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**PREDICTION OF ALFALFA DIALLEL HYBRID PERFORMANCE USING  
DNA MARKERS AND MORPHOLOGICAL TRAITS**

**BY**

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ABSTRACT

PREDICTION OF ALFALFA DIALLEL HYBRID PERFORMANCE USING DNA  
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Understanding genetic parameters of populations that are being considered for inclusion into a plant breeding program provides critical knowledge to enhance economic traits of interest. Use of genetic distance information based on molecular markers has been proposed to help reduce the time required, and resources needed, for selecting proper parents that produce heterosis among their  $F_1$  progenies. In this study, nine populations from the alfalfa (*Medicago sativa*) core collection that possessed differing fall dormancy responses were evaluated for their DNA marker diversity, forage yield combining ability, and heterosis among their 36 diallel hybrids. Simple and multiple linear regression models based on DNA markers, combining ability, and morphological trait data of the nine populations were evaluated to identify models that were best able to predict the performance and heterosis of the 36 diallel hybrids.

Genetic diversity among the nine parents, and an out-group check of *M. sativa* subspecies *falcata* was estimated by using amplified fragment length polymorphism (AFLP) markers. Previously published genetic distance data based on hypervariable regions of chloroplast DNA among the nine populations were also re-evaluated in this study. The hierarchical arrangements of the populations within the dendrograms that were based on AFLP markers, or chloroplast markers, agreed in many cases with the information on each population's pedigree, historical, and/or geographical origin.

Dry matter yield of the nine parents and their 36 diallel hybrids were collected over three harvests in each of two years. Variation among hybrids for forage yield was primarily attributed to general combining ability (GCA) effects, which was 5.5 times greater than specific combining ability effects. The frequency of hybrids showing significant midparent heterosis was twofold greater for hybrids generated between parents with different fall dormancy responses, as compared to hybrids generated from parents with similar fall dormancy responses.

Regression models based on DNA marker genetic distance estimates, GCA effects, variety effects (VE), and the morphological traits of fall regrowth (FR) and winter-hardiness (WH), were conducted alone or in various combinations, to identify parameters that were useful for predicting hybrid yield and heterosis. The best single model to predict hybrid performance included both FR and WH, and was able to identify 84% of 19 superior hybrids. Simple models containing GCA or VE or FR alone, and two and three factor models containing VE+FR, VE+WH, or FR+VE+WH were all able to identify 79% of 19 superior hybrids. High parent heterosis was

identified significantly by FR and WH. The implications of these results is that evaluation of variety effects (VE) and FR or WH could offer a practical approach to predict hybrid performance and heterosis among these nine parental populations.