



International Journal of
**Plant Breeding
and Genetics**

ISSN 1819-3595



Academic
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Genetic Mechanisms Controlling Salt Tolerance in F₃ Populations of Rice

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ABSTRACT

Salinity is a serious constraint to rice production in Niger. The release of rice cultivars with improved performance in saline environments is reliant on an understanding of genetic control of traits of plant exposed to salinity. This is vital in the choice of methods of generation advancement and evaluation. Thus, this study aims to know the genetic mechanism controlling salt tolerance in rice in Niger. One hundred and twenty F₃ families derived from a full diallel cross of four parents including two tolerant and two susceptible genotypes were evaluated in farmer's fields affected with high salt levels in two sites. The experimental design was 25×5 alpha lattice with 3 replications. Data on the duration, height, tiller number, panicle number, panicle weight, grain weight and yield were recorded. The intra-class correlation, heritability and gene action were estimated. Additive effects for tiller number, panicle number and panicle weight, additive maternal effects and partial dominance effects for height and duration were observed. The heritability was high and varied according to the site and the common parent.

Key words: Rice, salinity, salt tolerance, heritability, gene action

INTRODUCTION

One of the major inputs for increasing crop productivity is irrigation. But irrigation over a long period of time exacerbates soil salinity problems (Singh and Singh, 2000). Genetic manipulation of crop plants to develop genotypes tolerant to saline conditions is, one of the most cost effective means of maintaining crop production in areas with salinity problem (Blum, 1988; Singh and Singh, 2000). Successfully changing the characters of the population using hybridization is predictable only from knowledge of the degree of correspondence between phenotypic values and breeding values. An important function of the heritability parameter is expression of the degree of correspondence between the phenotypic and genotypic values (Munshower, 1994). Narrow sense heritability, expresses the extent to which phenotypes are determined by the genes transmitted from the parents and the proportion of the total variance that can be attributed to the average gene effects (Falconer, 1989; Falconer and Mackay, 1997; Fahlani *et al.*, 2010). Genotypic expression is, however, influenced by environmental factors (Falconer, 1989).

The release of rice cultivars with improved performance in saline environments is reliant on an understanding of genetic control of traits of plant exposed to salinity. This study focused on

studying genetic control of salt tolerance in F₃ populations. The specific objectives were to: (i) Assess the degree of inheritance of salt tolerance in rice and (ii) Determine the gene action involved in salt tolerance of rice.

MATERIALS AND METHODS

The study was carried out on two sites namely, Saga with a latitude of 13°28' N and a longitude of 2°08' E and Sekoukou latitude of 13°15' N and a longitude of 2°22' E. The soils characteristics are presented in the Table 1.

Two salt tolerant parents IRRI113 and NSIC RC106 and two susceptible farmers ‘varieties IR1526 and Gambiaka have been crossed in full diallel. The first generations F₁ from these crosses were bulked and selfed to get 12 F₂ families (Kol-2, Kol-15, Kol-14, Kol-11, Kol-5, Kol-4, Kol-31, Kol-29, Kol-27, Kol-25, Kol-23 and Kol-21). The F₂ families were advanced to have F₃ families. A random sample of one hundred and twenty F₃ families derived from F₂ individual plants were taken for evaluation in farmer’s field affected by salt problem. In addition, 4 parents and a farmer preferred variety (NERICA-L49) served as check were also evaluated in the same condition. The experimental design was 25×5 alpha lattice with three replications. Each block was constituted with 25 lines with 10 plants on lines and each line was constituted of one F₃ family. The inter-plant space was 0.2 m and the between line space was 0.5 m. At the maturity plant height, total tillers per plant, reproductive tillers per plant, number of panicle, panicle weight and paddy yield were scored. The time to 50% flowering, time to 85% maturity were also recorded. Data was analyzed using SAS software version 9.2. A general ANOVA was performed using SAS Glm procedure with random effect model. The Intra-Class Correlation (ICC) was calculated as follow:

$$ICC = \frac{\delta^2_A}{\delta^2_A + \delta^2}$$

Where:

δ^2_A = Among group variance = [MSa (among families means square)-MSe (Error means square)/n
 δ^2 = Within group variance: $\delta^2 = MSe$

The heritability was estimated using REML method. Proc mixed asycov and proc iml were used. The replication, block and entries were considered as random. Mid parent offspring regression was also used for heritability estimation. The Hayman diallel model (Hayman, 1954) was used for gene action study.

RESULTS

The intra-class correlation varied among traits and among sites for the same trait (Table 2). Thus, of the total variance in yield 81 and 15% were due to the differences among the families at Saga and Sekoukou, respectively. From the total variance of the traits the amount that was explained by families ranged from 57% for the duration (time to flowering) to 82% for total panicles

Table 1: Physical and chemical characteristic of the study sites soils

Sites	pH	SAR	CEC (meq/100 g)	EC (dS cm ⁻¹)	Na/k (%)	Clay (%)	Silt (%)	Sand (%)
Saga	5.4	14.38	11.94	12.30	118.6	11.6	13.1	75.3
Sekoukou	5.2	12.46	18.96	8.60	60.8	48.4	26.6	25.0

Table 2: Intra-class correlation of traits variances across sites

Traits	Yield	Pwt	Tpwt	Gwt	Pnum	Tnum	Height	Mat	Flw
	----- (%) -----								
Sekoukou									
ICC	15	11	23	15	44	43	46	74	74
R-square	14	8	24	14	22	22	37	50	50
Saga									
ICC	81	63	82	81	70	61	82	57	57
R-square	47	35	57	47	38	31	58	21	21

Pwt: Panicle weight, Tpwt: Total panicle weight, Gwt: Grain weight, Pnum: Panicle number, Tnum: Tiller number, Mat: Time to maturity, Flw: Time to flowering, ICC: Intra-class correlation

Table 3: Traits broad sense heritability (H^2)

Sites	Flw	Mat	Height	Tnum	Pnum	Tpwt	Pwt	Gwt	Yield
Sekoukou									
h^2_f	66	65	24	41	47	28	0	27	27
SE	0.040	0.040	0.07	0.06	0.055	0.07	0.070	0.057	0.057
Saga									
h^2_f	38	38	76	53	61	81	69	77	77
SE	0.052	0.052	0.028	0.05	0.043	0.024	0.035	0.026	0.026

Pwt: Panicle weight, Tpwt: Total panicle weight, Gwt: Grain weight, Pnum: Panicle number, Tnum: Tiller number, Mat: Time to maturity, Flw: Time to flowering, ICC: Intra-class correlation

weight at Saga. At Sekoukou, the part of variance that can be attributed to family differences varies from 11% for panicle weight to 74% for the duration. The percentage of the explainable sums of squares among the total individuals in the study is given by the R-square.

The proportion of phenotypic variance of family means that was due to family genetic effects ranged from 66% for the duration to 0% for panicle weight at Sekoukou (Table 3). The most inherited traits were duration (66%), the number of panicle per plant (47%), tiller number (41%) and yield (27%). The heritability varied at Saga from 81% for total panicle weight to 31% for the duration. In general, the populations expressed higher genotypic effects for all the traits except duration (38%) at Saga. However, the pooled heritability which was the heritability across environments was high for the duration (61%). The tillers number, panicle weight and height were poorly heritable across environments with a respective heritability of 2, 14 and 0%.

A very low heritability was observed in term of time to flowering and time to maturity when IRR113 was used as female parent (6% at Sekoukou and 17.88% at Saga). For the same traits the heritability was much higher when IRR113 was the male parent: 40 and 58%, respectively at Sekoukou and Saga (Table 4). The total panicle weight, panicle weight, grain weight and yield had higher heritability when IRR113 was the female parent.

The most highly heritable traits are total panicle weight (70-81%) panicle weight (7.22-76.3%) grain weight and yield (66.8-98.94%). For these traits the narrow sense heritability was high either NSIC RC 106 was male or female parent (Table 5). The tillering ability and the panicle number had low heritability at Sekoukou but medium at Saga in all cross directions. For the duration high heritability was observed only when NSIC RC 106 was used as female parent.

All the traits were poorly heritable when Gambiaka was used as female except the panicle weight that showed high heritability at Saga (Table 6). On the two sites only two traits such as tiller number and total panicle weight were highly heritable when Gambiaka was used as male.

IR1529 offspring's revealed high heritability of total panicle weight (68%), panicle weight (74.35%), grain weight (67.23%) and yield (67.23%) when their common parent was male at Sekoukou, whereas only the height (76.21%), tillering ability (75.39%) and panicle weight (81.34%) were highly heritable at Saga. When the common parent (IR1529) was the female, only trait (panicle weight) showed high heritability at Saga (Table 7).

Table 4: IRR1113 offspring narrow sense heritability (h²)

Traits	Flw	Mat	Height	Tnum	Pnum	TPwt	Pwt	Gwt	Yield
Sekoukou									
Half sib (IRRI113 female)	5.90	5.90	40.58	63.00	58.00	75.60	41.29	77.25	77.25
Half sib (IRRI113 male)	40.00	40.00	65.58	71.00	40.00	25.64	24.69	12.86	12.86
Saga									
Half sib (IRRI113 female)	17.88	17.88	100.00	23.89	5.32	16.01	15.69	16.81	16.81
Half sib (IRRI113 male)	58.04	58.04	6.10	26.92	3.87	5.43	9.38	2.80	2.80

Pwt: Panicle weight, TPwt: Total panicle weight, Gwt: Grain weight, Pnum: Panicle number, Tnum: Tiller number, Mat: Time to maturity, Flw: Time to flowering

Table 5: NSIC RC 106 offspring narrow sense heritability (h²)

Traits	Flw	Mat	Height	Tnum	Pnum	TPwt	Pwt	Gwt	Yield
Sekoukou									
Half sib (NSIC RC106 female)	58.00	58.00	3.41	15.68	14.28	78.13	7.22	66.80	66.80
Half sib (NSIC RC106 male)	15.00	15.00	0.70	13.38	24.92	81.42	13.28	98.94	98.94
Saga									
Half sib (NSIC RC106 female)	68.00	68.00	72.40	62.00	58.00	70.10	66.30	85.20	85.20
Half sib (NSIC RC106 male)	17.58	17.58	51.45	52.90	58.00	73.01	76.30	78.20	78.20

Pwt: Panicle weight, TPwt: Total panicle weight, Gwt: Grain weight, Pnum: Panicle number, Tnum: Tiller number, Mat: Time to maturity, Flw: Time to flowering

Table 6: Gambiaka offspring narrow sense heritability (h²)

Traits	Flw	Mat	Height	Tnum	Pnum	TPwt	Pwt	Gwt	Yield
Sekoukou									
Half sib (Gambiaka female)	33.54	33.55	51.90	23.61	36.31	17.77	44.78	29.24	29.24
Half sib (Gambiaka male)	32.00	32.00	23.44	74.37	99.71	72.81	21.26	56.11	56.11
Saga									
Half sib (Gambiaka female)	19.92	19.92	44.94	41.18	8.20	32.06	74.30	4.48	4.48
Half sib (Gambiaka male)	19.01	19.00	20.30	89.71	22.52	91.36	35.28	8.60	8.60

Table 7: IR1529 offspring narrow sense heritability (h²)

Traits	Flw	Mat	Height	Tnum	Pnum	TPwt	Pwt	Gwt	Yield
Sekoukou									
Half sib (IR15 female)	62.46	62.46	16.80	54.80	70.10	25.72	28.68	2.00	2.00
Half sib (IR15 male)	12.35	12.35	42.45	12.32	13.62	67.88	74.35	67.23	67.23
Saga									
Half sib (IR15 female)	4.34	4.32	30.16	31.08	6.04	50.34	64.25	14.22	14.22
Half sib (IR15 male)	30.27	30.27	76.21	6.99	75.39	34.68	81.34	31.88	31.88

Pwt: Panicle weight, TPwt: Total panicle weight, Gwt: Grain weight, Pnum: Panicle number, Tnum: Tiller number, Mat: Time to maturity, Flw: Time to flowering

Table 8: Genes action on traits

Gene action	df	Flw	Tnum	Pnum	Height	TPwt	Pwt	Gwt
A	3	95.20 ^{ns}	157.09 ^{**}	138.12 ^{ns}	55.69 ^{ns}	142.25 ^{ns}	0.41 [*]	55.82 ^{ns}
b1	1	17.63 ^{ns}	0.15 ^{ns}	0.19 ^{ns}	23.73 ^{ns}	400.70 ^{ns}	0.25 ^{ns}	228.20 ^{ns}
b2	3	39.77 [*]	81.68 ^{ns}	42.09 ^{ns}	3.87 ^{ns}	100.33 ^{ns}	0.07 ^{ns}	52.70 ^{ns}
b3	2	7.19 ^{ns}	22.40 ^{ns}	20.68 ^{ns}	0.56 ^{ns}	20.94 ^{ns}	0.098 ^{ns}	14.09 [*]
B	6	25.22 ^{ns}	48.34 ^{ns}	27.97 ^{ns}	6.08 ^{ns}	123.93 ^{ns}	0.11 ^{ns}	69.08 ^{ns}
C	3	79.49 [*]	17.29 ^{ns}	49.06 ^{ns}	7.87 [*]	222.50 ^{ns}	0.27 ^{ns}	98.73 ^{ns}
D	3	7.3 ^{ns}	12.62 ^{ns}	10.48 ^{ns}	16.27 ^{ns}	10.41 ^{ns}	0.043 ^{ns}	2.44 ^{ns}

**Highly significant, *Significant, ns: Non significant. Pwt: Panicle weight, TPwt: Total panicle weight, Gwt: Grain weight, Pnum: Panicle number, Tnum: Tiller number, Flw: Time to flowering, A: Additive effects, B: Dominance effects, b1: Direction of dominance, b2: Tests asymmetry of alleles, b3: Shows that some dominance is peculiar to some crosses, C: Additive maternal effects, D: Maternal interaction effects

A highly significant additive gene action was observed for tiller number (Table 8). But, the dominance effect and maternal effect were not significant for this trait. The time to flowering (duration) was significantly influenced by dominance effect and maternal additive effect. For the height only maternal additive effect had significant influence. The grain weight and panicle weight were significantly impacted respectively by dominance effect and additive effect.

Salt tolerant parent had more recessive gene for grain weight and total panicle weight (IRRI113) and for duration (NSIC RC 106). IR1526 (susceptible genotype) had more dominant genes controlling duration and height. GAMBIAKA (susceptible genotype) had more dominant genes controlling grain weight and total panicle weight.

DISCUSSION

Heritability: The Intra-Class Correlation (ICC) indicated that significant percentage of the variance of all the traits can be attributed to family differences. The causes may be heredity, environment or both.

Results showed that the heritability on the family means basis was high for almost the traits at Saga. Thus, height, tiller number, panicle number, panicle weight, grain weight and yield were more heritable at Saga than at Sekoukou. It supposes that it is better to breed for these traits under high salt stress conditions. Sure enough, high heritability is good to achieve meaningful results for Saga. Many Reports on diallel analysis have indicated significant additive and dominance genetic effects and a high degree of heritability values in most trait studies (Moeljopawiro and Ikehashi, 1981; Akbar *et al.*, 1985). The duration was more heritable at Sekoukou than Saga. This means that we can easily breed for early, late or medium maturing under less salt conditions than high stress. The duration heritability across environments was high. This means a stability of the F₃ population for this trait. For the same trait the heritability differed according to the site and the parents used in the cross. This conformed with results of Betran *et al.* (2009), who found that heritability for the same trait and their magnitude depends on several factors. These factors are the environment, the reference population, the sample of genotypes evaluated, the generation or progenies. Heritability is used to estimate expected response to selection and to choose the best breeding approach to improve the target trait(s). Traits with high heritability can be selected on a single-plant basis, faster and in a low number of environments. In contrast, traits with low heritability require selection on a family basis and in a greater number of environments to determine breeding values of genotypes (Fehr, 1987; Betran *et al.*, 2009). For direct selection, the heritability of the traits to be subjected to selection is fundamental.

Traits were more heritable under salt stress when IRRI113 and NSIC RC106 were used as female parents. The results showed that heritability was high for tiller number (63%), panicle number (58%), total panicle weight (75.6%) and yield (77%) when IRRI113 was the female parent. For the same traits the heritability was low when IRRI113 was the male parent. The duration heritability was high across environment when IRRI113 was the male parent or when NSIC RC106 was the female parent. The yield was highly heritable across sites and crosses when NSIC RC106 was either female or male parent. But, when Gambiaka and IR15 were involved as female parents the traits had low heritability except for the duration that was highly heritable when IR15 was used as female parent. Panicle number, tillering ability and yield were more heritable across sites when Gambiaka was the male parent. This may be brought about by maternal or cytoplasm effect. The implications of this are that, for offspring that female parents were either IRRI113 or NSIC RC106 we can continue the selection on the plant basis to advance in one environment for traits such as yield, tiller and panicle number and height. But for duration family basis selection on multi-environment will be necessary to advance. For offspring that female parents were either Gambiaka or IR15 the plant based selection can work only for the duration. So, we have to use family means basis selection over several environments to select for the others traits.

Gene action: This study indicated additive effect for tiller number, panicle number and panicle weight. This means that these traits were not influenced by allelic inter-action and that segregation does not have any effect on them. This confirmed findings of Mishra *et al.* (1998) that indicated the role of few major genes along with numerous minor genes involved for salinity tolerance. However, additive maternal effect was noticed for duration and height this does not conform to the result of the same authors who inferred that salinity tolerance trait is polygenic in nature and lacks maternal influence. Partial dominance effect was detected in some traits such as height and duration. So, breeding for early maturing and plant height can be influenced by segregation. This is because dominance effect is an inter-action of alleles at the same locus. As, the study was on segregating populations these traits may change substantially over generations.

CONCLUSION

The rice F_3 populations evaluated were composed of families that were significantly different. The heritability was high at Saga, which could lead to higher response to selection. The later could prelude meaningful results achievement. The F_3 families derived from the cross of either IRRI113 or NSIC RC 106 as female parent had higher heritability. For these families, selection for advancement can be done on the plant basis. For the other families with low heritability, selection can only be done on a family mean basis in multi-environmental trials. Traits such as tiller number, panicle number and panicle weight were controlled by additive genetic effect. These traits were more stable than those controlled by dominance genetic effect. Multi-environmental trial should be used for the future fixed lines. This is because the genotype by environment interaction was highly significant for all the traits.

ACKNOWLEDGMENT

Alliance for Green Revolution of Africa (AGRA) for funding the study and International Rice Research Institute (IRRI) for providing salt tolerant rice germplasm are highly acknowledged.

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