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Identification of Superior Segregants through Exploitation of Genetic Variability in F_3 Families of Rice (*Oryza sativa* L.) under Aerobic Cultivation

POTLANNAGARI ROOPA SOWJANYA, P. RAGHAVENDRA, R. VENKATESH GANDHI AND SHAILAJA HITTALMANI
Dept. of Genetics and Plant Breeding, College of Agriculture, UAS, GKVK, Bengaluru-560065

ABSTRACT

The present study was conducted to evaluate 35 and 30 F_3 families derived from MAS145 x MAS946-1 cross and IR 64 x IM 192 cross respectively. The results revealed that there is presence of adequate variability for traits under study. Slight difference between GCV and PCV estimates observed for most of the traits witnessing the lower influence of environment for expression of these traits. Most of the traits showed moderate narrow sense heritability coupled with moderate or low GAM indicating involvement of both additive and non-additive genes hence selection is effective with little intense. Further, based on the yield per plant, duration wise superior segregants were identified and these lines after stabilization with appropriate selection with homogeneity with higher will be highly suitable for cultivation under aerobic condition as the parents of the crosses have either one or both the parents for aerobic condition.

RICE (*Oryza sativa* L.) is a highly domesticated crop, and domestication processes are reported to be accompanied by genetic erosion, which causes a reduction in genetic variation (Khare *et al.*, 2014).Improvement in any crop largely depends on the genetic variability and the extent to which the traits are heritable. Therefore, there is dire need for creation of variability through artificial way to meet the food requirement of increasing population and also to cope up with water shortage situations. Hybridization is one of the way through which enormous variability can be created. It has been hypothesised that progress in breeding programme depends on amount of variability created during hybridization (Kayande and Debaje 2010). Segregating populations are more important for improving plant types by operating selection (Kiran *et al.*, 2013; Farhad Kahani and Shailaja Hittalmani 2015; Shantavva *et al.,* 2014). Therefore the knowledge of genetic parameters present in segregating population for the improvement of character under study has paramount importance. Phenotypic coefficient of variation(PCV), genotypic co-efficient of variation (GCV), heritability, genetic advancement will be useful for efficient exploitation of variability (Savitha and Usha kumara 2015a; Shantavva *et al*., 2014).The genotypic coefficient of variation measures the range of variability available in a crop and also enables to compare the amount of variability present in different characters. The phenotypic expression of the character is the result of interaction between genotype and environment. Hence, the total variance needs to be partitioned into heritable and non-heritable components to assess the inheritance pattern of the particular character under study. Heritability indicates the relative degree at which a character is transmitted from parent to offspring. Heritability estimates along with GA are normally more helpful in predicting the gain under selection than heritability estimates alone. As both will serve as important selection parameters (Ogunbayo *et al.*, 2014). One of the main constraints of rice cultivation and production is water shortage during periods of low rainfall, which affects the vegetative growth rate and grain yield (Tao *et al*., 2006). Aerobic rice cultivation is one such choice wherein the water required is half of that of irrigated puddled rice, without compromising the productivity (Gandhi *et al*., 2011a, Gandhi *et al*., 2011b).In this context the present investigation was undertaken to evaluate the genetic variability present in F_3 segregating populations and also to identify superior segregants suitable for aerobic condition.

MATERIAL AND METHODS

The experiment was carried out during *Kharif* season of 2013 at K block, GKVK, Bengaluru, representing the eastern dry zone which is located at the latitude of 12° 58' North; longitude 77° 35' East and altitude of 930 meters above mean sea level. The experimental material for the present study composed of 35 and 30 F_3 families derived from MAS 145 x MAS 946-1 cross and IR 64 x IM 192 crosses, respectively. They were evaluated in an augmented design (Federer, 1961) in 10 blocks under aerobic condition. The salient features of parents and checks used in the present study are furnished in the Table I.

Twenty plants were selected at random for each line from each family under aerobic condition for recording observations as per Standard evaluation system for rice (Annon. 1996). The characters observed for eliciting the information are as follows, Plant height at 30 days after transplanting (cm), Plant height at maturity (cm), Days to 50 Per cent flowering, Days to maturity, Total number of tillers per plant, Productive tillers per plant, 1000 grain weight (g), Harvest index, Grain yield per plant (g), Panicle length (cm), Panicle exsertion (± cm), Spikelets per panicle, Biomass, Panicle weight, Spikelet fertility (%), Grain yield per day (mg per day). The average of observations recorded on these twenty plants was considered for statistical analysis.

The potentiality of a cross is measured not only by mean performance but also on the extent of variability. Knowledge on nature and magnitude of genotypic and phenotypic variability present in any crop species plays an important role in formulating successful breeding programmes (Savitha and Usha kumari 2015b). Rahman *et al*., (2015) also highlighted the importance of variability in early segregating generations and suggested that magnitude of genotypic coefficient of variability and phenotypic coefficient of variability should be given importance.

The statistical analysis on the mean values of twenty randomly selected plants from each of population was recorded under aerobic condition statistical analysis was carried out on individual characters following Augmented design (Federer, 1956) WINDOSTAT version 9.0 developed by indostat services, Hyderabad. Adjusted trait mean of each of the genotype accession were estimated (Federer, 1956) and the same were used for all subsequent statistical analysis. The following descriptive statistics mean, Range and standardized range, Skewness and Kurtosis were calculated as per Raghavendra and S.Hittalmani (2015). Based on the direction and magnitude of skewness (g1) and kurtosis (g2), nature of genetic control of growth yield was inferred (Pooni *et al.*, 1977).Genetic parameters such as genotypic co-efficient of variation (GCV), phenotypic co-efficient of variation (PCV), heritability, genetic advance as percent mean were estimated. Superior segregants have been identified by considering the yield per plant further percent improvement over checks calculated.

TABLE I

Salient features of the parents and checks used in the study

Genotypes	Parentage	Special Feature	Source of seed
		Parents	
MAS 946-1	Cultivated variety (Aerobic)	High yielding under aerobic condition, WUE, Erect panicles	MAS LAB GKVK
IR 64	Cultivated variety	Semi dwarf, drought susceptible.	MAS LAB GKVK
IM 192	IR 50 X Moroberekan	Medium early maturing, drought tolerant	MAS LAB GKVK
MAS 145	IR 78875-131-B-1-2/IR 78877-208-B-1-1	Fine grain type, high yielding	MAS LAB GKVK
		Checks	
Rasi	Cultivated variety	Drought resistant	MAS LAB GKVK
Moroberekan	Landrace	Drought resistant	MAS LAB GKVK
MAS 99	Promising genotype	Aerobic rice	MAS LAB GKVK

RESULTS AND DISCUSSION

The mean performance of parents furnished in Table II indicated that they are contrasting for most of the traits under study. As it is the one of the important prerequisite for crop improvement through hybridization followed by selection (Savitha and Usha kumari 2015a).

*Genetic variability parameters for yield and yield attributing traits :*As evident from Table III, the analysis of variance are given for various morphological characters were statistically tested and found to be significant for all the characters in both the crosses derived F_3 progenies.

MAS 145 / MAS 946-1

The estimates genetic variability parameters of for yield and its attributing traits in F_3 families of a) MAS145/MAS946-1cross are provided in the Table IV and Fig.1. The variability parameters revealed that highest PCV and GCV values recorded for panicle exertion (32.93 & 32.28%), followed by spikelet fertility (22.98 &20.87%) and panicle weight (21.71 & 20.67%) indicated that presence of adequate

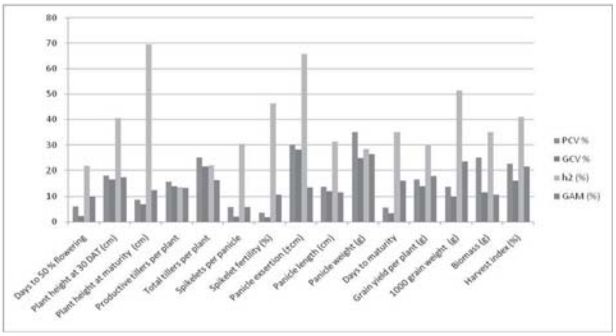

Fig. 1 : Genetic parameters for yield and its attributing traits in F_3 families derived from MAS145/MAS946-1 rice cross

TABLE II

Mean performance of Parents and checks for grain yield and its components

Traits	MAS 145	MAS 946 -1	IR 64	IM 192	Moroberekan	Rasi	MAS 99
Days to 50 % flowering	97.50	92.50	100.50	87.50	124.00	82.50	91.00
Plant height at 30 days after transplanting (cm)	25.23	40.00	33.0	27.50	31.00	33.00	32.00
Plant height at maturity (cm)	46.12	61.26	69.01	50.13	98.25	78.00	78.00
Productive tillers plant $^{-1}$	13.00	21.00	12.00	28.16	7.00	15.00	21.00
Total number of tillers plant^{-1}	15.00	23.00	13.02	15.32	8.00	17.00	24.00
Spikelets per panicle	100.00	117.00	80.00	113.00	81.00	100.00	82.00
Spikelet fertility (%)	83.00	67.35	82.35	68.40	86.00	96.00	88.00
Panicle exsertion (± cm)	0.02	0.00	0.00	0.00	0.00	0.00	0.02
Panicle length (cm)	18.00	20.00	16.12	19.00	22.00	21.00	16.00
Panicle weight (g)	1.03	1.80	3.56	1.02	1.20	3.70	3.95
Grain yield plant^{-1} (g)	18.50	23.60	20.01	25.50	20.64	30.21	37.25
1000-grain weight (g)	18.60	28.20	31.00	36.12	25.60	36.50	35.60
Days to maturity	135.36	120.26	110.03	101.32	155.00	128.00	127.00
Biomass (g)	51.20	79.30	61.00	85.00	78.00	68.00	56.00
Harvest index	0.40	0.29	0.36	0.40	0.35	0.43	0.40

TABLE III

Analysis of variance (mean sum of squares) for 15 quantitative characters in F_3 families derived from MAS 145 / MAS 946-1 (I) and IR64/ IM192 (II) crosses of Rice

Source of variation	Blocks		Entries (check + progenies)		Checks		Progenies		Check vs. progenies		Non Genetic (Error)	
	I	II	I	II	I	II	I	II	I	II	I	II
Degrees of Freedom (df)	1	2	40	35	5	5	34	29	1	1	5	10
Days to flowering	0.02	6.54	85.39	125.7	447.57	513.59	17.32 *	35.08 **	588.75	814.40	5.07	5.59
Plant height at 30 DAT (cm)	8.34	84.49	90.69	56.96	408.93	319.96	31.93 *	103.25 **	497.36	9.56	0.93	8.36
Plant height at maturity (cm)	0.00	0.16	178.3	194.92	906.25	1050.93	69.60 *	21.52 **	235.67	947.37	0.60	6.10
Productive tillers plant $^{-1}$	0.08	8.72	11.97	19.23	72.88	107.02	2.98 **	16.53 *	13.13	5.66	0.08	2.78
Total no. of tillers plant $^{-1}$	0.33	13.72	12.49	25.48	80.53	141.15	2.80 *	34.76 *	1.69	47.94	0.13	2.38
No. of Spikelets panicle^{-1}	0.08	0.05	90.65	81.46	599.15	441.65	5.71 *	21.45 **	504.19	20.67	4.88	3.92
Spikelet fertility (%)	0.42	2.51	33.98	50.05	210.84	291.36	7.96 *	6.65 *	34.39	102.19	0.45	1.57
Panicle exsertion (±cm)	0.00	0.00	0.37	0.15	0.00	0.00	0.41 *	0.10 *	1.04	2.21	0.00	0.00
Panicle length (cm)	2.08	0.00	4.26	3.39	6.35	18.40	5.08 *	0.54 *	0.19	11.10	1.83	0.39
Panicle weight (g)	0.03	0.00	1.40	2.04	0.97	3.08	0.80 **	1.68 *	24.08	7.12	0.05	0.65
Days to maturity	36.75	43.57	149.69	266.64	934.58	1355.64	41.36 *	70.18 *	74.62	518.92	35.34	38.89
Grain yield plant^{-1} (g)	0.67	0.61	35.90	48.93	77.89	71.08	25.88 **	21.25 *	166.54	740.91	0.30	12.79
1000-grain weight (g)	15.98	0.22	50.84	39.50	162.93	81.89	4.49 *	0.38	252.25	962.11	3.33	25.57
Harvest index	0.00	3.05	0.00	296.55	0.00	750.36	0.00 **	225.30 **	0.06	93.84	0.00	44.11
Biomass (g)	3.09	0.00	260.62	0.01	1091.78	0.00	143.74 **	0.01 *	78.97	0.12	1.44	0.00

TABLE IV

Estimates of genetic parameters for yield and its attributing traits in F_3 families of MAS145 / MAS 9461 of rice cross

Plant Traits	Range		Standardized range	Mean ± S.E	Variance	PCV (%)	GCV (%)	H^2 (ns) %	GAM (%)
	Max.	Min.							
Days to 50 % flowering	112.50	94.55	0.17	103.91 ± 0.70	17.33	5.39	3.39	32.26	6.92
Plant height at 30 DAT (cm)	56.45	24.95	0.86	36.71 ± 0.95	31.93	13.44	13.18	35.03	14.15
Plant height at maturity (cm)	93.70	56.35	0.54	69.36 ± 1.41	69.61	10.47	10.41	66.46	19.32
Productive tillers per plant	13.85	7.75	0.60	10.20 ± 0.29	2.99	14.79	14.52	17.82	18.62
Total tillers per plant	16.85	11.10	0.14	13.27 ± 0.28	2.81	11.06	10.71	19.05	17.39
Spikelets per panicle	94.75	86.35	0.09	90.47 ± 0.32	3.71	7.20	6.32	51.42	2.28
Spikelet fertility (%)	88.58	76.68	10.46	82.94 ± 0.47	7.96	22.98	20.87	61.42	7.83
Panicle exsertion (± cm)	2.95	-0.65	0.51	0.34 ± 0.10	0.41	32.93	32.28	32.09	28.40
Panicle length (cm)	23.80	14.20	1.08	18.90 ± 0.34	4.08	9.75	7.69	38.11	16.02
Panicle weight (g)	6.00	2.10	0.43	3.63 ± 0.15	0.80	21.71	20.67	60.63	21.97
Days to maturity	146.45	122.55	0.78	135.65 ± 1.03	37.36	4.47	3.90	61.33	18.75
Grain yield per plant (g)	38.40	15.40	0.93	24.16 ± 0.86	25.89	18.33	15.19	51.42	17.65
1000 grain weight (g)	42.29	22.21	0.95	30.51 ± 0.90	28.44	17.62	15.68	37.70	14.63
Biomass (g)	95.95	39.30	0.18	60.99 ± 2.06	14.74	17.11	17.00	63.67	24.58
Harvest index (%)	0.56	0.25	0.66	0.40 ± 0.01	0.01	17.08	16.97	66.73	24.53

Min.	Minimum	H^2 (ns) %	Narrow sense heritability
Max.	Maximum	GAM	Genetic advance as percent mean
S.E	Standard error	PCV (%)	Phenotypic coefficient of variation (%)
		GCV (%)	Genotypic coefficient of variation (%)

variability for these traits. Whereas, lowest PCV and GCV estimates for days to maturity (4.47 & 3.90%) and days to 50 Per cent flowering (5.39 & 3.39%) designated that presence of lower degree of variability for these traits. The narrow difference between PCV and GCV estimates for most of the traits studied indicated that slighter influence of environment for these traits. Which are in confirmatory with Gopal Reddy and Goud (1970), Bidhan *et al.* (2001), Thirugnana Kumar *et al.* (2007) and Kayande and Debaje (2010). High heritability coupled with high GAM was registered for panicle weight , biomass, harvest index, plant height at maturity, days to maturity suggested that preponderance of additive gene action in the expression of these characters. Therefore selection is effective for these traits. Which is in confirmatory with Kiran *et al.* (2013). Most of the traits shown moderate narrow sense heritability coupled with moderate or low GAM indicating involvement of both additive and non-additive genes. Selection is effective with little intense. These are in confirmatory with Shanthavva *et al.* (2014), Savitha and Usharani (2015a).

IR 64 / IM 192

The estimates genetic variability parameters of for yield and its attributing traits in F_3 families of IR64/ IM192 cross are provided in the Table V and Fig.2. Highest PCV and GCV estimates observed for panicle weight (34.96 & 24.80%) followed by panicle exertion

(30.06 & 28.62%) and total tillers per plant (24.98 & 21.54%) indicated the presence of high degree of variability for these traits. However lowest PCV and GCV estimates recorded for spikelet fertility (3.53 & 1.78%) and days to maturity (5.63 & 3.33%) suggested the presence of considerable degree of variability for these traits these results are in accordance with Chauhan (1996), Nath and Talekar, (1994), Rahman *et al.* (2015). The slighter difference between GCV and PCV estimates observed for most of the traits witnessing the lower influence of environment for expression of these traits. Most of the traits shown

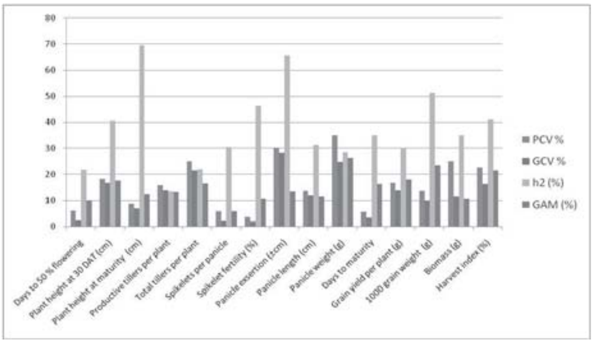

Fig. 2 : Genetic parameters for yield and its attributing traits in F_3 families derived from IR 64 / IM192 rice cross

TABLE V

Estimates of genetic parameters for yield and its attributing traits in F_3 families of IR 64 / IM192 of rice cross

Plant Traits	Range		Standardized range	Mean ± S.E	Variance	PCV (%)	GCV (%)	H^2 (ns) %	GAM (%)
	Max.	Min.							
Days to 50% flowering	120.00	96.00	0.22	107.59 ± 1.08	35.09	6.06	2.29	21.64	10.06
Plant height at 30 DAT (cm)	41.05	24.85	0.47	34.58 ± 0.66	13.26	18.11	16.54	40.54	17.41
Plant height at maturity (cm)	79.00	62.30	0.24	69.16 ± 0.84	21.53	8.62	6.98	69.54	12.31
Productive tillers per plant	17.45	8.65	0.69	12.74 ± 0.39	4.57	15.67	14.01	13.43	13.36
Total tillers per plant	18.45	9.00	0.15	13.71 ± 0.39	4.76	24.98	21.54	21.86	16.36
Spikelets per panicle	94.70	75.35	0.22	88.76 ± 0.84	21.46	5.81	2.06	30.34	5.67
Spikelet fertility (%)	93.93	80.19	-2.95	89.37 ± 0.47	6.65	3.53	1.78	46.24	10.60
Panicle exsertion (±cm)	0.15	-1.15	0.16	-0.44 ± 0.06	0.11	30.06	28.09	65.83	13.57
Panicle length (cm)	19.30	16.40	1.52	18.01 ± 0.13	0.54	13.67	11.89	31.24	11.58
Panicle weight (g)	6.30	1.30	0.69	3.29 ± 0.23	1.69	34.96	24.80	28.35	26.46
Days to maturity	152.35	118.80	1.00	136.02 ± 1.59	70.19	5.63	3.33	35.06	16.21
Grain yield per plant (g)	40.35	18.70	0.88	27.95 ± 0.84	0.38	16.70	13.86	30.05	18.01
1000 grain weight (g)	23.78	20.82	0.77	22.09 ± 0.11	225.30	13.83	9.85	51.42	23.48
Biomass (g)	101.04	40.23	0.25	69.23 ± 2.74	21.25	24.99	11.56	34.92	10.64
Harvest index	0.69	0.26	0.13	0.42 ± 0.01	0.01	22.63	16.17	41.07	21.51

Min. Minimum H^2 (ns) % Narrow sense heritability

Min. Minimum H^2 (ns) % Narrow sense heritability

Max. Maximum GAM Genetic advance as percent mean S.E

Standard error PCV (%) Phenotypic coefficient of variation (%)

GCV (%) Genotypic coefficient of variation (%)

moderate narrow sense heritability coupled with moderate or low GAM indicating involvement of both additive and non - additive genes.Selection is effective with little intense. These are in confirmatory with Panwar and Mathur (2007), Shanthavva *et al.* (2014), Savitha and Usharani (2015b).

Third (skewness) and fourth (kurtosis) degree statistics in F_3 families' : The study of distribution properties such as coefficients of skewness and kurtosis provides insight about the nature of gene action and number of genes controlling the traits respectively. They are more powerful than first and second degree statistics which reveal interaction genetic effects. The skewness and kurtosis values for 15 quantitative traits are presented in Table VI. It infers that the frequency distribution F_3 families for all traits shown positively skewed (+ve values) plautykurtic (<3) indicated the involvement of large number of genes controlling these traits with majority of them displaying complementary epistasis. Hence, intenseselection is required for rapid genetic gain for these traits (Pooni *et al.*, 1977). Similar observations were reported by Kiran *et al.* (2013), Raghavendra and S. Hittalmani (2015). However spikelet's per panicle and grain yield per plant in MAS 145 / MAS 946-1 cross and plant height at 30 days, spikelet's per panicle, spikelet fertility, panicle exertion, panicle length in IR 64 / IM 192 cross shown negatively skewed (-ve values) plautykurtic (<3) distribution indicated that they may be under control of large no. of genes with duplicate epistasis. Hence, mild selection is expected to result in rapid genetic gain for these traits. Plant height at 30 DAT and panicle exertion in MAS 145 / MAS 946-1 cross derived progenies showed leptokurtic (>3) distribution suggested that few genes controlling these traits (Pooni *et al.*, 1977).

Identification of superior segregants in F_3 families : The top five superior segregants for grain yield in early, mid, late duration and percent increase over check by F_3 progenies of MAS 145 X MAS 946-1and IR64/IM192 are presented in table VII and VIII

TABLE VI

Description of frequency distribution of grain yield and its component characters in F_3 segregating progenies under study

Traits	MAS 145 x MAS 946-1		IR 64 x IM 192	
	Skewness	Kurtosis	Skewness	Kurtosis
Days to 50% flowering	0.057	-0.247	0.508	-0.057
Plant height at 30 days after transplanting (cm)	1.191	3.413	-0.598	0.557
Plant height at maturity (cm)	0.536	0.788	0.411	-0.573
Productive tillers plant^{-1}	0.681	-0.579	0.333	0.249
Total number of tillers plant^{-1}	0.724	-0.517	0.210	0.387
Spikelets per panicle	-0.097	-0.019	-1.668	2.812
Spikelet fertility (%)	0.365	0.124	-0.988	2.424
Panicle exsertion (± cm)	2.047	6.826	-0.145	-0.671
Panicle length (cm)	0.200	0.438	-0.326	-0.321
Panicle weight (g)	0.674	0.355	1.006	0.892
Grain yield plant^{-1}(g)	-0.144	-0.848	0.140	-0.731
Days to maturity	0.103	-0.898	0.407	0.824
1000-grain weight (g)	1.014	1.817	0.184	-0.650
Harvest index	0.876	2.051	0.682	0.813
Biomass (g)	0.037	-0.555	0.577	-0.209

TABLE VII

The top five superior segregants for grain yield in early, mid and late duration and percent increase over check by F_3 progenies of MAS 145 x MAS 946-1 cross

Sl. No.	Duration	Plant No.	Duration (days)	Yield per plant (g)	Yield per Plant (g) per day (mg)
1		16-5	120	40.32	336.0
2		24-11	120	38.50	320.8
3	Early duration (120) days	8-14	120	35.63	296.9
4		3-5	120	34.13	284.4
5		2-3	120	32.26	268.8
Mean			120	36.16	301.3
Check	MAS 99		120	35.21	293.4
% increase over check				2.70	2.70
1		11-6	130	40.32	310.1
2		4-5	127	38.14	300.3
3	Medium duration (120-130)days	17-14	122	35.10	287.7
4		18-7	120	31.26	260.5
5		6-6	128	24.98	195.1
Mean			125.4	33.96	270.8
Check	Rasi		125	28.20	225.6
% increase				20.42	20.0
1		15-8	132	44.26	335.3
2		2-5	131	41.03	313.2
3	Late maturing (>130) days	21-5	140	40.59	289.9
4		33-14	141	39.98	283.5
5		35-4	142	32.06	225.7
Mean			138	39.58	286.8
Check	Moroberekan		140	20.60	147.1
% increase over check				92.13	94.96

TABLE VII

The top five superior segregants for grain yield in early, mid and late duration and percent increase over check by F_3 progenies of MAS 145 x MAS 946-1 cross

Sl. No.	Duration	Plant No.	Duration (days)	Yield per plant (g)	Yield per Plant (g) per day (mg)
1	Early duration (120) days	21-15	120	40.15	334.5
2		12-6	120	35.65	297.0
3		1-3	120	35.16	293.0
4		5-18	120	34.16	284.6
5		18-14	120	32.26	268.8
Mean			120	35.47	295.5
Check	MAS 99		120	35.21	293.4
% increase over check				0.80	0.80
1	Medium duration (>120-130)days	14-6	128	45.32	354.0
2		3-7	125	41.23	329.8
3		2-7	125	40.00	320.0
4		5-12	124	33.56	270.6
5		27-16	130	28.39	218.3
Mean			124	37.77	304.5
Check	Rasi		125	28.20	225.6
% increase over check				34.0	35.0
1	Late maturing (>130) days	29-20	135	40.25	298.1
2		24-11	140	32.56	232.5
3		7-13	130	32.13	247.1
4		4-7	132	30.50	231.1
5		27-16	145	20.16	139.0
Mean			137	31.12	227.1
Check	Moroberekan		135	20.60	152.5
% increase over check				51.10	48.9

respectively. The percent yield increase over checks was highest for late maturing superior segregants followed by mid maturing and early maturing segregants respectively in both cross derived progenies.

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