Journal of Applied and Natural Science
10 (2): 773 - 778 (2018)
ISSN : 0974-9411 (Print), 2231-5209 (Online)
journals.ansfoundation.org

Genetic variability study in F_2 population of tetraploid dicoccum wheat crosses

Channappagouda Patil
Department of Genetics and Plant Breeding, University of Agricultural Sciences, Dharwad- 580005 (Karnataka), India
Deepak Koujalagi*
Department of Genetics and Plant Breeding, G. B. Pant University of Agriculture and Technology, Pantnagar-263153 (Uttarakhand), India

*Corresponding author. E-mail: Koujalagi.deepak@gmail.com

Article Info
DOI:10.31018/jans.v10i2.1777
Received: March 1, 2018
Revised: April 14, 2018
Accepted: May 17, 2018

How to Cite
Patil, C. and Koujalagi, D. (2018). Genetic variability study in F_2 population of tetraploid dicoccum wheat crosses. *Journal of Applied and Natural Science*, 10 (2): 773 - 778

ABSTRACT

The aim of the present investigation was to estimate the genetic variability parameters in Wheat (*Triticum dicoccum*) F_2 population of the cross DDK1025 X ML-1. The traits involved in study were grain yield, threshability, rachis percent and other yield contributing traits such as tiller number, number of grains per spike, number of spikelet's per spike, etc. and the genetic variability parameters estimated are mean, range, Phenotypic coefficient of variation (PCV), Genotypic coefficient of variation (GCV), heritability and genetic advance over mean. The results obtained from the study reveals higher mean and wider range for all the traits especially for plant height, tiller number, spikelets per spike, number of grains per spikelet, spike length, grain yield per plant, threshability and rachis. High degree of PCV with moderate GCV was observed for the traits like number of tiller per plant (20.96 PCV and 15.96 GCV), number of grains per spike (21.92 PCV and 18.79 GCV), rachis % (22.5 PCV and 19.10 GCV) and grain yield per plant (20.07 PCV and 18.10) . Heritability and genetic advance was recorded to high for all the traits in both the populations. On the basis of an overall consideration of the genetic variability parameters it may be concluded that F_2 population of the cross, DDK-1025 x ML-1 have the potential source for improving the yield and its associated traits and also offering some scope in altering the plant height.

Keywords: Coefficient of variation, Genetic advance, Heritability, Threshability, Variability

INTRODUCTION

Wheat (*Triticum spp*), the versatile cereal food is also described as the stuff of life. It continues to retain this pride of place with its roots ramifying into the depths of human culture with evolutionary history parallel with the human civilization itself. Even today, it occupies primary position among all the cereal crops due to its feeding bowl to mankind. It is consumed by 2.5 billion people in 89 countries. It super-cedes maize or rice as a source of protein in low- and middle-income nations and is second only to rice as a source of calories and proteins. Nearly US $50 billion-worth of wheat is traded globally each year (CGIAR, 2018). Grown on more land than any other crop, more than 215 million hectares of wheat are harvested annually to generate a world production of almost 700 million to, making it the third most produced cereal after maize and rice (Islam *et al.* 2017). In India, wheat is the second most important crop after rice occupying 30.22 million hectares with a production of 93. 501 million tones and the average productivity is 3093 kg ha^{-1} (DES, 2018). These cultivated plants produced non-shattering inflorescences and soft fruiting bodies, which made them suitable for human planting and harvesting. The cultivated plants can be easily distinguished from their progenitors based on a suite of characters known as “domestication syndrome” (Doebley *et al.,* 2006). The important step in the evolution of modern polyploid wheat was the domestication of tetraploid emmer wheat (*Triticum dicoccum* Schuebler) from its progenitor *Triticum turgidum* subsp. *dicoccoides*. The remains of cultivated emmer have been discovered at several archaeological sites in Syria dating to 7500 BC (Zohary and Hopf, 1993). Unlike the wild progenitor, domesticated tetraploid wheats have a non-brittle rachis but the early domesticated emmer wheat, *T. turgidum* subsp. *dicoccum*, has hulled seeds (Dubcovsky and Dvorak, 2007).

Wheat is known to be temperate crop, however it is being cultivated in tropical ecosystem of India, where prevalence of high temperature during crop growth and peculiar climatic conditions coupled with rain fed cultivation of the crop leads to the lower productivity. In this context, dicoccum wheat assumes greater importance as it adapts well to high temperature stress, resistant to rust diseases (leaf and stem) than Durum and Aestivum, which is attributed to internal genetic makeup and morpho-physiological mechanisms (Tandon and Hanchinal, 1992). The desirable traits of dicoccum wheat have been successfully used in inter specific hybridization for improvement of aestivum and durum wheats (Gill, 1979). Dicoccum hulled wheat, commonly called by the name as "Jave, Sadaka, Samba, Khapli *etc.*" In India, it is traditionally cultivated in Northern Karnataka, Southern Maharashtra, Sourashtra region of coastal Gujarat, Nilgiris and Palani hilly areas of Tamil Nadu and Telangana region in Andhra Pradesh (Mahanteshivagogayya *et al.,* 2002). Looking to its quality traits and resistance to fungal diseases, there is a great need to develop dicoccum varieties with free threshing habit. Further, understanding the genetic variability, gene action of the threshability is of prime importance. Development of superior gene pool needs the genotypes with desired traits of both qualitative and quantitative. But owing to their economic importance quantitative characters receive more attention. The presence of variability for economic traits in the working population is must for profitable exploitation following recombination breeding and selection (Koujalagi *et al.,* 2017). Realizing the importance and need for such a study, evaluation of various qualitative and quantitative traits in F_2 population derived from the cross made between a dicoccum variety and a advanced mutant line (DDK1025 X ML-1) in order to isolate the superior free threshable lines.

MATERIALS AND METHODS

The experiment consists of F_2 population derived from the cross DDK1025 X ML-1 planted during Rabi 2013-14 at in the experimental area of Dr. Sanjay Rajaram Wheat Laboratory, All India Coordinated Wheat Improvement Project (AICWIP), Main Agricultural Research Station (MARS), University of Agricultural Sciences, Dharwad. The experimental site is located between 15^0 26'N latitude and 75^0 07'E longitude and has altitude of 678m above the mean sea level. It comes under transitional tract of Karnataka state where red soil is found to be predominant soil type and the area receives 1150 mm of average rainfall and irrigation schedule involved irrigation at every 15-20 days intervals during the entire crop growth period. The material for the present investigation was generated using one non free threshable dicoccum variety DDK1025 and a threshable mutant line ML-1(Mutant line was generated using ethyl methane sulfonate as chemical mutagen at AICWIP, University of Agricultural Sciences, Dharwad). The crossing was done by taking dicoccum as female and mutant lines as male during Rabi 2011-12 and Kharif 2012-13, the F_1 was freshly generated during Kharif 2013-14. The mutant line was selected from advanced free threshable mutant populations. The F_2 population was planted in augmented design (In an augmented design, a large set of experimental lines is divided into small incomplete blocks. In each incomplete block, a set of checks is included; every check occurs in each incomplete block, but the experimental lines are included in only one block) which consist of four blocks and four checks namely P_1 (DDK-1025), P_2 (ML-1) and two comercial durum varieties viz HD-4502 and DWR-1006. All five checks were allotted randomly once in each block at fixed interval of entries.

Observations recorded: Observation were recorded for following 11 traits: Plant height (cm), Number of tillers per plant, Number of spikelets per spike, Number of grains per spikelet, Number of grains per spike, Spike length (cm), Spike density (cm), Thousand grain weight, Grain yield per plant (g), Rachis (%): Spikes were observed for presence of rachis (100%) and absence of rachis (0%) while threshing of individual spikelet's and expressed as percentage.

Threshability (%): Observation on threshability of individual spikes was recorded after the crop was harvested. Spikes were threshed with hand and based on the ease of threshing and percentage of husked seeds obtained individual plants are classified as free threshable, medium free threshable and hard to thresh/ non free-threshable. The classification is represented in table 1.

Statistical analysis: Statistical analysis was done using INDOSTAT v8.1 to obtain basic statistics using the ten tagged plants in each genotype for all parameters.

General mean (X) = Sum of observations of selected plants in each genotype/ Number of plants selected

Range = the minimum and maximum values for each trait within a genotype.

Estimation of genetic parameters: Genotypic variance, phenotypic variance and coefficients of variances were computed based on the expected mean sum of squares from the ANOVA table as follows (Singh and Chaudary, 1985). The treatment mean sum of squares due to genotypes is made up of environmental variance along with 'r' times the genetic variance (Equation 1&2).

$$s^2p = M_t - M_e / r + M_e \text{ or } s^2g + s^2e \qquad \text{….Eqn(1)}$$

$$s^2g = M_t - M_e / r \qquad \text{….Eqn(2)}$$

Where, Mt = Mean sum of squares due to treatments, Me = Mean sum of squares due to error, r = Number of replications, s^2g = Genotypic variance, s^2p = Phenotypic variance, s^2e= Environmental variance.

Phenotypic coefficient of variance (PCV): Phenotypic coefficient of variation was calculated using the method suggested by Burton and Devane (1953) (Eqn. 3).

PCV =ÖVp / X´ 100 ….Eqn(3)

Where, Vp = Phenotypic variance,`X = General mean of the character

Low = 1-10%, Moderate = 10-20%, High = More than 20%

Genotypic coefficient of variance (GCV): GCV was calculated by the following formula (Eqn. 4).

GCV =ÖVg / X ´ 100 ….Eqn(4)

Where, Vg = Genotypic variance, X = General mean of the character

Low = 1-10%, Moderate = 10-20% High = More than 20%

Heritability: Heritability in broad sense was estimated by following formula and expressed in percentage. (Eqn. 5)

Heritability (h^2_{bs}) = s^2g /s^2p´ 100 ….Eqn(5)

Where, s^2g = Genotypic variance s^2p = Phenotypic variance

The heritability estimates were categorized according to Robinson *et al.* (1949) as given below: Low = 1-30%, Moderate = 30-60%, High = More than 60%

Genetic advance: The extent of genetic advance to be expected from selecting five per cent of the superior progeny was calculated using the following formula (Eqn. 6)

GA = I. s_p. $h^2_{(bs).}$ ….Eqn(6)

Where, i = Intensity of selection, sp = Phenotypic standard deviation, h² (bs) = Heritability in broad sense. The genetic advance estimates were categorized according to Johanson *et al.* (1955) as given below: Low = 1-10%, Moderate = 10-20%, High = More than 20%.

Genetic advance as percentage over mean (GAM):

GAM =GA / X x 100 ….Eqn(7)

Where, `X = General mean of the character. Genetic advance is categorized based on reports of Johanson *et al.* (1955) as follows: Low =1-10%, Moderate=10-20%, High=More than 20%

RESULTS AND DISCUSSION

Analysis of variance: Mean sum of squares for all the traits clearly indicated significant variation for all the in F_2 populations (Table.3). The significant differences indicates presence of large genetic variability for characters under study hence they are amenable to selection to achieve desirable improvement.

Table 1. Classification of threshability traits in Dicoccum wheat.

Threshability traits	Per cent range	Score value
Hard to thresh	0 to 30	1
Medium free threshable	40 to 60	5
Free threshable	70 to 100	7

Table 2. Analysis of variance for eleven quantitative characters in F_2 population of DDK-1025 X ML-1

Source of variation	DF	PH	NTP	NSS	NGSK	NGS	SL	SD	TH	RA	TW	GYP
Block	3	27.44 *	3.26	0.733	0.05	13.49	0.089	0.001	0.015	0.088	0.461	13.164
Entries	124	115.99 **	15.63 *	5.25 **	0.25 *	136.79 **	1.685 **	0.142 **	7.52 **	7.645 **	33.42 **	33.43 **
Checks	4	384.94**	41.92 **	20.20 **	0.115	116.86 *	5.58 **	0.25 **	17.61 **	16.99 **	0.74	12.65
Varieties	119	103.45 **	13.89 *	4.706 *	0.25 *	129.65 **	1.36 **	0.13 **	6.61 **	6.80**	34.71 **	32.9 **
Checks vs. Varieties	1	531.85 **	116.63 **	10.51*	1.72 **	1065.78 **	24.44 **	0.53 **	75.60 **	69.95**	10.41	168.7 **
Error	12	5.06	5.39	1.400	0.08	31.12	0.34	0.025	1.243	1.483	4.285	5.313
CD (5%)		5.98	6.17	3.14	0.75	14.83	1.55	0.42	2.96	3.23	5.50	6.13
S.Em±		2.7	2.83	1.44	0.34	6.81	0.71	0.19	1.36	1.48	2.52	2.81

PH – Plant height (cm) , SD – Spike density (cm), NTP – No. tillers per plant, TH –Threshability trait (%), NSS– No. spikelets per spike, RA – Rachis (%), NGSK – No. grains per spikelet, TGW – Thousand grain weight (g), NGS – No. of grains per spike, GYP – Grain yield per plant (g), SL – Spike length (cm).

Table 3. Estimation of variability parameters for eleven quantitative characters in F_2 segregating population of two dicoccum crosses.

characters	DDK-1025 X ML-1					
	Mean	**Range**	**PCV (%)**	**GCV (%)**	**h² (bs)**	**GAM (%)**
PH	91.54	63-113	10.43	10.13	94.4	20.29
NTP	17.09	10.0-33.0	20.96	15.96	57.9	25.04
NSS	19.68	13.0-27.0	10.52	8.64	67.3	14.61
NGSK	2.52	2.0-3.0	19.07	15.34	64.72	25.43
NGS	49.41	30.0-69.0	21.92	18.79	73.47	33.18
SL	9.75	6.0-12.5	11.39	9.68	72.16	16.93
SD	2.05	1.4-3.8	16.97	15.08	78.99	27.62
TH	2.80	1.0-7.0	24.10	22.4	79.09	35.8
RA	2.50	1.0-7.0	22.5	19.10	75.8	33.15
TGW	45.24	31.5-73.5	12.29	11.4	86.14	21.8
GYP	27.07	14.5-48.0	20.07	18.18	82.01	33.91

PH – Plant height (cm) , SD – Spike density (cm), NTP – No. tillers per plant, TH –Threshability trait (%), NSS – No. spikelets per spike, RA – Rachis (%), NGSK – No. grains per spikelet, TGW – Thousand grain weight (g), NGS – No. of grains per spike, GYP – Grain yield per plant (g), SL – Spike length (cm).

Range of variation: Bhushan *et al.* (2013) and Tambe *et al.* (2013) reported ranges for all the quantitative characters observed under the present study. For most of the characters (plant height, tiller number, spikelets per spike, number of grains per spikelet, spike length, grain yield per plant, threshability and rachis) wide range was observed in F_2 population.

A critical examination of range for some of the traits provided some interesting and useful information. The range of 63-113 for plant height recorded to be the maximum among all the traits. Plant height in wheat is a character for which there is a requirement of both dwarf and tall types. Dwarf types for some situations like non lodging types whereas, tall types for developing fodder or dual purposes. From this point of view, it would give ample opportunities for the breeder to select the segregants with desired height. Similarly in respect of thousand grain weight, segregants with test weight of 49 g and above have been recovered, surpassing the mean grain weight of 45g in DDK-1025 variety. This is again a positive feature of crosses to the breeder for improving grain yield. For the traits like threshability and rachis also noticed higher range of variation (0.0 to 7.0). Likewise, the upper value of range for grain yield was nearly two to three times higher than mean grain yield of highest yielding parental genotype DDK-1025. These results are in accordance with Naik *et al.* (2015) and Arpitha *et al.* (2017).

Genetic parameters: Absolute variability values of different characters do not reveal which of the characters are showing high variability. This could only be accessed through standardized values of the phenotypic and genotypic variance estimates by obtaining the coefficients of variability (Arpitha *et al.* 2017). The coefficient of variation indicates only the extent of total variability present for a character and does not demarcate the variability into heritable and non heritable portion (Basavaraj *et al.* 2017). The extent to which variability could be transferred from parent to offspring would suggest how far the variation is heritable which has close bearing on response to selection. The results obtained in the present study are presented in the Table.3.

High degree of Phenotypic Coefficient Variation was recorded for the traits like number of tillers per plant, number of grains per spike, rachis percent, threshability and grain yield per plant whereas other traits exhibited moderate PCV. Similarly for GCV most of the traits were recorded to exhibit moderate GCV except for threshability which recorded high GCV whereas number of spikelet's per spike exhibited low GCV. These various results of moderate PCV and GCV are in accordance with the findings of Ajmal *et al.* (2009) and Subhashchandra *et al.* (2009) whereas of High PCV and GCV with Manal H. Eid (2009), Kahrizi *et al.* (2010) and Arpitha *et al.* (2017). This suggested the greater effectiveness of selection and improvement to be expected for these characters in future breeding programme as the genetic variance is mostly due to additive gene expression.

The heritability of almost all the traits was found to be high which is in agreement with the results of Banshi *et al.* (2010), Tazeen *et al.* (2009). However, number of tillers per plant exhibited moderate heritability in F_2 population DDK-1025 x ML-1 which is in agreement with the Shukla and Singh (2004).

Genetic advance as percentage over mean for all the traits exhibited the same trend as of heritability and recorded to be high GAM for almost all the traits except for the traits like number of spikelets per spike and spike length. High genetic advance as per cent of mean, results are in accordance with Kashif *et al.* (2004) and Ajmal *et al.* (2009).

In general, the magnitude of GCV was low as compared to PCV values for all the quantitative characters indicating variability was not only due to genotype but also influenced by environment. Broad sense heritability estimate and expected genetic gain (GA) were high for number of grains per spikelet, number of grains per spike, spike density, thousand grain weight) and grain yield per plant. Therefore, it is clear that these traits were less influenced by the environmental changes and the improvement in these traits would be more effective through selection and hybridization owing to their dominance gene effects. In fact, PCV was high for all the traits and high heritability estimates coupled with high genetic advance which suggests that phenotypic selection for these characters may be effective (Sharma and Sharma 2007 and Tazeen *et al.,* 2009).

Conclusion

DDK-1025 x ML-1 may be regarded as potential source population for some of important yield component traits like number of spikelets per spike and spike length. Selective inter population inter mating involving this population might help in further increasing variation for productivity and its components providing better scope for achieving high genetic gain. Threshability trait coupled with yield per plant and some of its components like number of tillers, number of grains per spike and thousand grain weight exhibited considerable variation indicating the scope for effective selection to improve these characters. However, less variations was observed for some of the characters like, number of grains per spikelet, spike density (DDK-1025 x ML-1) indicating the limited scope for improving these characters by selection.

REFERENCES

Islam, A.U., Chhabra, A.K., Dhanda, S.S. and Munjal, R. (2017). Cell membrane stability-an important criterion for selection of heat tolerant genotypes in wheat (*Triticum aestivum* L.) *Journal of Applied and Natural Science,* 9 (4): 1894

Arpitha, H.R., Naik, R.V. and Anil Kumar, G. (2017). Study of Genetic Variability Parameters For Yield And Yield Attributing Traits in F5 Population of Dicoccum Wheat. *Bull. Env. Pharmacol. Life Sci.,* 6(1):189-193

Ajmal, S.U., Zakir, N. and Mujahid, M. Y. (2009). Estimation of genetic parameters and character association in wheat. *J. Agric. Biol. Sci.,* 1(1): 15-18.

Banshi, D. K., Arpita, D. and Choudhury, B. K. (2010). Genetic variability and association of characters in wheat (*Triticum aestivum* L.). *Asian J. of Crop Sci.*, 2 (3): 155-160.

Basavaraj, P.S., Biradar, B.D. and Rathod, R. (2017). Genetic Variability Studies for Quantitative Traits Of Maintainer (B) Lines In Pearl Millet [*Pennisetum Glaucum* (L.) *G.J.B.B.,* 6 (2): 357-362

Burton, G.M. and Devane, E.M. (1953). Estimating heritability in tall Fescue from replication clonal material. *Agronomy J.,* 45: 478-481.

Bhushan, B., Sonu, B., Ashish, O., Manoj, P., Shailendra, S., Gourav, B., Singh, T. and Gyanendra, S. (2013). Genetic variability, correlation coefficient and path analysis of some quantitative traits in bread wheat. *J. Wheat Res.,* 5(1):21-26.

CGIAR (2018). Wheat in the world. http://wheat.org/wheat-in-the-world/

DES (2018). Directorate of Economics and Statistics (DES), Ministry of Agriculture.

Doebley, J.F., Gaut, B.S. and Smith, B.D. (2006). The molecular genetics of crop domestication. *Cell.,* 7: 1309–1321.

Dubcovsky, J. and Dvorak, J. (2007). Genome plasticity: a key factor in the success of polyploid wheat under domestication. *Sci.,* 316: 1862-1866.

Gill, K.S. (1979). Effect of soil salinity on grain filling and grain development in barley. *Biologia Plantarum,* 21 (4): 241-244.

Johanson, H.W., Robinson, H.F. and Comstock, R.E. (1955). Estimates of genetic and environmental variability in soybean. *Agron. J.,* 47: 314-318.

Kahrizi, D., Kianoosh, C., Mehdi, K., Reza, M. and Abdolghafar, E. (2010). Heritability and genetic gain of some morphophysiological variables of durum wheat (*Triticum turgidum* var. *durum). African J. of Biotech.* 9(30): 4687-4691.

Kashif, M. and Khaliq. I. (2004). Heritability, correlation and path coefficient analysis for some metric traits in wheat. *International J. Agric. Biol*., 6(1): 138-142.

Koujalagi, D., Desai, S.A., Biradar, S.S., Naik, R.V., Yashavantha, K.J., Satish, T.N. and Kumar, N.C. (2017). Study Of Genetic Variability Parameters In Different Segregating Generations Of Bread Wheat (*Triticum Aestivum* L.). *Environment & Ecology,* 35 (3B): 2056—2060.

Mahanteshivagogayya, K. (2002) Genetic and breeding investigations for improving heat tolerance and productivity in dicoccum wheat (*Triticum dicoccum* Schrank Suhulb). *Ph. D. Thesis, Univ. Agric. Sci., Dharwad, Karnataka (India).*

Manal, H. E. (2009). Estimation of heritability and genetic advance of yield traits in wheat (*Triticum aestivum* L.) under drought condition. *International J. of Gen. and Mol. Biol.,* 1(7): 115-120.

Naik, R.V., Kumar, Y.L.M., Biradar, S.S., Desai, S.A. and Veeresha, B.A. (2015). Genetic variability parameters for micronutrients, yield and quality traits in wheat. *Int. J. Agric. Sci.*, 7(2):520-522.

Robinson, H.F., Comstock, R.E. and Harvey, P.H. (1949). Estimates of heritability and degree of dominance in corn. *Agronomy Journal*, 41: 353-359.

Sharma, S.N. and Sharma, Y. (2007). Estimation of variation and heritability of some quantitative and quality characters in *Triticum turgidum* L. ssp. Durum (Desf.). *Acta Agronomica Hungaria.,* 55(2): 261-264.

Shukla, R.S. and Singh, C.B. (2004). Genetic analysis for screening of high temperature and moisture stress tolerance traits in bread wheat. *JNKVV Res. J.,* 38(1): 22-25.

Singh, R.K. and Chaudhary, B.D. (1985). Biometrical Methods in Quantitative Genetics Analysis. Kalyani Publishers.

Subhashchandra, B., Lohithaswa, H.C., Desai, S.A., Hanchinal, R.R., Kalappanavar, I.K., Math K.K. and Salimath, P.M. (2009). Assessment of genetic variability and relationship between genetic diversity and transgressive segregation in tetraploid wheat. *Karnataka J. Agric. Sci.,* 22(1): 36-38.

Tandon, J.P. and Hanchinal, R.R. (1992). Nutritious emmer deserves more attention. *Indian Farming,* 42: 18 -19.

Tambe, A., Mehta, D.R., Chovatia, V.P. and Bhatiya, V.J. (2013). Genetic variability, character association and path coefficient analysis in durum wheat (*Triticum durum* Desf.). *Electronic J. Plant Breed.*, 4 (4): 1303-1308.

Tazeen, M., Nadia K. and Farzana N.N., (2009). Heritability, phenotypic correlation and path coefficient studies for some agronomic characters in synthetic elite lines of wheat. *J. Food, Agric. Env.,*7(3):278-282

Zohary, D. and Hopf, M. (1993). Domestication of plants in the Old World. The origin and spread of cultivated plants in West Asia, Europe and the Nile Valley. *Clarendon Press, Oxford, England*.