

# Relationship Between SNPs Density & Prediction Accuracy in Alfalfa Genomic Selection

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Effect of individual SNPs markers and size of 'training' and 'test' populations affect prediction accuracy in genomic selection (GS). This study evaluated 11 sub-sets of 4,932 SNPs using six genetic additive models to understand marker density in GS prediction in alfalfa (*Medicago sativa* L.). In the models, effect of 'training' to 'test' population size was also evaluated. Fourteen alfalfa populations sampled from long-term grazing sites were genotyped using genotyping-by-sequencing for identification of SNPs. These populations were also phenotyped for six agro-morphological and three nutritive traits from 2018-2020. The accuracy of GS prediction improved across six GS models when the ratio of 'training' to 'test' population size increased, ranging from 0.82 to 0.92 for the most informative 500 and 1000 SNPs. However, the prediction accuracy of the six GS models significantly reduced to -0.02 to 0.19 when random, uninformative SNPs were used. In this study, five Bayesian models had similar GS accuracies, outperforming rrBLUP. These findings can enhance application of GS in alfalfa genetic improvement.