

## Study Samples

**TROPICS and trios:** A TROPICAL Synthetic (TROPICS) maize population was developed for another study. The inbred lines used as parents of TROPICS were chosen based on a set of publications by Nelson et al. (Nelson 2009 Ch. 4 and 5; Nelson et al. 2006; Nelson and Goodman 2008) in which a collection of 71 tropical and semi-tropical lines were evaluated for grain yield in testcrosses with U.S.-temperate adapted lines. Among the aforementioned studies, CML10, CML258, CML277, CML341, CML373, Tzi8, and Tzi9 were top candidates as exotic germplasm for U.S. maize improvement; thus, the potential for these lines to contribute unique variation in the context of temperate maize improvement was the basis of selecting them. The inbred parental lines and their corresponding hybrids were used to assess genotyping accuracy (see Materials and Methods). Seed from each parent and hybrid were grown in a greenhouse with one seed per 4-inch pot filled with Pro-mix soil. Pots were watered daily and the whole plant excluding the root was collected and lyophilized once the V2 growth stage was reached. DNA was extracted from lyophilized leaf tissue.

**CML373/CML341-F<sub>2</sub> population:** The CML373/CML341-F<sub>2</sub> population, derived from one of the founding hybrids of TROPICS, was chosen to analyze segregation of copy number polymorphisms. The population was produced from three separate crosses of CML373 (female) with CML341 (male), and the seed from those three ears were bulked. From the bulked sample, 300 individuals were grown in a greenhouse with one seed per 4-inch pot filled with Pro-mix soil. Pots were watered daily and the whole plant excluding the root was collected and lyophilized once the V2 growth stage was reached. DNA was extracted from lyophilized leaf tissue.

**NAM parents:** The 26 inbred parents of the nested association mapping population (McMullen et al. 2009) were genotyped using RASP-1.0 GBS. These are previously characterized inbred lines from tropical, temperate, sweet corn and popcorn germplasm (Liu et al. 2003). Seed from each parent were grown in greenhouse settings with one seed per 4-inch pot filled with Pro-mix soil. Pots were watered daily and the whole plant excluding the root was collected and lyophilized once the V2 growth stage was reached. DNA was extracted from lyophilized leaf tissue.

## References

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Mcmullen, M. D., S. Kresovich, H. S. Villeda, P. Bradbury, H. Li, Q. Sun, *et al.*, 2009 Genetic properties of the maize nested association mapping population. *Science* 325(5941):737-40.

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