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Genetic Variability and Association of Various Heat Stress Relevantindices for Selecting Heat Tolerant Chickpea (*Cicer arietinum* L.) Genotype

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Abstract

Given the global climate change and frequent episodes of heat stress (HS), global crops including chickpea are receiving serious challenge of yield loss across the globe.A wide range of genetic variability for various phenological traits and yield related traits were recordedin 42 chickpea genotypes including two checks under both normal and HS sown conditions. Aiming at selection of superior genotype and to estimate yield loss, various HS indices were calculated and their significant association analyses were worked out based on the plot yield performance of the given genotypes under both conditions. Based on the results of evaluated stress indices, YI and MP could be deployed to select superior HS tolerant genotypes. In parallel, principal component analysis (PCA) reduced all the calculated HS tolerance indices into two major components; PCA1 explained 57.6% and PCA2 explained 41.6% of the total variation. Moreover, cluster analysis grouped all the genotypes into distinct 4 groups. Thus, a comprehensive assessment of genetic variability and screening of HS tolerant genotype recruiting various selection indices could hasten development of HS tolerant chickpea variety.

Keywords: Selection indices, genetic variation, heat stress, correlation, chickpea

1. Introduction

Chickpea is an important global grain legume crop mainly grown in semi arid and arid regions across the globe (Gaur et al., 2012). It is serving as an important component of global food security. It also helps in fighting malnutrition by providing essential protein, micronutrients and vitamins to the undernourished human population especially in the developing countries across the globe (Upadhyaya et al., 2016). Moreover, given the unique property of fixing atmospheric N_2 by symbiotically efficient root inhabiting bacteria, chickpea enables in enriching soil nitrogen content(Graham and Vance, 2003). It stands the third most important pulses crop grown across the globe (FAO, 2014). Importantly, India stands at the top of the chickpea growing countries across the globe, supplying 14.2 mt to the global food basket from 14.8 mha areas with productivity of 0.96 t ha^{-1} (FAO, 2014). Abiotic stresses remain one of the leading constraints to the global chickpea productivity, causing serious yield loss (Jha et al., 2014a). Add to this, recent global climate change has brought serious challenge to crop productivity including chickpea (Krishnamurthy et al., 2011). Most importantly, increasing evidences of heat stress (HS) is receiving serious attention and, is going to be an emerging threat to the cool season grown global food crops including chickpea (Jha et al., 2014b, 2017, 2018). In the context, consequences of increasing HS have significantly impacted upon chickpea growth in tropical and subtropical regions including Northern part of India, causing serious concern for chickpea yield (Jha et al., 2017; Krishnamurthy et al., 2011). In Indian condition, since last decade consequences of increase in environment temperature during the reproductive phase witnessed significant constraints in reproductive development processes resulting in significant yield loss in chickpea (Gowda et al., 2009). Thus, achieving optimum grain yield under HS remains prime criteria to chickpea breeders. Implication of various indices helps in measuring yield loss and screening HS tolerant genotype under stress condition (Sio-Se Mardeh et al. 2006). Therefore, to sustain the global chickpea productivity under HS, a comprehensive assessment of existing genetic variability under HS and yield based indices for selecting superior HS tolerant chickpea genotype with higher yield potential under prevailingHS condition is urgently needed. Hence, to select heat tolerant chickpea genotype, we assessed the genetic variability and yield based selection indicesaiming at selection of superior chickpea genotypes grown under normal sown and late sownconditions.

2. Materials and Methods

2.1. Experimental materials

The present study was conducted at Phanda farm, Bhopal, regional station of Indian Institute of Pulses Research (IIPR), Kanpur. The experiment was carried out in augmented design in 2015–16 under normal sown and late sown HS conditions, constituting 42 chickpea genotypes including two heat tolerant checks JG14 (Gaur et al., 2012) and ICC4958 (Krishnamurthy et al., 2011) replicated each in three blocks. Each genotype was sown in two rows having 4×0.3 m^2 plot size. Crop was grown in accordance with the recommended package of practices under both conditions. Data on various phenological viz., days to first flower initiation (FI), days to 50% flowering (FI 50%), days to pod initiation (DPI), days to pod filling (DPF), days to maturity (MAT), primary branch (PB), plant height (PH), and yield related traits such as seeds/pod (SP), filled pods $plant^{-1}$ (FPP), empty pods (EP), total pods (TP), empty pod% (EP%) 100 seed weight (100SW), yield/plant (Y/Plant) and plot yield (YPlot), were recorded from 5 randomly selected plants for each genotype under both conditions. Seven heat tolerance indices were estimated using the following formulae. Heat susceptibility index (HIS)=(1-(Y_s/Y_p))/ SI where SI=1–($\hat{Y}_s$ / $\hat{Y}_p$), Tolerance index (TOL)=(Y_p – Y_s)(Hossain et al. 1990),Mean productivity (MP)=(Y_s + Y_p) / 2(Rosielle and Hamblin, 1981),Geometric mean productivity (GMP)= $(Y_p \times Y_s)^{½}$(Fernandez, 1992) , heat tolerance index (HTI) =(Y_p× Y_s)/X_{p2}) (Fisher and Maurer, 1978), Yield index (YI) = Y_s / $\hat{Y}_s$(Gavuzzi et al., 1997; Lin et al., 1986). Ys and Y_p are the grain yield of individual genotype in HS condition and normal condition, respectively. While, $\hat{Y}_s$ and $\hat{Y}_p$ are the means of all genotypes under stressed and nonstressedconditions, respectively. Superiority measure π= [$\sum_j^n$=1(Xij-Mj)2/2n] Where, n=number of environments; X_{ij}=Grain yield of ith genotype at the jth environment, and M_j = Grain yield of the genotype with maximum yield at jth environment. The average weekly temperature recorded during the crop growth period from 1st week of November 2015 to last week of April 2016 is given in Figure 1.

2.2. Statistical analysis

We used 'Analyse-it' statistical analysis for all the data for genetic variability. For correlation analysis weemployedR statistical package. Principal component analysis (PCA) and hierarchical cluster analysis were analyzed by running SAS, version 9.3. While, biplot analysis and three dimensional plots were obtained by performing 'R', versions 2.15.

3. Results and Discussion

3.1. Genetic variation

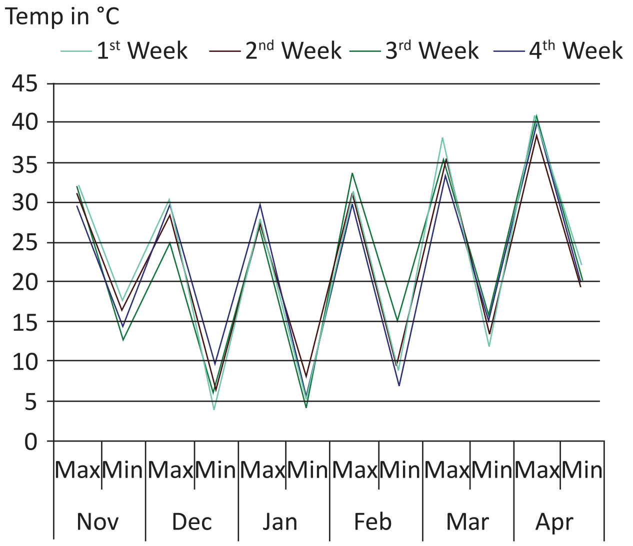

Figure 1: Average weekly day temperature recorded from Novemeber 1st week to April last week

A wide range of genetic variability for various phenological traits ranging from FI (49-79 days), 50% F (61-93 days), PI (55-95 days), DPF (88-121) and MAT (117-130 days) was noted under normal condition. In context of yield related traits viz., FPP (67-139), TPP (70-145) with 19.2% CV, 100SW (9.3-27 g) with 27.8% CV, Y/Plant (7.7-24.3 g) with 41.7% CV and for PlotY (256-871 g) were observed, see (Table 1). Likewise, under HS condition moderate variability for different phenological traits such as FI (49-63 days), 50% F (55-71 days), DPI (65-77 days), DPF (79-93 days) and for MAT (88-102 days) were registered. However, for yield related traits wide range of variability for FPP (32-112) with 25.8% CV, TPP (35-123) with 27.2% CV, 100SW (8.7-24 g) with 29.3% CV, Y/plant (6.3-16.3 g) with 29.9% CV and for Plot Y (138-745 g) with 18.1% CV were recorded given in (Table 2). Likewise, Jha et al. (2015a, b) reported wide range of genetic variability tested in chickpea under HS. Based on higher value of YI, MP and lower value of HSI three important HS tolerance indices, the following genotypes GNG1958, ICC 15955, IPC09-102 and ICC 15104 appeared to besuperior toICC4958 check genotypeunder field condition. Similarly, Jha et al. (2016) suggested significance of these indices for selecting superior genotypes under drought stress in chickpea.

3.2. Correlation analysis

Association between various HS tolerance indices and plot yield under normal vs HS conditions are given in (Table 3). Given the positive and high association of indices with plot yield under both conditions, could enable us in selecting superior HS tolerant genotype. In the current study, high and positive significant association of Y_p with Y_s, YI, MP, GMP, SSI and TOL were recorded. However, Y_p showed high and significant negative association with SM. Similarly,Sabaghina and Janmohammadi (2014) obtained positive correlation of Y_p with various stress indices under drought stress in

Table 1: General statistics of various parameters recorded under normal sown condition

Traits	Range	Mean	Mean SE	SD	CV%	Skewness	Kurtosis
FI	49-79	66.1	1.10	6.8	10.3	0.0	-0.12
50% F	61-93	78.7	0.98	6.1	7.7	-0.6	1.04
PI	55-95	85.0	1.28	7.9	9.3	-1.6	4.36
DPF	88-121	111.0	0.95	5.9	5.3	-1.6	5.70
MAT	117-130	122.3	0.62	3.8	3.1	0.6	-0.94
PB	3.7-7	4.83	0.085	0.53	10.9	0.0	-0.19
PH	45-60	49.983	0.6462	3.983	8.0	0.6	-0.04
Seed pod^{-1}	1-2	1.39	0.039	0.24	17.5	0.0	-0.81
FPP	66-139	97.38	3.193	19.68	20.2	0.5	-0.17
EP	1-8	4.35	0.306	1.89	43.4	-0.2	-0.39
TPP	70-145	101.9	3.18	19.6	19.2	0.5	-0.13
EP%	1-8	4.41	0.348	2.15	48.7	0.2	-0.78
100 SW (g)	9.3-27	16.83	0.758	4.67	27.8	0.6	-0.88
Y plant^{-1} (g)	4.7-24.3	17.05	1.154	7.11	41.7	0.8	1.06
Plot Y (g)	256-871	660.0	21.82	134.5	20.4	-0.6	0.72

SD: Standard deviation; CV: Co-efficient of variation; SE: Standard error

Table 2: General statistics of various parameters recorded under HS condition

Traits	Range	Mean	Mean SE	SD	CV%	Skewness	Kurtosis
FI	49-63	56.9	0.54	3.3	5.8	0.0	-0.36
50% F	55-71	65.5	0.60	3.7	5.6	-0.5	0.15
PI	65-77	71.1	0.45	2.8	3.9	-0.1	0.19
DPF	79-93	84.8	0.49	3.0	3.5	0.7	1.01
MAT	88-102	94.9	0.53	3.3	3.4	0.4	-0.31
PB	3-5.	3.5	0.09	0.6	16.5	0.6	-0.17
PH	37.7-60.7	46.06	1.016	6.26	13.6	0.7	-0.27
Seed pod^{-1}	1-2.2	1.35	0.048	0.29	21.8	1.0	0.58
FPP	32-112	69.95	2.924	18.03	25.8	0.1	-0.35
EP	2-10	4.53	0.294	1.81	40.1	0.7	-0.02
TPP	35-123	75.67	3.344	20.61	27.2	0.3	-0.32
EP%	2-13	6.10	0.498	3.07	50.3	0.9	-0.05
100 SW (g)	8.7-24	15.34	0.729	4.49	29.3	0.7	-0.75
Y plant^{-1} (g)	6.3-16.3	11.30	0.549	3.38	29.9	0.2	-0.20
PlotY (g)	138-745	576.6	16.93	104.4	18.1	-2.3	7.93

chickpea.Importantly, Y_s showed high and positive significant association with YI, MP, and GMP in the present study. While, HSI showed high and significant negative association with Y_s. This result was in agreement with the result suggested in wheat (Ali and El-Sadek, 2016). Likewise, YI exhibited positive significant correlation with MP and GMP indices. But it exhibited high and significant negative association with SSI index. These results remain in accordance to the result reported by Jha et al. (2016). In context of GM, it exhibited positive and significant high correlation with GMP and TOL. While, SSI showed high and significant positive association with TOL and high significant negation correlation with SM. These results were in consistence to the result revealed in the investigation conducted by Sabaghina and Janmohammadi (2014) under moistures stress in chickpea. High and negative significant correlation was recorded between TOL and SM

Table 3: Correlation analysis of calculated various HS indices

	Y_p	Y_s	YI	MP	GMP	SSI	TOL	SM
Y_p	1	0.659**	0.657**	0.933**	0.924**	0.364*	0.641**	-0.575**
Y_s		1	1**	0.886**	0.896**	-0.442**	-0.155	0.205
YI			1	0.884**	0.895**	-0.444**	-0.158	0.207
MP				1	1**	0.013	0.321*	-0.257
GMP					1	-0.007	0.299	-0.24
SSI						1	0.929**	-0.948**
TOL							1	-0.965**
SM								1

depicted in (Figure 3).

3.3. *Three dimensional plots analysis*

Given the selection of superior genotypes performing well under normal and HS conditionbased on various selection indices, a three dimensional plot was drawnrelying on Y_s, Y_p and MP indices. All the 42 genotypes were classified into 4 groups depicted in (Figure 2). The first group containing genotypes such as ICC12907, ICC15955, ICC16865, KWR 108 exhibited superior plot yield recorded under HS condition to the plot yield obtained under normal condition. However, genotypes viz., PBG5, IPC09-35, ICCV07110, and ICC10685 performed higher yield under HS condition than normal condition. The genotypes BG256, ICC10492, ICC10685, and Pusa 1103 showed poor plot yield under both conditions. Importantly, ICC15955, ICC8950, IPC09-102, ICC1205, and ICC15104 performed higher yield under the both conditions.

3.4. *Principal component analysis*

To discern the relationship among genotypes and various HS indices PCA analysis was performed.PCA analysis reduced all the calculated HS tolerance indices into two major components (Figure 3). PCA1 explained 57.6% of the total variation with Y_s, SM, GMP and MP indices. Whereas, PCA2 explained 41.6% of the total variation with SSI, TOL and Y_p indices. Equally, Golabadi et al. (2006); Zabet et al. (2003) reported similar results in wheat and mungbean, respectively under drought condition.

3.5. *Cluster analysis*

In concerned to cluster analysis, all the genotypes were classified into four distinct clusters. First cluster contained two genotypes; six genotypes remained in second cluster, the third cluster retained 23 genotypes and a total of 4 genotypes appeared in the fourth cluster given in (Figure 4 and Table 4). The genotypes such as BG256 and Pusa1103 appeared together in cluster 1, performing poor under both conditions. While, the genotypes prevailing in cluster 2 viz.,

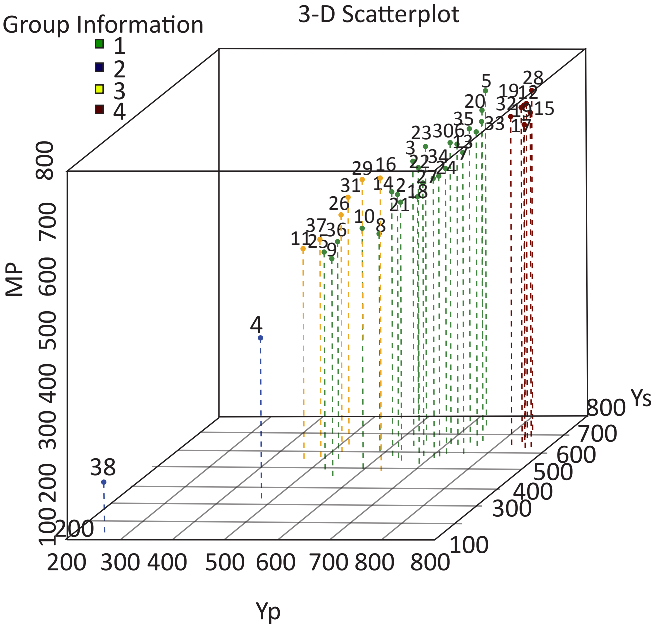

Figure 2: 3D scatter plot of genotypes

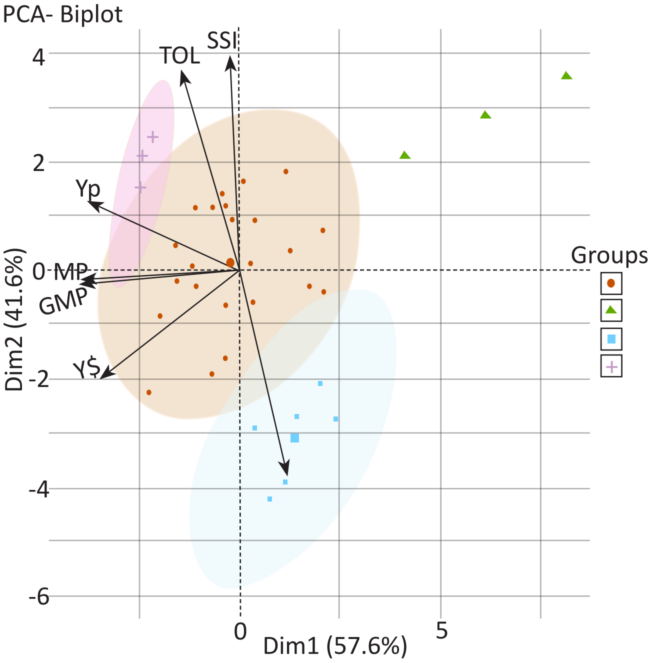

Figure 3: Principal component analysis of various HS tolerance indices

Table 4: Various HS tolerance indices measured in 42 genotypes

Genotype	Y_p	Y_s	YI	MP	GMP	HSI	TOL	SM	Group
ICC 15104	758	660	1.13	709	707.3	0.97	98	178.61	1
ICC 15854	639	562	0.97	600.5	599.26	0.91	77	220.5	1
P 1232	635	641	1.1	638	637.99	-0.07	-6	429.25	1
BG 256	466	341	0.59	403.5	398.63	2.02	125	131.22	2
GNG 1958	730	745	1.28	737.5	737.46	-0.15	-15	456.02	1
ICC-4958(ch)	722.67	627	1.08	674.83	673.13	0.99	95.67	183.18	1
ICC 10150	726	571	0.98	648.5	643.85	1.6	155	87.12	1
ICC 10487	639	474	0.81	556.5	550.35	1.94	165	74.42	1
ICC 10492	552	468	0.8	510	508.27	1.14	84	206.05	1
ICC 10528	590	514	0.88	552	550.69	0.97	76	222.61	1
ICC 10685	464	545	0.94	504.5	502.87	-1.31	-81	677.12	3
ICC 1205	848	644	1.11	746	738.99	1.81	204	34.45	4
ICC 12907	752	590	1.01	671	666.09	1.62	162	78.13	1
ICC 15041	620	581	1	600.5	600.18	0.47	39	307.52	1
ICC 15198	870	611	1.05	740.5	729.09	2.24	259	3.92	4
ICC 15562	570	643	1.11	606.5	605.4	-0.96	-73	648	3
ICC 15849	871	584	1	727.5	713.21	2.48	287	0	4
ICC 15879	695	523	0.9	609	602.9	1.86	172	66.13	1
ICC 15914	843	641	1.1	742	735.09	1.8	202	36.13	4
ICC 15955	746	690	1.19	718	717.45	0.56	56	266.81	1
ICC 16030	656	534	0.92	595	591.86	1.4	122	136.13	1
ICC 16865	657	613	1.05	635	634.62	0.5	44	295.25	1
ICC 1882	649	665	1.14	657	656.95	-0.19	-16	459.05	1
ICC 8950	720	554	0.95	637	631.57	1.73	166	73.21	1
ICC15923	525	499	0.86	512	511.83	0.37	26	340.61	1
ICCV 07110	518	590	1.01	554	552.83	-1.04	-72	644.41	3
ICCV 10	689	557	0.96	623	619.49	1.44	132	120.13	1
IPC 09-102	850	665	1.14	757.5	751.83	1.64	185	52.02	4
IPC 09-161	530	660	1.13	595	591.44	-1.84	-130	869.45	3
IPC 09-186	709	636	1.09	672.5	671.51	0.77	73	228.98	1
IPC 09-35	514	633	1.09	573.5	570.41	-1.74	-119	824.18	3
JG 14(ch)	827.33	627.33	1.08	727.33	720.39	1.81	200	38.67	4
JG 315	759	632	1.09	695.5	692.6	1.26	127	128	1
K 1058	708	557	0.96	632.5	627.98	1.6	151	92.48	1
KATILA	738	653	1.12	695.5	694.2	0.87	85	204.02	1
KWR 108	546	511	0.88	528.5	528.21	0.48	35	317.52	1
PBG 5	497	546	0.94	521.5	520.92	-0.74	-49	564.48	3
PUSA 1103	256	138	0.24	197	187.96	3.46	118	142.81	2

IPC09-35, ICCV07110, PBG 5 showed higher performance in HS condition. Importantly, the high performing genotypes such as GNG1958, ICC 15955 and ICC15041 remained in cluster 3. In this context, Jha et al. (2015b) grouped 62 chickpea

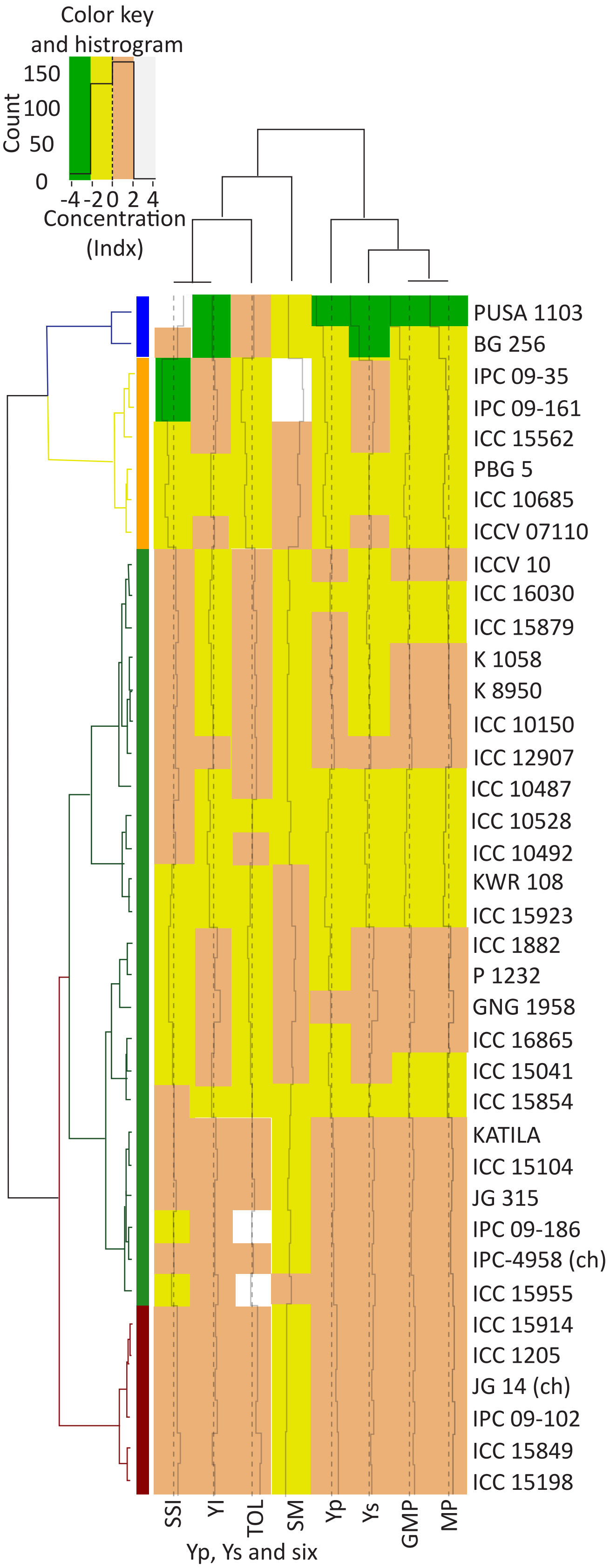

Figure 4: Cluster analysis of 42 genotypes based on various HS tolerance indices

genotypes into eight distinct clusters while assessing genetic variability for HS tolerance. Here, the cluster analysis results also supported the results obtained in three dimensional analyses above. Thus, incorporation of genotypes existing in the distant clusters into crossing programme could help in widening the genetic base for improving HS tolerance breeding in chickpea.

4. Conclusion

Availability of genetic variation remains a prerequisite to develop HS tolerant chickpea genotype. Based on the higher values of YI and MP, two important HS indices assisted in identification of GNG1958, ICC 15955, IPC 09-102 and ICC15104 genotypes to be tolerant to HS. In parallel, employment of various stress indices relying on yield parameter could help in measuring yield loss under HS, and alsofacilitate plant breeders to select superior HS tolerant chickpea genotypes under field condition.

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6. Author's Contribution

This work is based on a part of Ph.D. thesis of the first author. All authors contributed for the manuscript finalization except last two authors helped in statistical analyses.

7. Conflict of Interest

The authors declare no conflict of interest

8. References

Ali, M.B., El-Sadek, A.N., 2016. Evaluation of drought tolerance indices for wheat (*Triticum aestivum* L.) under irrigated and rainfed conditions. Communications in Biometry and Crop Science 11(1), 77–89.

FAOSTAT, 2014. FAO Statistics Division, Available at: http://faostat3.fao.org/compare/E (accessed 27.02.16.).

Fernandez, G.C.J., 1992. Effective selection criteria for assessing plant stress tolerance. In: Proceedings of the international symposium on adaptation of vegetable and other food crops in temperature and water stress. Taiwan, 257−270.

Fischer, R.A., Maurer, R., 1978. Drought Resistance in Spring Wheat Cultivars, I. Grain Yield Response. Australian Journal of Agriculture Research 29, 897−912.

Gaur, P.M., Jukanti, A.K., Varshney, R.K., 2012: Impact of genomic technologies on chickpea breeding strategies. Agronomy 2, 199—221.

Gavuzzi, P., Rizza, F., Palumbo, M., Campaline, R.G., Ricciardi, G.L., Borghi, B., 1997. Evaluation of field and laboratory predictors of drought and heat tolerance in winter cereals. Canadian Journal of Plant Science 77, 523−531.

Golabadi, M.A., Arzani, S.A., Maibody, M., 2006. Assessment of drought tolerance in segregating populations in durum wheat. African Journal of Agriculture Research 1, 62–171.

Gowda, C.L.L., Parthasarathy Rao, P., Tripathy, S., Gaur, P.M., Deshmukh, R.B., 2009. Regional shift in chickpea production in India. In: Ali, M., Kumar, S. (Eds.), Milestones in Food Legumes Research. Kanpur: Indian Institute of Pulses Research, 21–35.

Graham, P.H., Vance, C.P., 2003. Legumes: Importance and Constraints to Greater Use. Plant Physiology 131, 872–877.

Hossain, A.B.S., Sears, A.G., Cox, T.S., Paulsen, G.M., 1990. Dessication tolerance and its relationship to assimilate partitioning in winter wheat. Crop Science 30, 622–627.

Jha, U.C., Chaturvedi, S.K., Bohra, A., Basu, P.S., Khan, M.S., Barh, D., 2014a. Abiotic stresses, constraints and improvement strategies in chickpea. Plant Breeding 133, 163–178.

Jha, U.C., Bohra, A., Singh, N.P., 2014b. Heat stress in crop plants: its nature, impacts and integrated breeding strategies to improve heat tolerance. Plant Breeding 133(6), 679–701.

Jha, U.C., Shil, S., 2015a. Association Analysis of yield contributing traits of chickpea genotypes under high temperature condition. Trends in Bioscience 8, 2335–2341.

Jha, U.C., Basu, P., Singh, D., 2015b. Genetic variation and diversity analysis of chickpea genotypes based on quantitative traits under high temperature stress. International Journal of Bio-resource and Stress Management 6, 700–706.

Jha, U.C., Basu, P.S., Shil, S., 2016. Evaluation of Drought Tolerance Selection Indices in Chickpea Genotypes. International Journal of Bio-resource and Stress Management 7(6),1244–1248.

Jha, U.C., Bohra, A., Jha, R., Parida, S., 2017. Integrated 'omics' approaches to sustainmajor global grain legume productivity under heat stress. Plant Breeding 1–23.

Jha, U.C., Jha, R., Bohra, A., Parida, S.K., Kole, P.C., Thakro,V., Singh, D., Pratap Singh, N.P., 2018. Population structure and association analysis of heat stress relevant traits in chickpea (*Cicer arietinum* L.). 3 Biotech 8(1) 1–43.

Krishnamurthy, L., Gaur, P.M., Basu, P.S., Chaturvedi, S.K., Tripathi, S., Vadez, V., Rathore, A., Varshney, R.K., Gowda, C.L.L., 2011. Large genetic variation for heat tolerance in the reference collection of chickpea (*Cicer arietinum* L.) germplasm. Plant Genetic Resources 9(1), 59–69.

Lin. C.S., Binns, M.R., Lefkovitch, L.P., 1986. Stability analysis: where do we stand? Crop Science 26, 894−900.

Rosielle, A.A., Hamblin, J., 1981. Theoretical aspects of selection for yield in stress and non- stress environment. Crop Science 21, 943−946.

Sabaghnia, N., Janmohammadi, M., 2014. Evaluation of Selection Indices for Drought Tolerance in some Chickpea (*Cicer arietinum* L.) Genotypes. Acta Technologica Agricultuarae. DOI: 10.2478/ata-2014-0002.

Sio-Se Mardeh, A., Ahmadi, A., Poustini, K., Mohammadi, V., 2006. Evaluation of drought resistance indices under various environmental conditions. Field Crops Research 98(2−3), 222–229.

Upadhyaya, H.D., Bajaj, D., Das, S., Kumar, V., Gowda, C.L., Sharma, S., Tyagi, A.K., Parida, S.K., 2016b. Genetic dissection of seed-iron and zinc concentrations in chickpea. Scientific Report 6, 24050.

Zabet, M., Hosseinzadeh, A.H., Ahmadi, A., Khialparast, F., 2003. Effect of water stress on different traits and determination of the best water stress index in Mung Bean (*Vigna radiate*). Iranian Journal of Agriculture Science 34, 889–898.