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Short Communication

Genetic base of advanced urdbean breeding lines developed in India as revealed by pedigree analysis

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Development of high yielding varieties in urdbean has led to increase in area and production. But, this has narrowed down the genetic base in urdbean through the replacement of land races by a few improved varieties and, thus, need was felt to examine the genetic diversity in urdbean. Ancestor-offspring relationship, being used for studying the changes of genetic diversity during the course of cultivars improvement can be measured by relative genetic contribution. This parameter has been used as indicator of genetic diversity among genotypes in wheat [1], peanut [2], rice [3], soybean [4] and lentil [5] to provide information about the ancestor relationship of varieties. No such information is available in urdbean. The objective of this study therefore, was to (i) determine the number of ancestors present at least once in the pedigree, and (ii) estimation of relative genetic contribution of ancestors to urdbean genotypes bred during the last ten years.

Pedigree analysis was conducted to quantify the ancestral contributions of 308 advance breeding lines (Initial Varietal Trial entries) introduced into All India Coordinated Research Project during the ten years period (1996-2005) for multi-locational testing across the agro-climatic zones. Relative genetic contributions of different ancestors to a given genotype were computed following Lin [3]. Relative genetic contribution partitions the genetic constituents of each genotype into theoretical percentages attributable to different ancestors. The mean genetic contribution of a given ancestor was estimated by the means of relative genetic contributions of this ancestor to all the IVT genotypes.

The pedigree analyses of 308 advanced breeding lines were performed to identify the ancestors of the genotypes. The pedigree of these advanced breeding lines was traced back to 119 ancestors (Table 1), of which 59 appeared only once. Although these ancestors imparted little in mean relative genetic contribution, twenty-eight of 59 contributed 20% or more of genetic constituent of individual genotypes. Further, the most frequently used parent in crossing programme was T 9 followed by D 6-7, Netiminmu, UM 201, G 31, NP 21, Chikkudinimu, PLU 131, Sel. 1, Bihar Local in that order (Table 2). Further, T 9 was used 37 times directly and 206 times indirectly in hybridization. D 6-7 was used 28 times indirectly and 9 times directly; Netiminmu, 20 times indirectly and 14 directly; UM 201, 5 times directly and 27 indirectly; G 31, 8 times directly and 19 indirectly; NP 21, 21 times directly and 4 indirectly; Chikkudinimu, 7 times indirectly and 18 directly; PLU 131, 10 times directly and 12 time indirectly; Sel. 1, 11 times directly and 6 indirectly while Bihar local was used twice directly and 13 times indirectly and other ancestors once or twice directly or indirectly.

The ten most important contributors of 308 advanced breeding lines are presented in Table 1. These 10 ancestors collectively comprised 65% of the germplasm released in time period of 1996 to 2005. The mean genetic contribution revealed that ancestor T 9 contributed maximum to the genetic base followed by D 6-7, Netiminumu, UM 201, G 31 etc. T 9 was not only higher yielder but it was more suitable for unfavourable environments. Apart from its cultivation in India, it is also under cultivation in Srilanka at present. Further, among advanced breeding genotypes developed through hybridization and mutation, T 9 was involved in more than 78% of advanved breeding lines. Similarly, D 6-7 occurred in more than 12% advanced breeding lines

Table 1. Ancestors and frequency of their occurrence in the pedigree of 308 urdbean advanced breeding lines entered in IVT of AICRP (1996 to 2005)

Ancestors		Ancestors		Ancestors		Ancestors	
T 9	(243*)	L 151	(3)	S 8-5	(1)	LU 109	(1)
D 6-7	(37)	PH 32	(3)	K 1	(1)	KU 82-1	(1)
Netimininmu	(34)	LU 220	(3)	Sindh local	(1)	KU 309	(1)
UM 201	(32)	169	(2)	M 46	(1)	HPU 410	(1)
G 31	(27)	Pahelo	(2)	Gujarat local	(1)	HPU 133	(1)
NP 21	(25)	AB 1-33	(2)	P 225	(1)		
Chikkadiminumu	(25)	Kanpur local	(2)	Badnapur local	(1)		
PLU 131	(22)	Musiri local	(2)	Banglore local	(1)		
Sel. 1	(17)	Gurdaspur local	(2)	Pink mutant	(1)		
Bihar local	(15)	Reva 1-1	(2)	570	(1)		
NP 19	(14)	L 479	(2)	Koenzhar local	(1)		
H 76-1	(11)	Kullu local	(2)	446	(1)		
U 196	(11)	Uanno local	(2)	Shre Vaiukuntham local	(1)		
PLU 91	(11)	LBG 167	(2)	No. 55	(1)		
IC 8219	(10)	TAU 14	(2)	BG 51	(1)		
Punjab local	(10)	Farrukhabad local	(2)	P 160	(1)		
Khargone 3	(10)	IC 84206	(2)	UG 157	(1)		
UK 17	(8)	IC 43647	(2)	UPUG 40-4	(1)		
Jalgaon local	(8)	UL 144	(2)	Meghat local	(1)		
Bhawanipatna local	(6)	PLU 414	(2)	UL 1	(1)		
PDU 90-3	(5)	UL 2	(2)	UG 750	(1)		
7368/48	(5)	216	(2)	F 33	(1)		
UG 562	(5)	4201	(1)	F 338	(1)		
88-5	(4)	89-67	(1)	UG 620	(1)		
Barabanki local	(4)	B 7368	(1)	F 38	(1)		
Line 400	(4)	Adhuthurai local	(1)	PW 112	(1)		
Nagpur local	(4)	Barreminumu	(1)	PLU 770	(1)		
IC 11008	(4)	EC 168200	(1)	7378 / 2	(1)		
KE 70	(4)	H 70-1	(1)	L 64	(1)		
UPU 89-667	(4)	IU 8-6	(1)	U 201	(1)		
7368	(3)	K 10	(1)	L 196	(1)		
9022	(3)	K 66-110	(1)	7570/7	(1)		
No. 1766	(3)	K 8219	(1)	Shillongani local	(1)		
K 3	(3)	Karaikal	(1)	PLU 1149	(1)		
MCK 2	(3)	9-5/B	(1)	NULS 11-2	(1)		
P 133	(3)	London	(1)	NULS 86-2-1	(1)		
UZM 189	(3)	NPBR	(1)	NDU 95-6	(1)		
Tiruneleveli local	(3)	Phule 3	(1)	NDU 94-4	(1)		

*The frequency of occurrence in the 308 pedigrees is given in parenthesis

Table 2. Mean genetic contribution and frequency of occurrence of 10 important ancestors of urdbean advanced breeding lines entered in IVT of AICRP

Ancestors	Mean genetic contribution	Cumulative genetic contribution	Frequency occurrence in pedigrees
T 9	0.3500	0.3500	0.7889
D 6-7	0.0430	0.3930	0.1201
Netiminumu	0.0417	0.4347	0.1103
UM 201	0.0368	0.4715	0.1038
G 31	0.0354	0.5069	0.0876
NP 21	0.0340	0.5409	0.0811
Chikkudimimu	0.0312	0.5721	0.0811
PLU 131	0.0298	0.6019	0.0714
Sel. 1	0.0271	0.6290	0.0551
Bihar Local	0.0229	0.6519	0.0487

followed by Netiminmu, UM 20-1, G 31 etc. Among the important contributors, Netiminmu has resistance against powdery mildew whereas D 6-7 and T 9 has resistance against YMV. Ancestor Sel 1, originated from M.P., is a bold seeded with 100 seed wt. 5.3 g/100 seed and was used in the development of Narendra Urd 1 and KU 301 varieties.

Since 1996 to 2005, seventeen varieties have been released from these advanced breeding lines. Out of these, four varieties *viz*., AKU 4, Mash 414, Azad Urd 1 and RBU 38 were developed through selection. Twelve varieties *viz*., Birsa Urd 1, Mash 338, LBG 623, TU 94-2, LBG 685, KU 96-3, Uttrara, WBG 26, KU 300, NDU 99-2, KBG 512 and KU 301 were developed through hybridization. One variety i.e. Vamban 2 was developed through mutation breeding. Further, T 9 was directly involved in the development of four varieties *viz*., Uttara, WBG 26, KU 300 and NDU 99-2. Indirectly, T 9 had been involved in the development of six varieties like Birsa Urd 1, Mash 338, LBG 623, TU 99-2, LBG 685 and KU 96-3. Further, among tweleve varieties developed through hybridization and one through mutation since 1996-2005, T 9 was involved in 10 varieties developed through hybridization and all varieties developed through mutation. Thus, more than 83% of the varieties released so far, through hybridization and 100% of the varieties developed through mutation are more or less related because of the involvement of T 9 in their pedigree.

Among thousands of accessions available, only a small number were utilized in the breeding programme and variety development. Extensive use of T9, D6-7, Netiminmu, UM 201 and G 31 in the urdbean breeding programme of India led towards genetic erosion and narrowing of genetic base in this crop. This study quantify the genetic base of breeding lines that provides indirect information about the relatedness of the varieties and breeding lines. Knowledge of the degree of relationship among advanced breeding lines and varieties is useful in choosing superior yet genetically diverse parents for mating that would generate trangressive segregants in later generations.

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