Implementation of Marker-Assisted Selection For Lodging Resistance in Pea Breeding

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Abstract

Lodging resistance is a key criterion in pea breeding programs. In traditional breeding, a large number of lines are discarded in F₃ or later generations, because of susceptibility to lodging and much labor and other costs are wasted. Implementation of selection using molecular markers for lodging resistance at earlier generations will significantly enhance the efficiency of the pea breeding process. Ten F₂ populations consisting of a total of 869 plants were grown in the field in Saskatoon in the summer of 2002. These 10 populations were derived from crosses between the lodging susceptible variety Carrera, crossed with ten other lodging resistant lines. DNA samples were extracted from each individual plant. Each plant was scored for the presence of coupling phase linked SCAR markers A001 and A002, as well as a repulsion phase linked SCAR marker A004. The results showed that the frequency of marker presence is similar to the estimated frequency, obeying the rule of independent single gene segregation. Chi-Square analysis showed that the combination of A001 and A004 markers also followed a two gene model (P>0.05) in 8 populations. Due to linkage between A001 and A002 markers, population No. 3 and No. 4 did not follow the two or three independent gene segregation model. F₃ populations will be planted in the field in 2003 to evaluate the effectiveness of Marker Assist Selection for lodging resistance in pea.