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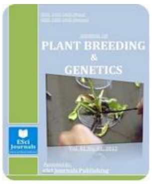

GENES ACTION IN SALINITY TOLERANCE AND THE IMPLICATION IN RICE BREEDING

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ABSTRACT

The current study was to understand the genes action in salt tolerance of rice and its use in the future breeding program. The research was carried out in Niger Republic. 120 F_3 lines derived from F_2 individual plants were evaluated along with their parents in farmer's field affected by the salt problem. The experimental design was 25*5 Alpha lattice with three replications. Data were analyzed using SAS software version 9.2. Hayman method was used to estimate gene effect. A significant additive gene action was notified in terms of tiller number (at P= 0.01), panicle number (P=0.05) and panicle weight (P=0.05). Suggesting that selection for high tillering ability, tillers fertility and panicle fertility in salt stress conditions at early generation would be fruitful. Partial dominance effect was detected in traits including the height and duration. This implied that breeding for early maturing height can be influenced by segregation. The additive maternal effect was found for duration and height. Thus, to improve the duration and height under salt stress the progeny should have a salt tolerant female parent.

Keywords: Rice, breeding, gene action, salinity, implication.

INTRODUCTION

In agricultural systems, a huge gap exists between yield potential and harvestable yield. The abiotic stresses account for most of this trend (Boyer 1982). Among these stresses, salinity leads to changes in development, growth, productivity and may threaten rice survival (Kawasaki *et al.* 2001). The development of salt tolerance rice offers the hope of increasing rice yield on current saline lands and bringing millions of hectares idle lands in rice production without costly input (Saha Ray and Amirul Islam 2008). Many studies have been conducted to know the mechanisms of genes that might confer salt tolerance to plants. Akbar and Yabuno (1977) reported that rice sterility in saline conditions is determined by many genes. Shannon (1985) found evidence of a genetically complex trait, with dominance and additive effects. Studies on salinity effects on the seedling stage and on sterility suggested both additive and dominance effects (Moeljopawiro and Ikehashi 1981; Akbar *et al.* 1985). According to Lin *et al.* (2004) and Hu *et al.* (2012), salt tolerance of rice is the genetics of quantitative characters, which is controlled by multiple genes, with the additive and dominant effects, the former playing a major role (Moeljopawiro and Ikehashi 1981; Gregorio and Senadhira 1993; Gu *et al.* 1999). Akbar *et al.* (1985) reported that the dry matter weight of rice seedling under salt stress was affected by at least two groups of genes with an additive effect. Thi Lang et *al*. (2010) reported that a dominant gene controls resistance to salt stress in the allelism test.

For developing salinity tolerant rice, it is important to understand the nature of gene action governing the trait. Knowledge of the relative importance of additive and non-additive gene action is essential to identify breeding strategies for different traits. According to Gamble (1961), the estimation of gene effects is interesting in order to formulate the most advantageous breeding procedures for improvement. Hence, Saharay (2008) found that significant additive gene effect may facilitate fixation of the desirable combination of genes.

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Furthermore, he suggested that the use of hybrid rice is feasible when dominance genes effect was significant. Mohammadi *et al.* (2014) stated that additive gene action is correlated to narrow sense heritability. Thus, significant additive gene action means high heritability and implies that selection at early generation on plant basis. The present study was carried out to estimate the effects of the gene involved in salinity tolerance of rice and the implications on the improvement methods.

MATERIAL AND METHODS

The study was carried out at National Institute for Agricultural Research of Niger (INRAN) on two sites of Niger country namely, Saga with a latitude of 13°28'N and a longitude of 2°08' and Sekoukou latitude of 13°15'N and a longitude of 2°22'. The research was conducted from December to May corresponding to the dry season. The soils characteristics are presented in the table1 showed that the two sites were saline with a high electrical conductivity (EC) of 12.3 dS/m and 8.6 dS/m at Saga and Sekoukou respectively. The pH was acidic and the sodium adsorption ration high. The average temperatures range from 25°C to 40°C.

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

Sites	pH	SAR	CEC (meq/100g)	EC (dS/m)	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	8.6	60.8	48.4	26.6	25

SAR=sodium adsorption ration, CEC= cation exchange capacity, EC= electrical conductivity, Na/K = sodium and potassium ration.

Two salt tolerant parents IRRI113 and NSIC RC106 (Souleymane *et al.* 2016) imported from IRRI (International Rice Research Institute) and two susceptible farmers 'varieties IR1526 and Gambiaka have been crossed in full diallel. The first generations F_1 from these crosses were bulked and selfed to get 12 F_2 families (Kol-2, Kol-15, Kol-14, Kol-11, Kol-5, Kol-4, Kol-31, Kol-29, Kol-27, Kol-25, Kol-23, Kol-21). The F_2 families were advanced to F_3. A random sample of one hundred and twenty (120) F_3 families derived from F_2 individual plants was taken for evaluation in farmer's field affected by the 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 F_3 family. The transplanting was performed at 4 leaves stage. The inter-plant space was 0.2 m and the between line space was 0.5 m. Fertilizer was applied before transplanting concerning NPK (15-15-15) and urea at panicle initiation. Irrigation was done regularly to avoid drought effect. At the maturity plant height, total tillers per plant, reproductive tillers per plant, number of panicles, panicle weight, and paddy yield were scored. The time to 50% flowering, time to 85% maturity were also recorded (Souleymane *et al.* 2015). Data were analyzed using SAS software version 9.2. A general ANOVA was performed using SAS GLM procedure with random effect Model.

The Hayman diallel model (Hayman 1954) was used for gene action study. The model used is:

Y = U + rep + a + b + c + d + a*rep + b*rep+ c*rep+ d*rep

Where: U = grand mean; rep= replication effects; a = additive effects; b = dominance effects;

b = is partitioned into: b1 that indicates the direction of dominance (unidirectional if significant; equiv. to Parent vs. crosses contrast); b2, tests asymmetry of alleles; b3, shows that some dominance is peculiar to some crosses. c = additive maternal effects; d = maternal interaction effects.

a*rep + b*rep+ c*rep+ d*rep = interaction of the reps with the model components

RESULTS

A highly significant (P= 0.01) additive gene action was notified in terms of tiller number (Table 2). However, the dominance effect and maternal effect were not significant for this trait. The duration was significantly influenced by dominance effect and maternal additive effect (P = 0.05). For the height, only maternal additive effect had significant influence (P = 0.05). The panicle number, total panicle weight and individual panicle weight were significantly (P = 0.05) impacted by and additive effect. The height was significantly influenced by the additive maternal effect. For grain weight, significant dominance effect was noticed with the dominance peculiar to some crosses.

Table 2. genes action on traits.

Gene action	d.f	Flw	Tnum	Pnum	Height	Tpwt	Pwt	Gwt
A	3	95.20^{ns}	157.09**	138.12*	55.69^{ns}	142.25*	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*	48.34^{ns}	27.97^{ns}	6.08^{ns}	123.93^{ns}	0.11^{ns}	69.08*
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 = not significant. Pwt= panicle weight, Tpwt = total panicle weight, Gwt = grain weight, Pnum = panicle number, Tnum= tiller number, and Flw= time to flowering. a = additive effects; b = dominance effects; b1 indicates direction of dominance, b2, tests asymmetry of alleles; b3 = dominance is peculiar to some crosses. c = additive maternal effects; d = maternal interaction effects.

The covariance (Wr) is related to the variance (Vr) by straight regression of a slope less than 1.0 implied the presence of non-allelic interaction and with the dependent distribution of genes among the parents for the trait time to flowering (Figure 1). This non-allelic interaction was the additive maternal effect. The regression line cuts the Wr above the origin (positive intercept) this suggested a partial dominance. The parents with most dominant genes were IRRI113 and IR1529 (they were close to the origin) where Gambiaka had equal dominant and recessive genes. NSIC RC106 was the parent with most recessive genes.

A slope less than 1.0 and a positive intercept suggested a presence of gene interaction and partial dominance for the trait height (Figure 2). The parents with more dominant genes controlling plant height were IRRI113, NSIC RC106 and IR1529. Gambiaka was the parent with the most recessive gene for height.

For tiller number (Figure 3) and panicle number (Figure 4) an absence of non-allelic interaction with the independent distribution of genes among the parents was suggested, this was explained in the flowing Figures by Wr that is related to Vr by straight regression of unity slope, 1.0.

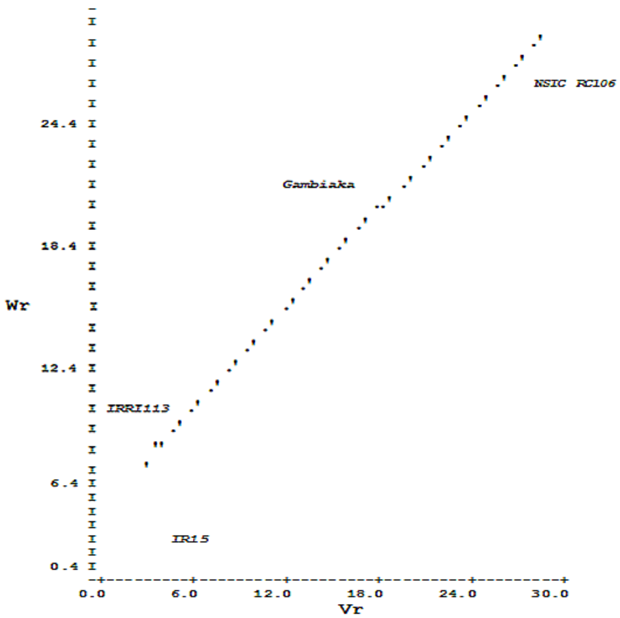

Figure 1. Variance and covariance regression for duration.

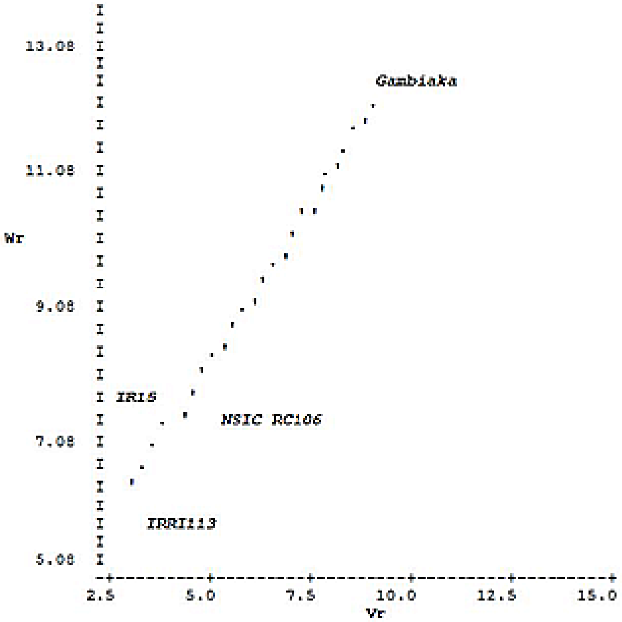

Figure 2. Variance and covariance regression for plant height.

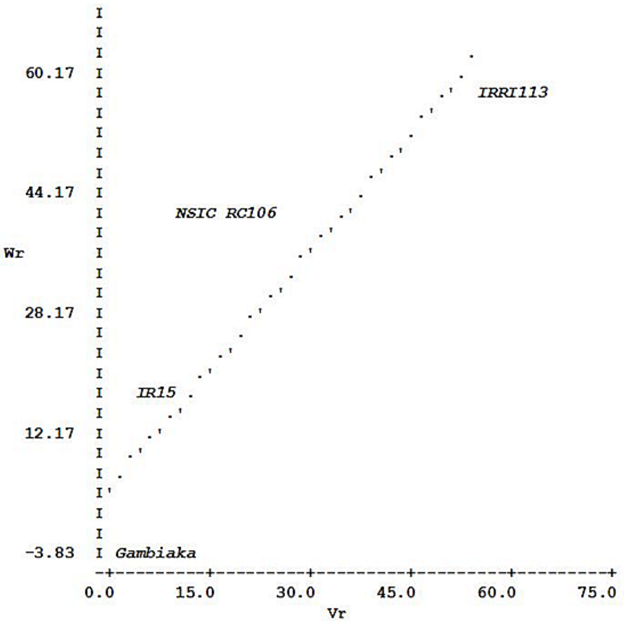

Figure 3. Variance and covariance regression for tiller number.

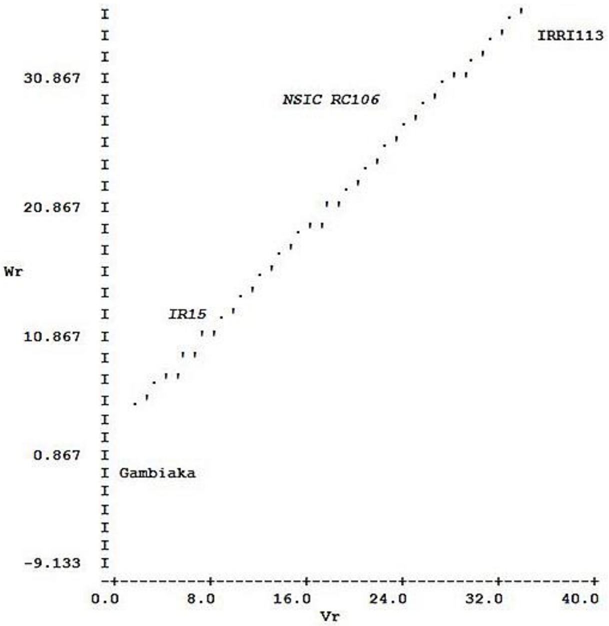

Figure 4. Variance and covariance regression for panicle number.

Figure 5 showed partial dominance effect on total panicle weight. This is indicated by a positive intercept of the regression line with the covariance. The parents with most dominance genes were NSIC RC106, Gambiaka and IR1529 were IRRI113 bears most recessive genes. Panicle weight variance and covariance regression (Figure 6) showed an absence of allelic interaction. However, partial dominance (positive intercept) affected grain weight (Figure 7). The parents with most dominant genes (P>75%) were NSIC RC106 and Gambiaka where IR1529 and IRRI113 had most recessive genes (P< 25%).

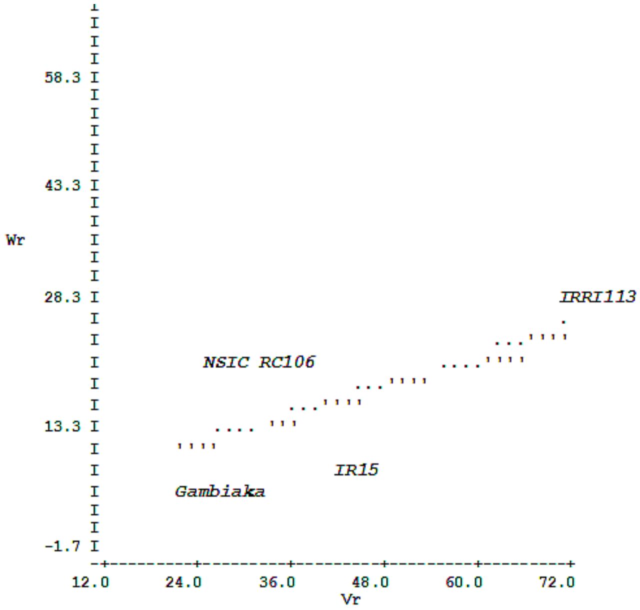

Figure 5. Variance and covariance regression for Total panicle weight.

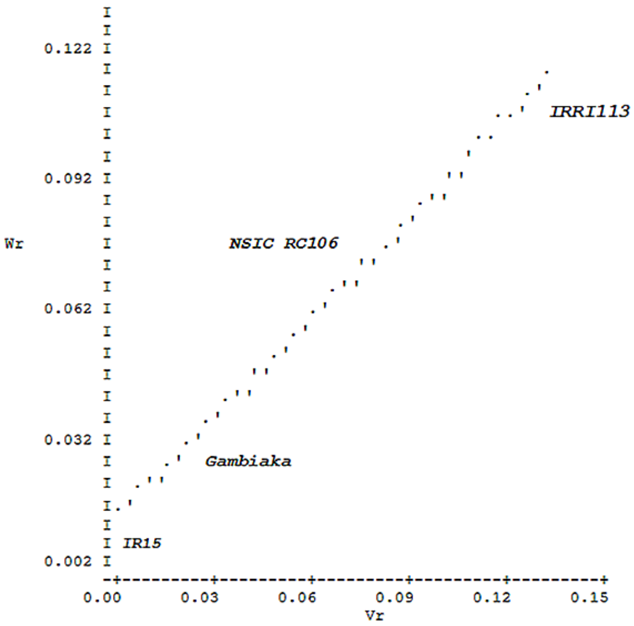

Figure 6. Variance and covariance regression for individual panicle weight

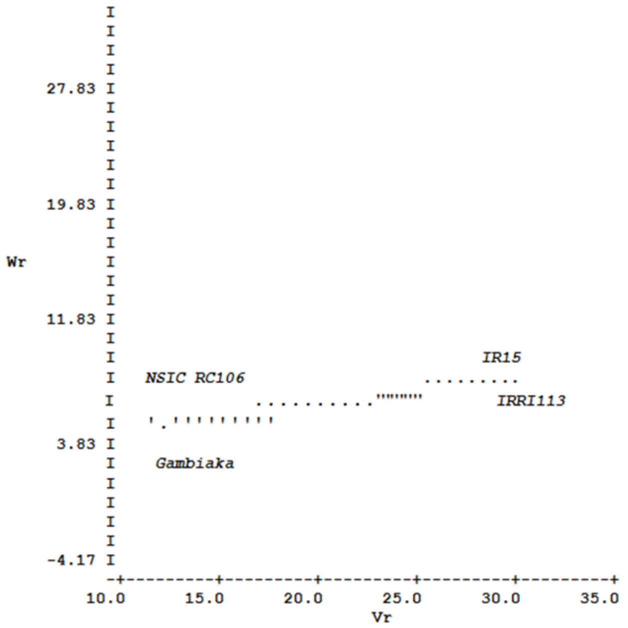

Figure 7. Variance and covariance regression for grain weight.

DISCUSSION

Additive effect has been found in the study for tiller number, panicle number, panicle weight and total panicle weight. Thus, these traits were not influenced by allelic inter-action and segregation will not affect them under salt stress. Mishra *et al.* (1998) indicated in their study the involvement of few major genes along with numerous minor genes for salinity tolerance. Rice panicle weight under salt stress condition is controlled by at least three pairs of genes (Akbar and Yabuno 1977). Chaubey and Senadhira (1994), observed highly significant additive gene effect under salt stress for grain yield. These authors author indicated significant dominance gene action under the saline condition for panicle weight and a number of tillers. Other studies indicated that plant yield was controlled by highly significant additive effects (Moeljopawiro and Ikehashi 1981; Akbar *et al.* 1985; Mishra *et al.* 1990).

Selection of traits such as: tiller number, panicle number, panicle weight and total panicle weight in salt-affected conditions may be done at early generation and therefore may be important promising and fruitful. Because the additive effects would give a better response (Saharay and Amirul Islam 2008). Falconer and Mackay (1996) had the useful insight that high narrow sense heritability is caused by high additive effects and low dominant gene action. Thus, the presence of additive gene action is indicated by higher narrow-sense heritability (Mohammadi *et al.* 2014). Furthermore, the usefulness of one individual in selection is determined by the breeding value. The latter being associated with additive effects and the variation among breeding values is attributed to these effects (Betrán *et al.* 2009).

However, the additive maternal effect was found for duration and height this was not conform to the results of (Mohammadi *et al.* 2014) who inferred that salinity tolerance trait lacks maternal influence. Deepa Sankar *et al.* (2011) stated that plant height was controlled by additive gene action. Traits controlled by maternal effect can be improved in rice breeding by selecting maternal plant (Shi and Zhu 1998). Thus, to improve the duration (early, medium or late) and height (dwarf, medium or tall) in salt stress conditions the progeny should have a salt tolerant female parent. Selection of these criteria could be done at early generations on a plant basis. This is because the additive maternal effect would imply high maternal heritability.

However, partial dominance effect was found in some traits such as height and duration. So, breeding for early maturing height may be partially influenced by segregation (Shi and Zhu 1998). The selection of these traits in early generations may not be effective. Nevertheless, this partial dominance can be exploited by intermating the selected F_3 families and delaying the selection to the advanced generations (Saharay and Amirul Islam 2008). Jensen (1970) proposed a diallel selective mating system to improve those traits in salt-affected conditions. The recurrent selection procedures can also be used (Singh and Power 1990).

CONCLUSION

Significant additive effects were noticed in term of tiller number, panicle number, panicle weight and total panicle weight. The additive maternal effect was noticed for duration and height. Partial dominance effect was detected in some traits such as height and duration. The improvement methods included early generation selection for tiller number, panicle number, panicle weight and total panicle weight, and intermating the selected segregants and delaying of the selection to the advanced generations for height and duration.

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