

Isolating quantitative kernel traits with NIR Spectroscopy and Genetic Diversity in *Vernonia*

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Abstract

The Functional Genomics of Maize Endosperm Development Project has developed a mutagenic inbred known as UniformMu. UniformMu was generated by introgressing the *Robertson's Mutator (Mu)* class of DNA transposons into a W22 inbred. Over 36,000 M₂ families were generated, which allows screening and molecular cloning of kernel mutants based on the *Mu* tags. We used Near Infrared Reflectance (NIR) spectroscopy to detect quantitative kernel composition mutants from visibly normal UniformMu transposon-tagging families. In a screen of 370 families, we found 48 putative *nir* mutants. Heritability test with 17 of the *nir* isolates suggests that a large fraction of the mutants are heritable kernel composition modifiers. To determine if single-kernel NIR accurately reports internal kernel composition, we developed calibrations between NIR spectra and analytically determined constituents. Partial least square regression (PLRS) models derived from the NIR spectra and constituent data have a good predictive power based on validation statistics and suggest that the NIR spectra report internal kernel constituents. These data indicate that single-kernel NIR can be used as both a qualitative tool to identify novel seed mutants and as a quantitative tool to determine the changes in kernel composition.

Vernonia galamensis is a wild plant from the family *Asteraceae* which is endemic to tropical countries and has the potential to become a new oil crop for industrial uses. Its seed oil is rich in vernolic acid, a naturally epoxidized fatty acid of high interest for oleochemical applications, as a raw material for manufacturing paints and coatings. In order to study the existing molecular and morphological traits diversity, a total of 480 *vernonia* populations were studied. Shannon-Weaver Diversity Index (H') showed that most traits are polymorphic and the highest H' was noted for internode size (0.93) and the lowest for stem color (0.47). The overall diversity index for all traits was 0.76. The majority of the genetic diversity, 89% and 95%, was observed within region of origin and altitudinal group, respectively. Principal component analysis and dendrogram constructed from H' indicated the close relationship of some of the populations both at molecular (RAPD) and morphological marker level. Though clustering matches, there was low correlation between the RAPD based molecular diversity and phenotypic traits diversity.