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B. Alarcon-Zuniga Universidad Autonoma Chapingo, Mexico

A. Bata-Valverde Universidad Autonoma Chapingo, Mexico

A. Betanzos-Betanzos Universidad Autonoma Chapingo, Mexico

M. Meneses-Mayo Colegio de Postgraduados, Montecillos, Mexico

M. Crosby-Galvan Colegio de Postgraduados, Montecillos, Mexico

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Heterosis and combining ability of morphological and forage quality predictors of silage corn in central valley of Mexico

B. Alarcon-Zuniga¹, A. Bata-Valverde¹, A. Betanzos-Betanzos¹, M. Meneses-Mayo², M. Crosby-Galvan² ¹Animal Science Department. Universidad Autonoma Chapingo. km. 38.5 Carr. Mexico-Texcoco, Chapingo, Mexico 56230. E-mail: b_alarcon_zuniga@yahoo.com.mx²Animal Sci. Program. Colegio de Postgraduados. Montecillos, Mexico.

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Introduction The livestock feeding in the Highland Valleys of Central Mexico is based on harvest, grazing and annual forage conservation, being forage maize the most important silage crop (Cervantes et al., 1978). Even though forage maize is extensively bred in Europe, USA and Asia since 1900's, this started in Mexico in the 1960's, and little is known about the genetic characterization in both agronomic and nutritive value traits. Our breeding program goals are to adapt temperate and tropical germplasm to Central Mexico, analyze combining ability of biomass and quality predictors and to study the genetic relationship of inbred lines between lowland tropical and temperate races using both genetic and molecular approaches.

Materials and Method Eight inbred populations (IPs) originated by single crosses from the tropical races : Chapalote, Celaya, Tuxpeno, Comiteco, Oloton, Zapalote Grande, Reventador, Vandeno, and tropical composites. The single crossbred Mexican IPs were recombined up to F13, and self pollinated up to S7 (Cervantes et al., 1978). In 2005, the IPs were hand crossed in a partial diallel design and field established in 2006 in a RCB with four replications. Agronomic and quality traits were evaluated when the kernel 2/3 milklined. 27 SSR markers covering the entire genome were used to estimate genetic similarities among IPs, and to compute a discriminatory analysis. The genetic components of variance, genotypic correlations and heritability were estimated by MANOVA and SE computed by the delta method (Lynch and Walsh, 1998).

Results The SSR markers amplified 117 alleles ranging from 2 to 7 alleles per locus (PIC= 0.74 ± 0.04). Based on the marker polymorphic information, the eight IPs were clustered into four groups arranged by Mexican race: a) tropical composite; b) tuxpeno and chapalote; c) comiteco; d) chapalote, reventador and zapalote grande; and e) oloton (Figure 1).

High parent heterosis across environments was 120%, 145%, 123% and 112% for stem, ear biomass, plant height, and grain yield, respectively, and no significant heterosis was identified for total biomass, ear number, and forage quality predictors (crude protein, *in vitro* DM digestibility, NDF, ADF, and soluble carbohydrates). IP TuxpenoxOloton (326) showed the highest GCA for plant height and silage biomass, considered as a good tester for Central Valley in both local and adapted populations. SCA was higher for the Comiteco and TuxpenoxOloton cross in all silage biomass traits, and no heterosis was identified for forage quality. Genetic distances based on SSR primers classified the IPs into four main clusters, and were positively

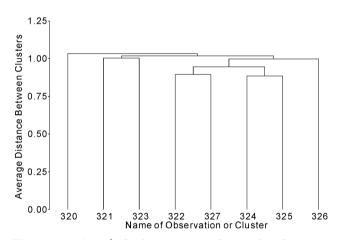


Figure 1 UPGMA's dendogram of eight IPs based on 27 SSRs, with 117 alleles clustered into four groups.

correlated with high-parent heterosis and combining ability in grain yield and ear number , but no correlation was found with silage biomass components and forage quality estimators .

Conclusions Selection of tropical races based on the proposed breeding scheme accomplished the adaptation of tropical IPs to Central Valley of Mexico at 2350 masl, which was expressed on plant health and grain yield. Biracial crosses of tropical and temperate Mexican races improved plant height, stem and total biomass, but no heterosis was found for other traits. A high correlation with SSR markers clustering IPs and genotypic data was identified, indicating markers can be useful in helping to define heterotic groups.

References

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