**Hans H. Ruthenberg-Graduierten-Förderpreis 2002/**

**Hans H. Ruthenberg Award for Graduates 2002**

Jochen Reif "Genetic Diversity within and between Seven Tropical Maize Populations Investigated with SSR Markers and Relation to the Heterosis of their Crosses"

University of Hohenheim, 2001

Supervisor: Prof. Dr. A. E. Melchinger

Summary

Genetic diversity in maize is a valuable natural resource and plays a key role for future breeding progress. The development of molecular markers provides a powerful tool for assessing the genetic diversity at the DNA level in plant species (Melchinger and Gumber, 1998). In particular, simple sequence repeat (SSR) markers show great potential for large-scale DNA fingerprinting of maize genotypes due to the high level of polymorphism detected (Smith et al., 1997), their analyses by automated systems (Sharon et al., 1997), and their high accuracy and repeatability (Heckenberger et al., 2001).

Most evidence in maize suggests that the genetic basis of heterosis is partial to complete dominance (Hallauer et al., 1988; Stuber et al., 1992). Overdominance has long been discussed as the basis of heterosis (East, 1936; Crow, 1948). However, many data supporting overdominance actually resulted from pseudo-overdominance, arising from dominant alleles in repulsion phase linkage (Crow, 1999; Stuber et al., 1992). Epistasis, particularly between linked loci, may also be an explanation for heterosis in maize (Cockerham and Zeng, 1996). No data exclude the possibility of all three mechanisms contributing to heterosis, albeit in different proportions.

Lamkey and Edwards (1999) coined the term panmictic midparent heterosis (PMPH) to describe the deviation in performance between a population cross and its two parent populations in Hardy-Weinberg equilibrium. Quantitative genetic theory shows that in the absence of epistasis and two alleles per locus, PMPH is a function of the product of the dominance effect and the square of the difference in gene frequencies at the respective locus (Falconer and Mackay, 1996, p. 255), which corresponds to the square of the modified Roger's distance (Melchinger, 1999). In fact, a linear increase in PMPH with increasing genetic distance (Hypothesis 1) was observed in a diallel of U.S. maize populations (Moll et al., 1962).

In contrast, experimental data reported by Moll et al. (1965) in a study with tropical maize populations of diverse geographic origin suggest that PMPH increases with increasing genetic distance only up to an optimum level but thereafter decreases in extremely wide crosses (Hypothesis 2). The authors explained this by fertility distortion in wide crosses and epistatic

interactions of genes. While Moll et al. (1962, 1965) inferred the genetic distance from the geographic origin of the populations, to our knowledge no attempts have been made to verify or falsify the above hypotheses with molecular marker data.

The choice of heterotic groups is fundamental in hybrid breeding (Melchinger and Gumber, 1998). While heterotic patterns in temperate maize were established more than 50 years ago, a clear heterotic pattern does not exist in tropical maize. Therefore, before embarking on a hybrid breeding program, CIMMYT conducted several diallel studies for identifying populations showing not only good *per se* perfomance but also high heterosis in their crosses (Beck et al., 1990; Crossa et al., 1990; Vasal et al., 1992a,b,c). Genetic distances based on molecular markers have been suggested as a tool for grouping of similar germplasm as a first step in identifying promising heterotic patterns (Melchinger, 1999).

The major goal of this study was to investigate the relationship between heterosis and genetic distance determined with SSR markers. The objectives of our research were to (i) compare the genetic diversity within and between seven tropical maize populations, (ii) test alternative hypotheses on the relationship between PMPH and genetic distances determined with SSR markers, and (iii) evaluate the use of SSR markers for grouping of germplasm and establishing heterotic patterns for hybrid breeding of tropical maize.

The results of this study suggest that molecular marker-based analyses, and in particular SSR technology, offers a reliable and effective means of assessing genetic diversity within and between maize populations. The AMOVA revealed a high within population variance, as expected from the origin and genetic background of the establishment of these populations. For the establishment of heterotic groups to be used in hybrid breeding, a higher variance between populations would have been advantageous because this should result in higher PMPH and, consequently, a higher performance of crosses between them.

SSR markers provide a valuable tool for grouping of germplasm and are a good complementation to field trials for identifying groups of genetically similar germplasm. Consequently, field trials for identification of promising heterotic patterns can be planned more efficiently based on prior information obtained from SSR analyses.