Genetic and molecular characterization of temperate and tropical forage maize inbred lines

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Introduction The livestock feeding in the Central highland of Mexico is based on harvest, grazing and annual forage conservation, being forage maize the most important silage crop (Alarcón, 1995). 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 diversity in both agronomic and nutritive value traits. Our breeding program goals are to analyze combining ability of biomass and quality predictors and to study the genetic relationship of inbred lines between lowland tropical and temperate races from Mesa Central, by genetic and molecular approaches.

Material and methods Fourteen inbred lines (IL) highly selected for forage biomass and quality value were used. 6 S_5 IL were collected from Mesa Central, Mexico, and 8 S_9 IL were originally single crosses from the tropical races: Tuxpeno, Vandeno, Olotillo, Naltel, Blandito, Reventador, Comiteco, Tepexintle, Celaya and Oloton. The single crossbred tropical races were recombined up to F_{13}, and selfpollinated up to S_9 (Cervantes et al., 1978). In early 2004, the ILs and temperate x tropical crosses were field established in two locations, and agronomic and quality traits evaluated when the kernel 2/3 milklined: total and per component dry matter, plant height (PH), days at flowering, soluble (SP) & insoluble protein (ISP), NDF, ADF & ADL, IVDMD, FAME, volatile fatty acids, sucrose and starch, were assayed. 27 out of 40 SSR markers were used to estimate genetic similarities among ILs, and to compute a discriminatory analysis by PCGA. The genetic components of variance, additive genotypic correlations and narrow sense heritabilities were estimated by MANOVA and standard errors computed by the delta method (Lynch and Walsh, 1998).

Results Genotypic effects were highly significant for all investigated traits ($P<0.001$), and much higher than genotype x environment interaction effects in all tropical ILs, but only higher in two of four temperate ILs. Transgressive segregations were observed in both tropical and temperate ILs for traits related to total DM, plant height, LSR, fiber predictors, free and volatile fatty acids; however, for each of the investigated digestibility traits, sucrose and starch, transgressive segregations were observed only on temperate Cacahuasintle and tropical ILs Tuxpeno y Vandeno. Narrow sense heritabilities on an entry basis ranged from low (~0.15; total and per component DM, IVDMD, FAME, ADL), medium (~0.3, PH, ISP, NDF, ADF, sucrose) and high (~0.6, days at flowering, volatile FA, starch). The average dry matter ear content was 51%, ranged 2-3% among ILs, and showed high heritability (0.5), with a high DM ear weight on ILs Cacahuasintle, Vandeno and Tuxpeno x Naltel. Positive additive genetic correlations between ear size, sucrose, starch or ADF content and IVDMD had similar absolute values, 0.55, so each of these two traits was an important but not the unique determinant of silage maize quality. A low genetic correlation was found between ADL/NDF and IVDMD, suggesting that digestibility can be improved in both tropical and temperate ILs independent on lignin content. The 27 SSR marker primers detected 86 alleles, with a range per locus from 2 to 7 (avg=3.19). The PIC values ranged from 0.09 to 0.75, with an average of 0.48. The marker analysis leads to the 14 inbred lines were classified into three distinct groups: temperate inbreds were included in group 1, with two distinct subgroups: Cacahuasintle and Chalqueno. The tropical inbreds were clustered into two groups: group 2 derived from dent grain germplasm included Tuxpeno, Blandito, Comiteco, and Tepexintle; and group 3 (flint germplasm) included Vandeno, Naltel and Oloton.

Conclusions These results suggest that tropical ILs Tuxpeno and Vandeno can be used as top parental ILs for forage maize in the highland Mexico; same was observed for Cacahuasintle as temperate IL. The primer loci of SSR markers did not cover all genomes completely, leading just to determine genetic similarities among ILs, and more SSR primers and ILs are ongoing to associate with loci that positively determine heterotic groups, supported by a field diallel analysis in 2005.

References

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