Evaluation of inbred lines derived from commercial hybrids and their utilization in developing high yielding field corn (*Zea mays* L.) hybrids

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Keywords: *Maize, Kernel row number, G×E interaction, Line×Tester, Inbred lines, Hybrids*

Abstract

Genetic enhancement and identification of genetically broad-based inbred lines for the development of new hybrids is the pre-requisite for the heterosis breeding. Newly derived 118 inbred lines were evaluated for their morpho-physiological characters in order to identify best suitable male and female parental lines. Total 10 best inbred lines were selected after thorough evaluation of 16 stable inbred lines, identified from the pool of 118 inbred lines. These inbred lines were crossed in line × tester manner, considering three inbred lines as male and rest as female, based on the Specific Combining Ability and General Combining Ability. Hybrids thus obtained were evaluated in two diverse agroclimatic situations and best heterotic hybrids were selected based on their standard heterosis and rank obtained in Duncan's Multiple Range Test analysis. Single location ANOVA for inbred lines and combined ANOVA for hybrids showed that selected inbreds and hybrids were significantly differing from each other. Since, there exists a Genotype × Environment interaction among hybrids, PCA also taken into consideration for giving weight as classification variable for the hybrids. Further, multi-location evaluation of these hybrids is proposed to identify stable hybrids suitable for large scale commercialization.

Introduction

Although India has achieved maize production of 28.72 mt by 2017-18, it would require 45 mt of maize by the year 2022 to meet out the increasing demand by maize based industries (Upreti, 2013). It in-turn demands development of market driven maize hybrids with higher genetic yield potentiality utilizing genetically enhanced germplasm/lines. Germplasm enhancement is the specific system approach which aims at the continuous increment in the genetic potentiality of the hybrids/varieties. In cross pollinated crops like maize, enhancement of genetic potentiality refers to the improvement of potentiality of the hybrid over existing hybrid in general and correlated improvement of potentiality of the parental lines in particular. For the fast track improvement of existing genetic potentiality, there is a need to target base populations which are enriched with positive alleles responsible for the expected traits.

The amount of heterosis exhibited by a cross is generally used as a measure of the genetic divergence of the parent stock. Without question, genetic divergence (difference in gene frequency) in the parents is required for heterosis to be manifested in the cross (Cress, 1965). Hence, success of the heterosis breeding resides with the development of divergent parents. In the present study new inbred lines derived from private/public bred hybrids were taken as parental lines to constitute new hybrids. According to the concept of heterotic grouping, recycling of hybrids to derive parental lines will surely mix up the heterotic pattern, thus it slows down the genetic improvement process of hybrid breeding (Moll *et.al.*, 1965; Hallauer *et.al.*, 1988; Melchinger, 1999). However, by the explanation of Cress (1965), one can be successful in exploiting heterosis by having diverse parent in a parent stock in subsequent crossing program. It was evident that by following the strategic selection, adapting customized methods, an inbred line with broad genetic base can be identified and heterosis can be exploited in positive manner (Mukri *et al.*, 2018). To derive genetically broad-based inbred lines, the choice and information on genetic composition of source population is very important (Duvick 1996). As a short-term strategy of breeding elite inbred lines, breeders were using F2 generations of public and private bred hybrids as base population and followed pedigree method to select elite lines. In the present study, similar approaches have been made and the homogeneous and homozygous lines so obtained were evaluated for their yield component traits, in general and kernel row number and cob length, in particular. Based on the information on heritability and genotypic variance of selected traits, these inbred lines were crossed and new hybrids with more genetic yield potentiality than existing best national checks were developed.

Material and methods

Selection of inbred lines

A total of one hundred eighteen newly derived inbred lines were grown in two seasons at ICAR-Indian Agricultural Research Institute (ICAR-IARI), New Delhi and Regional Research Centre, Dharwad during *kharif* 2016 and *rabi* 2016-17, respectively. ICAR-IARI, New Delhi is located at the latitude of 28.63° N and the longitude of 77.15° E having mean annual rainfall 800 mm. During the crop period in *kharif* 2016 (initial evaluation of inbred lines) and *kharif* 2018 (final evaluation of inbred lines), IARI location had received total rainfall of 1140 mm and 856 mm respectively. The annual minimum and maximum temperature recorded in the location was 1°C -46°C. During the cropping seasons the temperature recorded was ranged from 26°C -43°C. RRC-Dharwad is located at the latitude 15.46° N and the longitude 75.01° E and receives mean annual rainfall 885mm. Temperature during the cropping period ranged from 14.0°C to 39.0°C. Based on the morpho-phenological characters viz., days to anthesis and silking, ASI, tassel density, cob placement, stem girth and pollen duration, kernel row number, cob length, a total of 16 genotypes suitable either as male or as female parents were selected. Simple descriptive statistics viz., mean, range and standard deviations were used to select these genotypes. These 16 inbred lines were evaluated in *Kharif* 2018 at IARI, New Delhi, under randomized block design with two replications and finally 10 inbred lines were short listed based on their grain yield *per se*.

Hybrids and their evaluation

Among the 10 selected inbred lines, three inbred lines were designated as male parents based on their reported SCA and GCA measures (data not shown) and they were crossed to remaining seven inbred lines in Line × Tester manner. Out of 21 experimental hybrids thus obtained, 20 hybrids were evaluated along with one national check each from medium and late maturing categories across two diverse agro-climatic conditions, viz., 1. Northern Dry Zone (NDZ): Bijapur, Karnataka, 2. Transition Zones (TZ): Shivamogga, Karnataka, India. The NDZ receives total mean annual rainfall of <400mm and temperature ranges from 27°c to 42°c, where as TZ receives annual rainfall of < 600mm and temperature ranges from 17°c to 32°c. All genotypes, inbred lines as well as hybrids, were grown in a 3 m row with spacing: 75 cm between row and 20 cm between plants. All the recommended package of practices was followed to raise a healthy crop (Parihar *et.al.*, 2011). Data recorded included: days to 50% flowering, plant height (cm), ear height (cm), the number of plants, cob length (cm), cob girth (mm), kernel row number, kernels per row, shelling percentage and yield (kg/ha).

Statistical analysis

Genotypic coefficient of variance (PV), phenotypic coefficient of variance (GV), heritability, principal component analysis (PCA) and analysis of variance (ANOVA) to partition the different variance parameter were estimated using software, SAS 9.3v (http://stat.iasri.res.in/sscnarsportal/main.do). Descriptive statistics were performed using software, NCSS11 (http://www.ncss.com). Least Significant Difference (LSD) and Duncan's Multiple Range Test (DMRT) given by Ronald Aylmer Fisher (1935) and Gomez and Gomez (1984), respectively, were adopted to compare the performance of all possible pairs of genotypes. The correlation coefficients were worked out to determine the degree of

Table 1 - Analysis of variance for both inbred lines and hybrids evaluated in different environments

Mean Squares	**Location1**			**Location 2**	**Genotype × Location**
	Sources of variation				**p-value**
	Replication	Genotypes	Replication	Genotypes	
Mean Squares of Inbreds	€53.69 ^{NS} (p=0.8385)	€920281.64** p=<0.0001			
Mean Squares of Hybrids	®2.58 ^{NS} (p=0.5717)	®14.71** (p=0.001)	©1.41 ^{NS} (p=0.2544)	©12.06** (p=<0.0001)	0.0207*

€: IARI, New Delhi, ®: Northern Dry Zone (NDZ), Karnataka, ©: Transition Zone (TZ), Karnataka association of a character with yield and also among the yield components by using the formula given by Weber and Moorthi (1952).

Results

Inbred lines and their evaluation

One hundred eighteen inbred lines derived from the heterotic single cross hybrids were subjected to multi-seasonal evaluation. Based on the Least Significant Difference (LSD) among the yield component traits (Supplementary Table 1), 16 high yielding inbred lines were selected. Analysis of variance (Table 1) revealed that, these 16 inbred lines were differing significantly from each other with respect to cob length (cm), cob girth (mm), kernel row number (no.s), kernels per row (no.s) and per se grain yield (kg ha^{-1}), having trait range of 8.50-16.10, 26.00-41.00, 10.00-22.00, 11.00-33.00 and 900-3550, respectively (Table 2). Among the inbred lines tested PML 45 recorded highest yield (3550.00 kg/ha), followed by PML 93 (3118.60 kg/ha) and PML 102 (3040.20 kg/ha). The PV (Phenotypic variance) and GV (Genotypic variance) of cob girth (PV. 23.90, GV. 23.72), kernel per row (PV. 26.36, GV. 23.91), kernel row number (PV. 6.51, GV. 5.42) and cob length (PV. 4.57, GV. 4.52) were low in comparison with grain yield (PV. 460764.70, GV. 459516.94) (Table 3). As reported in Table 3, the analysis of trait association indicated that cob girth (r=0.66), kernel row number (r=0.49) and kernel per row (r=0.58) found to have significant correlation with the grain yield. The cob length had positive significant correlation (r=0.55) with kernel per row whereas, it had negative significant association with kernel row number (r=-0.36). The cob girth had negative correlation with cob length (r=-0.04) and positive association with kernel per row (r=0.13) (Table 3). The principal component analysis indicated that first principal component (PC1) had positive Eigen vector coefficients for all the traits under study. The PC1 explained 44.61% and PC2 31.85% of variation in the inbred lines (Fig.1). The second principal component (PC2) showed positive Eigen vector coefficients only for Cob length (0.72) and kernel per row (0.45) (Fig. 2). The PCA analysis was able to identify prominent trait which can be considered to select the genotypes for future utilization.

Hybrids and their evaluation

Analysis of variance of hybrids evaluated for their yield component traits both at NDZ and TZ showed that cross combinations differed significantly from each other for the traits under evaluation. Combined analysis of these hybrids indicated the presence of Genotype × Environmental interactions at p=0.05 (Table). Descriptive statistics indicated that, days to 50 per cent anthesis varied from 52 days to 68 days whereas days to 50 per cent silking varied from 54 days to 70 days. Ear height and plant height showed high variation, which ranged from 56-119 cm and 105.60-274.00 cm, respectively. The grain yield ranged from 3.47 -14.56 t ha^{-1} with the mean yield of 8.00 t ha^{-1}. Principal component (PC) analysis revealed that first PC (PC1) had positive Eigen vector coefficient for only days to 50 per cent anthesis (0.58) and days to 50 per cent silking (0.59), while second PC (PC2) had positive Eigen vector coefficient for all the traits viz., days to 50 per cent anthesis (0.18), days to 50 per cent silking (0.15), ear height (0.74), plant height (0.1) and grain yield (0.6).

Table 2 - Descriptive statistics, variance parameters of different yield component traits

Characters	Mean	Minimum	Maximum	Standard deviation
		Inbred lines		
Cob length (cm)	12.82	8.50	16.10	2.10
Cob Girth (mm)	35.47	26.00	41.50	4.81
Kernel Row Number (No.s)	13.84	10.00	22.00	2.51
Kernel Per Row (No.s)	21.49	11.00	33.00	5.05
Grain Yield (kg/ha)	2436.00	900.00	3550.00	667.75
		Hybrids		
Days to 50 percent anthesis	60.54	52.00	68.00	4.69
Days to 50 percent silking	62.38	54.00	70.00	5.00
Ear Height (cm)	86.86	56.00	119.80	13.13
Plant Height (cm)	201.68	105.60	274.00	46.87
Gain Yield (kg/ha)	10.36	3.47	14.56	2.72

Table 3 - Character association and variance parameters of inbred lines

Traits	CL	CG	KRN	KPR	GY	Phenotypic variance	Genotypic variance
CL	1.00000	-0.04 p=0.8081	-0.36 p=0.0386	0.55 p=0.0011	0.12 p=0.5050	23.90	23.72
CG		1.00000	0.27189 p=0.1322	0.13 p=0.4716	0.66 p=<0.0001	4.57	4.52
KRN			1.00000	0.15 p=0.4033	0.49 p=0.0044	26.36	23.91
KPR				1.00000	0.58 p=0.0004	6.51	5.42
GY					1.00000	460764.70	459516.94

CL= Cob Length, CG= Cob Girth, KRN=Kernel Row Number, KPR= Kernels Per Row, GY = Grain Yield

The contributions of PC1 and PC2 to the total variation of the hybrids were 54.43 % and 25.47 %, respectively (Fig.1). The standard heterosis of the tested hybrids ranged from -0.51.68 % to 35.59 % over Bio-9544 (medium maturing hybrid) and -54.38 % to 27.99 % over CMH- 08-282 (late maturing hybrid). Based on the PC obtained from the analysis, days to 50 per cent anthesis/silking was considered for further classification of hybrids and hybrids showing >10 percent standard heterosis against the check of each maturity category were selected.

Discussion

Inbred line selections

Utilization of inbred lines with broad genetic base for the hybridization is the foremost important cause of success of hybrid breeding. However, breeders can point to numerous examples of unexpectedly poor performing hybrids in spite of superior parental stock and genetic diversity (Cress, 1965). Hence systematized selection of inbred lines was done in the present study with the consideration of breeding for specific traits, market demanded maize hybrids. As yield components exhibit higher heritability and better stability across environment compared with yield (Dhillon and Singh 1977, Messmer *et.al*, 2009 and Peng *et.al*, 2011) selection was imposed on cob length (CL), cob girth (CG), kernel row number (KRN) and kernel per row (KPR). The selected 16 inbred lines exhibited high variance for grain yield and cumulative effect of all other component traits made individual genotype significantly different from each other, as it is evident from ANOVA. There existed a non-significant difference between

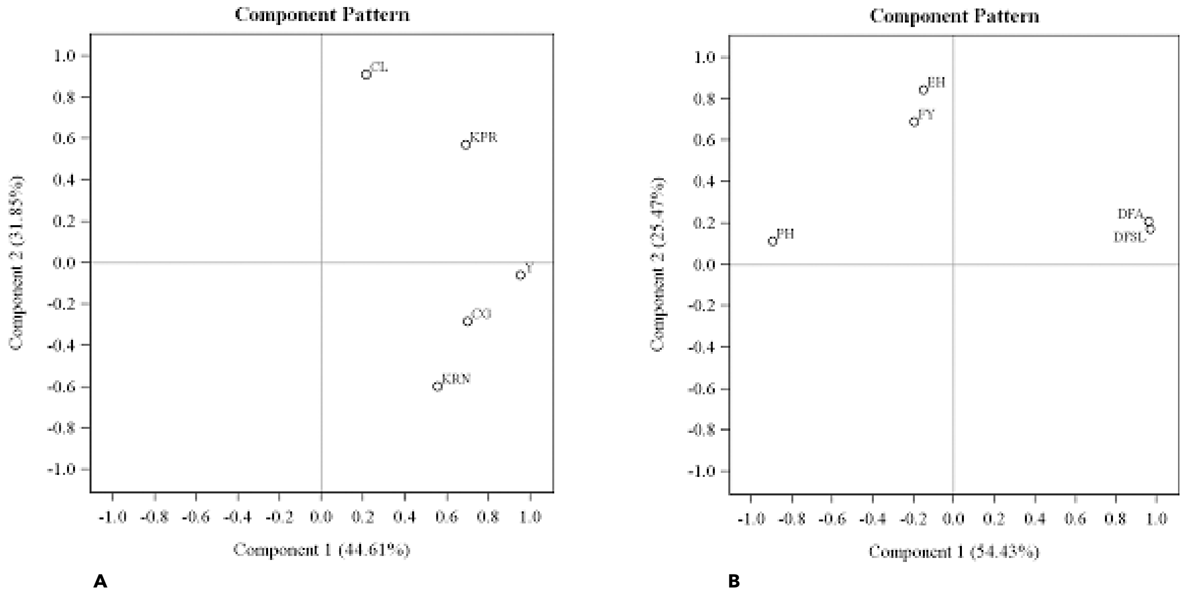

Fig. 1 - Principal components explaining variability in a)inbreds and b) hybrids

Table 4 - Performance and rank of the selected inbred lines

Inbred line	Mean grain yield (kg/ha)	Rank
PML 45	3550.00^{A}	1
PML 93	3118.60^{B}	2
PML 102	3040.20^{C}	3
PML 103	2950.00^{D}	4
PML 46	2860.65^{E}	5
PML 111	2845.00^{E}	6
PML 110	2785.50^{E}	7
PML 112	2606.50^{F}	8
PML 109	2473.50^{G}	9
PML 113	2426.50^{G}	10
PML 44	2215.00^{H}	11
PML 114	2183.88^{H}	12
PML 115	1736.39^{I}	13
PML 116	1714.11^{I}	14
DML-1913	1394.45^{J}	15
DML-1336	1072.99^{K}	16

phenotypic variance and genotypic variance of CL, CG, KRN and KPR traits, it can be hypothesized that, variation available for the selection is not under the control of environmental factors and any further selection will lead to trait improvement in the subsequent generations. Inter correlation among these four traits showed that they have significant association with each other and also influence the expression of grain yield in positive manner (Kumar *et. al.*, 2017, Nagarajan and Nallathambi, 2017; Yi Q *et. al.*, 2019). Finally, PC was taken into consideration along with all the above discussed parameters to decide the trait for which selection has to be operated. As PC1 and PC2 explained the maximum variation present among the inbred lines (Fig 1a), CL, KPR and grain yield were given due weight-age for the inbred lines selection. Hence, for the present study a total of 10 inbred lines viz., PML 45, PML 93, PML 102, PML 103, PML 46, PML 111, PML 110, PML 112, PML 109 and PML 113 were selected based on their grain yield *per se* and rank (Table 4). Though some of the inbred lines were statistically non-significant among the other lines for the grain yield per se, possibility of difference in their combining ability may not be ruled out. Hence the inbreed lines with high per se grain yield ranged from 2426 to 3550 kg ha^{-1} were selected.

Hybrid selection

Among the 10 selected inbred lines, male and female groups were made based on their combining ability. The PML 46, PML 93, PML 102 were used as tester to generate 21 test cross hybrids. The PML 46 and PML 93 had significant SCA effect for cob length and PML 102 had significant GCA effect for KRN. The ANOVA based on individual location as well as combined ANOVA across two locations along with the descriptive

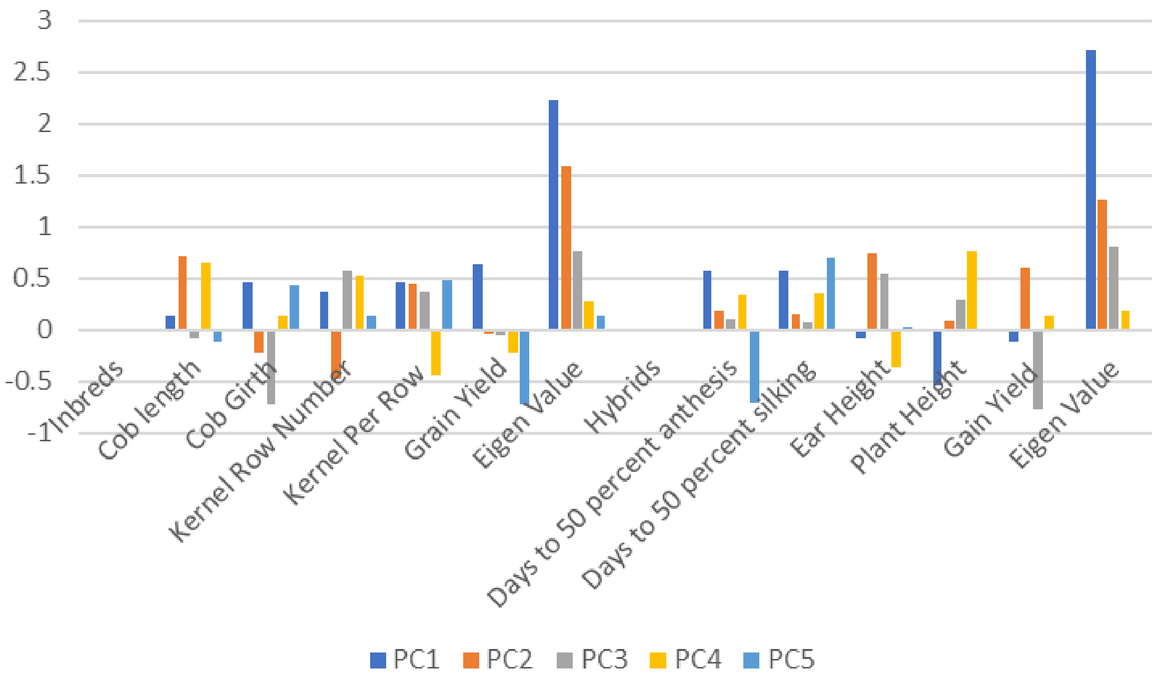

Fig. 2 - Eigen vector value of different principle components related to yield component traits and Eigen value of inbred lines and hybrids

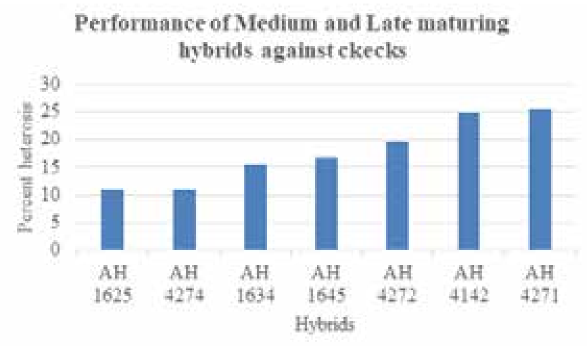

Fig. 2 - Standard heterosis of selected maize hybrids

statistics for the traits under consideration indicated that hybrids differed mainly for flowering behavior and grain yield. A wide range of grain yield in hybrid indicated that female lines selected might have different GCA effect, which can be studied separately (Larièpe *et. al.*, 2017, Mohan Singh *et. al.*, 2017). Since tested 20 hybrids (one was eliminated due to the smaller number of F1 seeds for multilocation trial) interacted with locations, identification of better performing hybrids across environment was little difficult. Hence, LSD technique along with quantum of standard heterosis (> 10 percent) was used as a criterion to shortlist the potential hybrids viz., AH1625, AH 1634, AH 1645, AH 4142, AH 4271, AH 4272 and AH 4274 (Fig.3). Indian maize evaluation network (AICRP system), majorly classifies field corn hybrids as per their maturity duration as, early maturing (≤ 85 days), medium maturing (85-95 days) and late maturing (> 95 days) hybrids (DMR, 2014), for their systematic evaluation to end with as national release. It is mandatory to classify and indicate the maturity group of our experimental hybrids before nominating them for their evaluation in respective maturity group under All India Coordinated Research Program (AICRP). The standard heterosis was calculated against the national checks used in the experiment. Interestingly, PCA analysis of tested hybrids indicated that flowering duration was the major component which contributed to maximum to the variability (Fawad Ali *et al.*, 2015, Sandeep *et al.*, 2017). Hence, selected seven hybrids were again classified into two groups in comparison with the flowering date of standard national checks (medium maturity: Bio-9544 and late maturity: CMH-08-282). Therefore, AH 1634, AH 1645, AH 4271, AH 4272 and AH 4274 were qualified as medium maturing, and AH 1625 and AH 4142 were qualified as late maturing field corn hybrids. These hybrids will be proposed for their multilocation evaluation in respective maturity group under AICRP testing.

Conclusions

Derivation of inbred lines from the potential hybrid is a short-term strategy. If genetic base of the hybrids under inbreeding is broad, then there is an ample possibility of getting distant inbreds in the derived population. As difference in the gene frequency of the parental line is the pre-requisite to develop heterotic hybrids, systematic evaluation can yield potential inbred lines for the strategic development of hybrids with high heterosis that can surely enhance the genetic gain in field corn. In the present study, PML 46, PML 93 was selected as specific combiner and PML 102 was selected as good general combiner for yield component traits. These lines were also promising with respect to their yield *per se*. Hybrids thus obtained from the possible combination of any one of the above lines were also high yielding. This supports the factual requirement of developing hybrid with the economically viable seed or pollen parents for its final commercial hybrid seed production. The identified hybrid viz., AH 13, AH 1645, AH 4271, AH 4272, AH 4274, AH 1625, AH 4142 become boon for the farmers to increase maize productivity.

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Supplementary Table 1- Details of inbred lines used in the study and per se yield of individual lines

S. NO.	Nomenclature	Pedigree	Yield (kg/ha)
1.	PML 1	Geo.Pre. Dia.-2-2-4	1132
2.	PML 2	Geo.Pre. Dia.-12-1-2	1138
3.	PML 3	KMH-25K60-2-1-2	1114
4.	PML 4	KMH-25K60-2-1-8	1130
1.	PML 5	KMH-25K60-12-1-2	1038
2.	PML 6	KH-2192-10-1-1	993
3.	PML 7	KH-2192-14-1-2	1140
4.	PML 8	GEO-2101-15-1-4	1198
5.	PML 9	POLO-1-2-2	1162
6.	PML 10	POLO-1-2-3	935
7.	PML 11	POLO-14-1-2	958
8.	PML 12	POLO-14-1-3	1189
9.	PML 13	KDMH-4086-15-1-5	1193
10.	PML 14	KDMH-4086-15-1-7	1157
11.	PML 15	CMH-08-282-14-1-1	909
12.	PML 16	HQPM5-13-1-1	904
13.	PML 17	RMH-3591-1-1-1	1005
14.	PML 18	RMH-3591-4-1-1	955
15.	PML 19	RMH-3591-4-1-2	987
16.	PML 20	RMH-3591-4-1-3	1180
17.	PML 21	DMH-119-1-1-4	1100
18.	PML 22	DMH-119-10-1-5	930
19.	PML 23	CP-999-9-1-3	1193
20.	PML 24	CP-999-15-2-4	973
21.	PML 25	KMH-218PLUS-1-1-3	1162
22.	PML 26	RASI-3033-2-1-1	901
23.	PML 27	RASI-3033-15-1-1	1108
24.	PML 28	PAC-745-2-1-1	977
25.	PML 29	PAC-745-2-1-2	914
26.	PML 30	PAC-745-9-2-1	1098
27.	PML 31	PAC-745-9-2-2	903
28.	PML 32	PAC-745-9-2-4	1000
29.	PML 33	PAC-745-9-3-4	1144
30.	PML 34	PAC-745-12-1-1	1080
31.	PML 35	PAC-745-12-1-2	1177
32.	PML 36	PAC-745-15-1-1	1157
33.	PML 37	PAC-753-4-1-1	1028
34.	PML 38	PAC-753-7-1-3	1062
35.	PML 39	PAC-753-8-2-2	982
36.	PML 40	PAC-753-9-1-6	1033
37.	PML 41	PAC-753-9-1-7	996
38.	PML 42	PAC-753-12-1-1	1106
39	PML 39	PAC-753-8-2-2	982
40	PML 40	PAC-753-9-1-6	1033
41	PML 41	PAC-753-9-1-7	996
42.	PML 42	PAC-753-12-1-1	1106
43	PML 43	PAC-753-12-1-4	1107
44	PML 44	PAC-753-13-1-2	2215
45	PML 45	PAC-753-13-1-4	3550
46	PML 46	SAFAL-X12-9-1-1	2860
47	PML 47	30B07-9-4	1116
48	PML 48	115-08-01-6-1	940
49.	PML 49	P-3501-3-1	1046
50	PML 50	P-3501-5-2	999
51.	PML 51	PMH3-11-1	1117
52	PML 52	EH 1974-6-3	1047
53	PML 53	KH-517GOLD-9-1-1	1180
54	PML 54	KDMH-755-12-1-1	1002
55	PML 55	KDMH-755-12-1-2	915
56	PML 56	HM4-10-1-3	906
57	PML 57	NK-6240-6-1-4	1185
58	PML 58	900M-GOLD-7-1-2	908
59	PML 59	(BML6 X CE18)-1-2	1158
60	PML 60	(BML6 X CE18)-1-3	951
61	PML 61	(HKI1105 X CML170)-1-2	929
62	PML 62	(CE8 X CE16)-2	1086
63	PML 63	(KML27 X V335)-3-1-1	1132
64	PML 64	(KML27 X V335)-2-1-1	1199
65	PML 65	(CE13 X HKI1128)-2-1-2	939
66	PML 66	IML307-1-1-1	997
67	PML 67	IML307-2-1-1	1047
68	PML 68	RMH-932-3-1-1	1070
69.	PML 69	SFAL-X2-11-1-5	1131
70	PML 70	GEO-2101-1-1-1	1044
71	PML 71	GEO-2101-15-1-4	1013
72	PML 72	KDMH-4086-15-1-5	959
73	PML 73	KDMH-4086-15-1-7	1122
74	PML 74	RASI-3033-15-1-1	900
75	PML 75	PAC-753-8-1-3	1011
76	PML 76	PAC-753-9-1-7	1088
77	PML 77	SUN-234-5-2-1	1148
78	PML 78	P-3501-3-1	1071
79	PML 79	LG-3281-11-1-1	1146
80	PML 80	(BML6 X CE18)-1-7	1094

S. NO.	Nomenclature	Pedigree	Yield (kg/ha)
81	PML 81	(VQL-1 X V-373)-1-1-1	1095
82	PML 82	PAC-745-6-1-1	979
83	PML 83	PAC-753-9-1-1	930
84	PML 84	PAC-753-13-1-2	925
85	PML 85	IML307-3-1-1	1050
86	PML 86	CP-888-14-1-1	1178
87	PML 87	CP-888-14-1-2	927
88	PML 88	POLO-11-2-1	978
89	PML 89	PAC-745-6-1-1	1100
90	PML 90	PAC-745-6-2-1	973
91	PML 91	V373-V6-17	1043
92	PML 92	PAC-753-13-1-3	1066
93	PML 93	KDMH-176-5-1-1	3118
94	PML 94	PAC-740-10-1-1	944
95	PML 95	P-3501-10-1-3	997
96	PML 96	V931-16	1141
97	PML 97	V931-16	920
98	PML 98	V929-7	1026
99	PML 99	V929-7	1195
100	PML 100	Z485-22	954
101	PML 101	SN-194-29	1149
102	PML 102	KDMH-755-12-2-1-1	3040
103	PML 103	CP-888-14-2-2-2	2950
104	PML 104	PAC-753-13-6-3	1176
105	PML 105	LG-3281-11-2-1	1067
106	PML 106	SFAL-X2-11-3-1-5	1043
107	PML 107	GEO-2101-15-2-1-4	1022
108	PML 108	POLO-11-2-1-2-1	927
109	PML 109	PAC-753-9-1-3-2-1	2473
110	PML 110	POLO-14-1-2	2785
111	PML 111	HQPM5-13-3-1	2845
112	PML 112	RMH-3591-14-1-2	2606
113	PML 113	PAC-753-4-1-1	2426
114	PML 114	115-08-01-10-2	2183
115	PML 115	KRISHNA GOLD -8-1-1	1736
116	PML 116	RMH-3591-14-5-2	1714
117	DML-1913	WNC-25-3-3	1394
118	DML-1336	JCY-36-2-2-1-1	1072