and genomic inbreeding to improve the management of Delle Langhe, a dairy Italian sheep population

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The Delle Langhe sheep breed is an autochthonous sheep population of about 4,300 heads mainly raised for dairy production in the homonym area of Northern Italy. In this work we compared parentage and inbreeding level (INB) estimated from traditional pedigree data with pairwise mendelian errors (ME) and runs of homozygosity (ROH) inbreeding (F_{ROH}) calculated from 50k medium SNPchip data. The objective was to check and improve the reliability of parentage testing and inbreeding estimates.

Data for the analysis were from two subsets of Delle Langhe individuals. The first subset (A) included 30 animals sampled from 10 farms (1 male and 2 females per farm). The second subset (B) included 74 animals sampled from only one farm (72 female and 2 male). All data were collected during *the Project Conservation, Health and Efficiency Empowerment of Small Ruminant (CHEESR)*, coordinated by the National Breeders Association.

ROH were calculated using PLINK software considering a minimum ROH length of 1 Mb and a sliding window of 20 SNP; F_{ROH} values were calculated as the proportion of the autosomal genome covered by ROH. ME of the pairwise comparisons between all sampled individuals were estimated using an in-house software.

Parentage mismatch rates comparing traditional pedigree data and genomic data was 19.5% and 6.6% for subset A and B, respectively. Correlation between ME and pairwise pedigree relationship was -0.62 ($p < 0.001$). A correlation of 0.44 ($p < 0.001$) was observed between F_{ROH} and INB. Genomic parameters are indeed efficient tools to identify possible parentage mismatch and to properly estimate genomic relationship among individuals. Both are essential prerequisites for the efficiency of any breeding program and an effective approach to improve animal management also in small populations.