

## **Evaluation of high-throughput phenotyping and genotyping for genomic selection in alfalfa**

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### **Abstract**

High-throughput phenotyping and genotyping have provided a vast source of information for evaluating the genetic merit of different breeding materials, but their implementation has been limited in alfalfa due to the complexity of the genome and the perennial nature of the crop. Vegetative indices (VIs) collected from an unmanned aerial vehicle (UAV) equipped with multi-spectral camera can be used to study forage growth and development throughout each growth cycle. Random regression models could be implemented to fit such longitudinal phenotypes like VIs collected over time to estimate growth curves, to access genetic variation in growth and the relations of VIs to end-use traits like forage yield and quality. The main objectives of this project are (1) to incorporate aerial high-throughput phenotyping to predict performance and genetic merit of the breeding materials, (2) to fit longitudinal random regression model to estimate genotype-specific growth curves, and (3) to develop a genotyping approach to estimate genetic relationships between alfalfa populations. The imaging of the alfalfa experimental trials was done every  $\sim 4.3$  days throughout the growing season. The Vegetative indices (VIs) close to the harvest date were extracted and used to fit multi-traits models to evaluate the genetic correlations between VIs and forage biomass yield. The VIs considered were Normalized Vegetative index (NDVI), Green NDVI, Red Edge NDVI, simple ratio of Near Infrared to Red (NIR), and Digital Surface Map (DSM). The preliminary results showed highest correlation of Green NDVI and biomass yield (0.4053, 0.7875, and 0.6779), followed by Rededge NDVI and biomass yield (0.417, 0.7898, and 0.6417) for the first, second and third cuttings respectively for the experimental trial located at Helfer, Ithaca. Heritability estimates ranging from 0.03 to 0.75 was observed indicating the presence of genetic variation in these VIs. Pairwise  $F_{st}$  values estimated from population-level genotyping approach was found to be efficient estimates of genetic relatedness between populations. Random regression models with a linear spline function and legendre polynomials including other environmental trials are under evaluation to see the potentiality of these models to fit VIs from multiple time points.