**Stage-wise analysis of multi-year phenotypic data for cranberry genotypic evaluation**

Multi-environment trials (METs) are used in plant breeding programs to identify superior genotypes for cultivar advancement or to use as parents in crosses. Stage-wise analysis of MET data using linear mixed-models is routine for genotypic evaluation programs for many annual crops, but the adoption of this procedure in perennial crop breeding programs is limited. MET data from evaluation trials of perennial fruit crops such as American cranberry (*Vaccinium macrocarpon* Ait.) introduce statistical challenges not present in annual crops, including the serial correlation of phenotypic observations across years. Our objective was to determine the most efficient and accurate stage-wise approach for analyzing data from cranberry genotypic evaluation trials. Using data on fruit weight, fruit yield, total anthocyanin content, and percent fruit rot from three multi-year trials of different sizes and designs, we compared two-stage mixed-models that applied different covariance structures to random spatial and genotypic effects across years. We conducted a cross-validation experiment to measure the accuracy of models to predict genotype means under sparse phenotypic designs or future years. Compared to traditional single-stage methods that compute simple fixed genotype means, mixed-models that explicitly accounted for the random correlation of genotype-harvest year effects led to superior fitting models and more accurate predictions of unobserved or future genotype means. By deploying statistical procedures that more accurately estimate genotypic values, phenotypic selection in cranberry and other perennial fruit crops can more reliably identify the true top-performing genotypes and increase genetic gain.