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ESTIMATES OF GENETIC PARAMETERS, COMPONENTS OF VARIANCE AND THEIR MAGNITUDE IN RICE (*ORYZA SATIVA* L.)

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Abstract

The relative contribution of males x females was higher than that of males and females for the expression of all the characters except total number of spikelets and number of fertile spikelets. Males exhibited maximum contribution for ear bearing tillers plant^{-1}. In general, phenotypic coefficient of variation was higher than genotypic coefficient of variation for all the characters. Phenotypic and genotypic variations were lower for days to 50% flowering, plant height, days to maturity, ear bearing tillers plant^{-1} and total number of spikelets plant^{-1}, indicating little opportunity of selection for these characters. Other characters showed more variation among phenotypic and genotypic values. Heritability in narrow sense (h^2n) ranged from 5.18 for days to maturity to 20.27 for ear bearing tillers plant^{-1}. Highest h^2n estimate was recorded for ear bearing tillers plant^{-1}. Moderate h^2n estimates were observed for remaining traits except days to 50% flowering, biological yield, harvest index, plant height and days to maturity which, were of lesser order. Estimates of h^2b were recorded high for all the characters except days to maturity.

***Keywords*:** Rice, GCV, PCV, heritability, gca (σ^2g), sca (σ^2s), degree of dominance $(\sigma^2s/2\sigma^2g)^{½}$

Introduction

The effectiveness of selection in improving a plant character depends largely on the extent of genetic variability in the breeding materials and transmissibility of the character in question. The information on coefficients of variation at genotypic, phenotypic and environmental level provides clear understanding of existing variability in a crop and relative importance of genetic and environmental components. The presence of high magnitude of variability in the germplasm or breeding materials only indicates the greater possibility of improvement through selection but the existence of high transmissibility is an important pre-requisite for realization of such possibility. The estimate of heritability is of immense value to the plant breeders in determining the index of transmissibility of a character from parents to the offspring. Lush (1947) defined the heritability in broad and narrow sense. In broad sense, heritability is the ratio of total genetic variance to the total phenotypic variance, while narrow sense heritability is the ratio of only additive genetic variance to total phenotypic variance. Heritability coupled with genetic advance in per cent of mean (Ga) provides more reliable information regarding transmissibility of traits, which is of great significance to plant breeders for developing suitable selection strategy. Breeding in rainfed lowland rice has primarily been confined to exploitation of available genetic variability resulting in development of homozygous lines as varieties. The information on the nature and magnitude of gene action controlling important agronomic traits is essential for devising a suitable breeding strategy for improvement in any crop. Furthermore, understanding of direct and indirect selection parameters also helps in effective application of selection in isolating superior genotypes for a particular environment or situation.

Materials and Methods

The investigation was conducted at Crop Research Station, Masodha, Faizabad (U.P.) during Kharif season of 2003 and 2004. The site falls under sub tropical to semi arid region in Indo-Gangatic plains and lies between 26.47ºN latitude, 82.12oE longitude and at an altitude of about 113 m above mean sea level. The two cytoplasmic male sterile (CMS) lines viz., IR 58025 A and NDMS 4A, possessing Wild Abortive (WA) type of cytoplasm, were crossed with thirty genetically diverse pollen parents in line x tester mating fashion. A total of 60 F1s were produced during Kharif 2003. The resulting set 60 F1's their 32 parents (30 male parents + 2 female parents) and a standard check variety i.e. Sarjoo-52 were evaluated in Randomized Complete Block Design with three replications. The fertilizers were applied @ 120 kg nitrogen, 60 kg phosphorus and 60 kg potash/ha through urea, di-ammonium phosphate and murate of potash recommended, for the rice crop. The full dose of phosphorus, potash and half dose of nitrogen were applied as basal and rest of nitrogen was applied in two splits as top dressing at tillering and panicle initiation stage. All the crosses were attempted during Kharif (wet season), 2003 at Crop Research Station, Masodha, Faizabad (U.P.). The F1's thus produced were evaluated alongwith their parents including standard check variety (Sarjoo-52) in Randomized Complete Block Design with three replications at Crop Research Station, Masodha, Faizabad. The seeds were sown on 21st June, 2003 in raised nursery beds. Twenty-five days old single seedling hill-1 were transplanted at a 20 cm inter and 15 cm intra-row spacing. Each test entry was raised in three rows of 3.0 m length. All the recommended cultural practices were followed to raise a good crop.

Statistical Analyses

Treatment and error mean sum of squares were taken as estimates of phenotypic (σ^2p), genotypic (σ^2g) and environmental (σ^2e) variances, respectively. The phenotypic variance being the summation of genotypic and environmental variance. Genotypic variance was calculated by subtracting the error mean sum of squares from mean sum of square due to treatments as proposed by Burton and de Vane (1953). Heritability in narrow sense (h^2n) and broad sense (h^2b) was calculated as suggested by Hanson *et al.* (1956) and Kempthorne (1957), respectively. The expected genetic advance (Gs) was estimated using formula suggested by Robinson (1965).

Results and Discussion

Estimation of Genetic Parameters

A perusal of genetic components and coefficients of variability indicated that phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for all the characters (Table 1). The differences in the magnitude of PCV and GCV were lower for 50% flowering, Plant height, days to maturity, ear bearing tillers plant^{-1} and total number of spikelets panicle^{-1}, indicating little opportunity of selection for these characters (Mamata *et al*., 2018). Similarly, Chauhan *et al.* (1989) reported considerable variation for spikelets panicle^{-1} and test weight of grains. High co-efficient of variability for various characters observed in the present study is in agreement with the findings of Chauhan *et al.* (1989), Sahu and Sahu (1990) and Rao and Srivastava (1994). Ganesan *et al.* (1995) reported moderate amount of variability (10-20%) for days to panicle emergence and plant height further confirming the present findings. High co-efficient of variation indicated that the traits under study can be improved through selection. Low values indicated the need to create variability either by hybridization or mutation followed by selection (Kumar *et al*., 2018).

Robinson *et al.* (1949) viewed that the knowledge of heritability of a character is important to the breeder since it indicated the possibility and extent to which improvement is possible through selection. It is a measure of genetic relationship between parents and progeny and has been widely used in determining the degree to which a character may be transmitted from parents to off-springs. High heritability alone is not enough to make efficient selection in the advanced generations unless accompanied by substantial amount of genetic advance. Burton (1952) pointed out that the heritability in combination with intensity of selection and amount of variability present in the population influences the gains to be obtained from selection. The genetic advance is yet another important selection parameter, which is although independent and represents the expected genetic advance under selection. It measures the differences between the mean genotypic values of the selected lines and the mean genotypic values of the original population from which these were selected.

Panse (1957) viewed that if character is governed by non-additive gene action, it may give high heritability but low genetic advances, whereas, if it is governed by additive gene action, heritability and genetic advance would be high. High estimates of heritability along with high genetic advance were provides good scope for further improvement in advance generations. In the present study, high heritability estimates in broad sense were obtained for most of the characters, indicating the major role of additive gene action in inheritance of these traits. While narrow sense, heritability estimates were high for ear bearing tillers plant^{-1} and moderate for rest of the traits except days to 50% flowering, biological yield, harvest index, plant height and days to maturity, which exhibited low heritability in narrow sense. High estimate of narrow sense heritability would mean that selection could be effectively made on phenotypic basis by mass selections. Whereas, progeny testing would be required if heritability is low and environmental influences are high. The broad sense heritability of these characters is in accordance with those of Maurya (1976) for spikelets panicle^{-1} and test weight; Bhattacharya (1978) for spikelet density and grain yield plant^{-1}; Huang (1984) for 1000-grain weight, number of spikelets panicle^{-1} and spikelet fertility per cent; Maurya *et al.* (1986) for spikelets panicle^{-1} and test weight; Mamata *et al*. (2018) for spikelets panicle^{-1}, biological yield, harvest index and Ganesan *et al.* (1995) for plant height, panicles plant^{-1} and harvest index.

High heritability coupled with high genetic advance was recorded for number of fertile spikelets panicle^{-1}, total number of spikelets, and number of sterile spikelets, biological yield and harvest index. The estimates of high heritability alongwith high genetic advance obtained are in close agreement with the findings of Rao *et al.* (1973) for number of spikelets panicle^{-1}; Sivasubramanian *et al.* (1973) for number of grains panicle^{-1} and yield; Bhattacharya (1978) for number of grains panicle^{-1} and grain yield; Wilfred and Prasad (1993) for spikelets panicle^{-1}, grain yield and harvest index and Ganesan *et al.* (1995) for grain yield plant^{-1} and harvest index. Singh (1992) recorded high heritability with low genetic advance for various characters further confirming the present observations.

Per cent contribution of males, females and females x males and estimates of components of variance and their magnitude:

The estimates of variance due to gca (σ^2g), sca (σ^2s) and average degree of dominance (σ^2s/2σ^2g)^{½} with per cent contribution of males, females and females x males for various plant characters are presented in Table 1. The average degree of dominance (σ^2s/2σ^2g)^{½} with a 1:1 ratio indicated an equal importance of additive and non-additive gene actions for expression of the characters, while deviation from this ratio indicated greater importance of σ^2g or σ^2s depending upon the magnitude of ratio. In general, the proportional contribution of female lines was lower than the males and females x males. A perusal of (Table 2) indicated that the maximum contribution of males was recorded for ear bearing tillers plant^{-1} (72.53%) followed by plant height (67.10%). The contribution of males ranged from 6.59 to 72.53 per cent. The per cent contribution of females x males was observed more than days to 50% for 50 flowering, Days to maturity and panicle length. Contribution of females x males towards different characters ranged from 5.69 ear bearing tillers plant^{-1} to 56.92 per cent days to maturity. None of the female lines contributed more than 21.77 per cent. The magnitude of σ^2s (sca variance) was found to be much higher than σ^2g (gca variance) for all the characters. The maximum variance σ^2g was recorded for total number of spikelets panicle^{-1} as well as σ^2s with the values of 30.70 and 61.39, respectively. It was further observed that sca variances were of higher (σ^2s/2 σ^2g)^{½} order and average degree of dominance (σ^2s/2σ^2g)^{½} was more than unity suggesting significant role of non-additive gene action which results from dominance, epistasis and various other interaction effects for all the characters.

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