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# Environmental influence on heritability and selection response of some important quantitative traits in greengram [*Vigna radiata* (L.) Wilczek]

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## ABSTRACT

**The phenotypic performance, heritability and selection response of quantitative traits vary due to genotypic differences, environmental factors and genotype by environment interaction. The present investigation was conducted with 36 greengram genotypes under three varying environments. Results of study indicated the significant differences among genotypes for almost all the traits studied under different environments. This study also revealed that heritability is affected by the environment. Some important traits *viz.*, plant height, number of primary branches per plant, number of secondary branches per plant, pod mass, seed mass, biological yield per plant, harvest index and seed yield per plant showed low environmental influence comprising high heritability coupled with high proportion of selection response. Due to preponderance of additive gene action simple plant selection may be rewarding to improve yield and yield components.**

***Key words:*** Environmental influence, Greengram, GCV, Heritability, PCV, Selection response, Yield contributing traits

Greengram [*Vigna radiata* (L.) Wilczek], belonging to family leguminoseae, is a tropical and sub-tropical grain legume, adapted to different types of soil conditions and environments (*kharif*, *spring, summer*). It ranks third in India after chickpea and pigeonpea. It has strong root system and capacity to fix the atmospheric nitrogen into the soil and improves soil health and contributes significantly to enhancing the yield of subsequent crops (Jat *et al.* 2012). However the production and productivity is very low in greengram mainly due to its cultivation in resource poor lands with minimum inputs, non-synchronous maturity and indeterminate growth habit. Greengram yield is also affected by insect-pests and diseases, especially by mungbean yellow mosaic virus (MYMV) and *Cercospora* leaf spot (CLS). There is a strong need to develop the lines/varieties which give outstanding and consistent performance in *kharif* season over diverse environment. Development of varieties with high yield and stable performance is a prime target of all mungbean improvement programmes.

Yield is a very complex trait and depends on several components highly influenced by environment. For any crop improvement programme selection of superior parents/ lines is essential that possess high heritability and genetic advance for various traits (Khan *et al.* 2005). Knowledge of genetic variability on different yield parameters is also an important criterion for yield enhancement. However, in greengram natural variation is narrow due to its self pollinating nature (Siddique *et al.* 2006), resulting in limited selection opportunity. The efficacy of selection depends upon the magnitude of genetic variability for yield and yield contributing traits in the breeding material. The knowledge of heritability and selection response (*R*) can provide useful information to select the trait for improvement and to select superior parents for hybridization and to choose appropriate breeding procedure for genetic improvement. Several plant researchers have emphasized upon the use of heritability and genetic advance to identify desirable populations in legumes (Ghafoor *et al.* 2000, Ullah *et al.* 2010, Ullah *et al.* 2011). However, yield and growth of greengram is highly influenced by environment (Ullah *et al.* 2011), thus screening of genotypes over environments can give good results for its improvement. Change in environmental factors affects the performance of genotypes; hence, the present experiment was conducted to find out the nature and extent of heritability and selection response of yield and its related traits under three environments.

## MATERIALS AND METHODS

The present experiment was conducted with 36 genotypes of greengram received from Pulse Breeding Section, Department of Plant Breeding and Genetics, Tirhut College of Agriculture (TCA), Dholi, Muzaffarpur, Bihar, India. The experiment was conducted at Crop Research Farm of TCA, Dholi ($25.5^0$N, $35.4^0$E, 52.12 m MSL) in district Muzaffarpur of North Bihar, India in Randomized Block Design (RBD) with 3 replications in three environments by adjusting the sowing dates at 15 days intervals *viz.,* 10 July 2012 (early sown $E_1$), 25 July 2012 (timely sown $E_2$) and 11 August 2012 (late sown $E_3$). Each genotype was sown in six rows of 4 m length each with 30 cm inter-row and 10 cm intra-row spacing. Five random plants were tagged from each plot to record the data for all the yield and agro-morphological traits (except days to 50% flowering) *viz.,* plant height (PH), number of primary branches per plant (NPBP), number of secondary branches per plant

(NSBP), number of clusters per plant (NCP), number of pods per cluster (NPC), pod length (PL), number of seeds per pod (NSP), shelling percentage (SP), seed index (SI), biological yield per plant (BYP), harvest index (HI) and seed yield per plant (SYP). Days to 50% flowering (DFF) was recorded on plot basis. Pod mass (PM) and seed mass (SM) were recorded by weighing the 10 pods and seeds from these 10 pods from five randomly selected plants and averaged. Pod wall mass (PWM) was obtained by subtracting the seed mass from pod mass. Pod wall proportion (PWP) is an index obtained by dividing the weight of pod wall by weight of whole pod. The data were subjected to analysis of variance and genetic parameters *i.e.* genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability in broad sense ($h^2bs$), selection response ($R$) and proportion of selection response ($pR$) by using online statistical package OPSTAT.

## RESULTS AND DISCUSSION

The analysis of variance (ANOVA) showed significant differences among the genotypes for all the traits studied in E2 and E3, whereas in E1 most of the traits showed significant differences except PWM, PWP & SP (data not shown). The range, mean, standard error (SE) and coefficient of variation (CV) have been presented in Table 1. DFF ranged from 29.00 to 49.00 days in E1, 29.00 to 41.00 days in E2 and 24.00 to 41.00 days in E3. The gradual reduction in variability for PH was also observed with extending the showing dates. It exhibited 34.08 to 72.46, 30.46 to 62.40 and 27.82 to 56.74 cm minimum and maximum limit under E1, E2 and E3, respectively. A significant reduction in variability for NPBP, NSBP, NPC, PL and PM were also recorded by extending the sowing dates. The range of PWP was recorded as 12.52 to 49.30 in E1, 16.23 to 47.95 in E2 and 34.30 to 58.80% in E3 which clearly reflected that proportion of pod wall increases with an extension in the showing dates and affects the seed yield. The good magnitude of variability for SP was recorded in E2 (52.5 – 83.77%) as compared to E1 (50.70 – 87.31) and E3 (33.62 – 65.70). The maximum variability for BYP was recorded in E3 as compared to other two environments. The maximum HI was recorded in E2, whereas maximum limit for SYP was recorded in E1.

The mean performance for various traits *viz.,* DFF, NPBP, NSBP, NPC, PL and SI showed gradual decrease with extended sowing dates. The maximum PH was observed in E1, whereas it was almost the same in E2 and E3, indicating the stability of this trait under E2 and E3. The tall PH in E1 might be due to prolonged vegetative period. Yimram *et al.* (2009) suggested that tall plant structure in greengram is beneficial for both manual and mechanical harvesting. NCP, NSP, PM, SM, SP, HI and SYP showed high magnitude in E2 as compared to E1 and E3. PWP and BYP was highest recorded in E3. The coefficient of variation (CV) was categorized in three groups *viz.,* high (>50%), moderate (20-50%) and low (<20%) (Singh *et al*. 1990). None of the traits exhibited high CV while it was moderate for HI and SYP in E2 and E3, and for PWM in E1. Rest of the traits showed low CV in all the environments.

The genetic parameters for 17 traits in all three environments have been presented in Table 2. Genotypic coefficient of variation (GCV) depends upon the heritable part

**Table 1. Range, Mean, standard error of mean (SEm) and coefficient of variation (CV) for yield and yield contributing traits in greengram**

| Traits | E1 | | | | | E2 | | | | | E3 | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | Range | | Mean | SEm | CV | Range | | Mean | SEm | CV | Range | | Mean | SEm | CV |
| | Min | Max | | | | Min | Max | | | | Min | Max | | | |
| **DFF** | 29.00 | 49.33 | 34.82 | 1.37 | 5.65 | 29.67 | 41.66 | 33.53 | 1.08 | 6.37 | 24.66 | 41.33 | 29.33 | 1.09 | 6.37 |
| **PH** | 34.08 | 72.46 | 53.97 | 1.24 | 3.97 | 30.46 | 62.40 | 45.08 | 0.99 | 3.59 | 27.82 | 56.74 | 45.03 | 0.94 | 3.59 |
| **NPBP** | 2.37 | 7.30 | 3.68 | 0.25 | 11.89 | 2.17 | 8.23 | 3.03 | 0.38 | 17.46 | 1.57 | 6.90 | 2.65 | 0.27 | 17.46 |
| **NSBP** | 2.33 | 12.67 | 3.84 | 0.32 | 14.57 | 2.07 | 9.53 | 3.23 | 0.25 | 18.84 | 1.10 | 5.67 | 2.30 | 0.25 | 18.84 |
| **NCP** | 8.10 | 15.23 | 11.52 | 0.81 | 12.13 | 8.86 | 17.63 | 11.99 | 0.38 | 15.64 | 3.67 | 17.80 | 6.80 | 0.58 | 15.64 |
| **NPC** | 3.27 | 10.10 | 4.88 | 0.37 | 13.12 | 3.26 | 6.10 | 4.70 | 0.31 | 15.60 | 2.12 | 5.30 | 3.39 | 0.31 | 15.60 |
| **PL** | 4.90 | 8.43 | 6.94 | 0.23 | 5.74 | 5.23 | 7.67 | 6.23 | 0.25 | 7.81 | 4.140 | 6.86 | 5.49 | 0.25 | 7.81 |
| **NSP** | 4.30 | 13.56 | 10.61 | 0.70 | 11.39 | 5.30 | 13.56 | 11.25 | 0.37 | 9.88 | 3.77 | 7.86 | 6.49 | 0.37 | 9.88 |
| **PM** | 0.30 | 0.58 | 0.42 | 0.02 | 7.11 | 0.25 | 0.52 | 0.64 | 0.01 | 4.01 | 0.30 | 0.52 | 0.39 | 0.01 | 4.01 |
| **PWM** | 0.05 | 0.18 | 0.15 | 0.02 | 25.27 | 0.05 | 0.21 | 0.14 | 0.01 | 11.20 | 0.15 | 0.28 | 0.20 | 0.01 | 11.20 |
| **PWP** | 12.52 | 49.30 | 35.62 | 4.07 | 19.78 | 16.23 | 47.95 | 34.66 | 3.12 | 10.62 | 34.30 | 58.88 | 50.95 | 3.12 | 10.62 |
| **SM** | 0.15 | 0.40 | 0.27 | 0.01 | 7.77 | 0.20 | 0.36 | 0.26 | 0.01 | 8.88 | 0.12 | 0.31 | 0.19 | 0.01 | 8.88 |
| **SP** | 50.70 | 87.31 | 64.48 | 4.71 | 12.60 | 52.50 | 83.77 | 65.39 | 2.67 | 9.44 | 33.62 | 65.70 | 49.05 | 2.67 | 9.44 |
| **SI** | 2.56 | 4.33 | 3.51 | 0.11 | 5.58 | 2.77 | 4.10 | 3.30 | 0.12 | 9.03 | 1.75 | 3.05 | 2.38 | 0.12 | 9.03 |
| **BYP** | 11.13 | 28.90 | 19.45 | 1.05 | 9.37 | 11.00 | 28.16 | 17.26 | 6.61 | 4.55 | 12.62 | 47.94 | 23.12 | 0.61 | 4.55 |
| **HI** | 11.16 | 48.85 | 26.09 | 2.69 | 17.79 | 14.70 | 50.52 | 30.76 | 2.19 | 28.08 | 6.33 | 27.24 | 13.51 | 2.19 | 28.08 |
| **SYP** | 2.58 | 11.20 | 4.76 | 0.37 | 13.40 | 3.07 | 9.86 | 5.09 | 0.41 | 24.39 | 1.80 | 5.43 | 2.92 | 0.41 | 24.39 |

DFF= Days to 50% flowering (Days), PH= Plant height (cm), NPBP= Number of primary branches per plant, NSBP= Number of secondary branches per plant, NCP= Number of clusters per plant, NPC= Number of pods per cluster, PL= Pod length (cm), PM= Pod mass (g), PWM= Pod wall mass (g), PWP= Pod wall proportion (%), SM= Seed mass (g), SP= Selling percentage, SI= Seed index (%), BYP= Biological yield per plant (g), HI= Harvest index (%), SYP= Seed yield per plant (g), E1= Environment 1 (Early sown condition), E2= Environment 2 (Timely sown condition), E3= Environment 3 (Late sown condition).

of variability. Therefore, it is expected to be more useful for the assessment of real variability. Success of any breeding programme is dependent on genetic variation present in breeding materials. The magnitude and extent of genetic variability existing in genotypes is very important. The more variability gives more chance to incorporate the traits/ genes from one genotype to another one, for effective utilization and improvement of crops. In the present study, the variability for all the traits was estimated on the basis of phenotypic and genotypic coefficient of variation. The phenotypic coefficient of variation (PCV) was higher than the corresponding GCV for all the traits studied over environment. This difference indicated that the traits were influenced by environmental factors. High magnitude of GCV and PCV were recorded for NPBP, NSBP, BYP, HI and SYP in all three environments. NCP, NPC exhibited high GCV and PCV only in E1. SM exhibited high extent of GCV and PCV in E1 and E3, whereas high PCV and moderate GCV in E3 indicated the influence of environment on this trait in E2. Among the pod traits, high PCV values were recorded for PWM and PWP in E1 and E2. High GCV and PCV have been reported earlier for HI, SYP (Suresh *et al.* 2010), PH & SYP (Rahim *et al.* 2010), PH & SYP (Baisakh *et al.* 2013), SYP & NCP (Narasimhan *et al.* 2013). Low magnitude of GCV and PCV were recorded for DFF, whereas rest of the traits exhibited moderate extent of GCV and PCV. Low magnitude of GCV and PCV indicated the lack of sufficient variability in the tested breeding material. Similar findings have also earlier been reported for DFF by Venkateshwarlu (2001), Biradar *et al.* (2007), Reddy *et al.* (2013). The moderate GCV and PCV values for PH, NBP, NCP, NPC, SI and low for PL, NSP were recorded earlier by Suresh *et al.* (2010).

Heritability ($h^2$) estimates give the best picture of the extent of advance to be expected by selection. In the present study, High $h^2bs$ were recorded for all the traits over different environments studied except for PWM, SP, DFF, NPC, NSP and NCP. PWM showed low, moderate and high $h^2bs$ for E1, E2 and E3, respectively. DFF and NSP exhibited high $h^2bs$ for E1 and E3, whereas moderate $h^2bs$ for E2. High $h^2$ for various yield contributing traits *viz.,* NPBP, NCP, NPC and PL (Veeramani *et al.* 2005), PH, TW (Makeen *et al.* 2007), DFF, PH and SI (Begume *et al.* 2013), SI (Verma *et al.* 2001), PH, NCP & PL (Narasimhan *et al.* 2013) have been reported earlier also. The variation in $h^2$ of these traits clearly reflected that $h^2$ is affected by changing the environments. Shimelis and Shiringani (2010) also suggested that $h^2$ of traits are environment specific and selection done on the basis of variance components and $h^2$ estimates alone may mislead. The selection response ($R$) was low to moderate for all the traits studied in all environments but the nature of $R$ was almost similar in all the environments. Thus, $R$ may be used as selection criteria for selection of traits. The maximum $R$ was recorded for HI in E1 and E2, whereas $R$ of PH was predominant in E3. High $h^2$ coupled with high genetic gain (GG) or proportion of selection response ($pR$) were found for PH, NPBP, NSBP, PM, SM, BYP, HI and SYP in all the environments. The pre-dominance of additive gene action to govern these important yield contributing traits in all three environments, indicated that these could be effectively utilized for improving the seed yield in greengram by simple plant selection method.

**Table 2. Genetic Parameters for yield and yield contributing traits in greengram**

| Traits | DFF | PH | NPBP | NSBP | NCP | NPC | PL | NSP | PM | PWM | PWP | SM | SP | SI | BYP | HI | SYP |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Genetic parameters | | | | | | | | | E1 | | | | | | | | |
| GCV | 9.27 | 18.72 | 26.19 | 42.10 | 17.32 | 24.35 | 8.44 | 14.19 | 15.21 | 11.02 | 14.74 | 20.71 | 8.14 | 9.92 | 30.94 | 33.80 | 37.67 |
| PCV | 10.85 | 19.80 | 28.77 | 44.55 | 21.15 | 27.65 | 10.20 | 18.31 | 16.79 | 27.46 | 24.68 | 22.12 | 15.59 | 11.38 | 32.33 | 38.52 | 39.98 |
| $h^2$ bs | 72.93 | 89.41 | 82.91 | 89.30 | 67.12 | 77.51 | 68.37 | 60.01 | 82.05 | 16.11 | 35.69 | 87.67 | 27.24 | 75.98 | 91.60 | 77.00 | 88.77 |
| *R* | 5.68 | 19.68 | 1.81 | 3.15 | 3.37 | 2.15 | 1.00 | 2.40 | 0.12 | 0.01 | 6.46 | 0.11 | 5.64 | 0.63 | 11.86 | 15.94 | 3.48 |
| GG (*pR*) | 16.30 | 36.46 | 49.13 | 81.96 | 29.24 | 44.15 | 14.37 | 22.64 | 28.38 | 9.12 | 18.14 | 39.95 | 8.75 | 17.81 | 61.00 | 61.10 | 73.11 |
| | | | | | | | | | E2 | | | | | | | | |
| GCV | 5.95 | 15.87 | 32.75 | 35.86 | 15.64 | 10.25 | 9.69 | 11.638 | 18.14 | 27.61 | 19.42 | 18.83 | 10.31 | 10.03 | 27.71 | 33.00 | 33.61 |
| PCV | 8.95 | 20.29 | 36.88 | 38.00 | 19.57 | 17.53 | 11.19 | 16.24 | 18.59 | 34.15 | 27.25 | 20.69 | 14.57 | 11.12 | 29.34 | 38.66 | 36.87 |
| $h^2$ bs | 44.10 | 61.18 | 78.87 | 89.06 | 63.86 | 34.17 | 74.99 | 51.36 | 95.23 | 65.39 | 50.79 | 82.80 | 50.06 | 81.34 | 89.17 | 72.83 | 83.07 |
| R | 2.73 | 11.53 | 1.81 | 2.25 | 3.09 | 0.55 | 1.11 | 1.93 | 0.15 | 0.07 | 9.88 | 0.09 | 9.82 | 0.62 | 9.31 | 17.84 | 3.21 |
| GG (*pR*) | 8.13 | 25.57 | 59.91 | 69.71 | 25.74 | 12.34 | 17.29 | 17.18 | 36.47 | 46.00 | 28.51 | 35.29 | 15.02 | 18.63 | 53.90 | 58.01 | 63.10 |
| | | | | | | | | | E3 | | | | | | | | |
| GCV | 8.62 | 17.22 | 30.41 | 38.03 | 7.79 | 18.02 | 6.82 | 12.92 | 15.89 | 16.28 | 12.35 | 24.92 | 12.85 | 11.39 | 28.95 | 42.93 | 28.68 |
| PCV | 10.71 | 18.79 | 35.06 | 42.45 | 62.18 | 23.84 | 10.36 | 16.26 | 16.39 | 19.77 | 15.30 | 26.45 | 15.92 | 14.53 | 30.06 | 51.29 | 36.57 |
| $h^2$ bs | 64.68 | 84.03 | 75.21 | 80.29 | 1.57 | 57.18 | 43.26 | 63.08 | 94.02 | 67.79 | 65.15 | 88.73 | 65.12 | 61.38 | 92.76 | 70.04 | 61.52 |
| *R* | 4.19 | 14.64 | 1.44 | 1.62 | 0.14 | 0.95 | 0.51 | 1.37 | 0.12 | 0.05 | 10.46 | 0.09 | 10.48 | 0.44 | 13.28 | 10.00 | 1.35 |
| GG (*pR*) | 14.27 | 32.52 | 54.32 | 70.20 | 2.01 | 28.08 | 9.24 | 21.13 | 31.75 | 27.61 | 20.54 | 48.35 | 21.36 | 18.37 | 57.43 | 74.00 | 46.34 |

GCV= Genotypic coefficient of variation, PCV= Phenotypic coefficient of variation, $h^2$bs= Heritability in broad sense, *R*= Selection response, GG= Genetic gain, *pR*= proportion of selection response, DFF= Days to 50% flowering (Days), PH= Plant height (cm), NPBP= Number of primary branches per plant, NSBP= Number of secondary branches per plant, NCP= Number of clusters per plant, NPC= Number of pods per cluster, PL= Pod length (cm), PM= Pod mass (g), PWM= Pod wall mass (g), PWP= Pod wall proportion (%), SM= Seed mass (g), SP= Selling percentage, SI= Seed index (%), BYP= Biological yield per plant (g), HI= Harvest index (%), SYP= Seed yield per plant (g), E1= Environment 1 (Early sown condition), E2= Environment 2 (Timely sown condition), E3= Environment 3 (Late sown condition).

Singh *et al.* (2009) has also observed high *pR* for HI, SYP, BYP, SI, NSP and PH. Similar findings for SYP, NSP and PH were reported earlier by Singh and Kumar (2009). The maximum *pR* along with high $h^2$ was recorded for NSBP followed by SYP, HI and BYP under E2, whereas in E1 it was recorded for SYP followed by NSBP, HI and BYP. This finding indicated the stability under varied environmental conditions (E1 and E2), as environment is less influential on highly heritable traits and could easily be improved by applying selection pressure and these traits showed greater importance for improvement of greengram. The maximum *pR* along with high $h^2$ under E3 was recorded for HI followed by NSBP. DFF and SI exhibited high heritability but low to moderate magnitude of GG, indicated the preponderance of non additive gene action governing these traits and improvement can be done by recombination breeding. NCP showed high $h^2$ coupled with high GG (*pR*) in E1 and E2, indicated that improvement of this trait could be done by single plant selection for E1 and E2 (timely and late sown conditions) although there is a need to identify the superior parents for trait manipulation by recombination breeding for improvement of NCP for very late sown (E3) condition.

Among all the 17 quantitative traits, some important traits *viz.,* PH, NPBP, NSBP, PM, SM, BYP, HI and SYP were found consistent for various genetic parameters (GCV, PCV, $h^2$, *R*, *pR*). Nevertheless, a perusal of additive gene action involved in governing these traits indicated that the simple selection method might give better response, while recombination breeding could be used for improving other traits of greengram.

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