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Identification of most promising genotypes for varietal development in fieldpea (*Pisum sativum* L. var. *arvense*)

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Abstract

The present investigation was carried out with one hundred twenty diverse genotypes with four check varieties viz., Ambika, Rachna, HUDP 15, HFP 8909 to identify most promising genotypes of fieldpea. To achieve this, data on various quantitative characters were recorded and on the basis of these data genetic variability, character association, path coefficient, mean performance of the genotypes and genetic divergence analysis were done in Augmented block design. Analysis of genetic variance revealed moderate to high level of genetic variability among all the genotypes in majority of the characters except number of primary branches per plant. Higher GCV were recorded for number of seeds per pod (30.414), seed yield per plant (28.874 g), for these characters PCV were 30.460 and 28.906, respectively, indicated very less influence of environment on the expression of these characters. Correlation and Path analysis indicated that harvest index, biological yield per plant, number of seeds per pod, pod length and 100-seed weight, had true relationship with seed yield. On the basis of non-hierarchical Euclidean cluster analysis, all the genotypes were grouped into twelve distinct non-overlapping clusters in which cluster XI was found largest having twenty genotypes while cluster VI had lowest number of genotypes e.g., FP 14-81, FP 11-72, EC-507770. The highest intra cluster distance was observed within cluster VII (16.392) followed by cluster IX (10.544). The maximum (58.308) inter cluster distance was recorded between cluster IV and XII and between cluster VI and cluster XI (54.180), indicating the possibility of high heterotic effect, if the individuals from these clusters are cross bred. On the basis of mean performance, correlation and path analysis, genotypes FP 14-81, FP 11-72, FP 2009-4, FP 11-108, FP 10-108 and FP 14-30 were found as the elite genotypes which can be utilized in breeding programme for development of high yielding varieties.

Keywords: Fieldpea (*Pisum sativum* L. var. *arvense*), Correlation coefficient, Genetic variability, Path coefficient, Genetic divergence

Introduction

Fieldpea (*Pisum sativum* L. var. *arvense*) is a popular pulse crop of India. It is a cool season crop which belongs to family Leguminosae (fabaceae) having 14 somatic chromosomes. It has unique position among all the pulses since it provides variety of vegetarian dishes and has multiple uses as food, feed and vegetable. Fieldpea has highest inherent productivity potential but the production of fieldpea is low due to unavailability of superior genotypes with wider adaptability and disease resistance. So, there is need to identify superior genotypes having disease resistance and wider adaptability with maximum production and protein content. Taking these problems under consideration the present investigation was carried out to identify most promising genotypes for varietal development.

Materials and Methods

One hundred twenty fieldpea genotypes with four check varieties viz., Ambika, Rachna, HUDP 15, HFP 8909 were evaluated to identify most desirable genotypes using Augmented block design during *Rabi* 2015-16 at Genetics and Plant Breeding Research Farm of Narendra Deva University of Agriculture and Technology, Narendra Nagar, Kumarganj, Faizabad (U.P.). The seeds of different genotypes were available with the Pulses Section, of the university. The entire experimental field was divided into 12 blocks of equal size and each block had 14 plots. Out of 14 plots in a block, 10 plots were used for accommodating the un-replicated test genotypes while 4 were allocated to the four check varieties. The four checks were randomly allocated along with the test genotypes in a block. Each plot consisted of a single row of 4 m length, following inter and intra row spacing 30 cm and 10 cm, respectively. Recommended cultural practices were practiced to raise a good crop. The observations were recorded on randomly selected five competitive plants from each genotypes for nine characters viz., plant height (cm), number of primary branches per plant, number of pods per plant, pod length (cm), number of seeds per pod, 100-seed weight, biological yield per plant, harvest index and seed yield per plant (g), while two characters viz., days to 50 percent flowering, days to maturity were recorded on the plot basis. Mean performance of genotypes for different quantitative characters, analysis of variance for augmented block design (Federer 1956) [7], GCV and PCV (Burton and de Vane 1953) [4], correlation coefficient (Searle 1961) [14], path coefficient (Dewey and Lu 1959) [6] and genetic divergence (Beale, 1969; Spark, 1973) [3, 18] were estimated.

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Results and Discussion

The analysis of variance revealed highly significant differences among all the genotypes for all the characters under study except number of primary branches per plant. It indicated that high amount of variability was present among all the genotypes (Table 1). Kumar (2008) ^[10], Khan *et al.* (2017) ^[18] and Pal and Singh (2012) ^[12] also found that the genotypes differed significantly for all the traits except the number of branches per plant. Phenotypic coefficients of variance (PCV) were higher than genotypic coefficients of variance (GCV), which indicated the effect of environment on the expression of characters (Table 2). Bashir *et al.* (2017) ^[2] and Meena *et al.* (2017) ^[11] also reported that relative magnitude of phenotypic coefficients of variation were higher than genotypic coefficients of variation for all the characters under study indicating environmental influence on the traits. Higher GCV were recorded for number of seeds per pod (30.414), seed yield per plant (28.874g), for these characters PCV were 30.460 and 28.906, respectively, indicated very less influence of environment on the expression of these characters. Other characters such as number of pods per plant, pod length, 100-seed weight, biological yield per plant and harvest index also showed very less environmental influence. Since the variations existed among the genotypes for these characters were due to their genetic makeup, these characters could be utilized for selection of elite genotypes. Correlation coefficients for different yield contributing traits in fieldpea (*Pisum sativum* L. var. *arvense*) are given in Table 3. The genotypic correlation coefficients between different characters were generally similar in sign and nature to the corresponding phenotypic correlation coefficients. However, in general the magnitudes of genotypic correlation coefficients were higher than their corresponding phenotypic correlation coefficients which indicated a strong inherent relationship in different pairs of character. Similar, results have also been reported by Chaudhary and Sharma (2003) ^[5] and Singh *et al.* (2014) ^[16]. Seed yield per plant exhibited highly significant and positive correlation with harvest index followed by biological yield per plant, seeds per pod, pod length and 100-seed weight. However, seed yield per plant had negative and non-significant correlation with plant height followed by days to 50 percent flowering, days to maturity, pods per plant and number of primary branches per plant. Singh *et al.* (2014) ^[16] also reported that biological yield per plant was highly significant with grain yield per plant. Earlier reports in fieldpea have also indicated existence of positive and highly significant association of weight of seeds per plant with the weight of pods per plant, biological weight per plant and harvest index recording (0.839, 0.694 and 0.505), respectively Tofiq *et al.* (2015) ^[19]. In addition Basaiwala *et al.* (2013) ^[1] also found that seed yield per plant was positively and significantly correlated with seeds per pod and harvest index. Another report in fieldpea also indicated that length and width of pod and 100-seed weight were associated positively and significantly with grain yield per plant (Singh *et al.* (2008) ^[17]). The direct and indirect effects of different characters on seed yield per plant are presented in Table 4. High positive direct contributions to the seed yield per plant were exhibited by harvest index and biological yield per plant. However, seeds per pod, pods per plant, 100-seed weight, days to 50 percent flowering and plant height exhibited considerable positive and direct effect on seed yield per plant. Tofiq *et al.* (2015) ^[19] also reported that biological weight per plant and harvest index exhibited maximum positive direct effect on weight of seeds per plant recording 0.630 and 0.456, respectively. Singh *et al.* (2014) ^[16] also reported that biological yield per plant, harvest index and plant height had positive and direct effect on grain yield per plant. Similarly, days to 50 percent flowering and pod length had positive and direct effect on grain yield per plant. Bashir *et al.* (2017) ^[2] also reported that 100-seed weight and number of seeds per pod had maximum direct effect on grain yield per plant. The occurrence of negative as well as positive indirect effects on seed yield by one or more characters present a complex situation where a compromise balance is required to attain proper balance of different yield components, for determining the ideotype of seed yield in fieldpea. The selection of suitable diverse parents for hybridization is an important step for any crop improvement programme to get desired recombinants. Through WARD's method all the genotypes were

grouped into twelve different non-overlapping clusters in which cluster VI had lowest number of genotypes namely FP 14-81, FP 11-72 and EC-507770. The cluster XI had highest number of genotypes (20). Highest intra cluster distance was observed in cluster VII (16.392). While, the lowest intra cluster value was recorded in case of cluster VIII (5.336). The maximum inter cluster distance was recorded between cluster IV and XII (58.308) and between cluster VI and cluster XI (54.180), which suggested that the genotypes of these clusters are genetically very diverse to each other and the intermating among these genotypes would be rewarded for improving grain yield. Parihar *et al.* (2014) ^[13] also assessed one hundred forty genotypes of fieldpea to the genetic divergence for various agronomic traits and stated that all the accessions were significantly different for the traits and a wide range of variability exists for most of the traits.

The clusters mean for eleven characters in fieldpea genotypes are given in Table 5. Perusal of table showed considerable differences among the clusters mean for different traits. The genotypes of cluster I had highest mean value for 100 seed weight (20.585g). The genotypes of cluster III had highest mean value for seeds per pod (7.074) as well as for pod length (7.984). The genotypes of cluster V had lowest value for days to 50 percent flowering (62.250 days) as well as for days to maturity (114.531 days). The genotypes of cluster VI had highest mean value for harvest index (55.971) followed by biological yield per plant (37.407) and seed yield per plant (20.819). The genotypes of cluster VII had highest mean value for pods per plant (19.485).

The analysis of character contribution towards genetic divergence among one hundred twenty genotypes with four check varieties of fieldpea showed that maximum contributions in manifestation of total genetic divergence were made by plant height (77.52%), harvest index (14.56) and days to 5 percent flowering (2.50). Similar results have also been reported by Shrivastava *et al.* (2012) ^[15]. The overall review of the results obtained by genetic diversity analysis in the present investigation revealed that the crosses between the entries separated by the large inter-cluster distance and having high cluster mean value for one or more characters to be improved is likely to be more useful. The results of Non-hierarchical Euclidian cluster analysis obtained under present study are also in agreement with the results of Khan *et al.* (2016) ^[9], Parihar *et al.* (2014) ^[13], Shrivastava *et al.* (2012) ^[15]. The mean performance of one hundred twenty field pea genotypes and four check varieties for eleven characters are given in Table 6. The highest seed yield per plant was obtained in FP 14-81 and constituted the top significant group for high seed yield along with five entries. Among the high yielding genotypes, six most promising genotypes were FP 14-81 (22.496), FP 11-72 (21.819), FP 2009-4 (19.741), FP 11-108 (19.629), FP 10-135 (19.011) and FP 14-30 (18.336). These genotypes also exhibited average to high mean performance for biological yield, number of primary branches per plant, harvest index, and for other traits. Genotypes FP 14-89, FP 14-33, FP 14-30, FP 14-88, FP 14-93, FP 14-15, FP 14-24, FP 14-34 IMD-83, IPLK-85, FP 14-75, FP 14-31, were earlier for days to 50 percent flowering and days to maturity. Population mean for plant height was 74.659 cm, which ranged from 12.700 (FP 14-15) to 139.650 (FP 14-30). Out of one hundred twenty genotypes and four check varieties, fifty nine entries were significantly shorter in plant stature than the general mean. However, best four genotypes showing tallest plant stature in order of merit were FP 14-30 (139.650 cm), DMR-37 (139.317cm), FP 14-25 (120.3 cm), FP 13-90 (118.81 cm). Genotype FP 14-15 had shortest plant stature followed by FP 14-15, FP 14-79, FP 14-83, FP 13-97, FP 14-67, FP 13-98, FP 14-90 and genotype FP 14-30 had tallest plant stature followed by DMR-37 (139.317cm), FP 14-25 (120.3 cm), FP 13-90 (118.81 cm) as compare to general mean. The entries FP 10-172 had maximum number of pods per plant. The genotype EC-209288 had highest pod length as compare to the general mean. The entry FP 13-100 had maximum number of primary branches per plant and the maximum number of seeds per pod was recorded in EC-209288. FP 10-172 emerged with boldest seed size (28.38 g/100 seeds), whereas, P-1042 as smallest seed size (12.65 g/100 seed). The genotypes FP 14-81, DMR-48 and FP 13-99 have maximum biological yield per plant. The genotype FP 2009-4 showed highest harvest index.

Table 1: Analysis of variance of augmented block design for 11 characters in fieldpea genotypes

S.V.	df	Days of 50% flowering	Days to maturity	Plant height (cm)	Number of pods/ plant	Pod length (cm)	Number of primary branches/ plant	Number of seeds/ pod	100-Seed weight (g)	Biological yield/ plant (g)	Seed yield /plant (g)	Harvest index (%)
Blocks (ignoring Treatments)	11	38.383**	33.383**	3339.912**	16.654**	4.035**	0.747**	5.076**	11.367**	53.927**	25.134**	86.862**
Checks	3	40.076 **	51.028 **	11884.360*	9.629 **	0.449**	0.180	0.541**	11.369**	7.847**	1.604**	40.878**
ERROR	33	2.864	4.088	248.028	0.087	0.008	0.067	0.005	0.074	0.188	0.024	0.773

*,** Significant at 5% and 1% probability level respectively

Table 2: Range, mean, coefficients of variance and least significant differences for 11 characters of fieldpea genotypes

Characters	Range (Min-Max)	Mean Value	Coefficient of variance (%)			Range of parameters			
			PCV	GCV	Coefficient of variance (%)	LSD ₁	LSD ₂	LSD ₃	LSD ₄
						5%	5%	5%	5%
Days to 50 percent flowering	61.188-77.938	71.458	5.524	4.989	6.377	1.406	4.870	5.444	4.007
Days to maturity	111.875-130.375	122.415	3.169	2.703	3.768	1.679	5.818	6.504	4.787
Plant height (cm)	12.700-139.650	74.659	35.597	28.690	38.197	13.081	45.313	50.662	37.286
Number of primary branches/plant	0.718-2.697	1.433	28.317	21.789	29.253	0.215	0.746	0.834	0.614
Number of pods/ plant	10.885-26.060	15.282	14.571	14.442	16.863	0.245	0.850	0.950	0.699
Number of seeds/ pod	1.738-8.411	4.261	30.460	30.414	34.181	0.060	0.207	0.231	0.170
Pod length (cm)	3.005-9.018	5.293	22.786	22.720	25.659	0.076	0.263	0.294	0.216
100-seed weight (g)	10.872-27.432	18.348	14.463	14.386	16.163	0.226	0.783	0.875	0.644
Biological yield/plant (g)	15.999-38.913	26.101	15.047	14.955	17.107	0.360	1.247	1.394	1.026
Harvest index (%)	23.039-61.684	43.405	17.639	17.522	19.795	0.730	2.530	2.828	2.082
Seed yield/plant (g)	4.801-22.496	11.554	28.906	28.874	32.606	0.129	0.448	0.501	0.369

LSD₁ = difference between adjusted yield of two genotype in the same block.

LSD₂ = difference between two check means.

LSD₃ = difference between adjusted mean of two genotypes in the different block.

LSD₄ = difference between adjusted yield of genotype and check mean.

PCV = phenotypic coefficient of variance.

GCV = genotypic coefficient of variance.

Table 3: Simple correlation coefficients between different characters in fieldpea genotypes

Characters	Days to 50 percent flowering	Days to maturity	Plant height (cm)	Number of primary branches /plant	Number of pods / plant	Number of seeds / pod	Pod length (cm)	100-Seed weight	Biological yield/ plant	Harvest index (%)	Seed yield/ plant (g)
Days to 50 percent flowering	1.0000	0.9412**	-0.1105	-0.1376	-0.1485	-0.0499	-0.0662	0.0176	-0.1773*	-0.0624	-0.1234
Days to maturity		1.0000	-0.0885	-0.1305	-0.1466	-0.0470	-0.0678	0.0485	-0.1526*	-0.0409	-0.0998
Plant height (cm)			1.0000	0.1887*	0.4387**	-0.2515**	-0.1829*	-0.1717*	0.0410	-0.2878**	-0.1487
Branches / plant				1.0000	0.4879**	-0.2380**	-0.1819*	-0.0712	0.0836	-0.1353	-0.0498
Pods / plant					1.0000	-0.4787**	-0.4199**	-0.0946	0.0519	-0.2130**	-0.0958
Seeds / pod						1.0000	0.9287**	-0.0334	0.6719**	0.7347**	0.7952**
Pod length (cm)							1.0000	-0.0503	0.6117**	0.6696**	0.7241**
100-Seedweight (g)								1.0000	0.1932*	0.4583**	0.3812**
Biological yield/ plant (g)									1.0000	0.5598**	0.8439**
Harvest index (%)										1.0000	0.9057**
Seed yield/plant (g)											1.0000

*,**Significant at 5% & 1% probability level Respectively

Table 4: Direct and indirect effects of different characters on seed yield in fieldpea genotypes

Characters	Days to 50 percent flowering	Days to maturity	Plant height (cm)	Number of primary branches / plant	Number of pods / plant	Number of seeds/ pod	Pod length(cm)	100-Seed weight (g)	Biological yield / plant(g)	Harvest index (%)	Seed yield / plant(g)
Days to 50 percent flowering	0.0145	0.0137	-0.0016	-0.0020	-0.0022	-0.0007	-0.0010	0.0003	-0.0026	-0.0009	-0.1234
Days to maturity	-0.0113	-0.0120	0.0011	0.0016	0.0018	0.0006	0.0008	-0.0006	0.0018	0.0005	-0.0998
Plant height (cm)	-0.0011	-0.0009	0.0102	0.0019	0.0045	-0.0026	-0.0019	-0.0017	0.0004	-0.0029	-0.1487
Number of primary branches /plant	0.0014	0.0013	-0.0019	-0.0102	-0.0050	0.0024	0.0018	0.0007	-0.0008	0.0014	-0.0498
Number of pods/plant	-0.0097	-0.0096	0.0287	0.0319	0.0654	-0.0313	-0.0275	-0.0062	0.0034	-0.0139	-0.0958
Number of seeds/pod	-0.0068	-0.0064	-0.0342	-0.0324	-0.0651	0.1360	0.1263	-0.0045	0.0914	0.0999	0.7952
Pod length(cm)	0.0013	0.0013	0.0036	0.0035	0.0082	-0.0181	-0.0195	0.0010	-0.0119	-0.0131	0.7241
100 seed weight (g)	0.0008	0.0023	-0.0081	-0.0034	-0.0045	-0.0016	-0.0024	0.0471	0.0091	0.0216	0.3812
Biological yield/ plant (g)	-0.0769	-0.0662	0.0178	0.0363	0.0225	0.2915	0.2654	0.0838	0.4339	0.2429	0.8439
Harvest index (%)	-0.0356	-0.0233	-0.1641	-0.0772	-0.1214	0.4189	0.3818	0.2613	0.3192	0.5702	0.9057

R SQUARE = 0.9867, Residual factor = 0.1151, Bold figures indicate the direct effects

Table 5: Cluster mean for different characters in field pea genotypes

Characters	Days to 50 percent flowering	Days to maturity	Plant height (cm)	Number of Primary branches/ plant	Number of Pods/ plant	Number of Seeds/ Pod	Pod length (cm)	100-Seed weight	Biological yield/ plant	Harvest index (%)	Seed yield/plant(g)
Cluster I	69.165	120.739	47.074	1.105*	12.813*	4.414	5.412	20.585**	24.793	45.332	11.325
Cluster II	74.708	125.706**	51.540	1.199	13.603	5.350	6.141	20.470	28.425	51.593	14.794
Cluster III	74.104	124.542	82.695	1.309	13.605	7.074**	7.984**	16.691	31.099	50.795	15.765
Cluster IV	66.250	116.500	28.531*	1.339	13.229	6.438	6.999	19.652	30.724	53.390	16.571

Cluster V	62.250*	114.531*	99.505	1.443	15.223	5.138	5.832	19.062	29.359	50.534	14.856
Cluster VI	68.271	119.292	91.942	2.085	18.635	5.542	6.260	20.346	37.407**	55.971**	20.819**
Cluster VII	69.243	120.403	75.954	2.027	19.485**	3.303	4.479	20.346	29.137	43.459	12.422
Cluster VIII	74.139	125.683	96.189	1.506	15.325	4.004	5.207	19.683	25.992	46.251	11.995
Cluster IX	74.964**	125.441	64.299	1.820	16.077	4.438	5.492	14.752*	25.450	40.502	10.308
Cluster X	67.304	117.542	95.543	1.147	16.305	3.230	4.449	15.263	23.896	33.149	7.908
Cluster XI	74.050	124.550	69.107	1.257	14.610	2.911	4.017	18.278	20.693*	36.544	7.599
Cluster XII	73.488	125.575	103.127**	2.135**	18.520	2.146*	3.695*	17.757	21.943	32.059*	6.936*

*,** indicated lowest values and highest values respectively, among different clusters for different characters

Table 6: Most desirable fieldpea genotypes identified for eleven characters

S. No.	Characters	Genotypes
1	Days to 50 percent flowering	FP 14-89, FP 14-33, FP 14-30, FP 14-88, FP 14-93, FP 14-15, FP 14-24, FP 14-34 IMD-83, IPLK-85.
2	Days to maturity	FP 14-15 (111.875), FP 14-93 (111.875), FP 14-24 (112.875), FP 13-104 (113.375), FP 14-6 (113.375), FP 13-24 (114.375), FP-34 (114.375), FP 14-34 (114.875), FP 14-31 (114.875), FP 14-3 (114.875) and FP 14-67 (115.375).
3	Plant height (cm)	FP 14-15, FP 14-79, FP 14-83, FP 13-97, FP 14-67, FP 13-98, FP 14-90 for dwarfness. FP 14-30 (139.650 cm), DMR-37 (139.317cm), FP 14-25 (120.3 cm), FP 13-90 (118.81 cm) for tallness.
4	Number of primary branches per plant	FP 13-100 (2.697), FP 13-99 (2.697), DMR-48 (2.298), EC-548810 (2.283), EC-384275 (2.328), FP13-40 (2.178), FP 14-87 (2.197), FP 14-81 (2.197), FP 10-172 (2.128), FP 11-33 (2.128), DMR-63 (2.17).
5	Number of pods per plant	FP 10-172 (26.060), DMR-63 (22.160), FP 14-3 (21.585), EC-384275 (20.960), HUDP-11 (20.860), DMR-48 (20.435), IPLK-85 (20.060), FP 13-24 (19.960), EC-281864 (19.960), FP 11-33 (19.060), FP 13-99 (18.835).
6	Pod length (cm)	EC-209288 (9.018), FP 11-112 (8.628), FP 2009-4 (19.741), FP 11-108 (8.408), FP-572 (8.265), FP 10-135 (8.163), FP 11-93 (8.015).
7	Number of seeds per pod	EC 209288 (8.411), FP-572 (7.141), FP 11-93 (7.131), FP 11-112 (7.328), FP 11-108 (7.718), FP 10-135 (7.471) and D-22 (7.188).
8	Biological yield per plant (g)	FP 14-81 (38.913), DMR-48 (37.488), FP 13-99 (37.348), FP 11-72 (35.821), FP 10-135 (34.143), FP 11-108 (33.431), FP 11-63 (32.933) and FP 14-30 (32.583).
9	Seed yield per plant (g)	FP 14-81 (22.496), FP 11-72 (21.819), FP 2009-4 (19.741), FP 11-108 (19.629), FP 10-135 (19.011) and FP 14-30 (18.336).
10	Harvest index (%)	FP 2009-4 (61.684), FP 11-72 (60.949), D-22 (60.074), FP 11-108 (58.739), EC-209288 (58.522), FP 14-81 (57.982), FP 11-51 (56.684) and FP 14-30 (56.442).
11	100-seed weight (g)	FP 10-172 (27.432g), FP 13-104 (26.542g), FP 11-51 (25.972g), FP 13-98 (22.572g), FP 2009-4 (22.392g), FP 10-122 (22.672g), IPLK-57 (21.972g) and EC-548810 (21.865g).

Conclusion

From all over the analysis, it can be concluded that high amount of variability was present in the genotypes under study which provided a better opportunity to select desirable genotypes for further utilization in breeding programme. Correlation and path analysis indicated that harvest index, biological yield per plant, number of seeds per pod, pod length and 100-seed weight had true relationship with seed yield and they are the major yield contributing traits. Hence, direct selection for these traits would be rewarding for yield improvement in fieldpea. Therefore, FP 14-81, FP 11-72, EC-209288, FP 2009-4, FP 14-30, FP 11-108, FP 10-108, FP-572, DMR-48 and FP 14-67 exhibiting higher mean performance for seed yield per plant, 100-seed weight, harvest index, biological yield per plant, plant height, number of primary branches per plant, pods per plant, seeds per pod, pod length and medium mean performance for days to 50 percent flowering and days to maturity, are the elite genotypes. These genotypes can be further utilized in breeding programme.

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