



Fast Neutron Induced Structural Variants and Seed Composition in Soybean Lines

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Abstract

Mutagenesis has been a useful tool in many crop species to create heritable genetic variability for trait improvement and gene discovery. In this study, fast neutron (FN) radiation was used to induce mutations for studying genes that effect soybean seed composition. Phenotypic screening of the FN population at the University of Minnesota has revealed mutant lines with modified seed protein, oil, and sucrose levels. A significant marker for increased oil was found on chromosome 10 near a known deletion using bulked segregant analysis (BSA). A similar BSA approach is being used to characterize FN lines with significantly increased sucrose levels. The elevated sucrose content in the seed will improve flavor of soy based products as well as provide more metabolizable energy in animal feed. These FN lines have approximately 9% sucrose compared to the FN parental line, M92-220, containing approximately 5% sucrose. The progeny of four different outcross populations from these mutants have been evaluated for sucrose content using a colorimetric assay. Overall, the populations vary in sucrose content between 3% and 8% sucrose. The DNA from the tails of the phenotypic distributions for each of the populations were pooled and sequenced for BSA. These studies will identify novel marker trait associations and provide molecular markers to be used in breeding programs.

High Sucrose Mutants

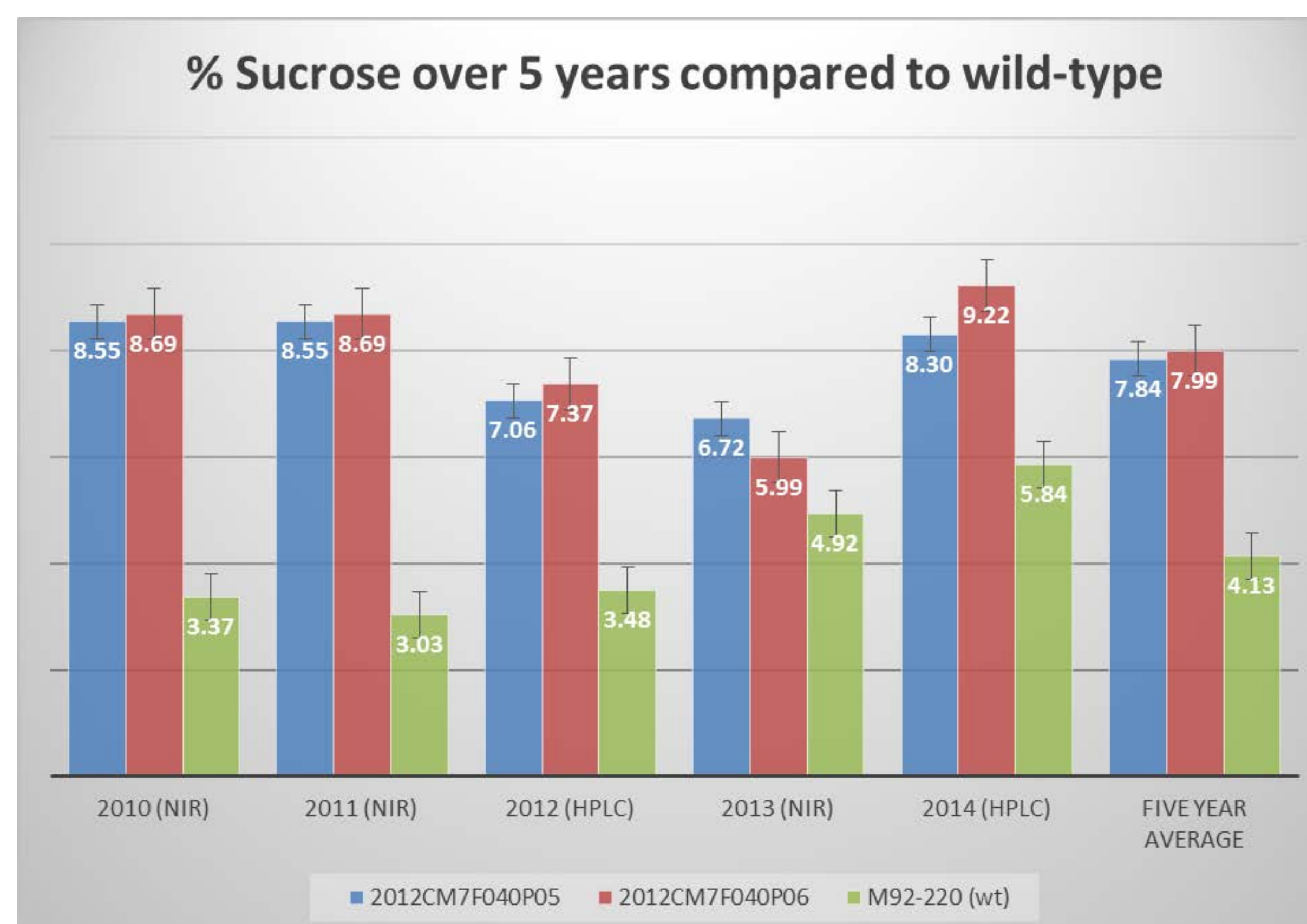


Figure 1. Two FN mutants show significantly elevated sucrose content compared to wt (M92-220) over five years of field data. There is also evidence of year to year variability for sucrose content.

Results

% Sucrose distribution in F2 populations

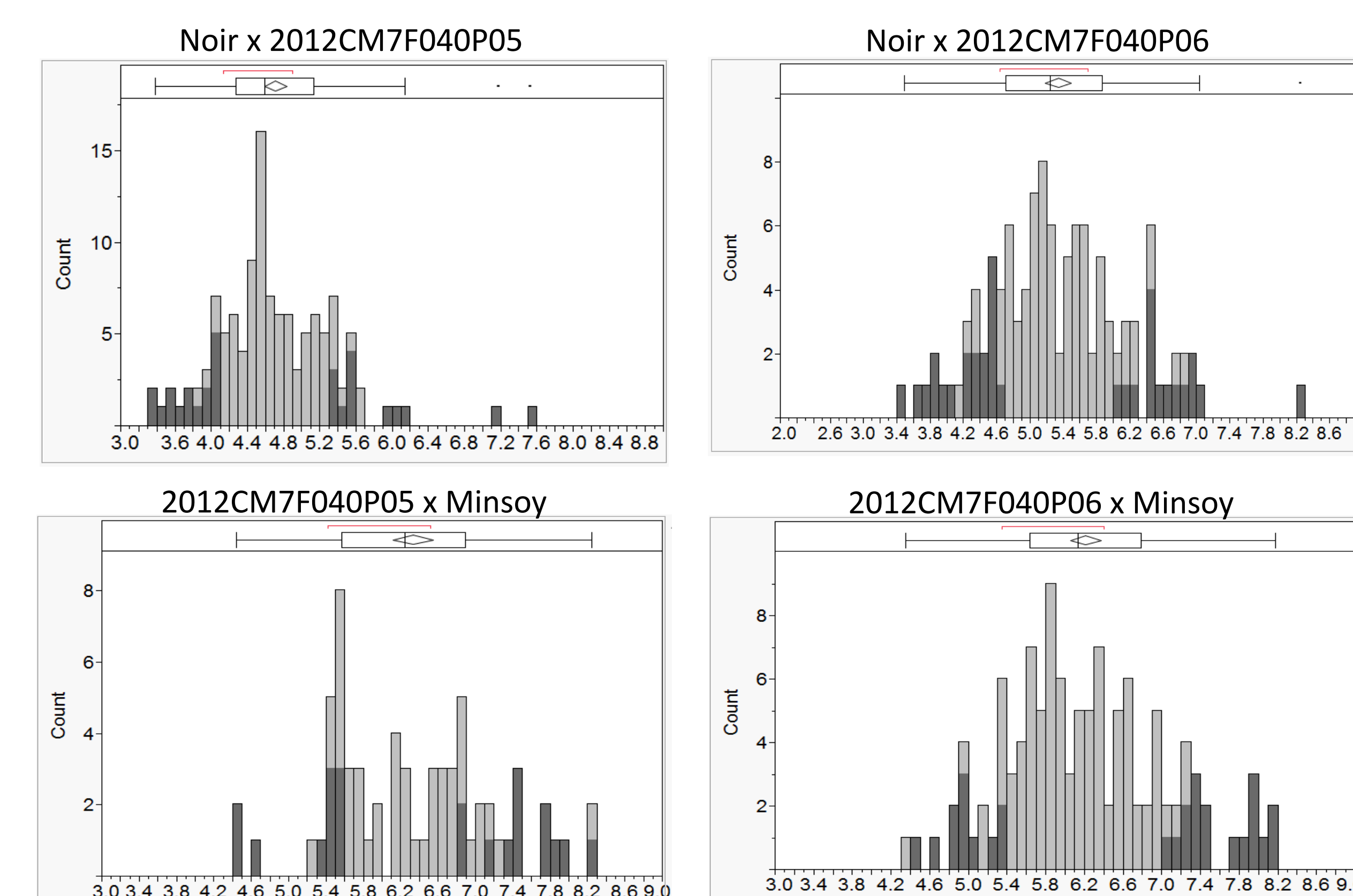
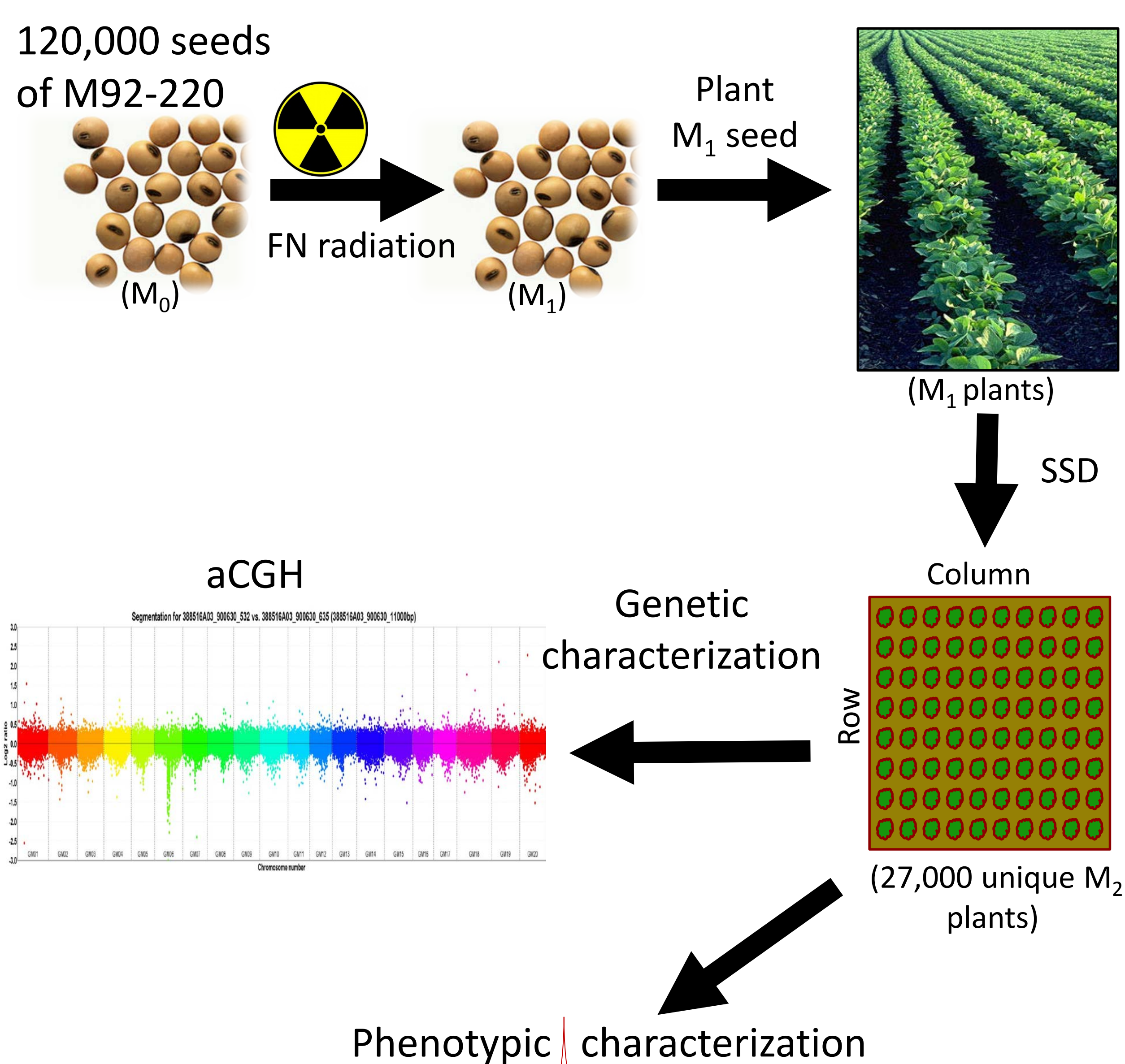


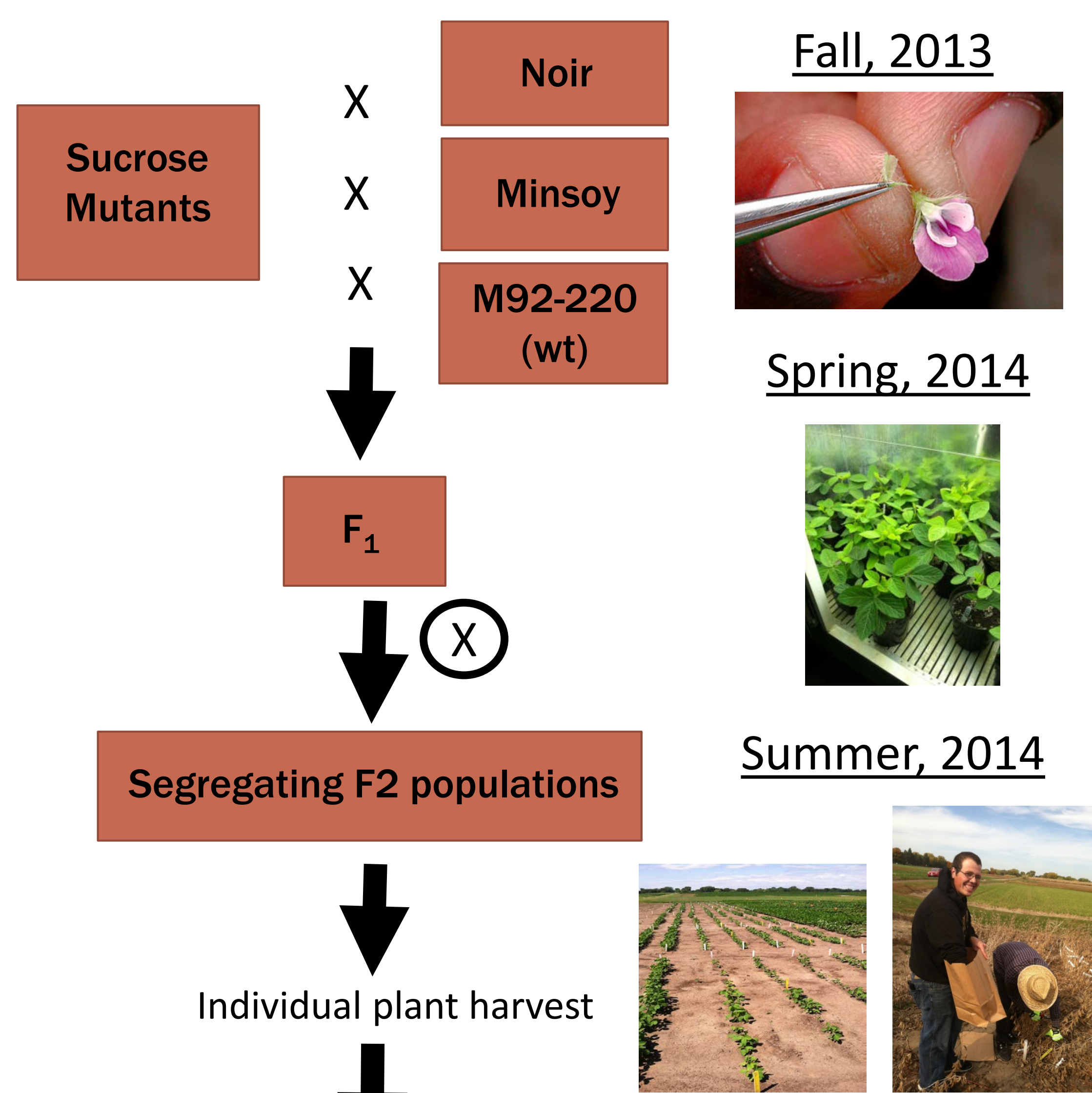
Figure 3. Distribution of sucrose content in each of the 4 F₂ populations analyzed in duplicate. Shaded bars indicate individuals selected for bulked segregant analysis (BSA).

Soybean FN Population



Materials and Methods

Mapping population creation



Analyzing sucrose content in soybeans

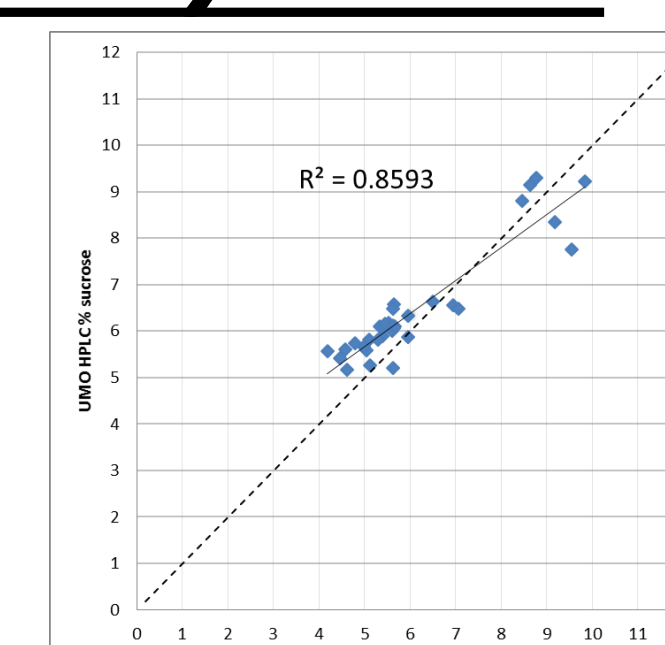
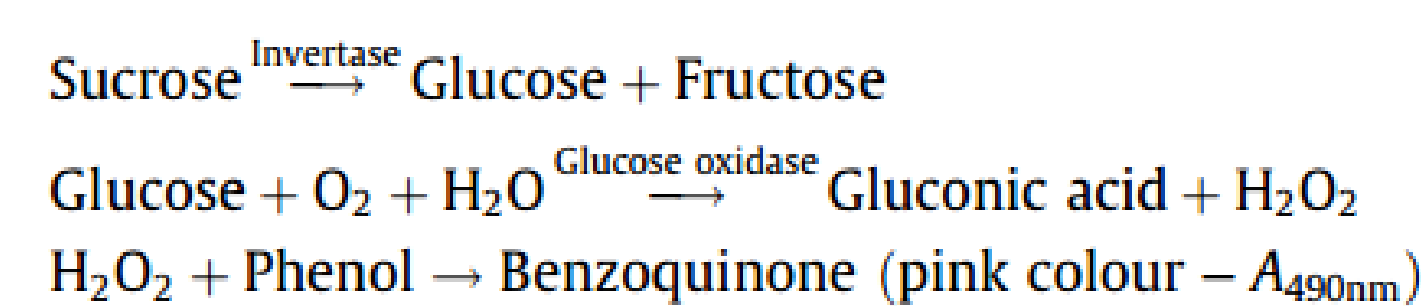


Figure 2. Comparison between HPLC measurements at UMO and enzymatic assay.

Conclusions

- Two mutants from the fast-neutron population show a heritable increase in sucrose content over 5 years
- Populations have been created to map structural variants associated with sucrose content
- An enzymatic assay has been modified and used to phenotype soybean seeds for sucrose

Future Work

- Complete bulked segregant analysis (BSA) with high sucrose mapping populations
- Map other seed composition mutants including lines with increased protein and oil content

Acknowledgements

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References

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- Telxaira, Arlindo I., Lucas F. Ribeiro, Sebastião T. Rezende, Everaldo G. Barros, and Maurílio A. Moreira. 2012. "Development of a Method to Quantify Sucrose in Soybean Grains." *Food Chemistry* 130(4):1134-36.