MOLNÁR, TERENCE LUKE. Evaluation of 50% Tropical Germplasm Maize Lines Derived by Two Selection Methods. (Under the direction of Dr. Major. M. Goodman).

Tropical maize germplasm can increase the diversity and yield potential of temperate maize in the US. After a period of per-breeding and adaptation to temperate growing conditions, incorporation of tropical germplasm into existing temperate germplasm can be undertaken. Novel breeding methods such as zygote selection may be a quick way to identify yield potential and combining ability in the early stages of inbreeding. For this technique, individual plants are selfed and crossed to a tester for immediate placement into yield trials. Advancement to another cycle of zygote selection is based on yield trial results.

The objective of this study was to determine if zygote selection was a viable method for determining superior material early in the breeding process, using the pedigree system as the ‘default’ method. Lines were derived using the above methodologies from the cross of NC258 and NC296. NC258 is an all-temperate germplasm line while NC296 is a 1st-cycle temperate adapted, all-tropical germplasm line. Results of three-year testcross yield trials revealed that the lines tested were competitive with commercial checks for yield, lodging resistance, and low kernel moisture at harvest. Zygote-derived and pedigree-derived material were also comparable suggesting that zygote selection is a valid way to identify families with good yield potential early in the inbreeding process. To determine if so-called ‘50% tropical lines’ indeed have that percentage of the tropical genome, 33 SSR markers were screened on 132 lines to determine parental contribution. Results showed that in general, the temperate genome is slightly favored, as on average ~54% of markers from the temperate parent are incorporated. However, 1st-cycle temperate adapted, all-tropical lines do contribute a significant portion of their genome to lines derived from their crossing to elite temperate lines.

Lines studied in this thesis by these methods were screened for resistance to the fungus (Cercospora zeae-maydis) at different generations over different years. Results
indicated that early testing may be inefficient in selecting resistant lines as many rank changes occurred between families tested as F₂ and Sib₂ testcrosses and their filial lines, likely due to dominance effects. Additionally, many of the most resistant lines from early screenings were discarded based on yield trial testcross performance. Therefore, it is a better use of resources to advance lines in inbreeding as well as yield testing before screening for GLS resistance.

Lines were also screened for the presence of the Ga₁-s allele or ‘super-gametophyte’. Homozygous Ga₁-s silks cross-incompatible with pollen haplotypes carrying the recessive ga₁ allele. Yellow-dent maize in the US is all homozygous ga₁, however NC296, a white endosperm line, carries the dominant Ga₁-s allele. Results of the screening were well out of line with expectations (30% of lines were homozygous ga₁). Two alternate hypotheses are proposed. One, the allele in NC296 is an unknown alternate allele, less ‘strong’ than Ga₁-s. Two, modifying genes or epistatic interaction from NC258 reduce the effect of Ga₁-s. Further testing is needed to fully explain our results.