Omonrice 10: 110-114 (2002)

SHORT COMMUNICATION

The choice of donor parents for salt tolerance in rice improvement through cluster distant analysis

Nguyen Thach Can and Nguyen Thi Lang

ABSTRACT

Cluster distant analysis among IR42, OM736 and OM80 indicated that the high values of cluster distance were obtained as 16.78 and 10.52 in terms of IR42 vs OM736 and IR42 vs OM80, respectively. Offsprings of two crosses were highly segregated. OM1348-5 was derived from IR42/OM736 and OM1352-5 from IR42/OM80. These rice varieties were released as new varieties by Ministry of Agriculture and Rural Development in 2002

INTRODUCTION

Salt tolerance is controlled by polygenes therefore quantitative genetic analysis should be dealt to have more effect in rice selection. Gregorio at al (1993) conducted 8x8 diallel set analysis on salt tolerance in rice. The authors sugested that rice selection for salt tolerance must be delayed and replicated to later generations when dominance gene effects are dissipated and selection must be done under controlled condition to minimize environmental effects. Modified bulk and single seed descent would be suitable to breeding methods to develop salinity tolerant rice. Gonzales (1996) indicated that the usefulness of the salt tolerance index for grouping donor parents to choose desirable hybridization materials. Lu (1974) reported that wide hybridization in rice obtaines high genetic variation in offspring generations and facilitates rice breeders easy to select desirable lines. In rice improvement for acid sufate soil areas, Tao et al. (2002) showed that AS996, an acid sulfate soil tolerant rice genotype was derived from highly segregated population by crossing between *O. sativa* and *O. rufipogon*. Currently, AS996 has been commercially produced in Mekong Delta. OM576, a salt tolerant rice also derived form the cross of Hungary/IR48 which expressed high value of genetic distance (Hoan 1984)

This study aims at selecting appropriate donor parents for salt tolerance improvement program in Mekong Delta

MATERIALS AND METHODS

Materials: 16 donor parents and 30 promising lines selected from pedigree nurseries were used. All of those were in multiplocation trials and screening experiments

Methods:

- Salt screening in Yoshida's solution with EC of 0 - 12dS/m following the method of Gregorio at al. (1997). The salt tolerant index (STI) was calculated for agronomic traits as survival days (SD) under salt stress, shoot length (SL), root length (RL), shoot weight (SW) and root weight (RW) after 7 days treated. STI(%) = 100 (IS/IC), where IS is the mean of saline solution indicator and IC is the mean of the control solution indicator (Gonzales 1996). The screening experiment was in completely randomized block design with 3 replications. Yoshida's solution with EC=0dS/m as control treatment
- Based on STI, Mahalanobis D^2 value was computed. Mahalanobis distance value was used to group genotypes into clusters following the method described by Tocher (Rao 1952) Genetic parameters were also computed by Singh and Chaudhary procedure (1985)

- These yield testing experiments were designed in randomized complete block with 3 replications. Agronomical traits were recorded as methods suggested by IRRI (IRRI 1980). Statistical procedures were computed following Gomez and Gomez described (1982)

RESULTS AND DISCUSSION

Compared performance of the genotypes in two different mediums (EC = 0 and 12dS/m) was noticed to calculate salt tolerant index (STI) and using Tocher's method in grouping different dornor parents into distinct clusters based on STI values of shoot length, root length, root weight, shoot weight in two mediums. It indicated that four distinct groups were established. First group included genotypes with the highest STI values (72.1% for shoot length, 68.6% for root length, 70.1% for shoot weight and 65.8% for root weight). It indicated that all of the genotypes in this group are highly tolerant to salinity (Table 1).

Table 1: Grouping into clusters based on salt tolerant index values

Cluster I	Cluster II	Cluster III	Cluster IV
OM723-7	OM80	OM736	OM739
IR42	IR64	IR66	OM344
A69-1	CR333	OMCS 7	IR29723
Pokkali	IR29		PUSA44-33
IR48			

Average intra and inter cluster distance values are shown in table 2. The measure of intra and inter cluster D^2 values between four groups showed that cluster I and cluster III separated by the largest statistical distance (D=16.78) and high genetic variation would be hopefully obtained. If crossing between cluster I and cluster III genotypes could be implemented.

Table 2 : Average intra and inter cluster distance (D) values

	Cluster I	Cluster II	Cluster III	Cluster IV
Cluster I	4.53	10.52	16.78	5.21
Cluster II		2.56	6.73	9.15
Cluster III			3.85	7.52
Cluster IV				1.57

Genetic variation of the genotypes into clusters with different D values was evaluated and it indicates that crossing between cluster I genotypes with cluster III genotypes will obtain the highest segregation frequency in progeny generations (table 3). Analysis on genetic variation and genetic parameters of the target crosses showed that two genotypes IR42/OM736 and IR42/OM80 with cluster D values of 16.78 and 10.52, respectively, expressed the highest phenotypic coefficient variation (%PCV), genotypic coefficient variation (%GCV), genetic advance (%GA) and broad sense heritability (h^2). %PCV did not differ from %GCV in case of spikelets per panicle. It indicated that this character cannot be much affected by environment. This character also obtained high %GCA and %GA values, so it should be considered that the better efforts for selection, the better perfomance will be gained in rice breeding

Similarly, panicles per hill and grain yield of OM1348-9 and OM1352-5 genotypes which were derived from IR42/OM736 and IR42/M80, respectively, have been well selected among segregants.

Table 3: Analysis of varience and genetic parameters of variation for quantitative characters in F_2 generation of two promising crosses

Designation	Character	Mean	Va. P	Va. G	PCV (%)	GCV (%)	h^2 (%)	GA (%)
IR42/OM736 (OM1348)	Growth duration (day)	130.1	50.3	38.0	5.5	4.7	81.0	11.0
	Plant heigh (cm)	98.7	59.9	38.8	7.8	6.3	60.0	10.3
	Panicle/hill (No)	9.6	125.2	81.6	116.5	94.1	70.0	15.0
	Spikelet/panicle(no)	100.2	93.7	88.1	19.7	19.4	90.0	18.7
	Sterility (%)	12.3	380.5	177.0	158.6	108.2	52.0	18.7
	Grain yield (g/hill)	14.6	104.1	80.6	69.9	61.5	80.0	16.3
IR42/OM80 (OM1352)	Growth duration (day)	132.4	23.4	11.0	3.6	2.5	47.0	4.7
	Plant heigh (cm)	102.4	32.6	21.3	5.5	4.5	65.0	7.6
	Panicle/hill (No)	10.2	35.3	25.0	58.2	49.0	70.0	8.6
	Spikelet/panicle(no)	108.6	26.3	19.6	15.7	15.0	84.0	7.8
	Sterility (%)	16.8	23.4	11.1	28.8	19.8	47.0	4.7
	Grain yield (g/hill)	15.3	26.3	20.7	33.5	29.7	78.0	8.3

Phenotypic coefficient variation (PCV),. Genotypic coefficient variation (GCV), Genetic advance (GA) and Heritability (h^2).

Some desirable agronomic characters, major pest and disease resistance (i.e. brown plant hopper, blast) of two promising improved genotypes as OM1348-9 and OM1352-5 indicated that these lines are mid-duration (135.2, and 130.6 days), with plant height of 103.6, and 101.4cm, respectively. They exhibit their salt tolerance as well as some leading varieties asTHDB, IR42 which have been grown in coastal areas of the Delta. Especially, they are resistant to major pests and disesases better than IR42 (Table 4)

Table 4: Agronomic characters, reaction to major pests and diseases of promising improved genotypes tolerant to salinity

No	Variety	Origin	Growth duration (days)	Plant height (cm)	Reaction to	
					BPH	Bl
1	OM1348-9	IR42/OM736	135.2	103.6	5	3
2	OM1352-5	IR42/OM80	130.6	101.4	5	3
3	THDB	Tep Hanh mutant	128.6	98.7	3	1
4	OM1351-2	IR42/PUSA44-33	127.3	100.1	5	3
5	OM723-7	NN6A/A69-1	126.8	98.8	3	1
6	IR42 (check)	IRRI	132.5	100.3	9	7

BPH: brown plant hopper, Bl: blast

Grain yield in multi-seasonal trials at Cuu Long Delta Rice Research Institute (CLRRI) is presented in Table 5. Average yields after 8 continuous seasons of OM1348-9 and OM1352-5 were the highest (5.1 and 5.0 t/ha, respectively). Particularly, these varieties obtained 6.1 - 6.2 tons/ha in 2000's dry season. OM1352-5 and OM1348-9 are considered as the most promising lines derived from above crosses

Table 5: Muti-seasonal yield trial of promising mid-duration rice genotypes in Mekong Delta (t/ha)

No	Variety	1998 Dry season	1998 Wet season	1999 Dry season	1999 Wet season	2000 Dry season	2000 Wet season	2001 Dry season	2001 Wet season	Mean
1	OM1348-9	6.2	3.5	6.8	4.2	6.2	4.2	5.8	3.0	5.10*
2	OM1352-5	5.6	4.2	6.4	3.5	6.1	3.8	6.4	3.6	5.00*
3	THDB	6.1	3.5	5.2	3.0	5.7	3.3	5.7	3.4	4.50
4	OM1351-2	6.2	3.6	5.2	3.0	5.4	4.1	5.3	2.8	4.50
5	OM723-7	5.4	3.1	5.3	3.0	5.2	3.4	5.3	3.5	4.30
6	IR42 (CHECK)	4.6	3.0	5.4	3.0	5.0	3.2	5.2	3.0	4.1
	CV%	12.3	9.8	10.2	8.9	12.1	10.2	12.3	9.2	10.4
	LSD5%	0.7	0.5	0.8	0.6	0.8	0.7	0.9	0.5	0.8

Scoring salt stress (EC=12dS/m) at seedling stage in Yoshida's solution among the traits as SD, SL, RL, SW, RW revealed that performance of OM1348 and OM1352 were better than IR29 (suceptible check) and IR42 for all these agronomic traits. As compared to Doc Do, a salt tolerant rice variety in Mekong Delta, OM1348 and OM1352 exhibited similarly salt tolerance concerned to the target agronomic traits (table 6). It indicated that unless Pokkali (tolerant check), two genotypes OM1348 and OM1352 were acceptable to develop under salt stress condition

Table 6: Peformance of OM1348-9 and OM1352-5 under salt stress of EC = 12dS/m at seedling stage

No	Variety	SD (days)	SL (cm)	RL (cm)	SW (g/100 seedlings)	RW (g/100 seedlings)
1	OM1348-9	26.3	16.7	6.8	8.1	2.1
2	OM1351-2	24.2	15.3	5.3	7.6	1.5
3	OM1352-5	25.7	17.8	7.1	7.6	1.9
4	OM2490	21.3	15.2	5.2	6.0	1.5
5	IR42	20.1	17.1	6.1	5.4	1.4
6	Doc Do	29.5	20.6	7.6	10.2	2.6
7	POKKALI *	29.7	21.3	8.0	15.4	2.7
8	IR29 **	15.3	10.1	4.2	3.6	0.8
	LSD5%	*1.1*	*2.4*	*1.3*	*2.3*	*0.5*

* Tolerant check ** Suceptible check SD – Suvival days ; SL – Shoot length ; RL – Root length
SW- Shoot weight ; RW- Root weight

Table 7: Muti-location yield trial in Mekong Delta (T/Ha)

Stt	Variety	Ben Tre	Soc Trang	An Giang	Caø Mau	Ba Ria Vung Tau	Bac Lieu	Mean
1	OM1348-9	4.0	6.2	5.7	5.8	6.1	5.8	5.6
2	OM1352-5	3.9	6.1	5.2	5.4	6.3	5.6	5.4
4	OM723-7	3.9	5.6	5.0	5.3	5.6	5.4	5.1
3	THDB	3.6	5.3	4.8	5.0	5.6	5.3	4.9
5	IR42	3.2	4.6	4.7	5.0	5.1	5.0	4.6
6	Local check*	3.0	4.6	4.2	5.0	5.1	5.0	4.5
	CV%	*9.1*	*12.7*	*9.8*	*11.5*	*12.6*	*9.2*	*10.3*
	LSD5%	*0.6*	*1.1*	*0.8*	*0.8*	*1.0*	*0.6*	*0.7*

(*) Local check is U17 in Ben Tre, Mahsuri in An Giang and IR42 in others

Multi-location yield trials were conducted in Ben Tre, Ba Ria Vung Tau, Soc Trang, Bac Lieu, An Giang provinces with salt tolerant rice nursery. OM1348 and OM1352 obtained the highest yield (5.1 and 5.0, respectively), significantly different to check variety IR42 at the level of 5% (table 7). In demonstrative plot (35 ha) at CLRRI, OM1348 and OM1352 obtained 7.5 and 7.3 tons/ha, respectively. In farmer fields of Long An province, OM1348 and OM1352 obtained 10.2 and 10.1 t/ha, respectively. Their grain yield is high and stable. OM1348 was released as a national variety and OM1352 as a regional variety for salt-affected areas in Mekong Delta

CONCLUSION

Genetic materials selected from two clusters which expressed high value of genetic distance, would offer high genetic variation among segregated progenies if the materials could be crossed together. IR42/OM736 and IR42/OM80 belong to the two clusters with genetic distance of 16.78 and 10.52, respectively. High opportunity to select and release the promising varieties as OM1348-9 and OM1352-5 is proved

OM1348-9 and OM1352-5 are mid-duration genotypes with high and stable yiels, suitable to salt-stress areas in Mekong Delta, resistant to blast and brown plant hopper. They have been recently recommended to be developed in rice-shrimp culture system.

REFERENCES

Gomez KA and AA Gomez. 1982 Statistical procedures for agricultural research. IRRI . P.O.Box 933 Manila - Philippines

Gonzales LM. 1996 Principal component analysis and variety classification in relation to rice seedling salinity tolerance in IRRN 21:2-3, IRRI P.O.Box 933 Manila Philippines

Gregorio B, D Senadhira and RD Mendoza. 1997 Screening rice for salinity tolerance. IRRI, P.O.Box 933 Los Banos Manila Philippines

Gregorio B, and D Senadhira. 1993 Genetic analysis of salinity tolerance in rice (*Oryza sativa* L) in Theor Genet 86:333-338 - IRRI P.O Box 933 Manila philipines

Hoan, Nguyen Tri. 1984. Result of selecting OM576 rice variety for salt effected areas in Mekong Delta (Vietnamese). Annual report 1984. Cuu Long Delta Rice Research Institute. Omon, Cantho, Vietnam

IRRI. 1980. Standar evaluation and utilization system for rice. IRRI P.O.Box 933 Manila Philippines

Lu, Dinh Van. 1974. Rice Plant, Hanoi Agricultural University (Vietnamese). Gia Lam, Ha Noi 104p

Rao, CR. 1952) Advanced statistical methods in biometric research, John Willey and Sons, New York, 348p

Singh RK and BD Chaudhary. 1985. Biometrical methods in quanlitative genetic analysis. Kalyani Publishers. New Delhi, India 318p

Tao NV, NT Lang, NT Tam, NT Can, TT Luy and BC Buu. 2002. The performance of AS996 in acid sulfate soil areas in Mekong delta (Vietnamese). This report presented in agricultural and plant protection session, organized by Ministry of Agriculture and Rural Development of Vietnam at Ho Chi Minh city 9/2002. CLRRI, Omon, Cantho, Vietnam

SUMMARY IN VIETNAMESE

Phân nhóm các vật liêu di truyền bằng phương pháp Tocher dựa vào chỉ số chịu mặn STI của một số tính trạng nông học như SL, RL, RW, SW và SD cho thấy IR42 và OM736 có khoảng cách nhóm lớn nhất 16.78 sau đó là IR42 với OM80 là 10.52. Chọn những vật liêu này lai với nhau có thể khai thác sự biến dị di truyền rất có lợi. Từ những kết quả phân tích những thông số về di truyền, hai cặp lai IR42/OM736 và IR42/OM80 có giá trị PCV, GCV, GA và h^2 của tính trạng số hạt trên bông, số bông trên bụi tốt nhất. Cũng từ cặp lai này, 2 giống lúa OM1348-9 và OM1352-5 được chọn ra. Kết quả khảo nghiệm trên nhiều vụ, nhiều điểm và thanh lọc mặn trong dung dịch Yoshida cho thấy chúng thể hiện tính chống chịu mặn. Hội Đồng Khoa Học Bộ Nông Nghiệp và Phát Triển Nông Thôn đã công nhận 2 giống lúa này là giống mới sản xuất trong vùng cơ cấu lúa-tôm vào năm 2002.