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Short Communication

Inheritance of seed protein expression in mungbean

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Molecular markers have emerged as a potential tool for studies on genome organization and its improvement. As compared to the DNA markers, detection of the seed protein markers involves simple and less expensive procedures. Polymorphism in electrophoretic banding patterns of seed proteins has effectively been employed to elucidate evolution, phylogenetic relationship and genetic variation in several crop plants.

Simple Mendelian segregation is a prerequisite for using a polymorphic protein as marker. Literature reveals seed protein expression to be under monogenic control with codominance of alleles for proteins with diverse molecular weight forms and complete dominance of presence over absence.

In mungbean, (*Vigna radiata* (L.) Wilczck), however, no information on inheritance of expression of seed proteins is available. Mungbean is an extensively grown pulse crop in India and other South East Asian countries. It contains about 23% seed proteins [1] and therefore, could be an ideal candidate for studies on genetics of electrophoretic banding patterns.

The present investigation reports, for the first time, on the employment of sodium dodecyl sulphate-polyacrylamide gel electrophoresis (SDS-PAGE) to delineate the inheritance of protein expression and linkage of seed proteins in mungbean. Two F_2 seed lots derived from the crosses, GDI 47-4 × Jyoti and TARM 18 × *Nagpuri* along with seeds of the parent genotypes were used for electrophoretic analysis. SDS-PAGE of crude proteins was done following Laemmli [2] with minor modifications as described elsewhere [3].

Preliminary studies of SDS-PAGE banding patterns of crude seed proteins in 10 mungbean cultivars revealed that a 62.4kD polypeptide was expressed in a variety Jyoti and a local land race of Orissa *Nagpuri*, while absent in the two varieties GDI 47-4 and TARM 18 [4]. Another polypeptide of 27.5/kD was present in *Nagpuri*, while absent in GDI 47-4, TARM 18 and Jyoti.

Electrophoregrams derived from SDS-PAGE of crude seed proteins of 78 seeds of the cross GDI 47-4 × Jyoti revealed 62 F_2 seeds had the 62.4 kD polypeptide as in the parent Jyoti and 16 seeds lacked the expression of this polypeptide resembling the parent GDI 47-4. It fitted to a segregation ratio of 3:1 (χ^2 = 0.837, p = 0.390).

In the second cross, TARM 18 × *Nagpuri*, the 62.4 kD polypeptide was expressed in 56 F_2 seeds as the parent *Nagpuri*, whereas no band was present in lanes of 24 F_2 seeds suggesting single gene control (χ^2 = 1.07, p = 0.322). Similarly, the 27.5 kD polypeptide was present in 54 F_2 seeds resembling the parent *Nagpuri*, while absent in 26 seeds similar to the parent TARM 18, evidencing for a monogenic segregating (χ^2 = 2.4, p = 0.133). Both these bands were present in 48 F_2 seeds, absent in 18 seeds and either of them was present in 14 seeds. Test for goodness of fit for a 9:3:3:1 ratio of independent assortment resulted in a χ^2 value of 42.67 indicating the presence of linkage between the two polypeptide. These two polypeptides exhibited a recombination of 17.5%.

Monogenic segregation of seed protein expression has been reported in several species of grain legumes including *Vigna*, such as cowpea [5] and urdbean [6]. The lack of expression of polypeptides has been attributed to a deletion of the structural genes encoding them, or a mutation in the structural or regulatory loci resulting in the inhibition of transcription or translation of these genes [7]. Linkage of protein bands *inter se* has also been reported in Frenchbean [8] and cowpea [5]. Information on inheritance and linkage of different

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polypeptides in mungbean could be useful in future breeding works for improvement of protein quantity and quality [8].

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