

# Optimization of Marker Density in Genomic Prediction in Alfalfa (*Medicago Sativa* L.)

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Alfalfa (*Medicago sativa* L.,  $2n = 4x$ ), is the most important perennial forage legume crop in the world. It is highly appreciated for its nutritive value and high biomass yield. Historically, genetic gain for yield has been lower in alfalfa compared to other crops. In recent years, the development of high throughput genotyping platforms and statistical models has enabled the use of genomic selection in alfalfa and promising results have been achieved to accelerate genetic gain in complex traits such as yield. Optimization of marker density could allow re-allocation of resources in genomic selection pipelines to increase the breeding population and improve genetic gain. The objectives of this study were to optimize marker density for genomic prediction and compare the predictive ability (PA) among genotyping platforms when predicting dry matter yield (DMY) by harvest and total accumulated DMY under varying training data. PA was measured with varying number of markers genotyped by Sequence capture (SC) and a fixed array developed by Breeding Insight (BI) through 11 harvests in a population of 160 families. The model used was GBLUP including the dominance effect (GBLUP-D). Genomic prediction with GBLUP-D model had on average similar results between genotyping platforms and PA decreased when using less than 500 markers from both genotyping platforms. The optimal number of markers for genomic prediction was 500 for BI and SC when using GBLUP-D predicting DMY by harvest. Genomic prediction of total accumulated DMY was similar between BI and SC and PA decreased when using less than 5 cumulative harvests to train the model.

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