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Rice Breeding for High Yield by Advanced Single Seed Descent Method of Selection

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ABSTRACT

Rice improvement for high yield is important to increase productivity of the crop. The success of breeding program depends on the choice of best parents and selection method. A research was conducted by applying Single Seed Decent (SSD) with Rapid Generation Advance (RGA) for speeding up the breeding cycle and to select elite line at F_7 in 2012. A total of 271 recombinant inbred lines (RILs) were obtained in this program. Augmented design in RCBD with 3 replications was performed using standard check varieties (PTT1, CNT1, SPR60, RD31 and RD41). Three lines were observed with significantly higher yield than the best check variety, CNT1. However, only one line was significantly higher for number of filled seed per panicle than the best parent, CH1. All ten top-yielding lines had significantly higher filled seed per panicle than CNT1. Plant height of mostly the top-ten high-yielding lines ranged between 110 to 120 cm and days to 50% flowering all early more than KDML 105. Positive transgressive segregation was observed for 11 of the traits evaluated; however, the frequency was higher for plant height, days to 50% flowering and number of panicles. The result of correlation analysis revealed highly significant and positive correlation between yield and all the eleven traits under study. Stepwise regression analysis identified panicle weight, number of panicle, days to 50% flowering, seed-setting rate and flag leaf length as traits contributing for linear increase in yield. These traits could be considered as critical criteria for selecting high-yielding lines in rice breeding programs.

Key words: Rice breeding, high yield rice, single seed descent

INTRODUCTION

Food shortage is one of the important problems for global food crops. Rice breeding for high yield is one of the important factors to increase rice production as a solution of food shortage. Breeding method for rice high yield include conventional hybridization and selection, F_1 hybrid breeding, ideotype (ideal plant type) breeding and enhancement of photosynthesis (Jeon *et al.*, 2011). The achievement of breeding program consisted the choice of parents for the potential of crosses in order to develop superior line (one parent should be selected on the basis of proved performance in the area of projected use and the second parent must complement the first in character under improvement) and the appropriate selection method (Chandraratna, 1964; Allard, 1966; Briggs and Knowles, 1967). Single Seed Descent (SSD) and Rapid Generation Advance (RGA) have been applied in many conventional breeding programs to speed up breeding cycle. SSD was used to develop cold-tolerant RILs. The results revealed higher spikelet fertility for the cold-tolerant lines (51-81%) than the cold-sensitive (7%) and the cold-tolerant (73%) parents

(Jena *et al.*, 2012). The efficacy of SSD with RGA was speeding up the breeding cycle, increasing the number of favorable genotypes and reducing breeding costs (Maruyama, 1987). Furthermore, SSD can be used to produce wide range of trait variation and high level of transgressive segregation (Moon *et al.*, 2003). The segregation of individuals in the F₂ or a later generation of a cross that shows a more extreme development of a character than either parent is referred to as transgressive segregation. Transgressive segregation is the segregation of F₂ or a later generation that reveals higher or lesser character than parents (Grant, 1975). Advantage of transgressive segregation is particularly attractive as a mechanism for rapid evolution of plant and animal (Rieseberg *et al.*, 2003). Transgressive segregant lines can be applied to breeding program improving for new cultivar or germplasm; especially, quantitative traits is particularly important for crop improvement.

The objective of the study was to develop high yielding rice varieties by using single seed descent method.

MATERIALS AND METHODS

Plant material: The plant materials used in this research include KDML105 and CH1 (New Plant Type (NPT) for high yield potential) as parents and five cultivated Thai varieties, PTT1, CNT1, SPR 60, RD31 and RD41.

Field experiment: The cross between KDML105 and CH1 was performed to produce F₁ seed. Growing F₁ plant and selfing to produce F₂ generation were done in nursery. The F₂ plants were grown under long day condition and photoperiod insensitive plants were selected. After that, the selected F₂ plants were self-pollinated until F₆ lines by SSD with RGA by growing individual plant in the small trays as 4×3 cm. The F₇ population was grown for preliminary yield trial by using Augmented Design in RCBD with four replications compared with the five standard check varieties and the parental lines.

The data were collected as Plant Height (PH), flag leaf length (FL), Number of Tillers (TN), Effective Tillers (ET), days to 50% flowering (DFF), Number of Panicles (PN), Panicle Length (PL), Panicle Weight (PW), filled seeds/panicle (FP), spikelets/panicle, seed-setting rate (SR), 1,000 grains weight (TW), Harvest Index (HI) and yield/plant (YP). The breeding procedure was conducted at the Department of Agronomy, Kasetsart University. The preliminary yield trial was conducted at Khlongsamwa district, Bangkok. Test of significance were analyzed using IRRISTAT for windows version 5.0, phenotypic correlation coefficients and stepwise regression were analyzed using MSTATC and seed-setting rate criteria was according to Department of Agriculture of Thailand (Department of Agriculture, 1988).

RESULT AND DISCUSSION

Selection of photoperiod insensitive lines from the F₂ population: The number of the selected lines for photoperiod-insensitivity and sensitivity were 288 and 784, respectively from the total F₂ population evaluated. The ratio of photoperiod sensitive to photoperiod insensitive lines was tested by Chi-square ($\chi^2 = 1.99$); it fitted the 3:1 segregation ratio and revealed that photoperiod sensitivity was controlled by a dominance gene while photoperiod insensitivity was controlled by a recessive gene.

Yield, yield component and agronomic characters: Three lines i.e., 76-1-1-1-1-1, 181-1-1-1-1-1 and 103-4-1-1-1-1 performed significantly higher in yield with 70.64, 61.38 and 57.69 g plant⁻¹,

Table 1: Means for yield, yield components and some agronomic characters for the top-ten high-yielding lines

Lines	PH (cm)	DFP	PW (g)	ET	PN	FP	TW (g)	YP (g)
76-1-1-1-1-1	113.10	114.80	5.34	100.00	19.54	235.80	19.57	70.64
181-1-1-1-1-1	106.10	114.40	4.81	86.96	26.39	186.60	22.52	61.38
103-4-1-1-1-1	190.10	102.80	7.46	100.00	10.54	270.30	24.59	57.69
176-4-1-1-1-1	115.10	103.40	6.76	84.06	12.89	262.30	23.52	53.75
15-2-1-1-1-1	116.40	103.20	5.78	100.00	13.32	211.50	24.95	51.82
69-2-1-1-1-1	170.00	90.79	7.11	95.79	11.54	251.30	25.25	51.60
90-3-1-1-1-1	101.00	85.79	5.14	94.08	16.04	204.30	22.48	51.42
202-3-1-1-1-1	97.27	104.40	5.61	87.59	13.89	224.60	23.40	49.73
102-4-1-1-1-1	122.80	103.80	5.46	96.44	13.54	192.30	26.02	49.21
193-4-1-1-1-1	111.00	99.36	4.38	91.25	15.89	186.30	22.12	48.92
KDML105	162.00	121.00	6.52	68.36	12.00	225.50	25.62	43.05
CH1	120.00	98.00	5.73	96.36	10.88	242.20	21.77	38.75
CNT1	116.40	112.50	4.07	97.47	17.12	134.60	26.96	44.84
CV (%)	5.51	2.12	12.41	7.70	15.23	15.43	4.59	20.82
LSD 0.05	7.69	2.60	0.62	7.94	2.41	27.40	1.36	9.47

PH: Plant height, DFP: Days to 50% flowering, PW: Panicle weight, ET: Effective tillers, PN: No. of panicles, FP: Filled seeds/panicle, TW: 1,000 grains weight, YP: Yield/plant

Table 2: No. of lines for seed-setting rate in RILs derived from KDML 105×CH1

Character	Seed-setting rate (%)	No. of lines
Highly fertile	> 90	32
Fertile	75-89	191
Partly sterile	50-74	44
Highly sterile	<50	4
Completely sterile	0	0

respectively than the best check (CNT1, 44.84 g plant⁻¹). The line 103-4-1-1-1-1 performed significantly higher in number of filled seed per panicle than the best parent (CH1 exhibited 242 seed/panicle). All the top-ten high-yielding lines had significantly higher number of filled seeds per panicle than CNT1. Plant height of mostly the top-ten high-yielding lines ranged between 110 to 120 cm and they were earlier in flowering than KDML 105 (Table 1). From the top-ten high-yielding lines, two lines had hundred percent effective tillers. In terms of seed-setting rate (Table 2), the 32 lines gave the higher seed-setting (>90%) than best check (CH1). However, most of the RILs (191 lines) showed the seed-setting rate in range of 75-89%, which were similar to CH1 (87.02%). The proposed yield component of NPT had low tillering capacity with 8-10 tillers when transplanted and 200-250 filled seed/panicle (Virk *et al.*, 2004). Seventy percent of the top-ten high-yielding lines were similar to NPT for filled seed per panicle but not for tillering capacity. In direct seeded conditions, most unproductive tillers and excessive leaf area may initiate unitary shading and a reduction sink size (Dingkuhn *et al.*, 1991). Although KDML 105 is the best for cooking quality in the world (Lanceras *et al.*, 2000), photoperiod sensitivity and susceptibility to lodging limited the use of KDML 105 in rice improvement for high yield. The result of this research showed that KDML 105 had heavy panicle weight (6.52 g) and high number of spikelets/panicle (297.8 spikelets/panicle) while CNT1 has 162.9 spikelets/panicle. However, partly sterile character (63.30% seed-setting rate) of KDML 105 could lead to decreased yield potential. Therefore, the inheritance of semi-dwarf, photoperiod insensitivity and fertile character (87.02% seed-setting rate) of CH1 is important to increase rice yield potential. Good agrobotanical characteristics in the

Table 3: No. of transgressive segregant lines for eleven traits in RILs derived from KDML 105×CH1

Traits	Parental mean values		Mid parent	No. of positive transgressive segregant lines	L.S.D. 0.05
	KDML105	CH1			
PH	162.00	120.00	141.00	171	7.69
FL	68.45	40.45	54.45	1	5.89
TN	18.00	11.38	14.69	9	3.50
DFF	121.00	98.00	109.50	110	2.60
PN	12.00	10.88	11.44	65	2.41
PL	33.12	27.30	30.21	1	2.20
PW	6.52	5.73	6.13	1	0.62
FP	225.50	242.20	233.85	3	27.40
TW	25.62	21.77	23.70	5	1.36
HI	0.26	0.49	0.37	11	0.05
YP	43.05	38.75	40.90	4	9.47

PH: Plant height, DFF: Days to 50% flowering, PW: Panicle weight, ET: Effective tillers, PN: No. of panicles, FP: Filled seeds/panicle, TW: 1,000 grains weight, YP: Yield/plant

superiority of potentials of the hybrid (DTPMFe+) is a results of the richness genetic variability in local rice germplasm (Oziegbe and Faluyi, 2008). KDML 105 is a thai local rice varieties that shows superior lines is as a result of the richness genetic variability in parents.

Evaluation of transgressive segregation: The evaluation of transgressive segregation (Table 3) revealed eleven traits had positive transgressive segregant lines. Higher number of positive transgressive segregant lines was observed for plant height (171), days to 50% flowering (110) and number of panicles (65). Phenotypic distribution of RILs derived from KDML 105×CH1 for yield/plant and traits for high number of positive transgressive segregant lines were controlled by polygenes (Fig. 1). The higher number of positive transgressive segregant lines were observed for plant height, days to 50% flowering and number of panicle. The finding was in agreement with Kjaer *et al.* (1991) who reported high number of positive transgressive segregant lines for plant height and days to heading in barley. The parents had comparable values for yield/plant and number of panicle. However, plant height and days to 50% flowering had contrasting values between CH1 and KDML 105 (Table 3, Fig. 1). The frequency of transgressive segregant implicate to genetic diversity that similarity phenotypic of parental and the frequency of recombinants with the number of recombination round (Kuczynska *et al.*, 2007). Number of panicle is yield component, breeding program can be used transgressive segregant lines in this trait for germplasm or selection superior lines.

Phenotypic correlation coefficients and stepwise regression: The estimates of phenotypic correlation coefficients (Appendix Table 1) showed highly significant ($p < 0.01$) and positive correlation between yield and the eleven traits. The results of phenotypic correlation coefficients between yield and filled seed per panicle ($r = 0.622^{**}$) had highly significant and positive correlation. Mulugeta *et al.* (2012) revealed that yield had positive and significant association with filled seed per panicle ($r = 0.847^{**}$). Highly significant and positive correlations were observed between effective tillers and all yield component traits (number of panicle, filled seeds/panicle and 1,000 grains weight). Highly significant and positive correlations were also observed between panicle weight and seed-setting rate; these traits also had highly significant and positive correlation with filled seeds/panicle and 1,000 grains weight.

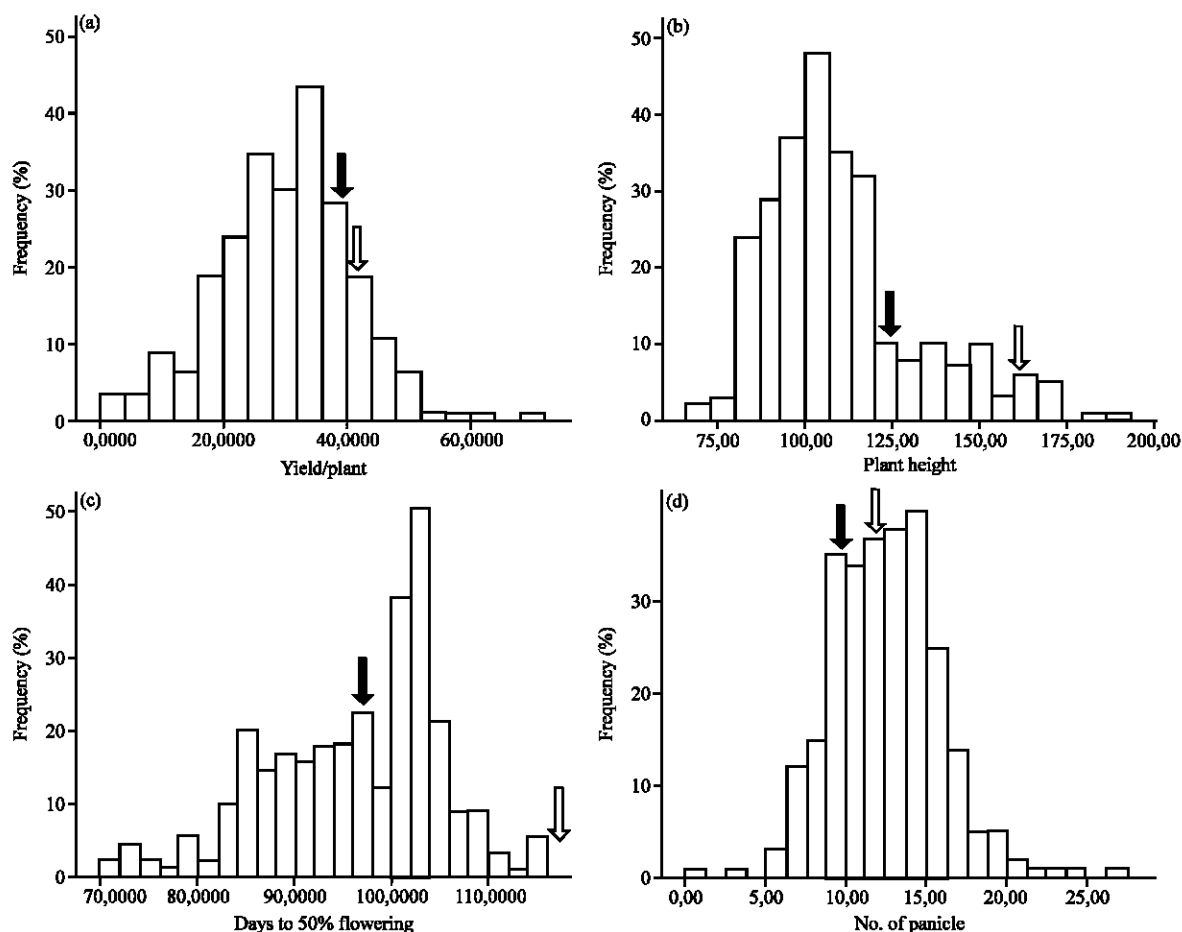


Fig. 1(a-d): Phenotypic distribution of RILs derived from KDML 105 × CH1 for yield/plant, (a) Traits for high number of positive transgressive segregant lines i.e., plant height, (b) Days to 50% flowering, (c) Number of panicles and (d) Black and white arrows indicate the mean values of the parental lines, CH1 and KDML 105, respectively

Appendix Table 1: Phenotypic correlation coefficients between 11 traits and yield/plant in RILs derived from KDML 105 × CH1, *, **Significant at the 0.05 and 0.01 probability levels, respectively

Traits	PH	FL	TN	ET	DFE	PN	PL	PW	FP	SR	TW
PH	1										
FL	0.240**	1									
TN	-0.309**	-0.077	1								
ET	0.213**	0.031	-0.193**	1							
DFE	0.289**	0.060	0.088	0.219**	1						
PN	-0.207**	-0.053	0.850**	0.332**	0.190**	1					
PL	0.342**	0.209**	-0.163**	0.142*	0.253**	-0.079	1				
PW	0.634**	0.310**	-0.385**	0.296**	0.221**	-0.226**	0.417**	1			
FP	0.524**	0.296**	-0.329**	0.252**	0.146*	-0.194**	0.368**	0.938**	1		
SR	0.108	0.016	-0.131*	0.361**	-0.180**	0.094	0.051	0.384**	0.437**	1	
TW	0.247**	0.026	-0.182**	0.319**	0.092	0.021	0.093	0.216**	-0.066	0.271**	1
YP	0.398**	0.158**	0.215**	0.488**	0.398**	0.459**	0.301**	0.661**	0.622**	0.408**	0.196**

Table 4: Stepwise regression for selection of traits

Traits	Regression coefficient	SE
PW	7.10**	0.30
PN	1.84**	0.09
DFP	0.17**	0.03
SR	0.09**	0.03
FL	-0.08*	0.04
Constant	-42.01**	4.24

* ,**Significant at the 0.05 and 0.01 probability levels, respectively, $R^2 = 0.843$

Stepwise regression analysis was performed to determine the traits contributed to yield. The result revealed that five out of the eleven traits had significant linear relationship with yield. The traits that had linear relationship include panicle weight, number of panicle, days to 50% flowering, seed-setting rate and flag leaf length (Table 4). The following model was obtained:

$$y = -42.01 + 7.10 (PW) + 1.84 (PN) + 0.17 (DFP) + 0.09 (SR) - 0.08 (FL)$$

The R^2 explained 84.3% from the total variations relative to yield. Similar to this finding, Ghaffar and Ghorbanali (2012) reported linear relationship of number of panicle with yield and 56.4% R^2 .

CONCLUSION

The three superior lines performed significantly higher for yield than the best check (CNT1). Single seed descent method can be used for quantitative traits selection because elite lines can be selected, wide range of trait variation and high transgressive segregation are produced. Higher number of transgressive lines was obtained for three traits, including plant height, days to 50% flowering and number of panicle. Panicle weight, number of panicle, days to 50% flowering, seed-setting rate and flag leaf length can be considered as critical criteria for yield improvement in segregating generations of rice. Seesang *et al.* (2013) revealed that the number of panicle and flag leaf length could be used for selection criteria of high yielding in inbred genotypes.

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