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Use of Seed Protein Marker in the Phylogeny Study of Sorghum Species

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Sorghum, the fifth important crop among the worlds cereals, shows immense morphological variability and adoption. The diversity and variability of sorghum make it especially difficult to deal taxonomically. Proper systematics, phylogeny and a well documented genomic relationship between different taxa of sorghum would avoid confusion. They would be more useful in breeding programmes on genetic manipulation and improvement of sorghum.

Proteins provide a more direct measure of gene homology than morphological and cytological observations. The seed protein profile has been found a characteristic feature of the species in several groups of plants (Johnson and Hall, 1965). This trait sometimes is so sensitive that it could differentiate types which are morphologically indistinguishable, but genetically considerably divergent from one another. Furthermore, the protein pattern of polyploidy species has been shown to display the additivity of the parental patterns (Murray *et al.*, 1970).

The present study was undertaken to investigate the phylogenetic relationship between *S. bicolor* (2n=20) and *S. halepense* (2n=40), and to study the exact relationship among *S. purpurosericeum* (2n=10), Parasorghum and Eusorghum.

Protein extracts were prepared as given below, from fully matured seed collected from *S. purpurosericeum spp* timidiatum (2n=10), *S. bicolor* (2n =20) and *S. halepense* (2n=40).

One gram of seed material was ground with 0.5 ml of 0.1 M phosphate buffer (pH=7.2) using pestle and mortar. The homogenate was centrifuged at 8000x9 for 20 min in refrigerated centrifuge. The supernatant was collected and its protein was estimated by the method of Bradford (1976).

Proteins were fractionated by SDS-PAGE (12.0%), following the method of Laemmli (1970). After electrophoresis, the gel was silver stained according to the procedure of Wary *et al.*, (1981).

Protein bands on the gel were compared between species with reference to the marker protein. The seed protein electrophoresis is a powerful tool in elucidating the origin and evolution of cultivated plants (Johnson *et al.*, 1967).

Unique bands at 3(40KD), 8(26KD), 10(22KD), 13(18KD) and 14(18 KD) of *S. bicolor* and 6(28KD), 12(19KD) and 15(17KD) of *S. halepense* were observed in the electrophoretic profile. Their proteins are species specific and characteristic of the particular species.

A similarity between the seed protein profile of wild species and their cultivated counterparts has been reported earlier in wheat (Johnson *et al.*, 1967) and in cotton (Johnson and Thein, 1975). In the present study, a similarity of protein profile between *S. bicolor* and *S. halepense* is observed, with respect to bands 16(15kD), 18(13kD) and 19(12kD). These similarities in protein suggest a similarity between two genomes. From the genetic point of view, these two species can be considered members of the same section sorghum. Thus, despite conspicuous morphological differences between them, these species share more or less the same protein pattern. This suggests that *S. bicolor* (2n=20) is probably one of the putative parents for evolution of *S. halepense* (2n=40). These results support the cytological studies of Hardley (1953), Gu *et al.*, (1984) and the molecular analysis of Lee (1986) and Huang Tang *et al.*, (1990).

Huang-Tang and Liang (1988) also reported *S. halepense* as a segmental auto allo-octoploid, *S. bicolor*, a tetraploid as one of the putative parents of *S. halepense*. The seed protein profile of *S. purpureosericeum* showed similarities to *S. bicolor* with respect to protein bands 7(26kD), and 11(18kD), and similarities to both *S. bicolor* and *S. halepense* with respect to the bands 16(15kD) and 18(13kD).

The results show that *S. purpureosericeum* (2n=10) is a para sorghum type and a primitive wild *spp* from which Eusorghum *spp* has evolved. Furthermore, this species (*S. purpureosericeum*) share common proteins with other evolutionarily higher order species (*S. bicolor, S. halepense*). The result is in accordance with the chromosome studies of sorghum (Sharma and Bhattacharijee, 1957).

A phylogenetic relationship between *S. bicolor* (2n=20) and *S. halepense* (2n=40) genome is confirmed by comparison of the protein profile of both species. Also, the protein profile of *S. purpureosericeum*, compared to other species, shows its relation to their earlier evolutionary history.

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