



OPEN ACCESS

Key Words

Rice, NCIII, gene action, heterosis, broad sense heritability, narrow sense heritability

Corresponding Author

Alireza Haghighi Hasanalideh,
Rice Research Institute of Iran,
Agricultural Research, Education and
Extension Organization (AREEO),
Rasht, Iran
haghighi.ag@gmail.com

Author Designation

¹Assistant Professor

Received: 10 August 2024

Accepted: 15 September 2024

Published: 16 September 2024

Citation: Alireza Haghighi Hasanalideh, 2024. Gene Action and Heterosis for Milling Traits in Rice (*Oryza Sativa L.*) Through North Carolina III Mating Design. *Res. J. Agron.*, 18: 1-5, doi: 10.36478/makrja.2024.1.1.5

Copy Right: MAK HILL Publications

Gene Action and Heterosis for Milling Traits in Rice (*Oryza Sativa L.*) Through North Carolina III Mating Design

¹Alireza Haghighi Hasanalideh

¹*Rice Research Institute of Iran, Agricultural Research, Education and Extension Organization (AREEO), Rasht, Iran*

ABSTRACT

This study conducted for assessing heterosis, genetic parameters, gene action and heritability of important milling traits in rice. The crosses of North Carolina design III with their parents were planted in a randomized complete block design with three replications in experimental field at Rice Research Institute of Iran, in 2015. The ANOVA analysis of NCIII showed that for all studied traits, there is a significant difference between the mean of progeny derived from F_2 , the means of progenies obtained from Gilaneh had a significant difference with the means of progeny derived from the Deylamani for these traits and Deylamani and Gilaneh varieties had affected on the offspring. Estimation of genetic parameters revealed that for BRW, WRW, HRW and KL, additive effects of gene action have more portion in genetic controlling of these traits. Over-dominance phenomenon revealed due to greater than one estimates of average degree of dominance (DD), for BRW and HRW. Results of mid-parent heterosis revealed a range of -0.22-5.51% in BRW, -3.46-4.06% for WRW, -21.26-16.19% for HRW and -2.9-19.22% in KL.

INTRODUCTION

Rice (*Oryza sativa* L.) is the most important staple food for about two-third of the world's population. It ranks the second position by production in the world. The increasing population pressure, the demand for cereal is increasing day by day. >90% of the rice produced and consumed in Asia as a staple food, which provides 35-60% of the required calories^[15]. Keeping in view of the future demand for rice as food for human, there is a continuous need to evolve new varieties, which should exceed the yields of existing ones. Variation present in the population is an important prerequisite for improvement of any crop species^[17]. It is very much essential to improve the rice with higher yield. The grain yield is a highly complex character, generally governed by genes and the interaction between them^[11]. To meet the future food demand, anticipated from the projected world population increase, there is an urgent need to take necessary steps for enhancing the productivity of this crop. Hybrid rice offers an opportunity to boost the yield potential of rice. It has a yield advantage of 15-20% over conventional high yielding variety. The breeding of yield rich and quantitatively better rice varieties is impossible without prior knowledge of their genetic properties^[15]. Successful application of biometrical procedures to understand genetics of quantitative characters helped the breeders to systematically plan for result oriented breeding programs^[12]. Conventional breeding strategy play a very important role for the screening, production of high yielding hybrids and exploitation of heterosis as well as the specific combining ability of crosses. The most important point for the plant breeders is to produce high yielding hybrids is the selection of the parents and their hybrids^[9]. Many combinations annually made and evaluated in hybrid breeding programs, only a few hybrids are selected. This means extremely intensive labor is required, time is consumed and the selection efficiency is low. Thus, it is very important to explore alternative approaches to enhance the selection efficiency and to predict hybrid performance^[16]. To breed an ideal cross with the highest grain yield is the ultimate goal of hybrid rice breeders. As parents with excellent agronomic traits do not always pass those traits on to their progenies, breeders often test the potential of a self-line by cross it to several other lines^[22]. Hybrid rice technology is one of the feasible options to meet the future food demand of 852 million tons in 2035, we need to enhance rice production to current production level of 676 million tons to fulfill the dietary requirements of ever growing populations^[8]. Heterosis expressed as percent, increase or decrease in the mean value of F_1 hybrid over better parent (heterobeltiosis) and over standard check (standard heterosis)^[4]. Heterosis breeding is a fundamental tool for the expression of various cross combinations and its potential for

commercial exploitation of heterosis under different environmental conditions. Overall positive heterosis desired for yield and yield relating traits and negative heterosis for days to flowering and plant height^[14]. Success of any plant breeding program depends on the choice of appropriate genotypes as parents in the hybridization program^[15]. The magnitude of heterosis helps in the identification of potential cross combinations to be used in conventional breeding program to enable create a wide array of variability in segregating generations. The knowledge of heterosis accompanied by the extent of inbreeding depression in subsequent generations is essential for maximum exploitation of such heterosis by adopting appropriate breeding methodology^[11]. In the breeder point of view, the estimation of genetics parameters such as, heritability, gene action and correlation among characters' are very important in order to formulate the most advantageous breeding procedures^[13]. Considering additive and dominance variance is useful for suggesting an appropriate breeding strategy to be followed for isolation of pure lines or exploitation of heterosis^[6]. Mating of randomly selected plants in segregating generation of a cross in between parent having contrasting characters will not only helpful in creating greater variability by breaking tight and unfavorable linkages for effective selection over the longer period but also creates new populations with high frequencies of rare recombinants. Before such populations can be used for the genetic improvement, an efficient breeding methodology has to be formulated. For this purpose, information would be required on the relative proportion of additive and non-additive variances^[2]. Information on the magnitude of various components of genetic variation is important in determining the best selection and breeding procedure for a particular set of material under given circumstances. The large range of variation and the high values of heritability for some traits suggested good potential for improvement through an intra-population selection program. However, the large dominance effects and the small additive effects for grain yield indicated that an inter-population selection program would be effective. The improvement of yield depends on the knowledge of the type of gene action involved in its inheritance and also the genetic control of related traits such as the capacity for production. Also the choice of breeding methods for genetic improvement of a crop depends upon the nature and magnitude of present genetic variability^[5]. Different mating designs are used in the estimation of genetic variability and other components of variance such as North Carolina Design I, II and III. North Carolina design I (NCI) is commonly used to estimate additive and dominance variances as well as for evaluation of full-sib and half-sib recurrent selection. It requires sufficient seed for replicated evaluation trials and

hence is not of practical application in breeding species that are not capable of producing large amounts of seed. As a nested design, each member of a group of parents used as males is mated to a different group of parents. NC design is a hierarchical design with non-common parents nested in common parents. This design is most widely used in animal studies. In North Carolina design II (NCII), each member of a group of parents used as males is mated to each member of another group of parents used as females. Design II is a factorial mating scheme similar to Design I. It is used to evaluate inbred lines for combining ability. The design is most adapted to plants that have multiple flowers, so that each plant can be used repeatedly as both male and female. In North Carolina design III (NCIII), a random sample of F_2 plants is backcrossed to the two inbred lines from which the F_2 was descended. It is considered the most powerful of all the three North Carolina designs^[1]. Wen^[18] conducted a NCII and reported that the ranking of factors affecting heterosis was dominance followed by dominance-by-dominance, over-dominance and complete dominance, respectively. Zhou^[19] constructed a both NCII and NCIII mating design. They reported that both kinds of gene effects were important for the inheritance of agronomic traits. traits plant height, heading date and grain weight per 1000 grains, mainly controlled by additive effects. Traits grain-filling degree, yield and spikelet per panicle, mainly controlled by non-additive effects. They also indicated that over-dominance contribute a lot to the heterosis of grain-filling degree, yield and seed-setting rate. Li^[10] used NCIII for understanding the genetic basis of heterosis. They reported that the relative contributions of the genetic components varied with traits. In hybrids, over-dominance was the most important contributor for yield, 1000-grains weight, seeding set, panicle length and plant height. Interactions with over-dominance also contributed to heading date and filled grains per panicle and with dominance contributed to plant height, grain density and 1000-grains weight. De Morais^[3] declared that non-additive genetic effects were more important than additive effects for the expression of yield, day to flowering and plant height. The dominance deviations were predominantly negative for yield and day to flowering and were positive for plant height. Crosses tended to be more productive (higher yield) and earlier (fewer day to flowering) than parental lines. Considering above contents, this study conducted for assessing heterosis, genetic parameters, gene action and heritability of important milling traits in rice.

MATERIALS AND METHODS

This experiment was conducted at Rice Research Institute of Iran (RRII), Rasht, Guilan province, during 2014-2015. Two cultivar including Deylamani and

Gilaneh and F_2 populations derived from their mating, were planted for crossing through NCIII, in 2014. In order to coincident in flowering and having enough time to conduct crosses, parental cultivars were seeded three times in a 10-day interval. The two lines were used as female parent and F_2 single plants were used as male parents. The crosses of NCIII with their parents were planted in a randomized complete block design with three replications in experimental field at RRII, in 2015. Each genotype was comprised of 4 rows and 10 plants per row. A composite sample of 15 plants from the middle row used to record observations for brown rice weight (BRW), white rice weight (WRW), head rice weight (HRW) and kernels length (KL). Analyses of variance and estimation of genetic parameters calculated according to Hallauer^[7].

Table 1: Analysis of Variance of Design III Progenies According to Hallauer *et al.*, (2010).

SOV	df	MS	variance component
Replications	$r-1^a$		
Parents (p)	1	M4	$\sigma^2 + r\sigma_{mp}^2 + rmk_p^2$
Males (m)	$m-1$	M3	$\sigma^2 + r\sigma_m^2$
$m \times p$	$m-1$	M2	$\sigma^2 + r\sigma_{mp}^2$
Error	$(r-1)(2m-1)$	M1	σ^2

^ar and m refer to number of replications and male plants, respectively

Mean square expectations to focus on in design III are the component of variance among males (σ_m^2) and the one for the interaction of males and inbred parents (σ_{mp}^2). Direct F-tests are possible for σ_{mp}^2 and σ_m^2 with the error term but they do not give us knowledge of the genetic structure of the progenies and how they relate to components of variance. Comstock and Robinson (1952) defined the genetic structure of progenies in the absence of linkage (independence of segregation) and epistasis (independence of action) as:

$$\sigma_m^2 = (1/2) \sum pqd^2$$

$$\sigma_{mp}^2 = \sum pqd^2$$

Since $p = q = 1/2$ is expected for F_2 populations, therefore, genetic parameters estimated as:

$$\sigma_m^2 [(M_3 - M_1)/2r] = (1/8) \sum a^2 = (1/4) \sigma_A^2$$

$$\sigma_{mp}^2 [(M_2 - M_1)/r] = (1/4) \sum a^2 = \sigma_D^2$$

From the expectations of the σ_m^2 and σ_{mp}^2 components of variance, a measure of the dominance of genes obtained. the average level of dominance estimated as.

$$[(M_2 - M_1)/r] [(M_3 - M_1)/2r]^{1/2}$$

From the components given in Table 1, an estimate of heritability based on the mean of r plots determined as follows.

$$h^2 = 4\sigma_m^2 / \left(\frac{\sigma^2}{r} + \sigma_{mp}^2 + 4\sigma_m^2 \right)$$

The magnitude of heterosis was expressed as heterosis over mid-parent (MPH). The following formulae were used for estimation of heterosis.

$$MPH = \left[\frac{F_1 - MP}{MP} \right] 100$$

$$SM = \sqrt{2MSE / r}$$

$$t = [(F_1 - MP) / SE] MPH$$

Where, MSE=Error mean sum of squares from RCBD ANOVA, F_1 =Mean of F_1 and MP=Mean of mid parent. SPSS software (IBM Corp 2011) and Excel were used for analysis of variance and estimation of NCIII genetic parameters.

RESULTS AND DISCUSSION

The ANOVA analysis of NCIII (Table 2) showed that mean square variances of male was significant for all studied traits. So, there is a significant difference between the mean of progeny derived from F_2 for these traits. Also, mean square variances of females was significant for all studied traits. Therefore, the means of progenies obtained from Gilaneh had a significant difference with the means of progeny derived from the Deylamani for these traits. Mean square of interaction between males and females was also significant. Therefore, F_2 genotypes reacted differently to Deylamani and Gilaneh genotypes for all studied traits. In other words, Deylamani and Gilaneh varieties had affected on the offspring.

Table 2: Analysis of Variance of NCIII, for Quantitative Traits in Rice.

SOV	df	Mean Square			
		BRW	WRW	HRW	KL
Replications	2	0.79 ^{ns}	8.42 ^{ns}	5.01 ^{ns}	0.06 ^{ns}
Parents (p)	1	8.71**	15.97**	198.79**	0.6**
Males (m)	14	102.19**	402.8**	3401.32**	0.26*
m × p	14	7.37**	7.58**	150.52**	0.08*
Error	58	0.76	1.92	4.64	0.04

ns * and **: non-significant, significant at 5% and 1% level respectively.

Investigating the genetic parameters through NCIII mating design (Table 3) revealed that variance of interaction between males and females and male variance was significant for all traits. Significance estimates of additive and dominance variances indicated the presence of additive and non-additive gene actions, in genetic controlling of traits BRW, WRW, HRW and KL. The estimates of additive variance were higher than the estimates of dominance variance for BRW, WRW, HRW and KL. So, additive effects of gene action have more portion in genetic controlling of these traits. However, slight difference between parameters A and D for BRW indicating the presence of non-additive gene effects in addition to the additive gene effects in genetic controlling of this trait. Over-dominance phenomenon revealed due to greater than one estimates of average degree of dominance (DD), for BRW and HRW. Estimates of broad sense heritability were high for all studied traits, indicating

that the expression of these traits affected more by genetic effects than environmental effects. The estimates of narrow sense heritability in all studied traits was moderate excepting KL and revealed presence of the dominance effects in genetic controlling of these traits.

Table 3: Genetic Parameters Estimation of NCIII, for Quantitative Traits in Rice.

Genetic Parameters	BRW	WRW	HRW	KL
mp	2.21**	1.89**	48.63**	0.01**
m	1.33**	2.34**	32.36**	0.09**
A	5.3**	9.37**	129.43**	0.37**
D	4.41**	3.78**	97.25**	0.03**
DD	1.29*	0.9*	1.23*	0.37*
h_b^2	0.93	0.87	0.98	0.91
h_n^2	0.51	0.62	0.56	0.85

mp= m × p variance, m=male variance, A=Additive variance, D=Dominance variance, DD=Average degree of dominance, h_b^2 = Broad sense heritability and h_n^2 = Narrow sense heritability.

^{ns} * and **: non-significant, significant at 5% and 1% level respectively.

Assessing the results of mid-parent heterosis (Table 4) revealed that Mid-parent heterosis for BRW ranged -0.22% in F_2 No. 6×Gilaneh to 5.51% in F_2 No. 9× Gilaneh. Evaluating mid-parent heterosis in WRW showed that the relative heterosis based on the average of the parents was in the range of -3.46% in the crossing of F_2 No. 5×Gilaneh and 4.06% in the crossing of F_2 No. 9×Gilaneh. For HRW, relative heterosis based on the average of parents was appeared in the range of -21.26% in the F_2 crossing No. 13×Gilaneh and 16.19% in the crossing of F_2 No. 11×Gilaneh. For the length of white rice, relative heterosis based on the average of parents appeared in the range of -2.9% in the crossing of F_2 No. 4× Deylamani and 19.22% in the crossing of F_2 No. 9×Gilaneh.

Table 4: Heterosis (%) Over Mid-Parent (MPH) for Quantitative Traits, in Rice Progenies Crossed Through NCIII.

Crosses	BRW	WRW	HRW	KL
F2 No. 1 × Deylamani	2.13*	1.27ns	6.1ns	0.65ns
F2 No. 2 × Deylamani	4.52*	3.06**	14.59**	-2.58ns
F2 No. 3 × Deylamani	3.19*	-0.59ns	1.15ns	0.92ns
F2 No. 4 × Deylamani	0.6ns	-1.17ns	2.5ns	-2.9*
F2 No. 5 × Deylamani	3.06**	1.08ns	6.84ns	-1.2ns
F2 No. 6 × Deylamani	2.53*	-1.59**	1.27ns	2.94ns
F2 No. 7 × Deylamani	1.09*	1.11ns	3.36ns	-0.73ns
F2 No. 8 × Deylamani	2.51**	1.75*	6.21*	12.7**
F2 No. 9 × Deylamani	3.65**	-0.5ns	-5.29**	-0.55ns
F2 No. 10 × Deylamani	1.8**	1.4*	5.41*	5.57*
F2 No. 11 × Deylamani	4.09**	3.48**	14.91**	1.29ns
F2 No. 12 × Deylamani	3.46**	-0.47*	1.93**	1.1ns
F2 No. 13 × Deylamani	0.76ns	-1.39*	3.03*	3.86ns
F2 No. 14 × Deylamani	3.27**	1.37**	6.47*	3.59ns
F2 No. 15 × Deylamani	2.29**	-1.11**	1.19ns	5.48ns
F2 No. 1 × Gilaneh	2.43**	-0.38ns	18.39*	-1.01ns
F2 No. 2 × Gilaneh	2.12**	0.48ns	-21.07**	-0.54ns
F2 No. 3 × Gilaneh	0.36*	-1.97ns	-7.36**	-2.73*
F2 No. 4 × Gilaneh	3.09**	-0.31ns	7.95**	-0.26ns
F2 No. 5 × Gilaneh	1.21**	-3.46**	3.9**	-1.75**
F2 No. 6 × Gilaneh	-0.22**	-1.84**	-8.63**	-3.2ns
F2 No. 7 × Gilaneh	-0.2ns	1.54ns	13.56**	0.91ns
F2 No. 8 × Gilaneh	0.8*	0.42ns	-4.17ns	0.39ns
F2 No. 9 × Gilaneh	5.51**	4.06**	19.22**	19.22**
F2 No. 10 × Gilaneh	1.29**	0.08ns	-3.53**	3.39ns
F2 No. 11 × Gilaneh	2.92**	0.22ns	19.16**	2.4ns
F2 No. 12 × Gilaneh	2.59**	0.54*	-21.08**	5.49ns
F2 No. 13 × Gilaneh	1.82**	0.61ns	-21.26**	2.45ns
F2 No. 14 × Gilaneh	3.25**	-0.71**	9.13**	2.08ns
F2 No. 15 × Gilaneh	1.68*	-5.72ns	2.94ns	3.06**

^{ns} * and **: non-significant, significant at 5% and 1% level respectively

CONCLUSIONS

This study conducted for assessing heterosis, genetic parameters, gene action and heritability of important milling traits in rice. The ANOVA analysis of NCIII showed that mean square the means of progenies obtained from Gilaneh had a significant difference with the means of progeny derived from the Deylamanifor these traits and, F2 genotypes reacted differently to Deylamanifor and Gilaneh genotypes for all studied traits. Significance estimates of additive and dominance variances indicated the presence of additive and non-additive gene actions. Over-dominance phenomenon revealed due to greater than one estimates of average degree of dominance (DD), for BRW and HRW.

REFERENCES

1. Acquaah, G., 2009. Principles of plant genetics and breeding.
2. Bainade, P.S., M.R. Manjare, S.G. Deshmukh and S.D. Kumbhar, 2014. Genetic analysis in green gram (*Vigna radiata* (L.) Wilczek) subjected to North Carolina mating design-I. *Bioscan*, 9: 875-878.
3. Comstock, R.E. and H.F. Robinson, 1952. Estimation of average dominance of genes. *Heterosis*, 2: 494-516.
4. De Moraes, O.P., J.A. Pereira, P.G.S. Melo, P.H.R. Guimarães and O.P. de Moraes, 2017. Gene action and combining ability for certain agronomic traits in red rice lines and commercial cultivars. *Crop Sci.*, 57: 1295-1307.
5. Fonseca, S. and F.L. Patterson, 1968. Hybrid vigor in a seven-parent diallel cross in common winter wheat (*Triticum aestivum* L.). *Crop Sci.*, 8: 85-88.
6. Hadini, H., N. Nasrullah, T. Taryono and P. Basunanda, 2015. Estimates of Genetic Variance Component of an Equilibrium Population of Corn. *AGRIVITA Jou Agric Sci.*, 37: 45-50.
7. Haghghi, H., E. Farshadfar and M. Allahgholipour, 2017. Genetic parameters and combining ability of some important traits in rice (*Oryza sativa* L.). *Genetika*, 49: 1001-1014.
8. Hallauer, A.R., M.J. Carena and F.J.D. Miranda, 2010. Quantitative genetics in maize breeding (Vol. 6). *Springer Science Business Media*, Vol. 0.
9. Khush, G.S., 2013. Strategies for increasing the yield potential of cereals: Case of rice as an example. *Plant Breed.*, 132: 433-436.
10. Kumar, S., N.K. Singh, R. Kumar, S.K. Singh, N. Jaya, C. Kumar and A. Kumar, 2017. Heterosis studies for various morphological traits of rice under drought conditions. *Int. J. Curr. Micro. Applied Sci.*, 6: 507-521.
11. Li, L., X. HE, H. ZHANG, Z. WANG and C. SUN et al., 2015. Genomewide mapping reveals a combination of different genetic effects causing the genetic basis of heterosis in two elite rice hybrids. *J. Genet.*, 94: 261-270.
12. Makwana, R.R., V.P. Patel, M.M. Pandya and B.A. Chaudhary, 2018. Heterosis and Inbreeding Depression for Morpho-Physiological Traits in Rice (*Oryza sativa* L.). *Intern Jour Pure Appl Bios.*, 6: 1477-1482.
13. NyaNayak, P., S.R. Ch and S. Vanisree, 2016. Heterosis and gene action studies involving aromatic lines for grain quality traits in rice. *Intern Jou Life Scie.*, 4: 517-528.
14. Nugraha, Y., S.W. Ardie, M. Ghulamahdi, S. Suwarno and H. Aswidinnoor, 2016. Implication of gene action and heritability under stress and control conditions for selection iron toxicity tolerant in rice. *Agri Jou Agric Scie.*, 38: 282-295.
15. Nuruzzaman, M., M.F. Alam, M.G. Ahmed, A.M. Shohael and M.K. Biswas, et al., 2002. Studies on parental variability and heterosis in rice. *Paki Jou Biol Sci.*, Vol. 5, No. 10.
16. Rahaman, A., 2016. Study of nature and magnitude of gene action in hybrid rice (*Oryza sativa* L.) through experiment of line x tester mating design. *Intern Jou App Res.*, 2: 405-410.
17. Tiwari, D.K., P. Pandey, S.P. Giri and J.L. Dwivedi, 2011. Heterosis studies for yield and its components in rice hybrids using CMS system.
18. Soni, S.K., V.K. Yadav, V.P. Bhadana, M.C. Yadav and R.M. Sundaram, 2017. Prediction of heterosis using hypervariable microsatellite markers in tropical japonica x indica rice hybrids. *Int J Curr Microbiol App Sci*, 6: 1-9.
19. Tejaswini, K.L.Y., B.R. Kumar, L.A. Mohammad, S.K. Raju and M. Srinivas, et al., 2016. Study of genetic parameters in F5 families of rice (*Oryza sativa* L.). *Intern Jour Envir Agric Biote.*, Vol. 1, No. 4.
20. Wen, J., X. Zhao, G. Wu, D. Xiang and Q. Liu et al., 2015. Genetic dissection of heterosis using epistatic association mapping in a partial nci mating design. *Sci. Rep.*, Vol. 5, No. 1. [10.1038/srep18376](https://doi.org/10.1038/srep18376).
21. Zhou, H., D. Xia, J. Zeng, G. Jiang and Y. He, 2017. Dissecting combining ability effect in a rice nci-iii population provides insights into heterosis in indica-japonica cross. *Rice*, 10: 1-9.