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EXPLORING GENETIC DIVERSITY FOR HEAT TOLERANCE IN CHICKPEA (*Cicer arietinum* L.) GENOTYPES

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ABSTRACT

An experiment was conducted during Rabi 2016-17 at Pulses Research farm, Bihar Agricultural University, Sabour (Bhagalpur) to study the existing genetic diversity in thirty six Desi chickpea genotypes. All the genotypes were grouped into eight clusters as per Ward minimum variance method revealed the presence of considerable amount of genetic diversity in the material with each other for different yield and yield attributing traits. The cluster IV containing the maximum of 10 genotypes followed by 8 genotypes in cluster II, 7 genotypes in cluster III, 5 genotypes in cluster I, 3 genotypes in cluster in cluster VI, 2 genotypes in cluster V and monogenotypes in cluster VII. The highest intra-cluster distance was exhibited by cluster V (399.87) followed by cluster VI (203.35) and II (148.26). The intra cluster distance was maximum in cluster V followed by cluster VI which indicates hybridization involving genotypes within the same clusters may result in cross combination. The highest inter cluster distance was observed between cluster III and VII (1992.64) followed by cluster IV and VII (1816.53) and cluster V and VII (1639.85). The above results indicate that these genotypes have maximum genetic diversity and useful for developing a large number of segregants through crossing programme by using maximum diverse genotypes. The genotypes of cluster V showed the highest mean values for grain yield per plant, grain yield per plot and chlorophyll index, while cluster VII showed the highest mean for total number of pods per plant, effective pods per plant, harvest index, secondary branches per plant, plant height, canopy temperature at reproductive stage, earliness in flowering and maturity. The cluster VI had highest mean value for 100 seed weight, primary branches per plant and biological yield per plant. The cluster II recorded highest mean value for plant height, lateness and delay in maturity. The promising genotypes for grain yield, number of pods per plant, 100-seed weight, harvest index and early maturity were identified from cluster V and VII on the basis of mean values which could be utilized for hybridization programme for the development of high yielding genotypes. Among the fifteen traits studied, maximum contribution was made by 100-seed weight (46.83%) followed by total number of pods per plant (22.22%) and grain yield per plant (12.54%). Therefore, these characters may be given importance during hybridization programme. Based on the mean performance, four genotypes have been identified PhuleG-13110, H12-55, BG3043 and Sabour chana-1(BRC-1) to have improved tolerance to high temperature and absolute yield equivalent to current commercial cultivars.

Key words : *Chickpea, genetic diversity, D^2 statistics, heat stress and grain yield*

Chickpea is the third leading grain legume in the world and first in the South Asia. It is even more important for India as the country's production accounts for 67% of the global chickpea production and chickpea constitutes about 40% of India's total pulse production. In spite of India being the largest chickpea producing country, a deficit exists in domestic production and demand which is met through imports. In India, the total area under chickpea is 8.25 M ha with 7.33 million tonnes production with productivity 889 kg/ha and the total area in Bihar reached 60.0 thousand ha with 57.50 thousand tonnes of production with productivity of 958 kg/ha (2014-15: Agricultural Statistics Division, Directorate of Economics and Statistics, Dept. of Agriculture and Cooperation).

Chickpea is a cool season food legume and incurs heavy yield losses when exposed to high temperatures (=35°C) at reproductive stage. Heat stress is increasingly becoming a major constraint to chickpea production in India because, increase in area under late sown conditions due to increasing cropping intensity or late maturity of rainy season crop, and expected increase in overall temperatures due to climate change. (1). Reproductive stages (flowering and podding) in chickpea are susceptible to changes in external environment and heat stress (2). The most important effects on the reproductive phase that affect pod set, seed set and yield are: flowering time, asynchrony of male and female floral organ development, and impairment of male and female floral organs. Frequent reductions in chickpea seed yields were observed when plants at flowering and pod development stages were exposed to high (> 35°C) temperatures. It is estimated that about 11.7 million ha of rice area in India, currently remains fallow after late harvest of rice during the winter season in the central and north-eastern India (3). These lands potentially offer expansion in chickpea cultivation provided genotypes

Table-1: Distribution of 36 Chickpea genotypes in various clusters.

Cluster	No. of Genotypes	Name of Genotypes
I	05	JG 74315-14, BRC-4, KWR108, PBC501, PG170
II	08	NDG14-24, GNF469, BRC-3,IPC2012-49, BRC-1, BG3067, GNG2215, JG24
III	07	KPG59, CSJ887, GNG2264, JG16, BG3068, DCP92-3,GL29098
IV	10	GNG2304, GNG2299, GN2207, H12-62, GL12003, GCP105, BRC-2, IPC2012-98
V	02	PhuleG-13110, H12-55
VI	03	NBeG507, ICCV15112, IPC2010-62
VII	01	BG3043

Table-2: Average intra and inter cluster distance values among eight clusters for thirty six genotypes of chickpea under heat stress condition.

Cluster	I	II	III	IV	V	VI	VII
I	113.37	294.12	364.49	293.61	636.37	607.92	878.84
II		148.26	435.29	362.14	660.98	542.89	1246.77
III			125.56	177.71	699.19	1300.70	1992.64
IV				115.05	524.86	1271.57	1816.53
V					399.87	1303.48	1639.85
VI						203.35	459.05
VII							0.00

capable of standing heat stress are made available. Finally, heat stress is expected to be an increasingly important constraint in near future due to climate change and global warming. By 2050, a rise in temperature by at least 2^0C, particularly the night temperatures, is being predicted with higher levels of warming in northern parts of India (4). Predicted climate change, particularly high temperature will reduce grain yield in chickpea. For example, the yield of chickpea declined by up to 301 kg/ha per 1°C increase in mean seasonal temperature in India (4). So, there is an urgent need to search the gene bank for diverse sources of heat tolerance. Heat tolerance is greatly needed in chickpea cultivars for realizing higher yields in all growing conditions that expose chickpea to high temperature, particularly at the reproductive stage. So, heat tolerant varieties are needed for improving chickpea yields in late sown conditions, Heat tolerant varieties will be resilient to climate change and enhance opportunities for expanding chickpea cultivation to new niches. In views of these facts, the current research was undertaken to assess the magnitude of genetic diversity and characters contributing to genetic diversity among late sown lentil genotypes. Therefore, identification of heat tolerant genotypes in available germplasm and their utilization can help to tackle situation of terminal heat stress through the development of heat tolerant cultivars. In views of these facts, the current research was undertaken to assess the magnitude of genetic diversity and characters contributing to genetic diversity among late sown lentil genotypes.

MATERIALS AND METHODS

The experimental material consisted of thirty six chickpea genotypes were sown on15th December 2016 at Pulses Research farm, Bhitti, Bihar Agricultural University, Sabour (Bhagalpur). Atmospheric temperature varied from 4.0°C minimum in January to 45.0°C maximum in May. The experiment was laid out in a randomized complete block design with three replications during Rabi 2016-17 under All India Coordinated Research Project on Chickpea. The plot size was 4.8 m^2, with 1 row of 4 m length. Inter row spacing distance was kept 30 cm and plant to plant spacing was 30 x 10 cm. The recommended packages of practices were followed to raise a healthy crop. Data were recorded on fifteen quantitative traits viz. days to 50% flowering, days to maturity, chlorophyll index, canopy temperature at vegetative stage, canopy temperature at reproductive stage, primary branches per plant, secondary branches per plant, plant height (cm), total number of pods per plant, effective pods per plant, 100 seed weight (g), grain yield per plant (g), biological yield per plant, harvest index and grain yield per plot (g).The days to 50% flowering, days to maturity, and grain yield per plot were recorded on a plot basis and plant height and number of pods per plant and 100-seed weight were recorded from a random sample of five plants in each plot. Genetic divergence was estimated by using D^2 statistics of (5) and clustering of genotypes was done according Ward minimum variance method. The per cent contribution of characters towards genetic divergence was calculated according to (6).

Table-3 : Mean values of clusters of different characters towards genetic divergence in thirty six chickpea genotypes under heat stress condition.

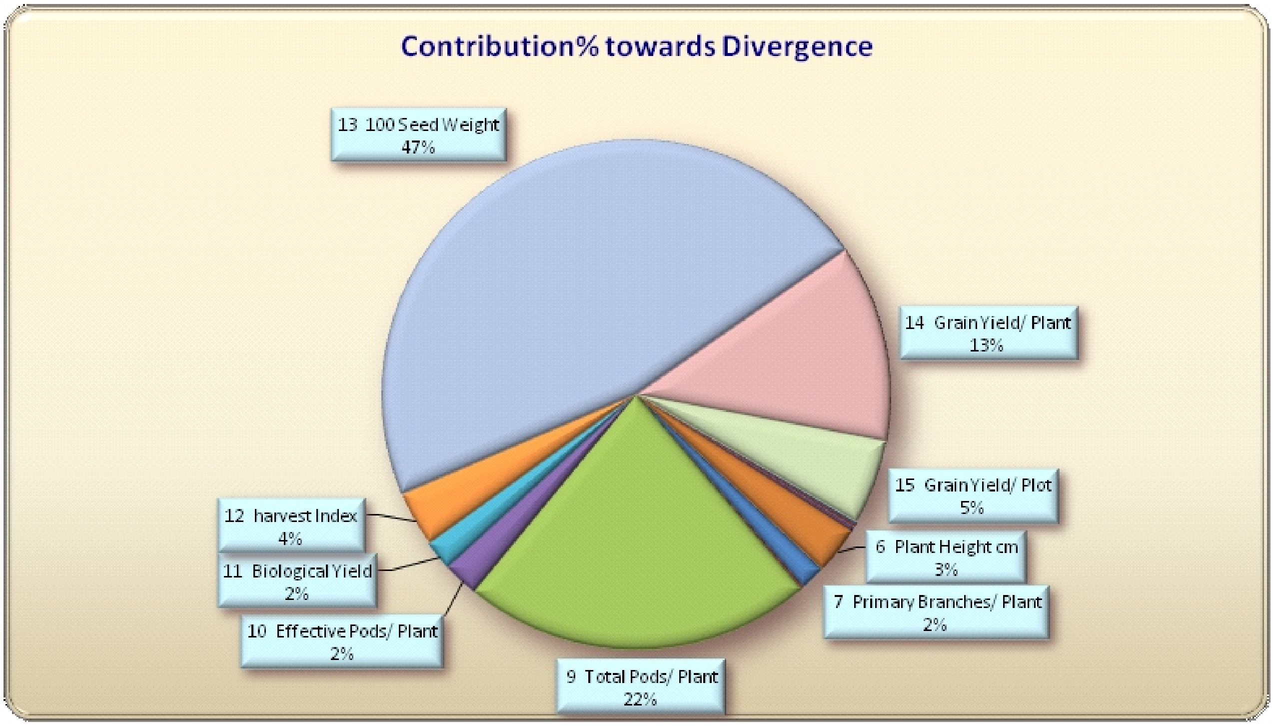
Clusters	Days to 50% Flowering	Days to Maturity	Chlorophy ll Index	Canopy Temperat ure @vs	Canopy Temperat ure @pfs	Plant Height cm	Primary Branches/ Plant	Secondary Branches/ Plant	Total Pods/ Plant	Effective Pods/ Plant	Biological Yield	harvest Index	100 Seed Weight	Grain yield/plant	Grain Yield/ Plot
I	66.300	113.800	59.194	27.570	42.630	45.460	2.000	5.240	44.764	38.056	21.641	43.002	19.450	8.286	1161.555
II	68.250	114.813	58.790	28.272	41.813	52.088	1.763	4.938	28.355	23.104	19.945	43.929	27.969	8.182	1187.076
II	68.429	114.786	57.910	27.211	42.086	41.421	1.357	4.371	22.479	18.209	14.353	33.292	16.429	5.998	1151.424
IV	67.600	113.400	57.976	27.557	42.730	50.100	1.660	4.650	23.048	19.210	11.853	42.225	17.125	6.299	1160.127
V	67.000	114.000	61.445	27.700	42.612	49.300	1.650	4.300	24.545	21.007	14.713	42.732	21.875	22.587	1316.978
VI	67.333	114.500	61.313	27.825	42.025	47.100	2.500	6.133	47.537	42.083	39.427	44.452	34.667	12.172	1170.785
VII	64.000	113.000	61.120	26.575	43.975	40.700	2.400	6.300	82.215	75.750	38.440	54.490	26.750	18.990	1288.340
Mean	67.569	114.153	58.871	27.653	42.356	47.654	1.761	4.892	30.900	26.075	18.692	41.529	21.715	8.682	1177.785
TreatMSS	6.099	2.862	10.252	1.163	1.546	113.551	0.720	2.082	1134.005	996.104	473.413	146.639	254.694	127.908	12220.829
ErrMSS	12.869	2.137	7.100	1.518	1.155	31.659	0.075	0.509	46.289	32.618	23.175	32.490	7.985	3.534	83635.248
F Ratio	0.474	1.340	1.444	0.766	1.339	3.587	9.624	4.094	24.499	30.538	20.428	4.513	31.897	36.193	0.146
Probability	0.793	0.275	0.237	0.582	0.275	0.012	0.000	0.006	0.000	0.000	0.000	0.003	0.000	0.000	0.980

RESULTS AND DISCUSSION

All the genotypes were grouped into eight clusters as per Ward minimum variance method, with cluster IV containing the maximum of 10 genotypes followed by 8 genotypes in cluster II, 7 genotypes in cluster III, 5 genotypes in cluster I, 3 genotypes in cluster in cluster VI, 2 genotypes in cluster V and mono-genotypes in cluster VII. (Table- 1). It means the overall genetic similarity was found in the germplasms were presented within the cluster and the pattern of distribution of genotypes in different clusters exhibited that geographical diversity was not related to genetic diversity as genotypes of same geographical region were grouped into different cluster and vice-versa, as supported by earlier finding of (7). The possible reason for grouping of genotypes of different places into one cluster could be free exchange of germplasm among the breeder of different region or unidirectional selection practiced by breeder in tailoring the promising cultivar for selection of different region. The intra-cluster D^2 value ranged from 0.00 to 399.87 while, inter-cluster D value ranged from 293.61 to 1992.64 (Table-2) in Ward minimum variance method. The highest intra-cluster distance was exhibited by cluster V (399.87) followed by cluster VI (203.35) and II (148.26). The intra cluster distance was maximum in cluster V followed by cluster VI which indicated that hybridization involving genotypes within the same clusters may result in cross combination. The highest inter cluster distance was observed between cluster III and VII (1992.64) followed by cluster IV and VII (1816.53) and cluster V and VII (1639.85). These lines may be utilized in further breeding programme for the exploitation of hybrid vigour. and suggesting wide diversity between them and genotypes in these clusters could be used as parents in hybridization programme to develop desirable type because crosses between genetically divergent lines will generate heterotic segregants. As heterosis can be best exploited and chances of getting transgressive segregants are maximum when generating diverse lines are crossed (8). Therefore, crosses between the members of clusters separated by inter-cluster distances are likely seemed to be beneficial for further improvement. Significant differences among the genotypes for different characters indicated variations among the genotypes favorable for their use in the breeding programs. Crosses between parents with maximum divergence would be more responsive to improvement since they are likely to produce higher heterosis and desirable genetic recombination (7). The genotypes of cluster V showed the highest mean values (Table-3) for grain yield per plant, grain yield per plot and chlorophyll index, while cluster VII showed the highest mean for total number of pods per plant, effective pods per plant, harvest index, secondary branches per plant, plant height, canopy temperature at

Table-4: Contribution of different characters towards genetic divergence of 36 chickpea genotypes.

Source	Contribution %	Contribution %
Days to 50% Flowering	0.16	1.000
Days to Maturity	0.16	1.000
Chlorophyll Index	0.01	0.000
Canopy Temperature @vs	0.32	2.000
Canopy Temperature @pfs	0.01	0.000
Plant Height (cm)	3.02	19.000
Primary Branches/ Plant	1.59	10.000
Secondary Branches/ Plant	0.16	1.000
Total number of Pods/ Plant	22.22	140.000
Effective Pods/ Plant	2.22	14.000
Biological Yield per plant (g)	1.90	12.000
Harvest Index (%)	3.49	22.000
100 Seed Weight (g)	46.83	295.000
Grain Yield/ Plant (g)	12.54	79.000
Grain Yield/ plot (kg/ha)	5.34	34.000



reproductive stage, earliness in flowering and maturity. The cluster VI had highest mean value for 100 seed weight, primary branches per plant and biological yield per plant. The cluster II recorded highest mean value for plant height, lateness and delay in maturity. The promising genotypes for grain yield, number of pods per plant, 100-seed weight, harvest index and early maturity were identified from cluster V and VII on the basis of mean values which could be utilized for hybridization programme for the development of high yielding genotypes. Among the fifteen traits studied, maximum contribution was made by 100-seed weight (46.83%) (Table-4) followed by total number of pods per plant (22.22%), grain yield per plant (12.54%), grain yield per plot (5.34%) and harvest index (3.49%). Therefore, these characters may be given importance during hybridization programme.

CONCLUSION

Genetic variability in response of 36 chickpea genotypes to imposed heat stress during the reproductive stage has been demonstrated. Four genotypes have been identified PhuleG-13110, H12-55, BG3043 and BRC-1 (Sabour chana-1) to have improved tolerance to high temperature and absolute yield equivalent to current commercial cultivars. The high inter cluster distance was observed between clusters, suggesting wide diversity between them and genotypes in these clusters could be used as parents in hybridization programme to develop heat tolerant lines because crosses between genetically divergent lines will generate heterotic sergeants. Among the fifteen traits studied, maximum contribution was made by plot yield followed by plant stand at harvest and number of pods per plant. Therefore, these characters may be given importance during hybridization programme and offers provides the opportunity for breeding programs to improve the tolerance of chickpea to heat stress, leading to better yield stability and profitability for growers. Further controlled studies are required to validate these early findings, refine screening methods and investigate mechanisms inferring tolerance.

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