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Short Communication

Pedigree analysis of soybean varieties

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Soybean [*Glycine max* (L.) Merr.] is an important oil seeds crop of India. The Jawaharlal Nehru Krishi Vishwa Vidyalaya [JNKVV], Jabalpur has evolved 12 varieties of soybean (Table 1). It includes short duration, determinate (JS 71-5), wide adaptive (JS 72-44 and JS 335), suitable for marginal land with poor management (JS 76-205), abiotic stress tolerance (JS 80-21), four-seeded pod coupled with early maturity (JS 90-41, JS 93-05 and JS 95-60) and multiple resistance (JS 97-52) varieties. Soybean varieties developed at JNKVV, Jabalpur are more popular across India.

The coefficient of parentage (r) is a direct measurement of the relationship between varieties, whereas relative genetic contribution (RGC) estimates the relationships between ancestors and their derivatives and provides indirect information about the relatedness of varieties. Low coefficient of parentage in Chinese and Japanese soybean cultivars showed potentially high level of genetic diversity [1,]. In India, pedigree of 66 varieties was traced back to 76 ancestors with 72.67% genetic contribution from 10 ancestors and Bragg as direct parent in 15 varieties [3].

Among the 12 varieties of soybean from JNKVV, Jabalpur eight were developed through hybridization involving 4-8 ancestors in their respective parentages. To identify the parentage of these varieties pedigree analysis was used with the assumption of no relationship among them. The *r* for all the pair-wise combinations of varieties [4], the relative genetic contribution [5], the theoretical proportion of genes coming from an ancestor to a given variety the mean RGC of a given ancestor (mean of the RGC of the ancestor to all the V varieties) and cumulative RGC (the successive summation of the mean RGC) \were estimated. Detailed pedigree information of the varieties was worked out from official record and personal contact with the concerned breeders. 'The assumptions used in the algorithm were that, a cultivar derived from a cross obtains half of its genes from each parent, all the lines used in crossing are homozygous and homogeneous (r = 1.0 between a cultivar itself), all ancestors are unrelated to each other, the *r* between a cultivar and a selection from that cultivar is 0.75 [6]. A dendrograph [7] was drawn based on the cluster analysis which was performed on the matrix of *r* between survey varieties and ancestral parents [8] to estimate the mean similarity between all the varieties within a cluster.

The ancestry and ancestral contribution of the 12 soybean varieties is presented in Table 1. The pedigrees could be traced to twenty-five ancestors distributed over five geographic regions with no information of eleven ancestors (Table 2). Out of 13 ancestors with known geographical origin five were from Chiria, four from India, two from Japan and one each from Korea and USA. Ancestors that appeared frequently in varietal parentages were PI 71569 (in eight varieties) followed by FC 30761 (in seven varieties), PI 54610 (in six varieties), and PI 8424 (in five varieties). Apart from three direct selection (100% contribution), 12 ancestors were present only once among 12 pedigrees contributing 50% to the variety (Table 2). The mean relative genetic contributions presented here reflect the relative importance of individual ancestors in the gene pool for all the varieties. Ancestor Roanake used only once (JS 80-21) with only 6.25% contribution. Maximum number

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Table 1. Ancestral contribution (%) to soybean varieties

Ancestors	JS 2	JS 72-280	JS 72-44	JS 71-05	JS 75-46	JS 76-205	JS 80-21	JS 335	JS 90-41	JS 93-05	JS 95-60	JS 97-52
D 69-3881	-	-	-	-	-	-	-	-	-	100	100	-
EC 14437		50	-	-	-	-	-	-	-	-	-	-
EC 7034			50	-	-	-	-	-	-	-	-	-
FC 3076		112.5	12.5	50	12.5	12.5	-	31.2	-	-	-	6.25
FC 31745			25	-	-	-	-	-	-	-	-	-
Tehri selection	100	-	-	-	-	-	-	-	-	-	-	-
JS 75-1	-	-	-	-	-	-	50	-	-	-	-	-
Kalitur	-	-	-	-	-	50	-	25	-	-	-	-
L85	25											
L129	50											
P 171569	-	12.5	12.5	50	12.5	12.5	3.12	31.2	-	-	-	6.25
PI 36653	-	-	-	-	-	-	-	-	12.5	-	-	-
PI 37335	-	-	-	-	12.5	-	-	-	-	-	-	6.25
PI 50523 Q	-	-	-	-	-	-	-	-	12.5	-	-	-
PI 54610	-	6.25	-	-	6.25	6.25	1.56	3.12	-	-	-	3.12
PI 60406	-	-	-	-	25	-	6.25	-	-	-	-	-
PI 70502-2	-	-	-	-	-	-	-	-	12.5	-	-	-
PI 71587	-	12.5	-	-	-	12.5	-	6.25	-	-	-	-
PI 81037	-	-	-	-	-	-	-	-	12.5	-	-	-
PI 8424	-	6.25	-	-	6.25	6.25	1.56	3.12	-	-	-	3.12
PI-229-358 (UPIR2)	-	-	-	-	-	-	-	-	50	-	-	-
Roanake	-	-	-	-	-	-	6.25	-	-	-	-	-
Tanloxi	-	-	-	-	25	-	6.25	-	-	-	-	-
UPSM 82	25											
No. of ancestors	1	6	4	2	7	6	8	6	5	1	1	7

of ancestors, eight were used in variety JS 80-21 followed by seven in JS 75-46 and JS 97-52; six in JS 72-280, JS 335 and JS 76-205. Minimum contribution (1.5625) of the ancestor PI 54610 and PI 8424 was recorded in variety JS 80-21 (Table 2). Although, as much as 67% of the genetic base for the notified soybean varieties was attributed to as few as eight ancestors, the interrelationships between varieties were not closed.

The coefficients of parentage (r) for pair-wise combinations of the varieties are presented in Table 3. The value of r ranged from 0.005 to 0.5 with an average of 0.21. This relatively small value resulted from the use of diverse germplasm in variety development. The genetic diversity among varieties was clearly shown by cluster analysis (Fig. 1) that produced six groups of varieties, designated A to F. Cluster A and C were the largest group, containing three varieties each. Since JS 2, JS 95-60 and JS 93-05 were developed from one (not common) ancestor of geographical origin of India (?) all fall in cluster A. The smallest groups contained only one variety i.e., E with JS 80-21 and F with JS 90-41. In Cluster C variety JS 72-280 and JS 76-205 had 50% common ancestor, whereas JS 76-205 and JS 335 had 100% common ancestors with the difference in percent contribution of the ancestors. Varieties representing Cluster B i.e., JS 72-44 and JS 71-05 had two common ancestors *i.e.,* EC 30761 (50% JS 71-5:12.5% JS 72-44) and PI 71569 (50% JS 72-44:12.5% JS 71-5). Cluster D was represented by variety JS 75-46 and JS 97-52 with five common parents out of nine.

Table 2. Relative Genetic Contribution (RGC) and the number of occurrences for the ancestors of the soybean varieties

Ancestors	Geographical origin	Mean RGC	Cumulative RGC	No. of occurrence	Maximum contribution variety^{-1}
D 69-3881	—	0.17	0.17	2	100
P 171 569	From Nanking China Rogue in Clemson	0.12	0.29	8	50
FC 30761	Selection from AK (Rogue in Illini)	0.114	0.404	7	50
Tehri selection	From Tehri Garwhal, India	0.083	0.487	1	100
Kalitur	From Malwa, India	0.062	0.549	2	50
EC 14437	—	0.042	0.591	1	50
EC 7034	—	0.042	0.633	1	50
JS 75-1	From Sagar, India	0.042	0.675	1	50
L129	—	0.042	0.717	1	50
PI-229-358 (UPIR2)	From India	0.042	0.759	1	50
PI 60406	—	0.026	0.785	2	25
PI 71587	From Nanking China	0.026	0.811	3	12.5
Tanloxi	—	0.026	0.837	2	25
FC 31745	—	0.021	0.858	1	25
L85	—	0.021	0.879	1	25
UPSM 82	—	0.021	0.9	1	25
PI 54610	—	0.02	0.92	6	6.25
PI 8424"	From Yokohama Japan	0.02	0.94	5	6.25
PI 37335	From Pingyang Korea Selection from Arksoy	0.015	0.955	2	12.5
PI 36653	Pehtuamlintza, NE China	0.01	0.965	1	12.5
PI 50523 Q	From Mukden NE China Selection from Mandarin	0.01	0.975	1	12.5
PI 70502-2	From Changling, NE China	0.01	0.985	1	12.5
PI 81037	From Sapporo Japan Selection from AK	0.01	0.995	1	12.5
Roanake	—	0.005	1.00	1	6.25

— = not known

Table 3. Coefficient of parentage between varieties of soybean evolved atJNKVV, Jabalpur

Ancestors	JS 2	JS 72-280	JS 72-44	JS 71-05	JS 75-46	JS 76-205	JS 80-21	JS 335	JS 90-41	JS 93-05	JS 95-60	JS 97-52
JS2	1.00											
JS 72-280	-	1.00										
JS 72-44	-	0.25	1.00									
JS71-05	-	0.125	0.125	1.00								
JS 75-46	-	0.375	0.250	0.125	1.00							
JS 76-205	-	0.500	0.250	0.125	0.375	1.00						
JS 80-21	-	0.005	0.004	0.016	0.006	0.006	1.00					
JS 335	-	-	0.082	0.312	0.082	0.082	0.011	1.00				
JS 90-41	-	-	-	-	-	-	-	-	1.00			
JS 93-05	-	-	-	-	-	-	-	-	-	1.00		
JS 95-60	-	-	-	-	-	-	-	-	-	0.500	1.00	
JS 97-52	-	0.02	0.016	0.0625	0.02	0.02	0.003	0.011	-	-	-	

The ultimate cytoplasm donors were traced to 11 ancestors (Table 4), indicating that diverse sources of cytoplasm were used in variety development. Considerable genetic diversity of cytoplasm and nuclear composition was found among these soybean varieties. Only one donor (PS 73-22) was common for two varieties (JS 93-05 and JS 95-60). Relative genetic contribution of the cytoplasmic parent EC 14437 (JS 72-280), FC 30761 (JS 71-05 and JS 75-1 (JS 80-21) was 50%. Whereas, the minimum genetic contribution (0.03125) among the cytoplasmic parent was of PI 8424 to JS 335. PI 71569 was the most important (frequent) nuclear gene donor. It kept the gene base of JNKVV varieties reasonably broad in comparison to overall narrow genetic base at the national level [1] making the varieties popular across the nation.

Table 4. Cytoplasmic parents and their Relatives Genetic Contribution (RGC) to soybean varieties

Variety	Cytoplasmic parent	RGC
JS 72-280	EC 14437	0.50
JS 72-44	FC 31745	0.25
JS 71-05	FC 30761	0.50
JS 75-46	Tanloxi	0.25
JS 76-205	PI 8424	0.0625
JS 80-21	JS 75-1	0.50
JS335	PI 8424	0.03125
JS 90-41	PI 50523 Q	0.125
JS 97-52	UPSM 82	0.25
JS2	Selection form Tehri garhwal	0.1
JS 93-05	PS 73-22	0.1
JS 95-60	PS 73-22	0.1

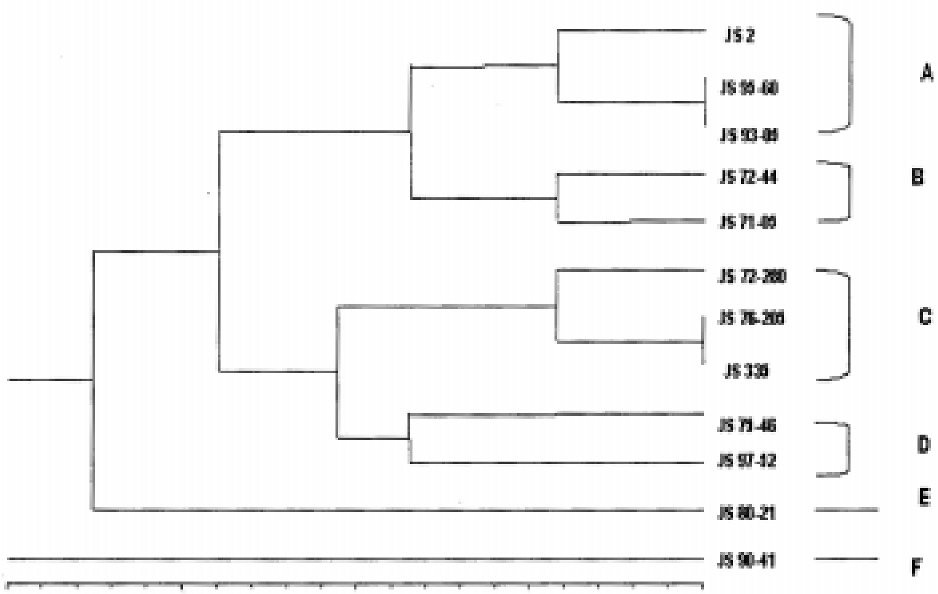

Fig. 1. Clustering dendrograph of the coefficient of parentage between soybean varieties

References

1. **Cui Z., Carter I. E. and Burton J. W.** 2000. Genetic diversity patterns in Chinese soybean cultivars based on coefficient of parentage. Crop Sci., **40**: 1780-1793.
2. **Zhou X., Carter I. E., Cui Z., Miyazaki S. and Burton J. W.** 2002. Genetic diversity patterns in Japanese soybean cultivars based on coefficient of parentage. Crop Sci., **42**: 1331-1342.
3. **Bhardwaj C. H., Satyavathi C. T., Tiwari S. P. and Karmakar P. O.** 2002. Genetic base of soybean varieties released in India as revealed by coefficient of parentage. Indian J. Agric. Sci., **72**: 567-469.
4. **Kempthorne O.** 1969. An introduction to genetic statistics. Iowa state University Press, Ames, Iowa.
5. **Delannay X., Rodgers D. M. and Palmer R. G.** 1983. Relative genetic contributions among ancestral lines to North American soybean cultivars. Crop Sci., **23**: 944-949.
6. **Cox T. S., Murphy J. P. and Rodgers D. M.** 1986. Changes in genetic diversity in the red winter wheat regions of the United States. Proc. Natl. Acad. Sci. USA, **83**: 5583-5586.
7. **McCammon R. B.** 1968. The dendrograph: A new tool for correlation. Geol. Soc. Am. Bull., **79**: 1663-1670.
8. **SAS.** 1985. SAS User's guide: Statistics. 5th edn. SAS institute, Inc., Gary, North Carolina.