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Genetic and Biochemical Analysis of Modifier Gene Action in opaque-2 Maize Using Recombinant Inbred Lines.

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Endosperm modification in *o2* maize genotypes results from the action of a system of genetic "modifiers" that were accumulated by backcross and recurrent selection. Despite the success of this approach, very little is known about the genetic and biochemical changes underlying the process of seed modification. A gradual increase in the proportion of hard to soft endosperm is consistently observed in reciprocal F1 hybrids developed by crossing *o2* and modified *o2* genotypes. In addition, continuous phenotypic variation ranging from completely opaque to completely modified kernels is found in single ears of F2 progenies segregating for kernel modification. Selfing of F2 individuals with extreme (modified and opaque) phenotypes indicated that the selected phenotype persists in the F2. These results strongly suggest that modifier genes act in a semi-dominant fashion. Previous studies have indicated that modified *o2* genotypes have increased contents of the storage protein gamma-zein, when compared to either *o2* or normal maize. Since gamma-zein genes function in a semidominant fashion, it is possible that the locus that encodes this protein corresponds to a modifier gene locus. We used a group of recombinant inbred lines with a wide range of seed phenotypes to further study the relationship between a candidate modifier gene and the vitreous trait. Physical and biochemical analysis of seeds were performed, and the association between seed modification and accumulation of endosperm proteins was assessed. The amount of gamma-zein increased in a continuous fashion, with continuous increases in the degree of seed modification and regression analysis indicated a positive correlation between its content and endosperm modification (R^2 = 82%). Also, positive correlations between endosperm modification and percentage of gamma-zein in the total storage protein fraction (R^2 = 79%), and content of total zein proteins (R^2 = 0.30) indicated that increases in the absolute content of storage protein occur as a consequence of increased gamma-zein accumulation. However, the magnitude of the calculated R^2 values indicated that gamma-zein, rather than total zein content, is better correlated with endosperm modification. Also, there is a negative correlation between endosperm modification and accumulation of the lysine-rich non-zein proteins.

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