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Genetic variability, heritability and genetic gain for yield and its contributing component in rice (*Oryza sativa* L.) at two environments

Anjali Singh and OP Verma

Abstract

Genetic variation, heritability and genetic advance were studied in rice during *Kharif* 2019-20 at Main Experiment Station (E1) with pH-9.5 and Agronomy Farm (E2) with pH-8.3 in randomized complete block design at Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya (U.P.). The present study was conducted with the objective of assessing the presence of genetic variability in seventy three diverse genotypes with three different checks (Sarjoo-52, Pusa-44 and NDU-3) at two different locations. A collection of genotypes were evaluated for quantitative characters *viz.*, days to 50% flowering, productive tiller per plants, panicle length (cm), fertile spikelet per panicle, spikelet fertility (%), biological yield per plants (g), harvest index (%), L/B ratio, 1000-grain weight (g) and grain yield per plant (g). Analysis of variance revealed highly significant differences among all the genotypes for all traits. Genotypic efficient of variation (GCV) and phenotypic coefficient of variation (PCV) indicated the presence of considerable amount variability in all the traits. Phenotypic coefficient of variability was higher than genotypic coefficient of variability at both the locations *i.e.*, Main Experiment Station (E1) and Agronomy Farm (E2). A perusal of coefficient of variability indicated that PCV and GCV were quiet high for biological yield per plant, productive tillers per plant and grain yield per plant and moderate for fertile spikelet per panicle, harvest index and L/B ratio while lowest for days to 50% flowering, panicle length and spikelet fertility at two different sodicity levels. A high estimate of heritability was found for all parameters at Main Experiment Station and Agronomy Farm. The presence of high heritability and high genetic advance in most of the traits indicated the presence of additive gene action. So, these traits can be improved through direct selection. The high broad sense heritability with moderate genetic advance in percent of mean were observed for days to 50% flowering, panicle length, spikelet fertility and 1000-grain weight indicating the presence of non-additive gene action suggesting heterosis breeding may be useful for the improvement of these traits. The overall results indicated the presence of enough variability for development of improved rice varieties and the studied traits can be used for selection.

Keywords: genetic advance, heritability, variability

Introduction

Rice (*Oryza sativa* L.) is a self-pollinated, short day monocotyledonous angiosperm has a place with the genus *Oryza* of family Poaceae (Graminae). Rice is mainly grown in hot humid tropical climate and its distribution varies from humid tropical to subtropical climate. It require mean temperature of 21 to 37 °C throughout the life cycle of crop and rainfall more than 100 cm. It is the only crop which withstand standing water for long period. Two important cultivated species of genus *Oryza viz.*, Asian rice (*Oryza sativa*) and African rice (*Oryza glaberrima*) and 22 wild species denoting 10 genomic types *viz.*, AA, BB, CC, BBCC, CCDD, EE, FF, GG, HHJJ and HHKK have been reported (Brar and Khus, 1986). Thus, the development of improved high yielding pure line and hybrid rice varieties suitable for adverse condition (salt affected soil), would be an important strategy to meet this challenge in context of production and productivity in sodic soil. We have tested certain traditional land races too at different sodicity levels to assess their potential / performance. Similarly, Verma and Shrivastava (2004) [26] have exploited certain traditionally adopted varieties for the creation of noble variability and their interactions may proof usefull for identifying superior hybrid combination possessing at least one major group of gene for enhancing grains yield in target environment. Utter Pradesh inland salinity areas are mainly concentrated in Raibareilly, Azamgarh, Sultanpur, Ayodhya, Lucknow, Unnao and Pratapgarh districts. India is world's second –largest producer of rice, and the largest exporter of rice in the world production

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increased from 53.6 million tonnes in FY 1980 to 120 million tonnes in FY 2020-21 and Uttar Pradesh production about 15.52 metric tonnes in FY 2020. The targeted rice production of the world, China and India for the year 2030 to feed the ever growing population, is conceptualized as 771.02, 168.90 and 130.02 million tonnes, respectively. To get achievement in accomplishing the objective, the expansion in rice profitability is the main choice left, since alternate choices like cultivable land, water and other regular assets are either stale or declining (Singh *et al.*, 2015). Biofortification is a genetic approach which aims at biological and genetic enrichment of food stuffs with vital nutrients like vitamins, minerals and proteins. In case of polished rice, zinc content ranged from 4.8 to 40.9 mg/kg in 170 rice germplasm of the present study. The reported ranges of grain zinc content in polished rice were 16.0 to 26.5 mg/kg in eight highly cultivated varieties (23), and up to 33 mg/kg zinc content in polished rice of 246 germplasm (Rao SD 2020) [3]. Protein content of milled rice is 6-7 per cent. The success of any breeding programme depends on the nature and amount of genetic variability available in the breeding material. Selection and hybridization approaches are easily followed in bringing about the quantitative improvement in economically important attributes like yield.

In recent years, a rapid advancement has been made towards the development of molecular marker technology and their applications in plant breeding programs Gopikannan M, Ganesh SK *et al.* (2014) [5]. SSR or microsatellite markers are proved to be ideal for making genetic maps Habib N, *et al.* (2013) [9], assisting selection Huyen *et al.* (2012) [10] and studying genetic diversity in different genotypes. Variability refers to the presence of differences among the individuals of plant population due to their genetic composition and the environment in which they are raised Falconer DS (1996) [4], Sumanth V, (2017) [20], Selection will be effective when there is a significant amount of variability among the breeding materials. The available variability can be measured using genotypic and phenotypic coefficient of variation which is used to partition genetic and environmental variance Onyia VN, *et al.* (2017) [15]. Therefore, the present study was conducted with the objective of assessing the genetic variability, heritability and genetic advance of yield and yield components of seventy three rice genotypes.

Materials and Methods

Two sets of the experiments were conducted during *Kharif* 2019-20 at the Main Experiment Station (pH -9.5) with EC range (3.1-3.3), organic carbon 0.21% and Agronomy Farm (pH- 8.3) with EC range of (0.30-0.32), organic carbon 0.30% at Kumarganj, Ayodhya. All the diverse seventy three genotypes including three checks (Sarjoo-52, Pusa-44 and NDU-3), were sown in Randomized Complete Block Design with three replications following 5 m row length (inter-and intra-row spacing 20 cm and 15 cm, respectively). The experimental materials of the study was comprised of seventy three diverse genotypes, collected from different agro-climatic zones. These genotypes were procured from germplasm lines available in rice section of the Department of Genetics and Plant Breeding, Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya. The observations *viz.*, days to 50% flowering, productive tiller per plant, panicle length, fertile spikelet per panicle, spikelet fertility, biological yield per plant (g), harvest-index (%), L/B ratio, 1000-grain weight and grain

yield per plant (g) were recorded on the basis of five randomly selected competitive plants in each plot. The fertilizers were applied @120 kg nitrogen, 60 kg phosphorus and 60 kg potash per ha through urea, DAP and murate of potash, respectively. Biometrical analyses were done with genetic variability parameters *viz.*, mean, variance, phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) (Burton and De Vane, 1953) [1], heritability (h^2) (Hanson *et al.*, 1956) [7] and genetic advance (GA) (Johnson *et al.*, 1955) [11] among characters were calculated by following the standard procedures with the help of MSTATC, Statistica 2 and Genres software's.

Results and Discussion

The analysis of variance for complete randomized block design for different characters in each environment given in Table 1(a), 2(a) highly significant differences were observed among the genotypes for all the ten characters. In two different locations mean sum of squares due to treatments, were highly significant for all the characters indicating the existence of sufficient variability in the materials at both sodicity levels. These findings are in conformity with those of Konate *et al.* (2016) [12] and Ravindra reddy *et al.* (2019) [19]. At Main Experiment Station (E1) the highest genotypic and phenotypic variance was recorded for fertile spikelet per panicle (429.49 and 458.41); while at Agronomy Farm this estimate ranged from 407.03 to 425.69, respectively for the same traits. According to Siva Subramanian and Menon (1973) [21], GCV and PCV more than 20% is considered as high whereas values less than 10% low and values between 10% and 20% being moderate. In this context, majority of the traits have high to intermediate GCV and PCV [Table 1(b) and 2(b)]. This indicated that these traits could be improved for breeding high yielding rice varieties through selection and hybridization. The genetic variation result showed that phenotypic coefficient of variation (PCV) was relatively higher than genotypic efficient of variation (GCV). According to Johnson, Robinson and Comstock (1955) [11], broad sense heritability is classified as low (<30%), medium (30% to 60%) and high (>60%). This shows most of the traits studied can be easily improved through selection. At Main Experiment Station (E1) and Agronomy Farm (E2) all the traits showed high heritability value (>60%) which reflects the more influence of environment. The broad sense heritability in the studied traits ranged from 61.95% to 97.68%. Since heritability do not always indicate genetic gain, heritability coupled with genetic advance is more effective for selection. Genetic advance indicates the expected progress as the result of selection Pratap *et al.* (2014) [16]. It is used to estimate the type of gene action in polygenetic traits. Genetic advance as percent of mean classified as low (<10%), moderate (10%-20%) and high (>20%). At Main Experiment Station (E1) it ranged from 12.23% for 1000-grain weight to 56.67% for biological yield per plant and at Agronomy Farm (E2) it ranged from 13.49% for panicle length to 63.95% for biological yield per plant. At both locations high heritability coupled with high genetic advance were recorded in majority of the traits indicating the preponderance of additive gene action which may directly be utilized for rice improvement. These results are in accordance with those of Khaire *et al.* (2017) [13], Kunkerkar *et al.* (2017) [14], Priyanka *et al.* (2017) [17] and SP Jadhav *et al.* (2019) (Table 1b,2b). High heritability values indicate though the character is least influenced by environmental factors yet the selection for

improvement of such characters may not be useful (Singh *et al.* 2018) [22] and Yadav *et al.* (2019) [27]. At Main Experiment Station and Agronomy Farm (at both the sodicity levels) days to 50% flowering, panicle length, spikelet fertility and 1000-grain weight have high heritability and moderate

genetic advance, indicating that these characters are governed by both additive and non-additive gene actions. This showed there is a possibility of direct selection for these characters including reduced duration. Therefore, heterosis breeding could also be used for such kind of traits.

Table 1(a): Analysis of variance (ANOVA) for ten characters in seventy three rice genotypes at Main Experiment Station Farm (2019-20)

Source of variation	DF	Days to 50% flowering	Productive tiller /plant	Panicle length (cm)	Fertile spikelet /panicle	Spikelet fertility (%)	Biological yield /plant (g)	Harvest index (%)	L/B ratio	1000-grain weight (g)	Grains yield per plant (g)
Repl.	2	106.03	0.05	2.05	1.69	13.84	9.44	0.90	0.05	0.69	0.31
Treatment	72	220.42**	9.68**	10.33**	1317.40**	126.02**	323.53**	69.22**	0.77**	9.39**	36.46**
Error	144	16.02	0.08	0.87	28.92	17.70	4.32	4.40	0.03	1.72	0.74

*, ** Significant at 5% and 1% probability levels, respectively

Table 1(b): Genetic variability- Main Experiment Station (2019-20)

Genotypes	Mean	Min	Max	var (g)	var (p)	Heritability bs (%)	GA	GA% mean	GCV (%)	PCV (%)
Days to 50% flowering	97.38	76.21	115.72	68.13	84.15	80.97	15.30	15.71	8.48	9.42
Productive tiller /plant	7.56	4.54	13.34	3.20	3.28	97.46	3.64	48.07	23.64	23.94
Panicle length (cm)	22.14	18.20	26.02	3.15	4.03	78.28	3.24	14.61	8.02	9.06
Fertile spikelet /panicle	115.63	60.25	154.30	429.49	458.41	93.69	41.32	35.74	17.92	18.52
Spikelet fertility (%)	79.67	44.55	89.42	36.10	53.81	67.10	10.14	12.73	7.54	9.21
Biological yield /plant(g)	36.76	19.62	66.29	106.40	110.73	96.10	20.83	56.67	28.06	28.63
Harvest index (%)	36.60	24.36	43.14	21.61	26.01	83.08	8.73	23.85	12.70	13.93
L/B ratio	2.69	1.61	3.94	0.25	0.27	90.18	0.97	36.22	18.52	19.50
1000-grain weight (g)	20.83	16.21	24.75	2.56	4.28	59.81	2.55	12.23	7.68	9.93
Grains yield per plant (g)	13.36	6.32	22.31	11.90	12.65	94.12	6.90	51.60	25.82	26.61

Table 2(a): Analysis of variance (ANOVA) for ten characters in seventy three rice genotypes at Agronomy Farm Mean sum squares genotypes (E2)-2019-20

Source of variation	DF	Days to 50% flowering	Productive tiller /plant	Panicle length (cm)	Fertile spikelet /panicle	Spikelet fertility (%)	Biological yield /plant (g)	Harvest index (%)	L/B ratio	1000-grain weight (g)	Grains yield per plant (g)
Repl.	2	18.57	0.15	0.48	30.88	27.39	1.42	9.88	0.01	4.67	0.78
Treatment	72	223.11**	6.71**	7.86**	1239.75**	125.28**	369.70**	67.56**	0.64**	8.73**	36.64**
Error	144	13.92	0.06	0.71	18.65	9.21	2.03	1.97	0.01	0.73	0.25

*, ** Significant at 5% and 1% probability levels, respectively

Table 2(b): Genetic variability- Agronomy Farm (E2)-2019-20

Genotypes	Mean	Min	Max	var (g)	var (p)	Heritability (bs) (%)	GA	GA% mean	GCV (%)	PCV (%)
Days to 50% flowering	95.28	74.01	113.54	69.73	83.65	83.36	15.71	16.48	8.76	9.60
Productive tiller /plant	6.02	3.21	9.45	2.22	2.28	97.47	3.03	50.36	24.76	25.08
Panicle length (cm)	20.69	17.21	25.37	2.38	3.09	77.03	2.79	13.49	7.46	8.50
Fertile spikelet /panicle	107.13	57.22	151.34	407.03	425.69	95.62	40.64	37.94	18.83	19.26
Spikelet fertility (%)	76.03	41.22	88.38	38.69	47.90	80.78	11.52	15.1	8.18	9.10
Biological yield /plant(g)	35.37	17.68	64.42	122.56	124.58	98.37	22.62	63.95	31.30	31.56
Harvest index (%)	34.40	23.01	42.05	21.86	23.83	91.74	9.23	26.82	13.59	14.19
L/B ratio	2.61	1.59	3.67	0.21	0.22	95.25	0.92	35.23	17.52	17.95
1000-grain weight (g)	20.52	17.06	23.40	2.67	3.40	78.56	2.98	14.53	7.96	8.98
Grains yield per plant (g)	11.98	6.23	20.48	12.13	12.38	98.00	7.10	59.27	29.06	29.36

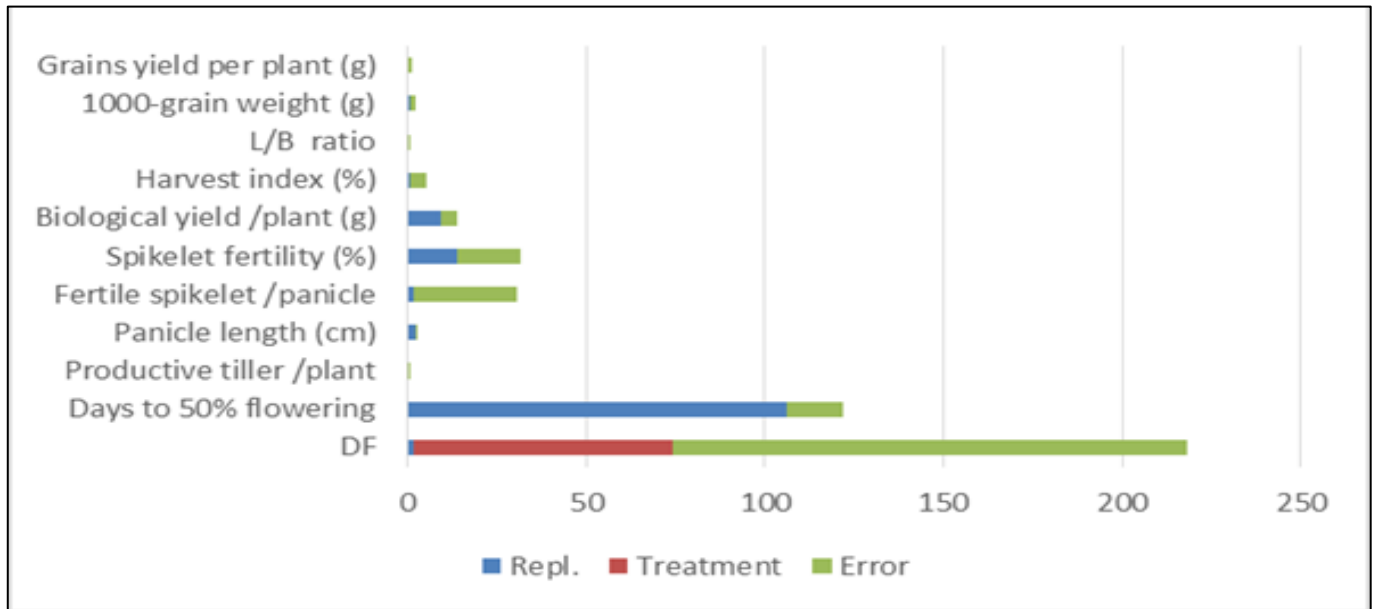


Fig 1(a): Graph represent Analysis of variance (ANOVA) for ten characters in seventy three rice genotypes at Main Experiment Station Farm (2019-20)

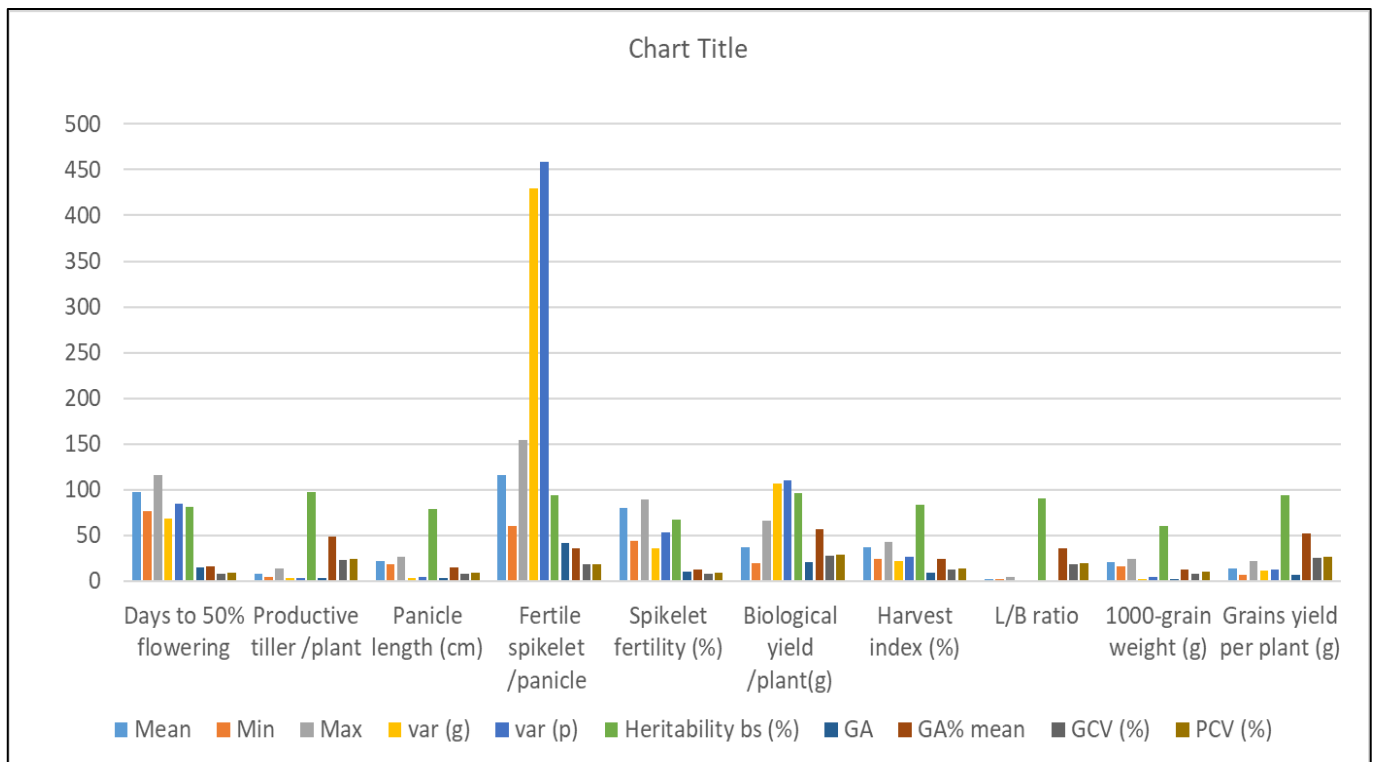


Fig 1(b): Graph represent genetic variability- Main Experiment Station (2019-20)

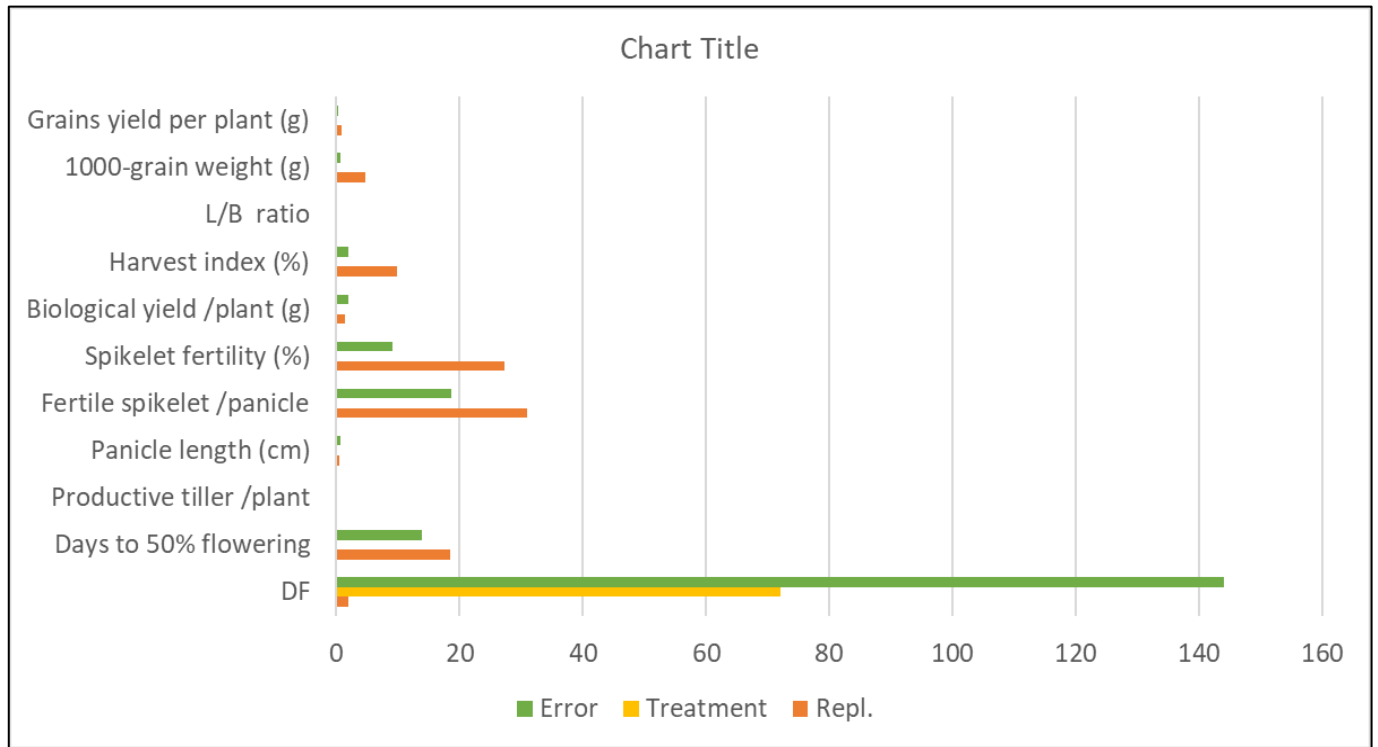


Fig 2(a): graph represent Analysis of variance (ANOVA) for ten characters in seventy three rice genotypes at Agronomy Farm Mean sum squares genotypes (E2)-2019-20

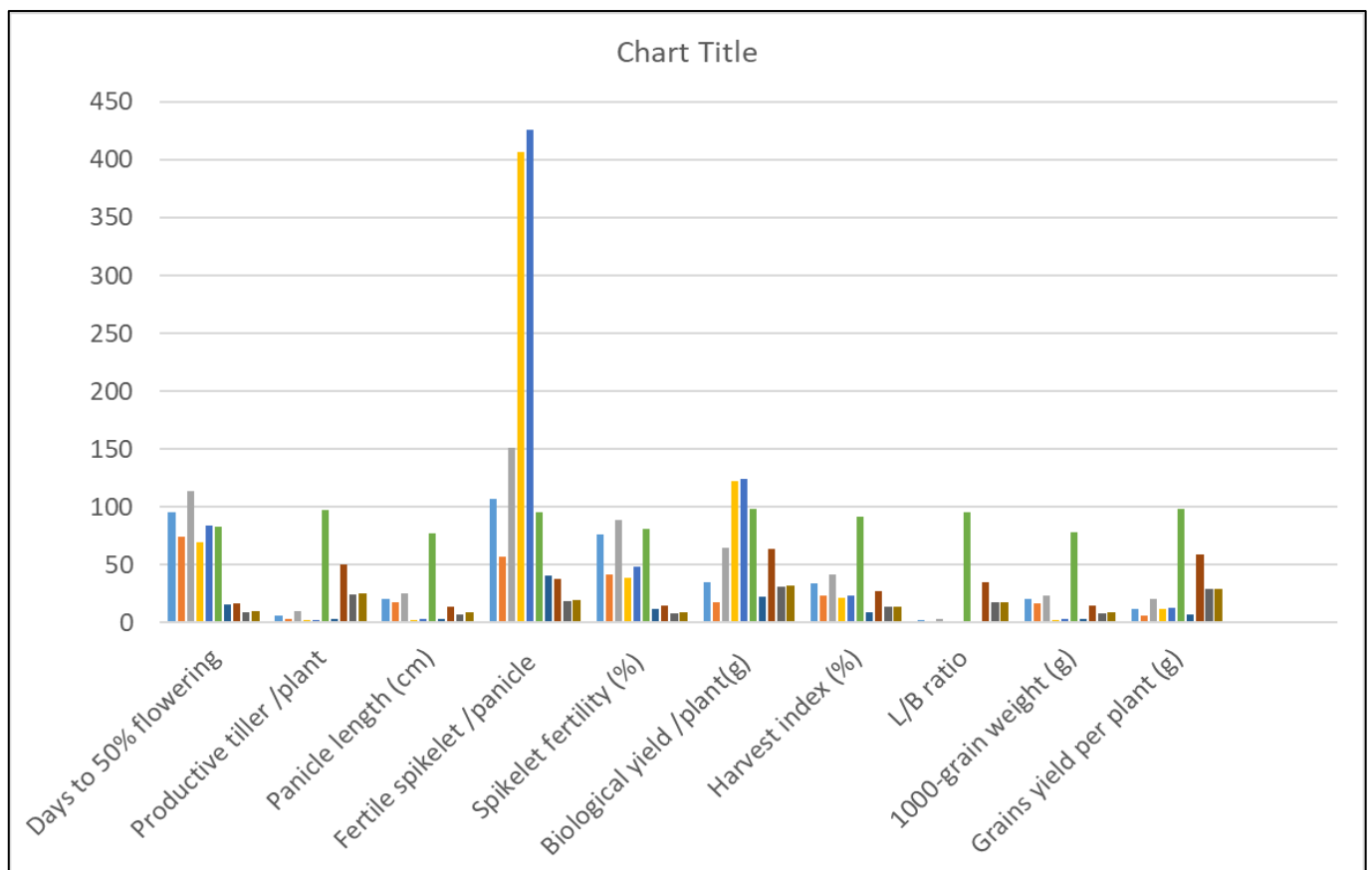


Fig 2(b): Genetic variability- Agronomy Farm (E2)-2019-20

Conclusion

Analysis of variance revealed highly significant differences among all the seventy three diverse genotypes for all the traits. Considering the evaluation of important variability parameters i.e. coefficient of variation, heritability and genetic advance together, it was found that productive tillers per

plant, fertile spikelet per panicle, biological yield per plant, harvest index and L/B ratio are most important characters at both the sodicity levels because they have high heritability coupled with high genetic advance indicating predominance of additive gene action in controlling the gene responsible for these traits. Therefore, these characters could be improved

through direct selection in segregating generations. The overall result showed the presence of adequate variability in the genotypes studied. This variation could be effectively manipulated using appropriate breeding techniques and program to develop improved varieties for target environment.

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References

- Burton GM, de Vane EH. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. *Agronomy Journal* 1953;45:471-81.
- Brar DS, Khush GS. Utilization of wild species of genus *Oryza* in rice improvement, In: Nanda, JS, Sharma SD (Eds.). Monograph on Genus *Oryza*. 2003, 283-309.
- Sanjeeva Rao D, Neeraja CN, Madhu Babu P, Nirmala B, Suman K, Subba Rao LV *et al.* Zinc Biofortified Rice Varieties: Challenges, Possibilities, and Progress in India Frontier. *Nutr* 2020
- Falconer DS. Introduction to quantitative genetics. New York: Longman 1996
- Gopikannan M, Ganesh SK. Genetic dissection for yield and yield components related to sodicity tolerance in rice (*Oryza sativa* L.) TNAU, Coimbatore, Tamil Nadu, India 2014.
- Girma BT, Kitil MA, Banje DG, Biru HM, Serbessa TB. Genetic Variability Study of Yield and Yield Related Traits in Rice (*Oryza sativa* L.) Genotypes. *Advance Crop Science Technology* 2018;6:381. doi:10.4172/2329-8863.1000381
- Hanson CH, Robinson HF, Comstock RE. Biometrical studies of yield in segregating population of Korean Lespedeza. *Agronomy Journal* 1956;45:268-272.
- Hossain H, Rahman MA, Alam MS, Singh RK. Mapping of Quantitative Trait Loci Associated with Reproductive-Stage Salt Tolerance in Rice. *Journal of Agronomy and Crop Science* 2015;201:17-31.
- Habib N, Ashraf M, Shahbaz M. Effect of exogenously applied nitric oxide on some key physiological attributes of rice (*Oryza sativa* L.) plants under salt stress. *Pakistan Journal of Botany* 2013;45:1563-1569.
- Huyen LTN, Cuc LM, Ismail AM, Ham LH. Introgression the salinity tolerance QTLs Saltol into AS996, the Eliterice variety of Vietnam. *American Journal of Plant Sciences* 2012;3:981-987.
- Johnson HW, Robinson HF, Comstock R. Estimates of Genetic and Environmental Variability in Soybeans 1. *Agronomy Journal* 1955;47:314-318.
- Konate KA, Zongo A, Kam H, Sanni A, Audebert A. Genetic variability and correlation analysis of rice (*Oryza sativa* L.) inbred lines based on agro- morphological traits. *African Journal of Agriculture Research* 2016;11(35):3340-46.
- Khaire AR, Kunkerkar RL, Thorat BS, Gavai MP, Bhawe SG. Studies on genetic variability for yield and yield contributing traits in local rice (*Oryza sativa* L.). *Journal of Pharmacognosy and Phytochemistry* 2017;6(5):1376-1378
- Kunkerkar RL, Ingale SN, Thorat BS, Devmore JP. Studies on genetic variability for quantitative and qualitative traits in North-East Indian Rice (*Oryza sativa* L.); *Journal of Rice Research* 2017;10(2):18-22.
- Onyia VN, Okechukwu EC, Atugwu AI, Akpan NM. Genetic Variability Studies on Twelve Genotypes of Rice (*Oryza sativa* L.) for Growth and Yield Performance in South Eastern Nigeria. *Notulae Scientia Biologicae* 2017.
- Pratap N, Singh PK, Shekhar R, Soni SK, Mall AK. Genetic variability, character association and diversity analyses for economic traits in rice (*Oryza sativa* L.). *SAARC Journal of Agriculture* 2014;10:83-94.
- Priyanka Rajpoot PK, Singh OP, Verma, Neeta Tripathi. Studies on genetic variability and heritability for quantitative characters in rice (*Oryza sativa* L.) under sodic soil. *Journal of Pharmacognosy and Phytochemistry* 2017;6(4):1162-1165.
- Reza M, Mendioro MS, Diaz GQ, Gregorio GB, Singh RK. Mapping Quantitative trait loci associated with yield and yield components under reproductive stage salinity stress in rice (*Oryza sativa*). *Journal of Genetics* 2013; 92:433-443. pmid:24371165.
- Ravindra Reddy G, Manikanta KL, Suresh Babu. Studies on Genetic Variability, Heritability and Genetic advance for Yield and Quality Components in Rice (*Oryza sativa* L.) Germplasm. *International Journal Current Microbiology Applied Science* 2019;8(10):580-584.
- Sumanth V, Suresh BG, Ram BJ, Srujana G. Estimation of genetic variability, heritability and genetic advance for grain yield components in rice (*Oryza sativa* L.). *Journal of Pharmacognosy and Phytochemistry* 2017;6:1437-1439.
- Sivasubramanian S, Menon M. Heterosis and inbreeding depression in rice. *Madras Agriculture Journal* 1973;60:1139.
- Singh KS, Singh M, Vennela RP, Singh KD, Kujur SN, Kumar D. Studies on genetic variability, heritability and genetic advance for yield and yield components in drought tolerant rice (*Oryza sativa* L.) landraces. *International Journal Current Microbiological Applied Sciences* 2018;7(3):299-305.
- Jadhav SP, Kunkerkar RL, Thorat BS, Gawai MP, Keluskar MH. Variability and genetic parameters studies in rice (*Oryza sativa* L.) *Journal of Pharmacognosy and Phytochemistry* 2020;9(1):1375-1377.
- Sala M, Shanthi P, Selvi B, Ravi V. Marker based Genetic Diversity of Rice Genotypes for Salinity Tolerance at Panicle Initiation Stage. *Vegetos* 2016;29:1.
- Thomson MJ, De Ocampo M, Egdane J, Rahman MA, Sajise AG, Adorada DL *et al.* Characterizing the Saltol quantitative trait locus for salinity tolerance in rice. *Rice* 2010;3:148-160.
- Verma OP, Srivastava HK. Genetic component and combining ability analyses in relation to heterosis for yield and associated traits using three diverse rice growing ecosystems *Field Crop Research* 2004;88:91-102.
- Yadav VP, Singh PK, Verma OP. Genetic variation and heritability for quantitative traits in rice (*Oryza sativa*) under sodic soil *Indian Journal of Agricultural Sciences* 2019;90(2):316-9, February 2020/Article