

## THE GENETIC ASSOCIATION BETWEEN THE YIELD, YIELD COMPONENT AND SALT TOLERANCE IN RICE

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### ABSTRACT

*Salt stress is the second largest abiotic stress affected rice productivity. The breeding for salt tolerance in rice involves selected parents at their F1s in all the combination. Identification and incorporation of salt tolerance gene into modern rice cultivars are important breeding strategies. In this study, the genetics of salt tolerance in rice was investigated in details. The reaction to salt stress gives well for resistance with salt at EC=18 dS/m such as: Mot Bui Do, Doc Do these are good for material in plant breeding. The F2 progenies from these crosses (OMCS2000/Pokkali, OM2395/Mot Bui do, OMCS2000/Doc Do, IR64/ Mot Bui Do segregated into 3:1 resistance to susceptible, suggesting that a dominant gene controls resistance to salt stress in the test varieties. This was confirmed by reaction of F3 progenies which segregated into 1:2:1 homozygous resistant to segregating to homozygous susceptible. The data on the reaction to salt of F1 hybrids, F2 and F3 lines of crosses among the resistant varieties were confirmed. For OMCS2000 Mot Bui Do, F2's lines segregated into 15:1 resistant to susceptible expected on the basis of independent segregation of two dominant duplicated genes. On the other hand, the F3 lines approximated a segregation ratio of 7:8:1 resistant to segregating to susceptible. For OM2395/Pokkali, F2's lines segregated into 3:1 resistant to susceptible. Some promising rice varieties in experiments will be continuously tested in next season. It should be recommended to be tested and evaluated at many sites to understand GxE interaction.*

**Keywords:** dominant, recessive, salt tolerance.

### INTRODUCTION

Salinity tolerance was determined by a more than one million hectares of land throughout the Vietnam. One of the limitations in the development of tolerant rice genotypes is our inadequate knowledge of salt tolerance genetics. In order to make more rapid progress in the development of improved tolerance genotypes to salinity, then combined with some good agronomic traits, it is essential to have more genetic knowledge, such as the identification of new genes for resistance, the mode of inheritance of different tolerant cultivars, the number of genes responsible, and the linkages between some traits and salt tolerance. As more tolerant genes are identified, the faster the development of tolerant varieties will be since many of the genes will be

incorporated systematically in our breeding works as has been done for pest resistance. There are genetic differences related of kind and degree of salt tolerance among varieties. Some landrace varieties are salt tolerance genotypes such as Pokkali, Mot Bui Do (Lang et al. 2006), but they are unadvantageous in other characters, such as tallness for lodging, paddy awning, low yielding. Therefore, one of the major objectives of rice improvement program at CLRRI is to deploy rice germplasm for our breeding goals. At present, a number of varieties and breeding lines with tolerance to the more important salt area have already been developed.

**Objectives:** To determine the genetic association between yield and salt tolerance and to identify the target genes for salt tolerance from our landraces.

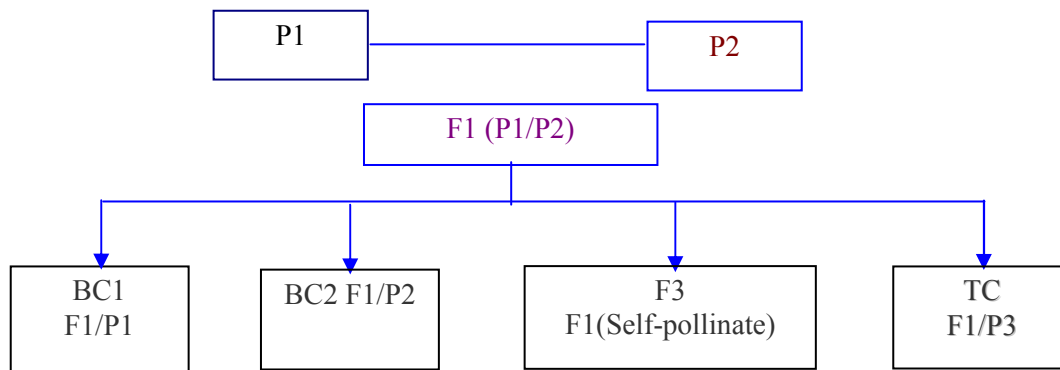
## MATERIALS AND METHODS

### Determination of rice yield

In the 2004-2008 wet and dry seasons, Pokkali, Mot Bui Do, IR64 were planted in CLRRRI hybridization block. The procedure following in the generation of the F1, F2, BC1, BC2 is designed in figure 1. The high yielding variety OMCS2000 as female (P1), was crossed with Pokkali as male (P2) to produce F1. Thirty seeds of OMCS2000 / Pokkali were planted in the green house on 2005 dry season. At flowering, the two

backcrosses namely F1/ P1 and F1 / P2 and test cross F1 / P3 were made. One hundred seeds of each cross combination were produced. Twenty F1 plants were also selfed to produce about 500g of F2.

Allelism test of genes governing salt tolerance of four landraces as Pokkali, Doc Do, Doc Phung and Mot Bui Do were used in this experiments. The crosses were made such as: OMCS2395/Pokkali; OM2395/Mot Bui Do, OMCS2000/Doc Do, IR64/Mot Bui Do.



**Figure 1:** The procedure following in the generation of the F1, F2, BC1, BC2 populations

Field experiments were conducted at CLRRRI. The experimental design was a randomized complete block design with five replications. Each plot, 2 m long and 10 m wide, was transplanted with space of 20 x 15 cm. Plot sites were located outside the commercial rice production areas of the respective states. Soil preparation and irrigation management were typical for the rice agricultural systems of CLRRRI. Evaluation of population lines and the parents of rice treated by NaCl (at EC = 6, 12 and 18 dS/m). The following variables were measured as plant height (measured from soil line to tip of flag leaf), date of first and 50% tillering, date of first, 50%, and last heading (heading defined as date of panicle emergence from the boot). Five panicles per plant and five plants per plot were harvested at physiological maturity. After collection panicles were carefully transported to a laboratory and rapped ten times against a plastic bucket. The percentage of seeds remaining on the panicle was used to give a seed. Total seed weight, 1000-seed weight, and total seed number were also determined. Panicles were stripped by hand into a

bucket; all seed returned to the sample envelope and allowed to dry for 3 days at 50°C. The seed were then passed through a small seed lot thresher to separate the blank florets from the seed. Both empty florets and total seed weights were obtained. A sample of 1,000 seeds was weighed and the total number of seeds was calculated.

### Statistical analyses

All analyses were completed on plot mean values. Analysis of variance was performed using the minimum model for all analyses of variance were comprised of entries and replications, with the entry replication interaction used as the error term. Replications and the entry replication interaction were considered random effects. Separation of means was performed using the Duncan's Multiple Range Test.

Data were subjected to analysis of variance. Variance components and their standard errors were estimated by equating observed mean squares to their expectations, following the method by Buu and Lang 2003

Estimates of broad-sense heritability ( $h^2_B$ ) based on progeny means were computed from variance components estimates

Genotypic coefficient of variation (GCV) was estimated according to the method suggested by Singh and Chaudhry (1977).

### Performance evaluation

For the performance test, agronomic characteristics such as plant height panicle length, tillers per hill, spikelets per panicle, spikelets per hill, and grain yield were investigated and compared with those of the original plant with

three replications per lines. Evaluations of lines were done at maturity. Analysis of variance and mean comparisons of the data from R- S fields were carried out. The t- test value at 5% and 1 % level of significance determined the superiority of the tested lines over.

## RESULTS

### Screening tolerance among parents

The screening results for salt tolerance (Table 1) showed that Doc Do, Mot Bui Do, and Pokkali were really tolerance.

**Table 1.** Reaction to salt stress of rice cultivars at seedling stage

Cultivar	EC=6 dS/m	EC=12 dS/m	EC =18 dS/m
OMCS2000	S	S	S
IR64	S	S	S
AS996	T	T	S
Doc Phung	T	T	S
Doc Do	T	T	T
Mot Bui Do	T	T	T
Pokkali	T	T	T:S

T: tolerance ; S: susceptible

Survival days at seedling of Doc Do, Mot Bui Do and Pokkali were recognized as 26 days. For OMCS2000 and IR64 – susceptible genotypes, they completely dead and only exhibited few green leaf sheaths at the treatment of EC=6 dS/m

### Segregation of salt tolerance

Inheritance of resistance and allelic relationships of genes for resistance:

The F<sub>2</sub> progenies from these crosses segregated into 3:1 resistance to susceptible, suggesting that a

dominant gene controls resistance to salt stress in the allelism test. This was confirmed by reaction of F<sub>3</sub> progenies, which segregated into 1:2:1 homozygous resistant to segregating to homozygous susceptible. The data on the reaction to salt of F<sub>1</sub> hybrids, F<sub>2</sub> expected the F<sub>1</sub> from all the crosses showed a resistance reaction. The F<sub>2</sub> populations from the crosses of OM2395/Pokkali and IR64/Mot Bui Do, OMCS2000/Doc Do were examined too.

**Table 2.** Reaction to salt stress of F<sub>1</sub>, F<sub>2</sub>, F<sub>3</sub> populations at 6dS/m

Cross	F <sub>1</sub>	F <sub>2</sub>		$\chi^2$	F <sub>3</sub>	$\chi^2$
		T	S	3:1		T
OMCS2000/Pokkali	T	564	204	1.35	91	1.30
OM2395/Mot Bui Do	T	531	201	2.24	81	2.70
OMCS2000/Doc Do	T	612	212	0.30	73	1.21
IR64/Mot Bui Do	T	611	213	0.29	74	1.20

T: tolerance ; S: susceptible

The F2 populations from OMCS2000/Mot Bui Do segregated into 15:1 resistant to susceptible, while the F3 lines approximated a segregation ratio of 7:8:1 resistant to segregating to susceptible. For OM2395 / Pokkali, F2 segregated into 3:1 resistant

to susceptible, while the F3 lines approximated a segregation ratio of 13:3 resistant to segregating to susceptible. This is the same figures by Singh et al. (2008).

**Table 3:** Reaction to salt stress of F1, F2, F3 populations at 6dS/m in OMCS2000/Mot Bui Do and OM2395/Pokkali

Designation	F <sub>1</sub>	F <sub>2</sub>		$\chi^2$	F <sub>3</sub>			$\chi^2$
		T	S		T	Segregating	S	
OMCS2000/Mot bui Do	T	751	50	0.03 (15:1)	69	72	10	0.72 (7:8:1)
OM2395/Pokkali	T	255	79	0.17 (3:1)	307	0	12	0.63 (13:3)

This study is useful for rice breeders in developing their improved varieties with multiple resistances to rice salt stress. Any one of newly identified genes for resistance to salt can serve as a source of resistance to this salt stress. Because various genes for resistance to salt are independent, they can be combined in cultivars of improved agronomic background. In order to exploit the variation in source material as efficiently as possible, the breeder needs to have knowledge of the genetic

architecture of the characters to improve. Means ranges, genotypic coefficients of variance (gcv), phenotypic coefficients of variance (pcv), and broad-sense heritability estimates for yield and yield components are shown in table 3. IR64 / Mot Bui Do recorded higher mean of yield than other. OM2395/Mot Bui Do offered better spikelet number per panicle as compared to IR64 / Mot Bui Do. In contrast, IR64 / Mot Bui Do obtained higher yield than OM2395/ Mot Bui Do.

**Table 3.** Means, ranges, genotypic coefficients of variation (gcv), genetic variances ( $\sigma^2_G$ ), phenotypic variance ( $\sigma^2_{Ph}$ ), and broad-sense heritability values ( $h^2_B$ ) for OM 2395/Mot Bui Do breeding populations.

OM2395/Mot Bui Do	Mean	Range	GCV (%)	$\sigma^2_G$	$\sigma^2_{Ph}$	$h^2_B$
Height (cm)	110	100-101.9	7.2	10.34	8.35	0.58
Duration(day)	97	95-105	5.8	1.37	2.81	0.49
Tilling	12.0	9-12	5.9	0.17	0.21	0.83
Panicle length (Cm)	28	23-27	4.4	3.8	3.2	0.34
Spikelets / panicle	145.7	100.-106.5	9.6	204.85	341.74	0.62
1000-grain weight (g)	26.8	25-27	11.8	5.34	7.82	0.77
Yield (ton/ha)	6.7	5.4-5.7	6.7	0.29	0.618	0.54

#### Field test of elite rice lines / varieties at CLRRRI

A total of 1,712 lines having been used as control, were tested in the field. Tens lines were selected for further observation. For the performance test agronomic characteristics such as plant height, panicle length, tillers per hill, and spikelets per panicle; panicles per hill and grain yield were investigated and compared with those of the original plant in the field. Analysis of variance and mean comparisons of the data from were carried out. The t-test values at 5% and 1% level of

significance determined the superiority of the tested lines over control. Almost varieties exhibited their early growth duration: 90-100 days, short plant stature. High yielding of 5-6 ton/ha in dry seasons were recorded. Four lines from IR64/ Mot Bui Do showed longer survival days under salt stress; they would be a strong selective advantage for these hybrid families resistance. Generally, increased tiller and grain filling exhibited among selected progenies.

**Table 4:** Reaction to salt stress of promising lines from IR64/Mot Bui Do and OM2395/Mot Bui Do

Designation	6dS/m	12dS/m	18dS/m	Origin
AS996 (check)	T	S	S	IR64 / O. rufipogon
OM 7368-2-4	T	S	S	OM2395/ Mot Bui Do
OM 7369-15-7	T	S	S	IR64 / MOT BUI DO
OM7369-14-115	T	T	S	IR64 / MOT BUI DO
OM7369-9-27	T	T	S	IR64 / MOT BUI DO
OM7369-1-225	T	T	S	IR64 / MOT BUI DO
OM7369-1-225	T	T	S	IR64 / MOT BUI DO
OM 7368-147	S	S	S	OM2395 / Mot Bui Do
OM 7368-2-14-9	S	S	S	OM 2395 / Mot Bui Do
OM 7368-2--89	S	S	S	OM2395 / Mot Bui Do
Pokkali	T	T	T	
Mot Bui Do	T	T	T:S	
OM2395	S	S	S	
IR64	S	S	S	

S: susceptible T: tolerance

**Yield testing on rice varieties**

This study aims at selecting rice varieties with high yield potential, brown plant hopper resistance in Mekong delta, and finding out rice varieties with desirable traits.

They are including lines rice varieties with Pokkali for checked, growing 2006 dry seasons. Yield testing experiments were laid out in completely randomized block designs with three replications

in CLRRRI's experimental field. Statistical analysis was cited (Gomez and Gomez 1982). Data records on agronomic characters, yield and yield components were also guided as SES (IRRI, 1996). Insect, disease-screening experiments were laid out in single replication. Evaluation of insect and disease reaction at seedling stage (IRRI, 1996). Agronomic characters were presented in table 6.

**Table 5:** Yield and yield components of lines from

Designation	Duration (days)	Height (cm)	Panicle/m <sup>2</sup>	Yield (t/ha)
AS996( check )	100	107.00 b	303.66 ab	4.473 bcde
OM 7368-2-4	95	109.33 b	266.66 bc	5.13 ab
OM 7369-15-7	96	107.33 b	242.00 c	5.16 ab
OM7369-14-115	100	108.00 b	274.00 bc	4.72 abcde
OM7369-9-27	105	108.33 b	284.00 abc	4.95 abcd
OM7369-1-225	98	95.66 d	284.33 abc	3.84 cde
OM7369-1-225	98	115.00 a	272.66 bc	4.69 abcde
OM7368-147	95	106.66 b	290.33 abc	5.84 a
OM7368-2-14-9	94	98.67 cd	293.67 abc	4.35 bcde
OM7368-2--89	100	101.67 c	338.33 a	4.32 bcde
POKKALI	115	109.67 b	318.67 ab	3.66 e
Mot Bui Do (Check)	131	101.33 c	285.33 abc	3.80 de
OM2395 (Check)	95	99.33 cd	287.67 abc	4.07 bcde
IR64	105	107.33 b	320.00 ab	5.09 abc
CV (%)		2.16	10.16	14.26

It is indicated that almost of rice varieties in experiment are less than 100 days duration. Plant height ranged in 100 days for Pokkali and Mot Bui Do, IR 64

Grain yield and yield components of 10 genotypes were presented in table 6. It was indicated that OM7368-2-4 and OM7369 obtained the highest yield in experiment (5.13- 5.16 t/ha) and higher than AS996 and IR64 (check).

### CONCLUSION AND SUGGESTION

Results of analysis of variance for the seven traits measured indicated that significant amounts of genetic variability exist among the progenies for almost all traits in both populations. This variability could be exploited for future improvement of the essential traits in the populations. The wide range of phenotypic variability existing for yield in both populations might be due to the fact this trait was easily influenced by the environment.

Some promising rice varieties in experiments will be continuously tested in next season.

It should be commended to be tested and evaluated many sites to get stability in performance. It is one of the most desirable properties of a genotype to be released as a variety for wide cultivation.

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### Đặc điểm di truyền của những giống lúa chống chịu mặn có triển vọng ở đồng bằng sông Cửu Long

Công tác chọn tạo giống chống chịu mặn ở ĐBSCL trong chương trình hợp tác với IRRI đã được thực hiện, thông qua đánh giá vật liệu bố mẹ và con lai F<sub>1</sub>s. Phản ứng với stress do mặn được khảo sát trong điều kiện EC=18 dS/m. Các giống Một Bụi Đỏ, Đốc Đỏ thể hiện là nguồn donor tốt cho chương trình chọn tạo giống. Quần thể F<sub>2</sub> của những cặp lai OMCS2000/Pokkali, OM2395/Một Bụi Đỏ, OMCS2000 / Đốc Đỏ, IR64/Một Bụi Đỏ phân ly theo tỷ lệ 3:1 (Kháng : Nhiễm), cho thấy alen trội chiếm ưu thế trong điều khiển tính kháng. Xác nhận lại phân ly của F<sub>3</sub> với tỷ lệ 1:2:1. Đối với cặp lai OMCS2000 / Một Bụi Đỏ, các dòng phân ly F<sub>2</sub> thể hiện tỷ lệ 15:1 (kháng : nhiễm) cho thấy 2 gen trội lặp đoạn điều khiển tính trạng này. Quần thể F<sub>3</sub> phân ly với tỷ lệ 7:8:1. Đối với cặp lai OM2395/Pokkali, F<sub>2</sub> phân ly theo tỷ lệ 3:1 (kháng: nhiễm). Phân tích tương tác giữa kiểu gen và môi trường (GxE) cũng được thực hiện.