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Research Article

Genetic divergence among greengram (*Vigna radiata* (L.) Wilczek) germplasm collections

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Abstract
Four hundred and forty five genotypes of greengram were evaluated for eight quantitative traits *viz.* plant height, number of branches/plant, number of clusters/plant, number of pods /clusters, number of pods/plant, pod length, 100- seed weight and seed yield /plant. The data was subjected to cluster analysis, and the genotypes were grouped under three discrete clusters. This study concluded that an effective hybridization programme including the genotypes between the clusters I, II and III would produce wider segregation that might be used for development of improved greengram varieties.

Keywords
Greengram, diversity, seed yield, clustering

Introduction

Greengram (*Vigna radiata* (L.) wilczek, 2n=22, Fabaceae) is one of the most important edible food legumes of Asia widely cultivated and consumed throughout India (Datta *et al.,* 2012). It is cultivated in tropical, sub-tropical and temperate zones of Asia including Bangladesh, India, Pakistan, Myanmar, Indonesia, Philippines, Srilanka, Nepal, China, Korea, and Japan (Shanmugasundaram, 2001). It is regarded as quality pulse due to its excellent digestibility and rich protein (25-28%), especially when combined with cereals (Thirumaran & Seralathan 1988). India is the leading greengram cultivator with upto 55% of the total world acreage and 45% of total production (Rishi, 2009: Singh *et al*. 2013). On account of its short duration, photosensitivity and dense crop canopy, it assumes special significance in crop intensification, diversification and hybridization.

The yield of green gram has not increased substantially due to lack of sufficient genetic diversity for desirable traits in the germplasm used for improvement (Skrotch and Nienhuis, 1995). It is essential to have knowledge on variability of different characters for crop improvement. Tabasum *et al.* (2010) reported that the biometrical traits are useful for establishing selection criteria for hybridization program. Crop improvement is mainly depending upon the amount of genetic variability existing among the selected populations. Genetic diversity is one of the important key factors and also necessary in any hybridization program. Obtaining desirable recombination can be possible only by the activity of inclusion of diverse parents in hybridization program (Yimram *et al*., 2009). Study of genetic diversity in genetic resources is a critical factor for breeders to better understand the evolutionary and genetic relationships among populations, to select germplasm in a more systematic and efficient way and to perform and develop strategies to incorporate useful diversity in their breeding programs (lavanya *et al.,* 2008). The crosses between the parents with maximum genetic divergence are generally the most responsive for genetic improvement (Arunachalam, 1981). In the present study, 445 greengram germplasms were taken to assess diversity among them using quantitative data.

Materials and Methods

The experimental materials for the present study comprised of 445 diverse germplasms maintained at the National Pulses research center (NPRC), Vamban, were evaluated during *Rabi* 2016-17. Each entry was evaluated in 2.4 m^2 plot. Recommended crop management practices were followed. Eight quantitative traits *viz.* plant height (cm), number of branches/plant, number of clusters/plant, number of pods/clusters, number of pods/plant (g), pod length (cm), 100 seed weight (g), seed yield /plant (g), were observed on five randomly selected plants per genotype. The data collected on 445 genotypes were analyzed using Darwin5 (version 5.0.158) software with continuous dissimilarity index method with

Euclidean on standardized variables under 1000 as boot strap number with default method 'DICE'. The tree had been constructed using weighted neighbour joining method and the germplasms were grouped under various clusters.

Results and Discussion

The present study is also important on the account that India is the centre of origin for greengram and varieties released for cultivation are expected to be diverse because they are released from different states according to their suitability to respective agro-climatic regions. A comprehensive diversity analysis of yield contributing attributes in such a diverse set of germplasm accessions may assist the greengram breeders in deciding which one of the two is appropriate for the exploitation of transgressive segregants in the segregating populations.

In the present study all the 445 greengram genotypes were grouped under three major clusters (Table 1 and Fig.1). Those clusters were divided into sub clusters. The maximum number of clusters were included in the cluster I A (266 genotypes), followed by sub cluster II A (89 genotypes), sub cluster I B (51 genotypes), sub cluster II B (30 genotypes), and sub cluster I C and cluster III were found with less number of genotypes *viz.,* 7 and 2 genotypes respectively.

Characterization of the genetic diversity and phylogenetic relationships provides valuable information needed to broaden the narrow genetic base as well as enhance breeding and conservation strategies for crops (El-Esawi *et al*., 2016). Analysis of population structure also facilitates a deeper understanding of germplasm diversity and association mapping studies [El-Esawi *et al*., 2017]. Therefore, various approaches including coefficient of parentage, morphological traits and biochemical markers (storage proteins and isozymes) have been used for evaluating the genetic variation level and structure in many crops, including wheat, maize, soybeans and barley (De Lacy *et al*., 2000).

In the present study all the 445 greengram accessions were grouped into 3 three clusters with 5 sub populations. Accessions from Vamban (VGG), exotic collections and other accessions were grouped in all the three clusters viz., I (IA, IB, IC), cluster II (II A and II B) and cluster III. The overlap may be due to frequent germplasm exchange among the greengram breeding centers. This result is in accordance with the findings of Chen *et al*., (2017). Exchange of genetic resources and germplasms will benefit plant breeding research and cultivar development and will facilitate greater use of germplasm to develop new cultivars with a wider genetic base.

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Table 1. Clustering pattern of 445 of greengram germplasm accessions

Cluster	Subcluster	Genotypes
I	I A	LPUS93, EC391178, SPS352, WGG39A, RM11602, PLM3A, PDM841464, WGG62, COGG919, STU2651, ML703A, ML1367, GM8835B, GANGA7, VRD911B3, VGG87, WGG47B, SP29, NO2268, M705, HUM16, BDYR1, ML209SMU11, PDM8927A, GPR22G/A, PS16, PLM150, GP644, VGG124, GPR22G/A, GP1, SPLMBB, KMG2140A, PGSA9031, VGG2, VGG80, UPM0218, NL1B, VGG05006, PDM91242, LM6843, WGG478, VPM924, LGG460, IC296672, NL43A, ML1257, NL3B, COGG923, GPS272, LM70381, VPM92, GP58A, VGG10005, NPM31, NL23, COGG942, ML1059, PDM8414A, LM65, SP23, EC39885, VGG28, EC314288, PDP8926, ML935, VBN3, PLM12, CHINAMUNG2, HUM1, ML682, MHIK25, SEC2, ACC1729B, AGY1721, AKM961, AKN962, AKP/NP1819, ASHAMUNG, AVRDG3484, BDYR1, BHUTANLM1, BHUTANLM2, BOD1, CE514, CHINAMUNG, CHINAMUNG1, CHINAMUNG2, CO4, CO6, COGG8, COGG901, COGG917, COGG919, COGG923, COGG924, COGG940, COGG942, COPORGARN, EC200341, EC314288, EC314289, EC391178, EC39885, EC398886, EC398891, EC398894, EC398897, EC496839, EC496841, EC501566, EC52001, EC520011, EC520014, EC520016, EC520024, EC520026, EC52004, EC52034, EC522022, EC550831, EC59388, ES134, GANGA1B, GANGA5, GANGA7, GANGA8, GM208, GM8535A, GM8835B, GP1, GP162, GP163B, GP471, GP58A, GP644, GPP113, GPP131, GPR22G/A, GPS272, GPS280, HUM16, HUM161, HUM1 , IC296672, IP01539, IPM23, JR6, KMG2140A, KMG2, LB86, LDM, LGG22, LGG410, LGG460, LM44A, LM49YM, LM56B, LM70381, LM258, LM258, LM64, LM65, LM6843, LM701, LM95, LPUS93, M705, M905, MG3098MG3294, MHIC24, MHIK25, MI2A, ML2283,ML1367, ML209SMU11, ML3A,ML703A,ML1059,ML1108,ML1165,ML1257,ML13,ML130,ML17,ML1A,ML319,ML331,ML515, ML682, ML682, ML729, ML818, ML935, MT12A, NG1020, NG29A, NL13, NL61, NL12A, NL1B, NL23, NL3B, NL43A, NL7B, NO2268, NPM31, OMG1030, OMG1045, P166, PANAPAGILOCAL, PDM54, PDM841464, PDM8414A, PDM88271, PDM8927A, PDM91242, PDM139, PDM8934, PDP42, PDP8926, PGSA9031, PGSA9132, PGSA9531, PLM12, PLM12PD101, PLM150, PLM212, PLM299A, PLM3A, PLS248, PLS259, PLS265, PLS26839, PLS3001, PLS476B, PLS9630, PM4, PM5, PMG311, PS16, PUMTH3, PUSA109A, PUSA118A, PUSA95531, PVSA9030, PW1, RM11602, RM11605, RM11612, RM11614, RMG189, RMG216, RMG330, RMG341, RMG394, SAPTARI, SEC2, SM191, SM47, SM48, SML668, SP16, SP17, SP21, SP23, SP24, SP29, SP35, SP63, SP64, SP84, SPLMBB, SPS352, STU2651, STU2631, SU23, SU4146, SU4149, TAARM1, TAARM18, TARM20B, TMB37, TMR13, UH867,UPM0218,UPM981, VBN1, VBN2, VBN3, VGG03021, VGG04001, VGG04002, VGG04005, VGG04009, VGG04010, VGG04011, VGG04012, VGG04013, VGG04015, VGG04016, VGG04019, VGG04021, VGG04022, VGG04023, VGG04025, VGG04149, VGG0416, VGG05006, VGG06013, VGG07007, VGG10008, VGG10010, VGG10012, VGG10015, VGG10018, VGG29, VGG1, VGG10002, VGG10005, VGG10012, VGG113, VGG114, VGG116, VGG121, VGG123, VGG124, VGG127, VGG15, VGG2, VGG24, VGG26, VGG28, VGG80, VGG87, VGG90, VPM92, VPM922, VPM924, VRD911B3, VRD91/P3, WGG39A, WGG478, WGG47B, WGG62.
	I B	PLS259, WGG47B, NL10, RMG62, LM216, LM56, KOPERGAN, NL15B, STV26560, TNP7, NL67, SP26, BDYR2, PM2, ML18143, PLM113A, TAR3, CES4, M412B, EC314284, ML29, AKN961, GM84041A, EC5200246, RMG39A, NL14A, TMB962, GM9, VPM0217, MS12A, VGG117, PLS330, VGG04148, SP32, VGG77, VGG73, PLS313, PLM113DMG, RM1237, PM3, HUM12, K851, ML1100, STV2725, SP28, VGG20, PLS248, RMG348A, NL326, VGG119.
	I C	WGG47A, LM184B, LM520B, LM850A, PLS39A, VGG05001, COGG954.
II	II A	NL20B, OCGG931, NL161, PUSA118RMG, PLS476A, VGG120, LM388, VGG07003, PLM314, VGG70, NL209SM11, LGG422, LM122, GAPR22, CHINAMUNG, LGG160, IPM214, PLS303A, GPB262, NL101, SP18, VGG05009, GPLM87, HUM9, VGG04146, PLS3051, VGG9123, VGG04150, ML12, EC398889, PDM89226, ML1256, VGG070021, VGG10013, VGG128, VGG23, DUM115, ML148, ML2037, VGG10004, BM64, EC520029, PDM93366, PUSA9031A, RMG353, V1133, VGG10001, VGG040145, ML558, ML131, VGG148, VGG13, RM11604, PLS330, PDM84146, PUSA18A, MH981, LM68, COGG932, VGG05010, PLS311B, COGG936, TMB962, SU4137, WGG85, VGG04007, VGG07001, VGG10021, VGG06013, VGG006, VGG10016, VGG10009, VGG08003, TRM21, SP229, VGG10020, SAMRAT, S8, BM63, KMG341, LM1036, PLS282, IPUSYM6, PLU125, IPU917, M702, NL17A, PLS111, SP19, VGG11.
	II B	AKN994, CO5, CO7, COGG912, COGG915, LGG460, LM44B, LM65B, MH318, MH521, ML515, NL1914, NL30A, PDM89229A, PDM9929, PDM8929, PLS303B, PLS476A, PRATUKSHANEPAL, PUSA103, SP12, SP47, SU4135, TM200050, VGG06003, VGG08002, VGG10002, VGG10007, VGG10017, VGG112.
III		VGG127, ML331

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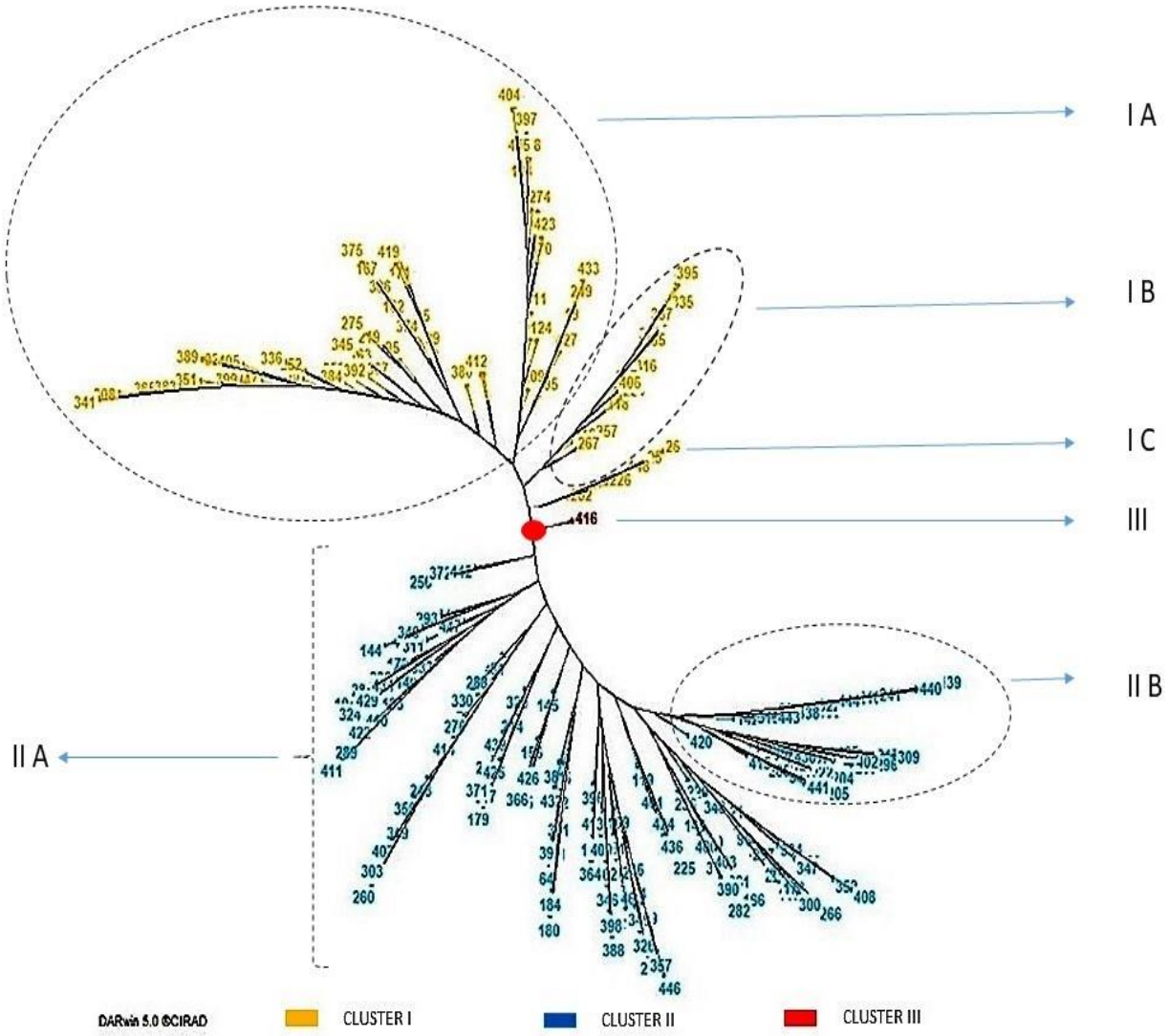

Fig. 1. Dendrogram of 445 greengram accessions based on neighbour joining method (radial)