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Assessment of heritability and genetic advance in segregating generations for grain yield and its attributing traits in rice (*Oryza sativa* L.)

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Abstract

The experiment was carried out during *kharif*-2021 at Regional Rice Research Station, N.A.U., Vyara to study the narrow sense heritability and genetic advance from segregating generations of four different crosses of rice *viz.*, Lal Kada × Tetep, Gurjari × Tetep, Lal Kada × IR-28 and Gurjari × NVSR-2756. Moderate to high heritability (narrow-sense) estimates coupled with moderate to high genetic advance was observed for most of the traits under study in all four crosses. High heritability coupled with a high genetic advance was most likely due to additive gene effects and selection for improvement of these traits would be rewarding.

Keywords: Heritability, genetic advance, rice, segregating generations

1. Introduction

Rice (*Oryza sativa* L.) is known as princess among the cereals and is the second most important cereal food crop, next to wheat in terms of annual production for human consumption in the world. Asia is considered to be the 'rice bowl' of the world, produces and consumes more than 90 per cent of world rice (Tyagi *et al.*, 2004) [17]. In Asia alone, more than two billion people obtain their calorie intake from rice and its derived products. Rice kernel is naturally cholesterol and sodium free. Rice is gaining importance in the making of infant foods, snack foods, breakfast cereals, beer, fermented products and rice bran oil, as it is the main source of calories constitutes as food. India ranks first position in area and second position in production of rice. The agricultural food production must continue to meet the demands of growing population. Therefore, rice production must be increased by 50% in order to meet the growing demand to ensure food and nutritional security of India's ever increasing population (Miah *et al.*, 2013) [9].

In crop improvement, only the genetic component of variance is important since, only this component can be transmitted to the next generation. As the estimates of heritability serves a useful guide to the breeder. It expresses the relative amount of heritable portion of variation, however, its estimate along with genetic advance which is more useful in predicting the resultant effect of selecting the best genotypes. It is necessary to have sufficient understanding of the inheritance of quantitative traits and information about heritability of grain yield, its components traits are essential to develop an efficient breeding strategy. Moreover, narrow sense heritability plays important role in the selection of the elite genotypes from the segregating populations and genetic advance is essential to know the effectiveness of selection. Considering these facts, grain yield and its contributing traits of rice are the most important, hence, estimation of heritability and genetic advance for yield and its contributing traits was undertaken.

2. Materials and Methods

The experimental material was comprised of five diverse elite lines of rice *viz.*, Lal Kada, Tetep, Gurjari, IR-28 and NVSR-2756, which were selected on the basis of variation in their morphological traits. Four different crosses *viz.*, Lal Kada × Tetep, Gurjari × Tetep, Lal Kada × IR-28 and Gurjari × NVSR-2756 obtained by crossing of five diverse parents during *kharif* 2020 at Regional Rice Research Station, Navsari Agricultural University, Vyara. F₁s were produced during *kharif*-2020. Selfing of F₁s and backcrossing were carried out during *rabi*-2020 to produce F₂s and backcrossed seeds, respectively.

The evaluation trial was conducted with all six generations of four crosses during *kharif*-2021 at Regional Rice Research Station, Navsari Agricultural University, Vyara. Six generations *viz.*, P₁, P₂, F₁, F₂, BC₁ and BC₂ of four different crosses were sown during *kharif*-2021 in compact family block design with three replications. Inter and intra row spacing was 20 cm and 15 cm respectively. All recommended agronomic practices along with necessary plant protection measures were timely adopted.

Ten plants from each of the P₁, P₂ and F₁, 40 plants from F₂ and 20 plants from each of the BC₁ and BC₂ generations were randomly selected per replication and observations were recorded for the characters *viz.*, days to flowering, days to maturity, plant height (cm), productive tillers per plant, flag leaf length (cm), panicle length (cm), grains per panicle, grain length (mm), grain breadth (mm), grain l:b ratio, 100 seed weight (g), grain yield per plant (g) and straw yield per plant (g).

High, moderate and low heritability are not rigidly defined as it varies with character to character, but the following values are widely accepted (Robinson *et al.* 1949) [14]. Low heritability (0 - 30%), Moderate heritability (30 - 60%) and High heritability (> 60%). The value of expected genetic advance for various characters is demarcated into three categories *viz.*, low, moderate and high, as follows (Johnson *et al.* 1955) [5]. Low genetic advance (0 - 10%), Moderate genetic advance (10 - 20%) and High genetic advance (> 20%).

If heritability of a trait is very high, selection for the trait should be fairly easy because there would be a close correspondence between the genotype and phenotype due to relatively smaller contribution of the environment to phenotype. Hence, in present investigation, narrow sense heritability may be more helpful in the selection of segregating populations and that is why the genetic advance was calculated on the basis of narrow sense heritability to ascertain more reliable results and improvement in the mean genotypic value of selected families over that of the base population.

3. Results and Discussion

In crop improvement, only genetic component of variation is important since that component is transmitted to the next generation. Heritability indicates the effectiveness with which the selection of genotypes could be based on phenotypic performance. This could be achieved through determining heritability and genetic gain under selection. The success of selection is governed by the degree to which the desired character is transmitted to the offspring's of the selected parents. Burton (1952) [2] stated that an understanding of the inheritance of quantitative characters could change the art of plant breeding into a science. Therefore, a reliable estimate of heritability can be a powerful tool in determining the breeding programme.

The results of narrow sense heritability and genetic advance for thirteen different traits studied in four crosses of rice are presented in the Table 1 and Table 2. High to moderate narrow sense heritability was recorded for most of the characters in all four crosses. High narrow sense heritability was recorded in all four crosses for days to flowering, days to maturity, plant height, flag leaf length, panicle length, grain length and grain breadth. It was also recorded high for productive tillers per plant in cross I; grains per panicle in cross II, III and IV; l:b ratio in cross II and IV; 100 grain weight in I and II; grain yield per plant in cross I and IV and straw yield per plant in cross I and III. These results are in correspondence with Kumar and Senapati (2013) [7], Nugraha *et al.* (2016) [10], Revathi *et al.* (2016) [13], Bharath *et al.* (2018) [1], Manohara and Shashidhar (2018) [8], Priyanka *et al.* (2019) [12], Patel and Patel (2020) [11] Harijan *et al.* (2021) [4] and Singh *et al.* (2021) [15]. Moderate narrow sense heritability was observed for productive tillers per plant in cross II and IV; grains per panicle in cross I and grain yield per plant in cross II. While, low estimate of narrow sense heritability was recorded for grain yield per plant in cross III.

Table 1: Estimates of heritability and genetic advance for days to flowering, days to maturity, plant height, productive tillers per plant, flag leaf length, panicle length and grains per panicle in four crosses of rice

| Estimates | Days to flowering | Days to maturity | Plant height (cm) | Productive tillers per plant | Flag leaf length (cm) | Panicle length (cm) | Grains per panicle |
|---------------------------------------|-------------------|------------------|-------------------|------------------------------|-----------------------|---------------------|--------------------|
| Cross I (Lal Kada × Tetep) | | | | | | | |
| Heritability (ns)% | 125.74 | 112.68 | 99.27 | 62.12 | 96.13 | 70.62 | 57.15 |
| Genetic Advance% | 21.30 | 14.45 | 14.22 | 44.02 | 33.88 | 19.35 | 13.30 |
| Cross II (Gurjari × Tetep) | | | | | | | |
| Heritability (ns)% | 134.61 | 136.77 | 82.04 | 49.23 | 129.83 | 68.08 | 144.52 |
| Genetic Advance% | 23.93 | 19.51 | 20.08 | 33.06 | 63.02 | 18.62 | 34.83 |
| Cross III (Lal Kada × IR-28) | | | | | | | |
| Heritability (ns)% | 111.59 | 113.32 | 139.47 | - | 90.72 | 76.26 | 64.24 |
| Genetic Advance% | 20.02 | 15.82 | 45.35 | - | 38.07 | 26.26 | 18.22 |
| Cross IV (Gurjari × NVSR-2756) | | | | | | | |
| Heritability (ns)% | 117.51 | 116.73 | 79.31 | 48.17 | 117.70 | 146.22 | 145.94 |
| Genetic Advance% | 19.21 | 14.10 | 16.79 | 26.12 | 55.09 | 50.95 | 33.70 |

" - " represent negative value

Table 2: Estimates of heritability and genetic advance for grain length, grain breadth, L:B ratio, 100 grain weight, grain yield per plant and straw yield per plant in four crosses of rice

| Estimates | Grain length (mm) | Grain breadth (mm) | L:B ratio | 100 Grain weight (g) | Grain yield per plant (g) | Straw yield per plant (g) |
|---------------------------------------|-------------------|--------------------|-----------|----------------------|---------------------------|---------------------------|
| Cross I (Lal Kada × Tetep) | | | | | | |
| Heritability (ns)% | 120.69 | 142.86 | - | 120.83 | 124.57 | 125.80 |
| Genetic Advance% | 3.00 | 8.55 | - | 14.43 | 164.83 | 96.57 |
| Cross II (Gurjari × Tetep) | | | | | | |
| Heritability (ns)% | 157.09 | 129.03 | 147.06 | 129.94 | 56.09 | - |
| Genetic Advance% | 8.47 | 7.22 | 11.62 | 12.99 | 56.67 | - |
| Cross III (Lal Kada × IR-28) | | | | | | |
| Heritability (ns)% | 121.62 | 134.97 | - | - | 16.39 | 156.42 |
| Genetic Advance% | 5.27 | 12.35 | - | - | 14.39 | 140.65 |
| Cross IV (Gurjari × NVSR-2756) | | | | | | |
| Heritability (ns)% | 162.46 | 143.94 | 154.81 | - | 105.21 | - |
| Genetic Advance% | 6.87 | 12.19 | 15.01 | - | 98.87 | - |

" - " represent negative value

The higher estimates of narrow sense heritability indicates that these traits were comparatively less affected by environment and their phenotypes are good reflection of genotypes and thus possessed paramount importance in making selection of superior genotype on the basis of phenotypic performance of these matric traits but in case of lower heritability, pedigree, sib or progeny test can be employed for genetic improvement. The moderate estimates of heritability indicated the preponderance of non-additive variance for yield and yield attributes in the material under study.

In present investigation, the estimates of genetic advance were recorded high for days to flowering in cross I, II and III; plant height in cross II and III; productive tillers per plant in cross I, II and IV; flag leaf length in all four crosses; panicle length in cross III and IV; grains per panicle in cross II and IV; grain yield per plant in cross I, II and IV and straw yield per plant in cross I and III. Moderate genetic advance was recorded for days to flowering in cross IV; days to maturity in all crosses; plant height in cross I and IV; panicle length in cross I and II; grains per panicle in cross I and III; grain breadth in cross III and IV; l:b ratio in cross II and IV; 100 grain weight in cross I and II and grain yield per plant in cross III. However, Low estimates of genetic advance were recorded for grain length in all four crosses and grain breadth in cross I and II. Similar results were also reported by Khaled Salem *et al.* (2015) [6], Revathi *et al.* (2016) [13], Bharath *et al.* (2018) [1], Priyanka *et al.* (2019) [12], Gupta *et al.* (2020) [3], Patel and Patel (2020) [11], Harijan *et al.* (2021) [4], Singh and Patel (2020) [16] and Singh *et al.* (2021) [15].

The present investigation revealed that the high heritability coupled with high genetic advance was observed for days to flowering, productive tillers per plant, flag leaf length, grain yield per plant and straw yield per plant in cross I (Lal Kada × Tetep); days to flowering, flag leaf length and grains per panicle in cross II (Gurjari × Tetep); days to flowering, plant height, flag leaf length, panicle length and straw yield per plant in cross III (Lal Kada × IR-28); flag leaf length, panicle length, grains per panicle and grain yield per plant in cross IV (Gurjari × NVSR-2756), which indicated the governance of additive gene action and selection for improvement of these traits would be rewarding. The high heritability coupled with moderate to low genetic advance was recorded for days to maturity, plant height, panicle length, grain length, grain breadth and 100 grain weight in cross I; days to maturity, panicle length, grain length, grain breadth, L:B ratio and 100

grain weight in cross II; days to maturity, grains per panicle, grain length and grain breadth in cross III; days to flowering, days to maturity, plant height, grain length, grain breadth and L:B ratio in cross IV, which indicated the role of non-additive gene action along with environmental influence. Hence, heterosis breeding would be beneficial for improvement of these traits. Low to moderate heritability coupled with high genetic advance for traits *viz.*, productive tillers per plant and grain yield per plant in cross II; productive tillers per plant in cross IV, which reveals the effect of additive gene action along with environmental influence. Hence, selection strategies would be useful for improvement of such traits.

4. Conclusion

The higher estimates of heritability indicating that these traits were comparatively less affected by environment and their phenotype is a good reflection of genotype and thus possessed paramount importance in making a selection of superior genotype based on the phenotypic performance of these matric traits, but in case of lower heritability, pedigree or progeny test can be employed to improve it. Moderate to high heritability (narrow-sense) estimates coupled with moderate to high genetic advance was observed for most of the characters in all four crosses under study. High heritability coupled with a high genetic advance was most likely due to additive gene effects. Therefore, characters having high heritability coupled with high genetic advance can be further improved by adopting selections in succeeding generations.

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