Application of Random Regression Models to Model Growth Curve in Alfalfa Using Phenotypes From High-Throughput Multi-Spectral Images

Ranjita Thapa, Cornell University
Nicholas Santantonio, Virginia Tech University
Nicholas Morales, Cornell University
Julie Hansen, Cornell University
Michael Gore, Cornell University
Virginia Moore, Cornell University
Kelly Robbins, Cornell University

Vegetative indices (VIs) collected from an unoccupied aerial vehicle (UAV) equipped with a multi-spectral camera can be used to study growth and development of alfalfa throughout each growth cycle. Random regression models are well suited to fit longitudinal phenotypes such as VIs collected over time to estimate growth curves using covariance functions. Using these functions genetic variation in growth through time can be estimated and the relationships between VIs and end-use traits, like forage yield and quality, can be assessed. The main objectives of this project are (1) to incorporate aerial high-throughput phenotyping to predict performance and genetic merit of the experimental populations, (2) to fit longitudinal random regression models to estimate genotype-specific growth curves and estimate the heritability of key growth parameters. Univariate and multivariate models were used to estimate heritability of image features for alfalfa trial of Helfer, 2020 and 2021. The heritability of different image features in alfalfa ranged from 0.19 - 0.78. 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 of the experimental trial located at Helfer, Ithaca for 2020, while the genetic correlation for 2021 were highest for Rededge NDVI and biomass yield (0.76, 0.74, and 0.66) followed by Green NDVI and biomass yield (0.75, 0.76 and 0.60) for the first, second and third cuttings. The potential of random regression models were investigated using Legendre polynomial functions. Random regression model converged for most of the time points and showed potential for modeling genetic parameters associated with growth and development. 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.