

Original Research Article

Genetic Variability studies in F₂ Population of the Wheat Cross DDK-1029 x GPM DIC 66

ABSTRACT:

The selection of breeding material heavily relies on genetic variation and its inherited components. A thorough understanding of genetic variation is necessary in order to develop an improved variety. Thus, genetic parameters were assessed in the F₂ population of the cross between DDK-1029 and GPM DIC 66. The genetic variability results indicated a moderate to high phenotypic and genotypic coefficient of variation for characters like days to 50% flowering, plant height, productive tillers per plant, spike length, spikelets per spike, grains per spike, thousand grain weight and grain yield. In contrast, the protein, iron and zinc contents exhibited low to moderate phenotypic and genotypic coefficient of variation. All the traits had higher heritability except for grain yield which exhibited a moderate heritability. All the characters exhibited significant GAM except for days to maturity, iron content and protein content which exhibited moderate GAM. This suggests that high genetic variation, heritability, and GAM for such traits will aid in their improvement through both direct and indirect selection.

Keywords: GCV, PCV, GAM, Heritability, Selection.

INTRODUCTION:

Wheat (*Triticum aestivum* L.), ($2n=2x=42$) is one of the world's most important food crops, supplying about 20 per cent of the world's dietary energy and total protein consumed [1]. In India, wheat is grown in an area of 31 million hectares and the production of 105.4 million tonnes with an average productivity of 3295 kg ha⁻¹ Anonymous [2]. Uttar Pradesh, Madhya Pradesh, Punjab, Haryana and Rajasthan are the major wheat growing states in India. The area under Karnataka is about 1.68 lakh hectare with annual production of 1.72 lakh tonnes with productivity of 1023 kg ha⁻¹ Anonymous [3].

Wheat contains 1,370 kilojoules (327 kilocalories) of food energy in 100 grams and is a rich source of several essential nutrients, such as protein, dietary fiber, manganese, phosphorus and niacin (20 per cent or more of Daily Value, DV). There are many essential B vitamins and other dietary minerals. Wheat accounts for 13% water, 71% carbohydrates and 1.5% fat. Its 13 per cent protein content (75-80% of the protein in wheat) is mainly gluten Shewry [4]. Micronutrient deficiency contributes to micronutrient malnutrition, which is a global issue, affecting more than 52 per cent of the world's population Hwalla [5]. Over two billion individuals are reportedly suffering from "hidden hunger" (deficiency of micronutrients). In particular, iron (Fe) and zinc (Zn) deficiencies are causing severe health problems in developing regions for pregnant women and children under 5 years of age. Around 24.8 per cent of the global population and more than 65 per cent of pre-school children in Africa and South-East Asia are affected by anaemia, the largest cause of which is Fe deficiency WHO [6]. Therefore, it is necessary to develop wheat varieties with improved yield, quality and resistance to pests and diseases in order to meet the world's growing demand for the grain. Considering the potential of this crop, there is scope for improvement and development of cultivars adapted for particular agro-ecological conditions. For the crop improvement program thorough understanding of the genetic variability is required for different traits. Limited variability makes it difficult to achieve much, thus the breeder must either enrich the germplasm or to shift for polyploidy breeding, hybridization and mutation to create more variability. Genetic improvement of any crop requires appropriate breeding techniques for the creation and utilization of variability. More variability is typically produced in the early generations than in the later segregating generations. A sound breeding program can be planned with the help of assessments of genetic variation and the degree of desirable characters transmission. To determine if selection will result in a superiority of genetic advance, we have to evaluate the variability among the different traits when partitioning the total variation into heritable and non-heritable components.

Any crop enhancement program success is mostly determined by the extent to which genetic variation exists in the base population. Identifying and selecting the best segregants from the diverse population in the initial segregating generation is crucial for self-pollinated crops like wheat. The current study aims to evaluate the genetic variability for yield and its associated characters in the F_2 population of the cross DDK-1029 × GPM DIC 66 .

MATERIALS AND METHODS

The present investigation was carried out from November to February 2020 at the College of Agriculture, Dharwad, Karnataka. The two parents DDK-1029, a high-yielding variety with a moderate Fe and Zn content released by UAS, Dharwad and GPM DIC 66 (rich in grain Zn content) were involved in the development of the F_2 population. The F_2 population, which was produced by selfing of F_1 was planted in an unreplicated trial along with P_1 , P_2 and F_1 and evaluated for yield and yield attributing traits. Twelve quantitative characters were recorded for each plant in the F_2 population. The following characters were examined: plant height (cm), productive tillers per plant, spike length (cm), spikelets per spike, grains per spike, thousand grain weight (g), grain yield per plant (g), days to 50% flowering (days), days to maturity (days), iron content (ppm), zinc content (ppm), and protein content (%).

Statistical Analysis:

The approach suggested by Burton [8] was used to compute statistical parameters such as mean, V_p , V_g , V_e and the phenotypic and genotypic coefficients of variation (PCV and GCV). The formula proposed by Lush [9] was utilized to calculate broad sense heritability. The Johnson's suggested method [10] was used to calculate the genetic advance as a percentage of mean (GAM). Microsoft Excel was used to calculate all of the above characters.

RESULTS AND DISCUSSIONS

Superior variety development will be largely depends on the availability of genetic variability. It is therefore essential to understand the degree of variability that exists. In the F_2 population of the cross DDK-1029 × GPM DIC 66 the results of mean, range, phenotypic variance, genotypic variance, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (h^2), and genetic advance as a percent of mean (GAM%) are shown in Table 1. Based on results, there is relatively less difference between the genotypic and phenotypic coefficient of variance. Traits such as productive tillers per plant (54.41, 47.74) and grain yield per plant (57.63, 41.77) had higher PCV and GCV, suggesting larger levels of variability for these traits. Moderate PCV and GCV were shown by the traits like days to 50 per cent flowering (12.30, 11.33), Plantheight (18.45, 17.87), spike length (16.97, 15.36), spikelets per spike (18.40, 17.16), iron content (14.25, 11.74), zinc content (14.79, 13.63) and low PCV and GCV values were shown by day to maturity (8.11, 6.95) and protein content (7.96, 6.38). For every character, there is an environmental influence because the PCV is greater than the GCV. That is low, though, because there is less of a difference between PCV and GCV. GCV can be used for the selection for further crop improvement. The level of PCV and GCV are depicted in Fig. 1. These findings were similar to Nagaraju [11] and Ashish [12] for the characters like day to 50 percent flowering, day to maturity, plantheight, productive tillers per plant, spike length, spikelets per spike, grains per spike, thousand grain weight and grain yield per plant. The results were in line with Heidari [13], Naik [14], Srivijay [15], Arati [16] and Fyroj [17] for characters like iron content, zinc content and protein content.

Table 1: Estimation of genetic variability parameters for yield, yield attributing traits and grain micronutrients in the F_2 populations of the cross DDK-1029 × GPM DIC 66.

SI.No.	Characters	Mean	Range		PCV(%)	GCV(%)	h^2 bs(%)	GAM(%)
			MIN	MAX				

1	DFF	77.90	54.00	94.00	12.30	11.33	84.96	21.52
2	DM	114.30	91.00	131.00	8.11	6.95	73.48	12.28
3	PH	75.87	45.00	108.00	18.45	17.87	93.76	35.64
4	PTPP	17.06	4.00	41.00	54.41	47.74	76.97	86.28
5	SL	9.44	6.00	12.00	16.97	15.36	81.93	28.64
6	SPS	22.80	14.00	30.00	18.40	17.16	86.97	32.96
7	GPS	40.70	24.00	60.00	20.63	18.32	78.83	33.51
8	TGW	37.66	27.95	49.16	20.82	19.64	89.02	38.18
9	GY	26.83	7.00	72.00	57.63	41.77	52.55	62.38
10	Fe	47.10	38.40	65.20	14.25	11.74	67.90	19.93
11	Zn	47.80	34.00	63.30	14.79	13.63	84.91	25.88
12	Protein	16.30	14.00	18.60	7.96	6.38	64.25	10.53

DFF- Days to fifty per cent flowering, DM- Days to maturity, PH- Plant height (cm), PTPP- Productive tillers per plant, SPS- Number of spikelets per spike, SL- Spike length (cm), GPS- Grains per spike, GY- Grain yield per plant (g), TGW- Thousand grain weight (g), Fe- iron content (ppm), Zn- Zinc content (ppm), Protein content (%).

The degree to which traits are passed on from parents to their offspring can be evaluated well by heritability. It facilitates the selection of superior genotypes from a range of genetically diverse populations. Heritability for the following characteristics was found to be high: days to 50% flowering (84.96), days to maturity (73.48), plant height (93.76), number of productive tillers per plant (76.97), spike length (81.93), spikelets per spike (86.97), grains per spike (78.83), thousand grain weight (89.02), iron content (67.90), zinc content (84.91) and protein content (64.25) except for grain yield, which had a moderate heritability (52.55). The level of heritability for all traits are depicted in Fig. 3. The results were in agreement with those of Ashish [12], Surya [18], Danial [19], Nagaraju [11] and Ranjana [20].

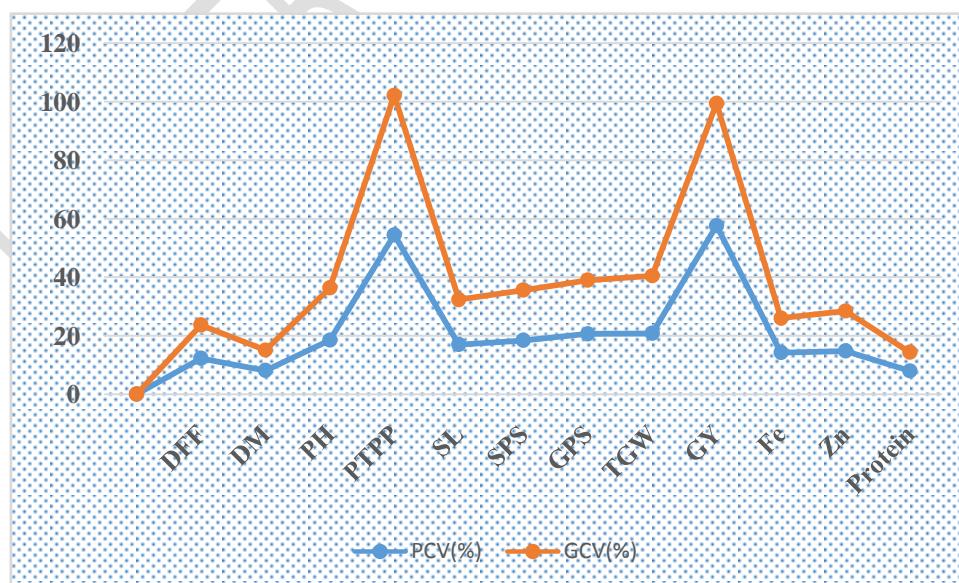


Fig. 1. Estimation of PCV and GCV for yield, its attributing traits and grain micronutrients in F₂ population of the cross DDK-1029 × GPM DIC 66.

For traits like days to 50 per flowering (21.52), plant height (35.64), number of productive tillers per plant (86.28), spike length (28.64), spikelets per spike (32.96), grains per spike (33.51), thousand grain weight (38.18), grain yield per plant (62.38), and zinc content (25.88), there was a high genetic advance as a percentage of mean. The genetic advance as a percentage of mean was low for characters like days to maturity (12.28), iron content (19.93), and protein content (10.53). The level of genetic advance as percent of mean for all traits are depicted in Fig. 3. The traits like days to 50 per flowering (days), plant height (cm), number of productive tillers per plant, spike length (cm), spikelets per spike, grains per spike and thousand grain weight (g) showed high heritability with high genetic advance. This indicates the presence of additive gene effects and selection is effective for these traits. These findings are similar to the results of Singh [21], Kyosev [22], Srinivas [23], Danial [19] and Nagaraju [11].

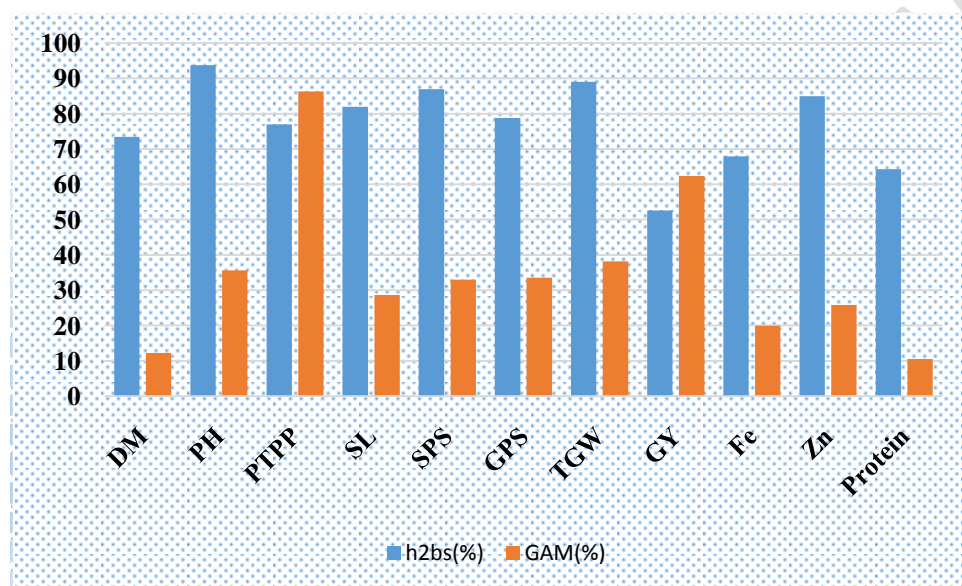


Fig. 1. Estimation of Heritability and GAM for yield, its attributing traits and grain micronutrients in F₂ population of the cross DDK-1029 × GPM DIC 66.

CONCLUSIONS

Higher levels of genetic variability was observed in the following characters: days to 50 per flowering (days), days to maturity (days), plant height (cm), number of productive tillers per plant, spike length (cm), number of spikelets per spike, number of grains per spike, thousand grain weight (g), number of grains yielded per plant (kg), and levels of iron, zinc, and protein (ppm). The same characters however, showed a significant degree of heritability along with genetic advance as a percentage of mean, suggesting that there is a greater potential for development in these traits by direct selection.

FUTURESCOPE

The results of this study showed that the F₂ segregating population possesses an enormous amount of genetic variation. Therefore, superior wheat varieties with high yield and quality can be developed by applying particular breeding techniques to harness the variance.

REFERENCES

1. Liu J, Bihua W, Ravi P, Govindan V. QTL mapping for micronutrients concentration and yield component traits in a hexaploid wheat mapping population. *Journ al of Cereal Science*. 2019; 88:55-64.

2. Anonymous, 2019, Agricultural statistics at a glance, Directorate of economics and statistics.
3. Anonymous, 2018, Area, production and productivity, Ministry of Agriculture and Farmers Welfare, Government of India, Website: -<http://www.indiastat.com>
4. Shewry PR, Halford NG, Belton PS, Tatham AS. The structure and properties of gluten: An elastic protein from wheat grain. *Philosophical Transactions of the Royal Society B: Biological Sciences*. 2002; 357 (1418):133-142.
5. Hwalla N, AlDhaheeri AS, Radwan H, Alfawaz HA, Fouda MA, Daghri NM, Zaghloul S, Blumberg JB. The prevalence of micronutrient deficiencies and inadequacies in the middle East and approaches to interventions. *Nutrients*. 2017; 9(3):229.
6. WHO, 2008, Worldwide Prevalence of Anaemia 1993-2005, WHO Report.
7. Robinson HE, Comstock RS. Biometrical studies of yield in segregating population of Korean lespedeza. *Agronomy Journal*, 1949; 48:268-272.
8. Burton GW, Dewane EH. Estimating heritability in tall fescues (*Festuca arvensis*) from replicated clonal material. *Agronomy Journal of Nepal*. 1953; 45:1476-1481.
9. Lush JL. Intra-sire correlation and regression of offspring on dams as a method of estimating heritability of characters. *American Society of Animal Production*. 1940; 33:293-301.
10. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybean. *Agronomy Journal of Nepal*. 1955; 47:314-318.
11. Nagaraju CH, Biradar SS, Desai SA, Rudra Naik V, Cheatna CK, Satisha TN. Genetic and association studies in segregating populations for yield and free threshability trait in tetraploid wheat. *International Journal of Agricultural Sciences*. 7:430-433.
12. Ashish O, Bharat B, Sonu B, Manoj P, Shailendra SG, Bhudeva ST, Gyanendra S. Genetic variability, correlation coefficient and path analysis of some quantitative traits in bread wheat. *Journal of Wheat Research*. 2013; 5 (1):21-26.
13. Heidari B, Padash S, Dadkhodaie A., Variations in micronutrients, bread quality and agronomic traits of wheat landrace varieties and commercial cultivars. *Australian Journal of Crop Science*. 2016; 10 (3): 377-384.
14. Naik RV, Suma SB, Arati Y, Desai SA, Veeraha BA. Study of genetic variability parameters in bread wheat (*Triticum aestivum* L.) genotypes. *Research Journal of Agricultural Science*. 2015; 6 (1):123-125.
15. Srivijay Malipatil, SS Biradar, SA Desai, SS Gundlur. Genetic variability studies for yield and its attributes under salt affected soils in wheat species. *Journal of Farm Science*. 2022; 35(2):169-173.
16. Arati Y, Hanchinal RR, Nadaf HL, Desai SA, Biradar S, Naik RV. Genetic variability for yield parameters and rust resistance in F₂ population of wheat (*Triticum aestivum* L.). *The Bioscan*. 2015; 10 (2):707-710.
17. Fyroj U. 2017, Genetic variability studies for grain nutrients, yield and yield attributes in tetraploid wheat. *M.Sc. (Agri) Thesis, Univ. Agric. Sci., Dharwad, Karnataka (India)*.
18. Surya K, Lamba R, Panwar I, Arya RK. Variability and inter-relationship among yield and quality parameters in bread wheat. *Journal of Wheat Research*. 2011; 3(2):50.
19. Danail K, Mahdi M, Reza M, Kianoosh C. Estimation of genetic parameters related to morpho-agronomic traits of Durum Wheat (*Triticum turgidum var. durum*). *Biharean Biologist*. 2010; 4 (2):93-97.
20. Ranjana J, Gaur SC, Sunil KJ, Anil K. An estimate of variability, heritability and genetic advance for grain yield and yield components in bread wheat (*Triticum aestivum* L.). *British Journal of Applied Science and Technology*. 2020; 39 (12):1-6.

21. Singh JB, Verma A, Prakash S, Patidar I, Prakash TL, Saiprasad SV, Singh AK, Mishra A N., Variability and interrelationship analysis in bread wheat under moisture stress conditions. *Journal of Wheat Research*. 2013; 5(2):27-34.
22. Kyosev, Desheva. Study on variability, heritability, genetic advance and associations among characters in emmer wheat genotypes (*Triticum dicoccon* Schrank). *Journal of Bioscience and Biotechnology Discovery*. 2015; 2:221-228.
23. Srinivas AD, Suma SB, Deepak K, Rudra Naik V, Yashvantha K, Sathisha K, Chourasia N., Study of genetic variability parameters in different segregating generations of bread wheat (*Triticum aestivum* L.). *Environment and Conservation*. 2016; 35(3B):2056-2060.

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