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Genetical studies on assessment of combining ability for grain yield and yield attributing traits in green gram (*Vigna radiata* (L.) Wilczek)

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Abstract

Combining ability determined through diallel analysis is useful to assess the nicking ability of the parents and at the same time, it elucidates the nature and magnitude of different types of gene actions involved. Superiority of parents depends on their ability to combine well and on the potentiality to produce transgressive segregants. Combining ability not only helps in developing improved hybrids and high yielding varieties but also aids to identify the best combiner in breeding procedure, thus it is an unavoidable phenomenon for the plant breeders. For any successful breeding programme to improve grain yield and component characters, it is essential to know precisely the genetic architecture of these characters under prevailing conditions. For appropriate breeding strategy, knowledge of nature of inheritance is essential. To understand the nature of inheritance of yield and its components, genetic parameters like gene action, combining ability are necessary. Hence, estimation of general combining ability and specific combining ability may be very helpful in selection of parents and identification of desirable crosses. In a crop improvement programme, much of the success rests upon isolation of valuable gene combination as determined in the form of lines with high combining ability.

Keywords: mungbean, gene action, combining ability, GCA, SCA, and yield components

Introduction

Pulses constitute an important ingredient of the vegetarian as well as non-vegetarin diet in the Indian sub-continent and play a significant role in Indian farming because of their value in providing quality food to teeming million and restoring soil fertility through biological nitrogen fixation. India is the largest producer and consumer of pulses in the world accounting 33 per cent of the area and 25 per cent of the global out-put. Green gram (*Vigna radiata* (L.) Wilczek) is the most important legume crop in India after chickpea and pigeonpea. It belongs to family Leguminaceae, subfamily Papillionaceae, genus *Vigna*, species *radiata* and its chromosome number is 2n = 2x = 22. According to Vavilov (1926) [56] and Zukoveskij (1962), green gram has originated from Indian Sub-continent. Green gram is extensively grown in India under varying soil types and climatic conditions. It is fairly well adapted to sandy loam soils and dry conditions. Besides being a rich source of protein, green gram enriches soil fertility through atmospheric nitrogen fixation with the help of rhizobium bacteria in nodules and humus thus, plays a crucial role in furthering sustainable agriculture. It is drought tolerant crop and suitable for dry land farming and predominantly used as intercrop with other crops. Among pulses, green gram has important place as it contains more digestible proteins. The seeds are easily digestible and form excellent source of food for infants in the absence of milk. It contains 25.0 per cent proteins with all essential amino acids, which is almost three times more than that of cereals (Saini *et al.,* 2010) [44]. The biological value improves greatly, when wheat or rice is combined with green gram, because of the complementary relationship of the essential amino acids, it is particularly rich in Leucine, Phenylalanine, Lysine, Valine, Isoleucine etc. India is the primary green gram producer and contributes to about 75 per cent of the world pulses production. Maharashtra, Rajasthan, Madhya Pradesh, Bihar, Punjab and Andhra Pradesh are the leading producers of green gram. In India, pulses are grown in nearly 25.4 million hectare area with production status of nearly 19.66 million tonnes at an average productivity level of 770 kg/ha. Among various pulse crops grown in India, green gram is grown on an area of 2.75 million hectares with a production of 1.19 million tonnes and productivity of 436 kg/ha (Economic Survey 2013-2014. The country has experienced progressive decline in per capita availability of pulses per day from 70.3 g in 1956 to 41.9 g in 2013 (Agril. Statistics at a glance, 2014). This decline is mainly attributed to the steady marginalization of their cultivation in the wake of the green revolution, meager productivity

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advances and burgeoning population. Several reasons have been suggested for low productivity of this crop, which include inherent low potential of yield, damages caused by several diseases like yellow mosaic virus, anthracnose, little leaf and pest, abiotic stress factors and poor management. It generally felt that there is an urgent need to break the bottleneck for increasing productivity of this crop.

Serious attention is required to develop high yielding varieties of green gram using various crop-breeding techniques. The diallel cross analysis technique (Griffing, 1956) [19] could be used as one of the approaches to identify superior parents and crosses. Further knowledge on genetic architecture and mode of inheritance of different characters related to yield and quality is necessary for the effective implementation of selection programme aimed at improvement of genotypes

Material and Methods
The statistical analysis of variance for randomized block design can be carried out for the data recorded on each character as per standard procedure given by Panse and Sukhatme (1985). Analysis of variance for combining ability can analyse according to method 2 (Parents and one set of F_1s without reciprocals) Model-I (fixed effects) of Griffing (1956) [19]. In this model, experimental material regarded as population about which inference was to be drawn and combining ability effects of parents could be compared when parents themselves are used as tester to identify good combiner. It can assumed that variety and block effects were constant but error (environment and other uncontrollable components) was variable and normally and independently distributed with mean zero and variance. Another important method to assess the nature of gene action involved and combining ability of parental genotypes for different characters utilizing Line × Tester mating design (Kempthorne, 1957). For testing significance of difference between two effects, the critical difference was divided by respective standard error of difference and compared with table value of 't' at error degree of freedom

Result and Discussion
Combining ability
The concept of combining ability was enunciated in maize by (Sprague and Tatum, 1942) [50]. They defined the term GCA as an average performance of a line involved in crosses, while SCA as those instances where certain cross combinations do relatively better or worse than would be expected based on average performance of parental lines involved. It has also been revealed that GCA is primarily due to additive gene effects and additive x additive interaction variance, while SCA is the consequence of non-additive genetic effects arising from dominance and epistatic deviations. It is also being realized that high yielding lines may not necessarily be able to transmit their superiority to their hybrids (Allard, 1960) [8]. Hence an estimate of GCA and SCA effects may be more reliable test rather than their *per se* performance. Choice of the parents is one of the important practical problems encountered by plant breeders, which plays important role in hybridization and produce superior off springs. Pedigree system would be more efficient method of obtaining lines with high pod and cluster numbers. Simultaneously, diallel selective mating among the good general combiners can be followed for release of greater genetic variability (Malhotra *et al*. 1980) [32]. The most useful technique that helps plant breeders in this direction is the analysis of combining ability. Non-additive gene effects were important for all traits except

100-seed weight and harvest index for which additive gene effects were more important. Significant specific combining ability for height and pod number and seed yield/plant while for general combining ability for all traits (Ahuja, 1980) [5]. The variance due to specific combining ability (σ^2 sca) was much higher than the variance due to general combining ability (σ^2 gca) indicating the operation of non-additive gene action for expression of grain yield (Basaeeruddin & Nagur 1981) [13]. The existence of both additive and non-additive gene action for days to flowering, days to maturity, plant height, pods/plant, pod length, seeds/pod, seed yield/plant, 100-seed weight and protein content. However, additive gene action was predominant in the expression of all the characters except protein content (Wilson *et al*. 1985) [57]. Parents T44 and K8S1 had significant positive estimates of gca effects for the nodulation traits and would be useful as parent in hyridization programmes. Some cross combinations showed significant heterosis for the three traits (Singh and Paroda 1985). The variance due to gca effects was more prominent for branches /plant and 100-grain weight, while sca variance was prominent for plant height, days to flower, clusters/plant, pods/cluster, pods/plant, seeds /pod and grain yield (Thimmappa *et al*. 1989) [52]. Both additive and non-additive gene action were important for plant height, clusters/plant, pods/plants, seeds/pod and seed yield. The additive gene action was predominant for plant height and seed yield (Natarajan et al. 1990) [35]. Mungbean parent ML 5 and Sabarmati were a good general combiners for seed yield, pods/plant, clusters/plant and tallness etc. The crosses showing high sca effects for yield also had significant and positive effects for two important yield components (Pathak *et al*. 1990) [38]. The additive gene action was predominant for days to flowering, maturity, plant height, seeds/ pod and 100-seed weight whereas non-additive gene action was predominant for seed yield/ plant (Reddy *et al*. 1992) [41]. Additive and non-additive variances were significant for branches/plant, pods /plant, seeds /pod and seed yield/plant. However, an additive component was higher than that of non-additive component (Saxena & Sharma 1992) [45]. The gca variance found higher than sca variance for branches/plant and test weight, while sca variance was higher than gca variance for days to maturity, plant height, pods/plant, seed yield/plant and protein content (Tiwari *et al*. 1993) [53]. Both gca and sca variances were significant for all the characters except branches/plant and pod length. The sca was predominantly higher in all the characters except days to flowering, 100-seed weight and seed yield (Holkar, 1994) [20]. The dominance gene action was involved in the expression of yield, pods/plant, plant height, pod length and custers/plant in mungbean. Additive x additive and dominance x dominance played important role in the expression of plant height, branches/plant, clusters/plant, pods/plant and grain yield/plant (Ram, 1997) [40]. Recorded that out of 28 F_1's only 4 F_1's exhibited positive significant sca effects (Aher *et al*. 1998) [4]. Additive gene effects were predominant for seed yield/plant, pods/cluster and harvest index. B1 and B105 were good general combiners for seed yield/plant. PS16 was a good general combiner for protein content. The three best specific combinations for seed yield/plant and other traits involved one parent with good GCA effects (Dasgupta *et al*. 1998) [14]. Additive gene effect was predominantly higher for all the characters except seed yield/plant (Kute *et al*. 1999) [31]. Days to 50% flowering, days to maturity, plant height, primary branches/ plant, seeds/ pod, 100-seed weight and protein content were under the control of additive gene actions. On

the other hand, pods/ plant and seed yield /plant were governed by non-additive gene actions (Aher *et al*. 1999) [2]. The specific combining ability (sca) effects were found to be higher in magnitude than the general combining ability (gca) effects for all the six characters. The ratio of gca to sca variance was less than unity for all the characters, indicating the presence of the non-additive gene action for all the characters studied (Joseph & Santhoshkumar, 2000) [24]. The variance due to both gca and sca were highly significant for all the characters except primary branches/plant, indicating the importance of both additive and non-additive gene effects. However, the additive gene effects showed pre-dominance for all the characters studied (Aher *et al*. 2001) [3]. Variances due to gca and sca were significant for all the characters studied. The good general combiners consisted of Kopargaon and TARM 18 for days to 50% flowering and maturity; PIP 3-85-2 for plant height, pods/ plant, 100-seed weight, and grain yield /plant; and AKM 8802 for pods/ plant, and grain yield /plant (Gawande and Patil 2002) [16]. All the characters *viz*., plant height, branches/plant, pods/plant and seed yield /plant displayed predominance of gca than that of sca variance in mungbean (Manivannan, 2002) [33].

Nature of gene action
Predominance of additive effects for days to flowering, pods/cluster, pods/plant and 100-seed weight in was recorded most of the crosses. The dominance effect was also noticed in most of the crosses for clusters/plant, pods/plant and seed yield/plant (Kute & Deshmukh, 2002) [31]. The estimates of sca variance were higher than gca variance for all the traits indicating the importance of non-additive gene effects in the expression of the traits. IPM 99-124 x IPM 99-125 was the best combination, because of its high and desirable sca effect for seed yield/plant (Singh & Dikshit, 2003) [46]. The ratio of gca : sca indicated the preponderance of non-additive type of gene action for all the traits. The parents VGG 77, MI 267, Vamban 2 and KM 2 were the best general combiners for most of the characters (Anbumalarmathi *et al*. 2004) [10]. The magnitude of sca variances for all ten characters indicated the influence of non-additive gene action (Kumar *et al*. 2005) [29]. Analysis of variance revealed highly significant differences for female and male parents and their interaction in F1 and F2 generations. Estimation of genetic components of variation revealed the significance of both additive and non-additive components in both generations (Aziz *et al*. 2005) [11]. General and specific combining ability mean squares were significant for 2 nitrogen fixation traits. Parents K-851, PS-7 and PIMS-2 showed significant positive gca effects and would be useful as parents in breeding programmes (Singh & Singh 2005) [48]. The mean squares due to LXT were significant for all the characters indicating greater variability among the parents. The interaction effects between lines and testers were significant for all characters except branches/ plant. The variances due to sca were of greater magnitude than gca indicating the majority of non-additive gene action (Gopi *et al*. 2006) [17]. The parent VC 3760-88 was the best general combiner for grain yield/plant, pods/plant, pods/ cluster and clusters/ plant. SML 668 x VC 3760-88 had the highest sca values for grain yield/ plant, clusters /plant, pods /cluster, pods/plant and seeds /pod along with their high *per se* performance in mungbean (Gupta *et al*. 2006) [18]. The additive genetic effects appeared to be important for pod length and 100-seed weight and non-additive effects were pronounced for pods/plant, seeds/pod, and grain yield/plant. Directional dominance was observed for pods/ plant,

seeds/pod, and grain yield/plant (Ajmal *et al*. 2007) [6]. The presence of additive, dominance and epistatic gene effects in almost all the crosses indicated importance of both additive and non-additive gene actions for the expression of the characters namely, days to 50% flowering, days to maturity, plant height, primary branches, pods/ plant, pod length, seeds/ pod and yield/plant (Singh *et al*. 2007) [49]. The sca variances were greater in magnitude than the gca indicating the preponderance of non-additive gene action for all the yield attributing characters. The parents LGG 450, LGG 410, ADT 3 and KM 2 were identified as good general combiners based on gca effect. The hybrids LGG 450/ADT 3, VRMGG Local/KM 2 and LGG 410/ADT 3 exhibited high sca effects for all the economic traits (Vasline *et al*. 2007) [54]. The additive gene action was involved in controlling days to flowering, days to maturity and seed yield /plant. While other characters *viz.,* plant height, clusters /plant, pods /plant, pod length, seeds/pod, 100-seed weight and protein content were under the control of non-additive gene action (Barad *et al.* 2008) [12]. The mean squares due to gca and sca were significant for all the characters thereby revealed preponderance of additive gene effects for days to 50% flowering, days to maturity and pods/plant. Vaibhav and BM 4 proved to be good general combiners with good *per se* performance for most of the characters (Dethe *et al*. 2008) [15]. Both the general and specific combining ability were significant for seed yield and its related traits. GM-4, VRMG$_g$-1,Pusa bold-1, and Pusa 9632 were good general combiner for seed yield and its related traits. Crosses VRMG$_g$-1 x SM-7 and GM-4 x Pusa bold-2 were the best on the basis of *per se* performance, sca effect, and heterobeltiosis (Intwala *et al.* 2009) [21, 22]. The sca variances were greater in magnitude than the gca indicating the preponderance of non-additive gene action for all the yield attributing characters. The parents, LGG 450, VRMGg Local, and ADT 3 were identified as good general combiners based on gca effect (Vasline & Suguna, 2009) [55]. The parents LGG 460, Pant M 4, and OGG 12 were judged as good general combiners for seed yield. The cross combinations OGG 12/LGG 460, LGG 460/Pant M 4 and TARM 1/OUM 11 5 were identified as potential on the basis of their mean performance and specific combining ability in mungbean (Rout *et al*. 2009) [43]. Parents GM-4 and GM-9918 were good general combiners for seed yield and yield attributing traits. The highest sca effect for seed yield was observed in cross PDM-11 x GM-4 followed by PDM-143 x GM9918. The crosses PDM-143 x GM-9918 and PDM-87 x GM-4 were superior for MYMV incidence (Patel *et al*. 2009) [37]. Eight diverse parents were selected for a diallel set of crosses to study the mode of inheritance. ANOVA showed the significance of additive and dominance effects for all the traits in both generations. Significance of D, H1 and H2 also confirmed the contribution of both additive and dominance effects in controlling the inheritance of traits (Rehman *et al.* 2010) [42]. Parent EC 30072 was a good general combiner for grain yield/plant, whereas VBN 1 and PMB 27 were a good general combiners for 100-seed weight. Cross combinations *viz.*, VRMGG Local/VBN 1, VRMGG 1/EC 30072, VRMGG 1/PMB 27, M 123/LGG 450 and VBN 1/PMB 27 recorded high specific combining ability (Kumar *et al*. 2010) [28]. The ratio of gca to that of sca indicated preponderance of non-additive type of gene action for most of the characters except for plant height and pods/plant. The good general combiners for seed yield /plant were GM-4, Pusa vishal and K-851. The best specific cross combiners were Pusa vishal x SML-668, GM-4 x GM-3, GM-2k3 x GM-

4 showed the highest sca effect for seed yield/plant (Patil *et al.* 2011) [39]. The variance due to female were significant for characters such as plant height, primary branches, cluster/ plant, pods/plant, seeds/ pod and 100-seed weight. Variance due to males were significant for all characters (Kujur & Lavanya, 2011) [27]. High magnitude of sca variance than gca variance was recorded for all characters indicating role of non-additive gene action. The parents, 'Co 6', 'Barimung 7' and 'Binamung 7' were identified as good general combiners for yield and yield contributing characters (Jayamani & Sathya, 2011) [23]. Studied mixing ability and inter-genotypic competition from 7x7 mechanical diallel mixtures excluding reciprocals of mungbean, the biblend BD-6901+BD-6922 was found as the best biblend mixture for different characters. Averaged biblends were 1.35% higher yielding than the mean yield of their uniblend components (Alam *et al.* 2012) [7]. MGG-351, WGG-42, LGG-460 and TM-96-2 were considered as superior parents as they recorded high *per se* performance with positive significant effects for seed yield /plant and other yield contributing traits. Cross combinations viz., MGG-351 x PM-115, MGG-295 x PM-110 and WGG-42 x PM-110 were good specific combinations for seed yield/ plant and other desirable traits (Narasimhulu *et al.* 2014) [34]. Out of thirty hybrids, seven cross combinations for plant height, six for branches per plant, six for pods/plant, 4 for grains/pod, 12 for 100-grain weight and 10 for grain yield/ plant exhibited significant sca effects (Katiyar & Kumar 2015) [25].

Conclusion
Combining ability analysis is useful in isolating superior genotypes and in identifying gene action involved in the inheritance of characters of economic importance. Yield is the most important character for improvement of a crop and it has a complex inheritance governed by large number of genes and greatly affected by environmental factors. Since high gca effect are due to additive and additive x additive gene action they can be readily exploited in breeding program and high sca effect due to dominance x dominance gene action can be used for exploiting heterosis.

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