



## Analysis of genetic distance by SSR in waxy maize

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**ABSTRACT.** We examined the genetic diversity of 80 inbred waxy maize lines using 22 SSR molecular markers that could be used to achieve heterosis in waxy maize. Eighty inbred waxy maize lines with different phenotypes, 40 yellow, 25 white, 13 black, and two red lines were analyzed by SSR molecular marker fingerprint and cluster analysis. Using a standard genetic distance of 0.55, the 80 waxy maize inbred lines were clustered into nine groups. Among them, group II, group V, groups VII and VIII, and group IX were divided into three subgroups at a genetic distance of 0.46, into two subgroups at 0.49, into two subgroups at 0.46, and into four subgroups at 0.493, respectively. All but one of the yellow waxy maize inbred lines were clustered in groups VI, VII, VIII, and IX. Group IX (30 lines) contained 28 yellow lines; the other 11 yellow lines were distributed among groups VI, VII and VIII. Among the 25 white lines, 21 were clustered in groups III, V, VI and the third subgroup of group II. The black line N72 was in a group of its own. The black lines N75, N76 and N78 were distributed in groups VII, VIII and IX, respectively. The other nine black lines were clustered in group II. The red lines were distributed in the second subgroup of group II and there was no difference in genetic distance between them. In conclusion, there were considerable genetic differences among waxy maize inbred lines of different colors. The mean genetic distance of inbred lines of the same color was significantly less than that of lines

of different colors. Therefore, we concluded that it was more accurate to determine the difference between the populations using the highly stable DNA genetic markers.

**Key words:** Waxy maize; SSR; Genetic distance