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Short Communication

Genetic variation in seed proteins of improved cultivars and local land races of finger millet from Garhwal Himalayas

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Finger millet [*Eleusine coracana* (L) Gaertn.] is cultivated over a wide area in India and possesses wide genetic diversity among land races. In Uttarakhand state, it is cultivated under low input, rain fed conditions from low to high hills. Modern cultivars show poor adaptation and lack stability for grain production at hills due to environmental constraints. It is difficult to identify desired traits associated with the development of cultivars through conventional breeding methods that show greater adaptability and better stability in grain production at high altitude [1,2]. In this investigation, the genetic variation of seed protein patterns [3] in finger millet was assessed for identifying the differences among land races and modern cultivars using SDS-PAGE analysis.

Genetically diverse seven finger millet cultivars were considered for this investigation. Seeds of three genotypes were obtained from All India Coordinated Small Millet Improvement Project, U.A.S., Bangalore, Karnataka (GPU 45, HR 374 and RAU 8), two from Vivekananda Parvatiya Krishi Anusandhan Shala, Almora, Uttaranchal (VL 146 and VL 316) and two from the collection of local land races (PRM 9801 and PRM 9803). Each genotype was made homogeneous through selfing over two consecutive years prior to experimentation at Ranichauri (30^{o} 15′ N latitude and 78^{o} 02′E longitude). The seeds harvested from the plants were subjected to SDS-PAGE on 15% gels following the procedure of Laemmli [4] with modifications. Statistica programme (version 4.1) was used to calculate the genetic similarities (squared Euclidian distances) and subsequently cluster analysis using UPGMA (unweighted pair group average method) based on Nei and Li [5] was performed. In order to determine the presence of heterogeneity in the population, randomly selected two different samples of the same population, designated by the subscript 1 and 2, were subjected to SDS-PAGE analysis.

Seed protein profile of seven finger millet genotypes differed considerably for the presence and absence of bands of differing intensity (Fig. 1). Based on molecular weight of the polypeptide bands, the gel could be arbitrarily divided into two parts. The major (upper) part entailed protein bands that ranged from 121 kD to 14 kD and were distinguished by the variation in 14 scorable polypeptides bands. The presence or absence of a band at a particular position across different lanes would indicate differences in constitution of genetic materials present among finger millet cultivars subjected to analysis. Variability in protein bands could be observed up to the polypeptide of 14 kD. Lane G8 (PRM 9803) had all the bands that were darker as compared to other genotypes and this genotype had one additional band of higher molecular weight (121 kD). The second (lower) part accumulated protein bands of lower molecular weight. Separation of bands for different protein segments was not distinct in this group, though an apparent similarity in the arrangement of lower molecular weight bands among genotypes could be easily noted. Major variation in the protein bands

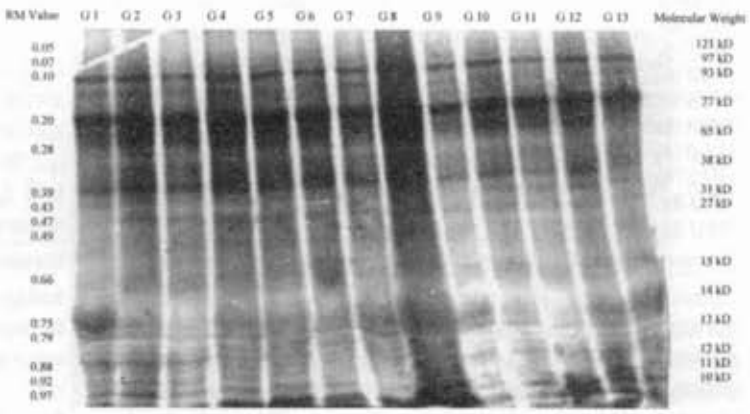

Fig. 1. Electrophoregram of total seed protein extracts of finger millet genotypes. Lane descriptions are : GPU-45 (lanes G1, G2); VL-146 (lanes G3, G4); VL 316 (lanes G5, G6); PRM-9803; (lane G7, G8), PRM-9801 (lane G9); HR-374 (G10, G11) and RAU8 (G12, G13)

was scored in lanes G7 (PRM 9803_1), G8 (PRM 9803_2) and G9 (PRM 9801). Two additional bands (27 kD and 11 kD) were observed for these three lanes, while the same were missing in the other genotypes. Conversely, the bands of molecular weight of 14 kD and 10 kD were absent in lanes G7, G8 and G9 but existed in the other lanes. These results showed that genotypes belonging to local land races exhibited protein bands different from the other finger millet genotypes and indicated the possible existence of genetic variation among improved and local genotypes of finger millet. Local genotypes *viz.*, PRM 9801 and PRM 9803, however, differed from each other with respect to a protein band at 12 kD. Variation in position of bands between two samples of a genotype indicated existence of heterogeneity in a population among individual plants. The result, therefore, indicated that the bands of various seed protein sub units in SDS-PAGE analysis could be utilized effectively for the identification and characterization different finger millet genotypes. The presence of common bands (65 kD) between local land races and improved cultivars suggested that genetically both the cultivars were closely associated for some characters.

Squared Euclidean distance (Table 1) and similarity coefficient ranged from "0" to "7" with values closer to "0" indicating increasing similarity amongst genotypes. Contrarily, differences in similarity indices exhibited heterogeneity in the population. In this investigation UPGMA cluster analysis (Fig. 2) corroborated the analysis given by SDS-PAGE and showed distinct separation between local and improved genotypes. Genotypes GPU 45, VL 316, and HR 374 shared close similarity possibly due to identical behaviour. Genotypes RAU 8 and PRM 9801 grouped into two separate clusters and maintained genetic distance to other cultivars of finger millet used for this investigation. Heterogeneity within the population, however, was observed in both improved (VL 146) and local (PRM 9803) genotypes. This led to suggest that genetic variation among finger millet genotypes could easily be identified on the basis of total seed protein variations revealed through SDS-PAGE gel and that the technique was sensitive and powerful.

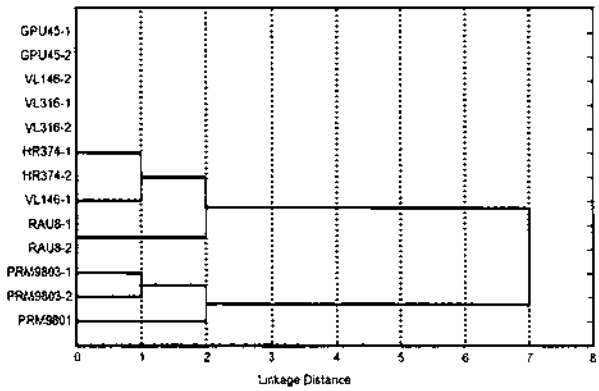

Fig. 2. Tree diagram for seven variables based on Squared Euclidean distance (unweighted pair-group averages)

Table 1. Squared Euclidean distances among seven finger millet genotypes*

Genotype	GPU 45_1	GPU 45_2	VL 146_1	VL 146_2	VL 316_1	VL 316_2	PRM 9803_1	PRM 9803_2	PRM 9801	HR 374_1	HR 374_2	RAU 8_1	RAU 8_2
GPU 45_1	0	0	1	0	0	0	7	6	6	0	0	1	1
GPU 45_2	-	0	1	0	0	0	7	6	6	0	0	1	1
VL 146_1	-	-	0	1	1	1	6	7	5	1	1	2	2
VL 146_2	-	-	-	0	0	0	7	6	6	0	0	1	1
VL 316_1	-	-	-	-	0	0	7	6	6	0	0	1	1
VL 316_2	-	-	-	-	-	0	7	6	6	0	0	1	1
PRM 9803_1	-	-	-	-	-	-	0	1	1	7	7	6	6
PRM 9803_2	-	-	-	-	-	-	-	0	2	6	6	5	5
PRM 9801	-	-	-	-	-	-	-	-	0	6	6	5	5
HR 374_1	-	-	-	-	-	-	-	-	-	0	0	1	1
HR 374_2	-	-	-	-	-	-	-	-	-	-	0	1	1
RAU 8_1	-	-	-	-	-	-	-	-	-	-	-	0	0
RAU 8_2	-	-	-	-	-	-	-	-	-	-	-	-	0

*Subscript 1 and 2 indicates two samples of the same genotype.

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