Characterization of Bioactive Compounds and Antioxidant Activity among Genetically Different Genotypes of Chilli (*Capsicum annum L.)*

ABSTRACT

This study evaluated the antioxidant power, flavonoids and the total phenolic contents of forty-five genotypes of chilli. The antioxidant activities were tested forextraction scavenging using diphenyl-2-picrylhydrazyl (DPPH), azinobisethylbenzothiazoline-6-sulphonic acid (ABTS), assay of ferric reducing antioxidant power (FRAP), and determining total phenolics (TP) and total flavonoids (TF) contents. There were a significant difference in the total phenolic content (17.38–131.5mg GAE/g dry weight), total flavonoid (14.07–56.15 mg quercetin/g dry weight), DPPH (0.55–5.60 mM AAE/g dry weight), ABTS (16.03– 38.12 mM AAE/g dry weight) and FRAP (0.80– 6.40 mM GAE/dry weight). Three genotypes viz. IC-561635, CITH-HP-22 and IC-561731 exhibited highest values for all the assays. Significant correlation coefficients were identified between TP–TF (r = 0.93) DPPH-ABTS (r= 0.71), ABTS-TP (r=0.81) and FRAP-TF (r=0.89). Hierarchical cluster analysis grouped the studied genotypes into seven clusters. The identified genotypes of chilli are powerful sources of natural antioxidants that slow down the oxidation processes in the body by protecting them from the active oxygen species.

Keywords: *Chilli, genotypes, antioxidant, Reactive oxygen species, agro-ecological regions*

INTRODUCTION:

The novel coronavirus disease-2019 (COVID-19) has infect the world, killing more than 5.5 million people and infecting more than 323 million people [1]. "The vaccine is now available against COVID-19 but nerveless the importance of natural forms of prevention and treatment cannot be overstated. In this regard, eating and eating habits play an important role in determining well-being and resistance" [2]. "Vegetables are a great way to build resilience against infection by having low calories full of vitamins, minerals, antioxidants and photo chemicals" [3]. Therefore, "the use of natural compounds may provide an alternative prophylactic and therapeutic support along with the therapy for COVID-19" [4].

Chilli (*Capsicum annuum* L.) is widely regarded as an excellent source of natural pigments and antioxidants compounds. Chilli have a variety of uses in a variety of conditions, used as a spice, beverage, traditional medicine, vegetable or ornamental plant. Chilli is an important spice in Indian cuisine because of its texture, color and aroma. The plant is a rich source of nutrients, including vitamins A, C, E and thiamine, minerals (i.e.,

molybdenum, manganese, potassium) carotenoids, and phenolic compounds [5], "These compounds provide nutritional and health benefits that includes antioxidant, anti-inflammatory and antimicrobial activities, reduce the risk of type 2 diabetes, protect against hypercholesterolemia, and reduce the spread of cardiovascular disease" [6,7] "Fresh green peppers contain more vitamin C than citrus fruits as well. and fresh red pepper is rich in vitamins then carrot" [8,9].

However, the composition and levels of certain phytochemicals with antioxidant potential present in vegetables do not basically mimic the total antioxidant capacity, depending on the type and concentration of phytochemicals, as well as the interaction or inhibition of molecules in the matrix. Therefore, it is important to study the phytochemicals present in important vegetables such as chilli, in order to generate information about its potential health benefits. These nutrients may be replicated in reducing the pathological effects caused by acute respiratory infection of acute coronavirus 2 (SARS-CoV-2). The aim of this study was to investigate the antioxidant properties (phenolic content and total flavonoid content) in forty-five Chilli plants grown in Kashmir.

Materials and Methods

Planting material/ samples:

Forty-five genetically diverse chilli genotypes collected from different Indian provinces representing different agro-ecological regions were analysed for various quantitative and quality traits at the Experimental Field, Division of Vegetable Science, SKUAST-Kashmir, Shalimar Srinagar, during Kharif 2021. The experiment was laid in a randomised block design (RCBD) with three replications. Seeds were sown in April. Seedlings were transplanted at a spacing of 60 × 45 cms after 30 days after sowing. Recommended package of practices was followed. Genotypes name sources are presented in the Table (1). The ripe red fruit was dried in the oven (40 ^{0}C) for 15 days and then powdered with pestle and mortar and passed through a 100- mesh sieves and extraction was carried out with methanolic extract, the material (5 g of fruits) was extracted with 70% ethanol (plant: solvent, 1:10, w/v) under mechanical orbital shaker at room temperature for 72 h. Extracts were filtered using a Buckner funnel and Whatman No. 1 filter paper and ethanol was allowed to dry. Each extract was suspended in methanol to make 50 mg ml^{-1} stock solution.

Table (1): Name and sources of chilli genotypes used in the present study.

S.No.	Genotypes names	Source	S.No.	Genotypes names	Source
1.	LSVT-Red -1	Gujarat	27.	IC-561627	NBPGR
2.	LSVT-Red-2	Gujarat	28.	SK-SC-1162	CITH-Srinagar
3.	LSVT-Red-3	Gujarat	29.	SKAU-078	SKUAST-K
4.	Kashmiri Long-1	SKUAST-K	30.	V0BC-0289	Orrisa
5.	IC-561652	NBPGR	31.	Jawahar Mirch	Jabalpur Madhya Pradesh
6.	IC-561614	NBPGR	32.	Guccha Mirch-1	Chamba-Himachal Pradesh
7.	IC-561610	NBPGR	33.	SK-SC-1161	CITH-Srinagar
8.	IC-561730	NBPGR	34.	Guccha Mirch-2	Chamba-Himachal-Pradesh
9.	IC-561665	NBPGR	35.	CITH-HP-17/13	CITH-Srinagar
10.	IC-572487	NBPGR	36.	ARCH-228	IIVR
11.	IC-561618	NBPGR	37.	SKAU-084	SKUAST K
12.	IC-561661	NBPGR	38.	G-4	Andhra Pradesh (ANGRAU)
13.	IC-561691	NBPGR	39.	CITH-HP-171/13	CITH-Srinagar
14.	Kashi Anmol	Varanasi (IIVR)	40.	CITH-HP-22	CITH-Srinagar
15.	IC-561657	NBPGR	41.	Sel-680/11	CITH-Srinagar
16.	CITH-HP-16	CITH-Srinagar	42.	CITH-HP-71/13	CITH-Srinagar
17.	IC-561731	NBPGR	43.	SKAU-089	SKUAST-K
18.	IC-561622	NBPGR	44.	CITH-HP-1154-1/13	CITH-Srinagar
19.	Sel-839-2	CITH-Srinagar	45.	SKAU-092	SKUAST-K
20.	CITH-HP-111	CITH-Srinagar	46.	SKAU-096	SKUAST-K
21.	Sel-917-111	CITH-Srinagar	47.	Goa-Sel-1	Goa
22.	CITH-HP-1154	CITH-Srinagar	48.	SKASU-111	SKUAST-K
23.	IC-561631	NBPGR			
24.	IC-561635	NBPGR			
25.	IC-561639	NBPGR			
26.	Pusa Sadabahar	New Delhi (IARI)			

Determination of total polyphenolic content (TPC):

Total phenolic content of different extracts was assessed using Folin–Ciocalteu method [10], with gallic acid as a reference standard. To make a calibration curve, 0.5 ml aliquots of 12.5, 25, 50, 100, 200, and 400 lg/ml methanolic gallic acid solutions were mixed with 2.5 ml Folin–Ciocalteu reagent (diluted tenfold) and 2.5 ml (75 g/l) sodium carbonate. After incubation at 25^0C for 30 min, the quantitative phenolic estimation was performed at 765 nm against reagent blank by spectrophotometer (MALDI-MS). A similar procedure was adopted for the extracts as described above in the preparation of calibration curve. All determinations were performed in triplicate. Total phenolic content was expressed as milligrams of gallic acid equivalent (GAE)/g dry weight.

Total flavonoid:

Total flavonoid was estimated using the method of [11]. A sample of 0.5 ml was mixed with an equal volume of 2 % $AlCl_3$ ethanol solution which was kept for 1 h at room temperature. Then the absorbance was measured at 420 using spectrophotometer (MALDI-MS). Total flavonoid content was calculated as mg quercetin/g dry weight based on calibration curve.

Antioxidant activity determination by 2,2-diphenyl-1-picrylhydrazyl (DPPH) Assay:

The DPPH scavenging assay is based on antioxidants' ability to donate electrons to the DPPH radical. A DPPH colour change detected at 517 nm corresponds to the reaction, and the variation serves as an indicator of antioxidant activity. The method is based on the assumption that antioxidant activity is equal to its electron giving capacity. For measuring DPPH radical scavenging activity 2 ml of each extract and control at various concentrations were added to 3 ml of freshly prepared DPPH solution (50 lM) in methanol [12]. The reaction was allowed for 30 min and absorbance was measured at 517 nm using a spectrophotometer ((MALDI-MS). Results were expressed in mM of ascorbic acid equivalent (AAE)/g dry weight.

Azino-Bis 3-Ethylbenzothiazoline-6-Sulfonic Acid (ABTS) Radical Scavenging Activity ABTS Assay:

For ABTS assay, stock solutions included 7.4 mM ABTS solution and 2.6 mM potassium persulfate solution [13]. The working solution was then prepared by mixing the two stock solutions in equal quantities and allowing them to react for 12 h at room temperature in the dark. The solution was then diluted by mixing 1 ml ABTS solution with 60 ml methanol to obtain an absorbance of 1.1 ± 0.02 units at 734 nm using the

spectrophotometer (MALDI-MS). Sample extracts (150 ml) were allowed to react with 2850 ml of the ABTS solution for 2h in a dark condition. Then the absorbance was taken at 734 nm using the spectrophotometer (MALDI-MS). Results were expressed in mM of ascorbic acid equivalent (AAE)/g dry weight.

Ferric reducing antioxidant power (FRAP) determination Assay:

The FRAP test is an ET-based approach that evaluates the reduction of ferric ion (Fe^{3+})–ligand complex to the brightly blue ferrous (Fe^{2+}) complex by antioxidants in acidic conditions. FRAP assay was conducted using method of [14] with some modifications. 200 ml of extract were added with 3 ml of FRAP reagent that was prepared with mixture of 300 mM sodium acetate buffer at pH 3.6, 10 mM 2,4,6- tri (2-pyridyl)-s-triazine (TPTZ) solution and 20 mM $FeCl_3 6H_2O$ at the ratio of 10:1:1. The reaction mixture was incubated in a water bath at 37^0C for 30 min. The increase in absorbance was measured using spectrophotometer (MALDI-MS) at 593 nm. The antioxidant capacity based on the ability to reduce ferric ions of the extracts was calculated as mM GAE/g dry weight from the GAE–FRAP standard curve

Statistical analysis:

The value for each sample was calculated as the mean ± SD. Each assay was performed with three replications. Analysis of variance and significant difference among means were tested by ANOVA with completely randomised design (CRD) of experiment mean were separated using Tukey's test at $\alpha = 0.05$. Statistical analyses were performed using R software [15].

Results and Discussion

Analysis of variance

Analysis of variance revealed highly significant difference among all genotypes of chilli Table (2) for all the characters observed. The result indicated presence of adequate amount of variability in the germplasm under study.

Table (2): Analysis of variance for various quantitative characters in chilli.

Source of Variations	df	Sum of Squares	Mean Squares	F Ratio
Varieties	44	1.1427	2.5970	2.391
Error	87	9.4480	1.086	
Total	131	1.1427	8.722	

Total phenolic content:

Genotypes collected from different Indian provinces representing different ecological zones revealed significant differences for total phenolic content. Table (3). The percent of total phenolic contents varied from 17.38 to 131.5 mg GAE/g dry weight, recorded for IC-561652 and IC-561635, respectively. Phenolic compounds and flavonoids contribute significantly to the antioxidant properties due to presence of bioactive compounds [16]. Phenolic compounds tend to prevent lipid autoxidation by acting as radical scavengers. Phenols are compounds have the potential to destroy radicals because they contain hydroxyl groups. These essential plant components hydrogen atoms from their hydroxyl groups to radicals and form stable phenoxyl radicals and, as a result, are important antioxidants that protect against the propagation of oxidative stress. The variation in the total phenolic content were in conformity with previous findings of [17,18]

Flavonoids:

Total flavonoid content also varied significantly among the population.The highest flavonoid content was exhibited by IC-561731 (56.15 mg quercetin/g dry weight), whereas the minimum was observed for IC-561652 (14.07 mg quercetin/g dry weight). Flavonoids are also involved for their antioxidant activities because of the ability of hydrogen donation to stabilize the phenoxyl radicals formed [19] and thus play an important role as antioxidant agent and eliminate the free radical reaction. The presence of high phenol and flavonoid content in the Chilli genotypes indicates their potentiality in Nutra pharmaceutical uses. The variation in the total phenolic content and total flavonoid content between the genotypes could be attributed to variability of habitat [20]. Our results are in agreement with the results of [17, 18]

Antioxidant Activities:

Antioxidant activity differ significantly among the population which was measured through DPPH , ABTS and FRAP assay (Table 2). The amount of DPPH

antioxidant activity varied from 0.55 mM AAE/g dry weight to 5.60 mM AAE/g dry weight, recorded for IC-561652 and IC-561635, respectively. ABTS antioxidant activity ranged between 16.03 to 38.12 mM AAE/g dry weight, recorded for IC-561652 and IC-561635, respectively. Antioxidant activity measured by FRAP assay varied from 0.80 to 6.40 mM GAE/dry weight, recorded for IC-56165 and IC-561731, respectively. The results are in agreement with the results of [18] who also found variation in the results of antioxidant capacity by the DPPH assay (2.28 to 15.6 µmol TEAC g-1) and by the FRAP assay (3.99 to 84.67 µmol TEAC g-1) in chili pepper. These variances may perhaps be described by diverse analytical methods. FRAP assay measures the ability to reduce a ferric tripyridyltriazine (Fe^{3+}-TPTZ) to a ferrous form (Fe^{2+}-TPTZ) of samples [21]. ABTS and DPPH assays are based on the reduction of ABTS and DPPH free radicals[22] of samples.

Table (3): Mean performance of different genotypes of chilli (*Capsicum annuum* L.)

S.No	Genotypes	Total Phenolic Content(mg GAE/g dry weight)	Total flavonoid mg quercetin/g dry weight	DPPH mM AAE/g dry weight	ABTS mM AAE/g dry weight.	FRAP mM GAE/dry weight
1	IC-561635	131.5	54.06	5.60	38.12	4.4
2	CITH-HP-22	130.00	53.00	5.30	31.25	3.50
3	IC-561731	129.20	56.15	5.50	38.00	6.40
4	IC-561730	127.30	54.14	5.20	36.10	4.20
5	IC-572487	125.53	51.07	4.80	34.08	4.00
6	LSVT-Red-1	120.43	50.05	4.50	32.22	4.10
7	LSVT-Red-2	119.13	49.05	4.20	36.11	3.90
8	SK-SC-1161	118.03	48.13	4.10	35.30	3.70
9	LSVT-Red-3	118.06	47.00	4.00	34.10	3.60
10	IC-561610	114.16	45.10	3.90	33.15	3.10

11	CITH-HP-16	112.20	43.03	3.50	32.16	3.00
12	IC-561665	110.20	42.18	3.40	30.15	3.90
13	Bhut Jolokia	108.06	40.16	3.30	29.08	3.75
14	Kashmiri Long - 1	107.05	40.07	3.40	29.00	3.90
15	Sel-917-111	106.37	39.05	3.90	30.11	3.60
16	IC-561639	103.21	41.00	4.10	31.22	3.00
17	IC-561661	102.26	36.16	3.30	31.13	3.40
18	IC-561622	100.48	29.09	4.10	20.33	2.50
19	SKAU-078	97.36	28.10	4.50	31.12	3.10
20	SKAU-084	95.16	27.22	4.30	30.00	2.90
21	CITH-HP-71/13	94.20	25.98	4.00	29.09	2.70
22	Sel-680/11	92.26	25.08	3.90	32.18	2.00
23	IC-561627	82.46	29.08	5.10	32.00	2.80
24	ARCH-228	78.10	27.03	3.10	33.10	2.08
25	Guccha Mirch-1	70.30	28.21	5.10	31.21	2.00
26	IC-561614	69.14	27.05	4.80	28.15	2.60
27	CITH-HP-111	58.11	28.08	5.20	24.11	2.10
28	VOBC-0289	56.20	27.14	2.50	29.10	1.50
29	Guchha Mirch-2	53.40	25.14	4.20	31.00	2.50
30	CITH-HP-171/13	51.30	24.11	4.10	23.10	2.70
31	SKAU-092	47.35	23.09	3.00	21.12	1.80
32	CITH-HP-17/13	45.13	25.00	3.20	22.07	2.80

33	SKAU-096	44.13	26.09	5.10	34.12	2.30
34	IC-561657	43.03	25.23	4.00	29.13	2.10
35	Jawahar Mirch	42.13	24.06	3.80	28.00	2.00
36	CITH-HP-1154-1/13	36.12	20.07	3.40	23.09	2.30
37	IC-561618	48.11	24.00	3.50	28.22	2.25
38	CITH-HP-1154	35.12	20.13	3.20	22.15	1.45
39	IC-561691	31.21	19.10	3.25	20.00	1.70
40	Sel-839-2	30.13	18.50	3.00	20.50	2.00
41	G-4	28.00	17.50	2.10	19.03	1.80
42	Goa-sel-1	23.83	17.00	2.50	18.50	1.50
43	SK-SC-1162	21.11	17.07	2.80	18.06	1.90
44	SKAU-089	20.08	16.03	2.00	17.19	1.10
45	IC-561652	17.38	14.07	0.55	16.03	0.80
CV (%)		0.28	0.90	2.14	0.67	0.48

Distribution of genotypes into different clusters:

Based upon the mean performance of the studied genotypes were grouped into seven clusters (Table-4, Fig 1). The cluster table and dendrogram indicated that the maximum number of genotypes fall in cluster III (11) followed by cluster I, II , cluster V, cluster IV, cluster VI and cluster VII. Cluster I, involved, IC-561610, CITH-HP-16, IC-561665, SKAU-111, Kashmiri Long -1, Sel-917-111, IC-561639, IC-561661. Cluster II included the following genotypes: IC-561635, CITH-HP-22, IC-561730, IC-572487, LSVT-Red-1, LSVT-Red-2, SK-SC-1161, LSVT-Red-3. Cluster III, involved CITH-HP-171/13, SKAU-092, CITH-HP-17/13, SKAU-096, IC-561657, Jawahar Mirch, CITH-HP-1154-1/13, IC-561618, CITH-HP-1154, VOBC-0289, Guchha Mirch-2. Cluster IV included the following genotypes: IC-561622, SKAU-078, SKAU-084, CITH-HP-71/13, Sel-680/11, IC-561627. Cluster V included following genotypes: IC-561691, Sel-839-2, G-4, Goa-sel-1,

SK-SC-1162, SKAU-089, IC-561652. Cluster VI involved ARCH-228, Guccha Mirch-1, IC-561614, CITH-HP-111 and cluster VII included one genotypes IC-561731. The emergence of various clusters with varying numbers of entries in each cluster suggested genetic diversity. The genotypes from various Indian states were discovered to be dispersed in various clusters, which revealed that a pattern of accessions' grouping was independent of their place of origin.

Table(4): Distribution of chilli genotypes into different clusters.

S. No	Cluster	No. of genotypes in the cluster	Name of genotypes
1	I	8	IC-561610, CITH-HP-16, IC-561665, SKAU-111, Kashmiri Long -1, Sel-917-111, IC-561639, IC-561661
2	II	8	IC-561635, CITH-HP-22, IC-561730, IC-572487, LSVT-Red-1, LSVT-Red-2, SK-SC-1161, LSVT-Red-3
3	III	11	CITH-HP-171/13, SKAU-092, CITH-HP-17/13, SKAU-096, IC-561657, Jawahar Mirch, CITH-HP-1154-1/13 IC-561618, CITH-HP-1154, VOBC-0289, Guchha Mirch-2
4	IV	6	IC-561622, SKAU-078, SKAU-084, CITH-HP-71/13, Sel-680/11 , IC-561627
5	V	7	IC-561691, Sel-839-2, G-4, Goa-sel-1, SK-SC-1162, SKAU-089, IC-561652
6	VI	4	ARCH-228, Guccha Mirch-1, IC-561614, CITH-HP-111
7	VII	1	IC-561731

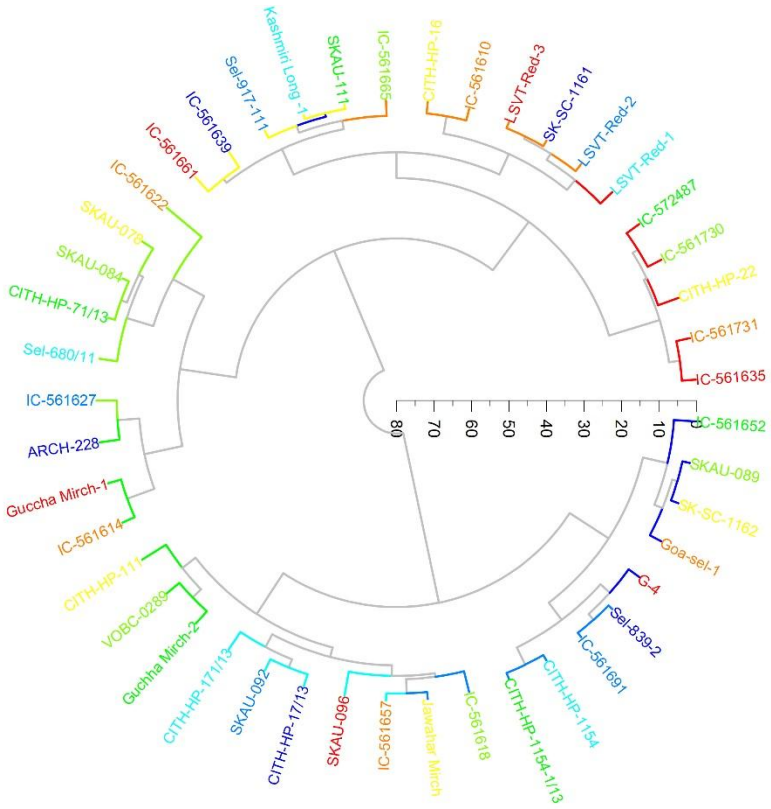

Fig 1: Dendrogram generated by hierarchical cluster analysis showing the relationships among the characterized chilli genotypes

Identification of diverse and desirable genotypes:

"Non- hierarchical cluster analysis was also performed in addition to combining of genotypes into different clusters to determine the desired genotypes in terms of inter and intra cluster distances and mean performance of clusters for various characters, respectively" [4]. Cluster distances, and the mean performance for the studied variables are present in Table (5).

The intra cluster distance ranged from 0.00 (cluster VII) to 12.30 (cluster VI) indicating dissimilarity for the studied variables among the evaluated chilli genotypes. The members of cluster VI exhibited maximum divergence (intra cluster distance12.30) followed by members of cluster III (10.09). The inter cluster distance were larger than the intra cluster distances indicating a wider genetic diversity between genotypes of cluster with respect to

the studied traits considered. A high inter-cluster distance indicates that genotypes falling in these clusters had wide diversity and can be used for hybridization programme to get better recombinants in the segregating generation. Low levels of intra-cluster distances reveal narrow genetic variation within clusters. The inter cluster distance values was highest for cluster VII and cluster V (88.02) followed by 81.43 for cluster V and cluster II.

The importance of different plant characters in the inter-cluster divergence can be studied further by comparing cluster mean for different characters. Based on mean of the clusters, the donors for different characters could be selected from clusters. The cluster mean values for five characters are presented in Table (6). The perusal of data indicated considerable differences for all the characters among clusters. It is inferred from the cluster means that each cluster has its uniqueness that separated it from other cluster. Highest cluster mean for total phenolic content (129.20) was observed in Cluster VII while the lowest cluster mean of (24.54) was found in cluster V. The highest cluster mean for total flavonoid (56.15) was found in cluster VII and lowest cluster of 17.04 was observed in cluster V. The highest cluster mean for DPPH (5.50) was found in cluster VII, whereas the lowest cluster mean of (2.31) in cluster V. The highest cluster mean for ABTS(38.00) was found in cluster VII and the lowest cluster mean for ABTS (18.47) was found in cluster V. The highest cluster mean for FRAP (6.40) was observed in cluster VII, whereas the lowest (1.54) was recorded in cluster IV.

Table (5): Average intra (Underlined) and inter-cluster (above diagonal) distance values in chilli (*Capsicum-annuum* L.)

	Group. 1	Group .2	Group .3	Group .4	Group .5	Group .6	Group .7
Group. 1	7.04	17.89	48.94	16.67	66.61	31.90	24.69
Group.2		8.76	63.23	31.03	81.43	45.70	12.86
Group.3			10.09	37.97	21.17	21.18	69.68
Group.4				9.18	55.22	21.52	37.57
Group.5					9.01	38.54	88.02
Group.6						12.30	52.36
Group.7							0.00

Table (6): Cluster means for various characters in different groups of chilli (*Capsicum annuum* L.)

	Total Phenolic Content	Total flavonoid	DPPH	ABTS	FRAP
Cluster-I	107.94	40.85	3.60	30.75	3.46
Cluster-II	123.78	50.81	4.71	34.68	3.93
Cluster-III	45.64	24.10	3.64	26.47	2.15
Cluster-IV	93.64	27.43	4.32	29.12	2.67
Cluster-V	24.54	17.04	2.31	18.47	1.54
Cluster-VI	68.91	27.60	4.55	29.15	2.25
Cluster-VII	129.20	56.15	5.50	38.00	6.40

Relationship Among Total Phenol, Flavonoid and Antioxidant Assay:

In order evaluate relative competence of antioxidant assays for determination anti-oxidant potential correlation matrix of diverse assays like DPPH and FRAP along with TPC, was performed. Correlation co-efficient determines the degree of association among two or more parameters. Pearson correlation analysis was performed to evaluate the suitability and reliability of the antioxidant assay for the measurement of total antioxidant activity in Chilli genotypes (Fig. 2). Correlation coefficient measures the degree of association between two or more parameters. Results revealed significant positive correlation among total phenol, flavonoid and antioxidant assay and suggest reliabilities of these methods. Significant positive correlation was found among Total Phenolic Content- Total flavonoid ($r = 0.93$), DPPH–ABTS ($r = 0.71$), ABTS–FRAP ($r = 0.73$) and FRAP- Total flavonoid ($r = 0.89$). Strong positive relationship of antioxidant assays suggested that all antioxidant assays used in this study are comparable and exhibit their suitability for chilli genotypes. These results are in accordance with the previous study [23]

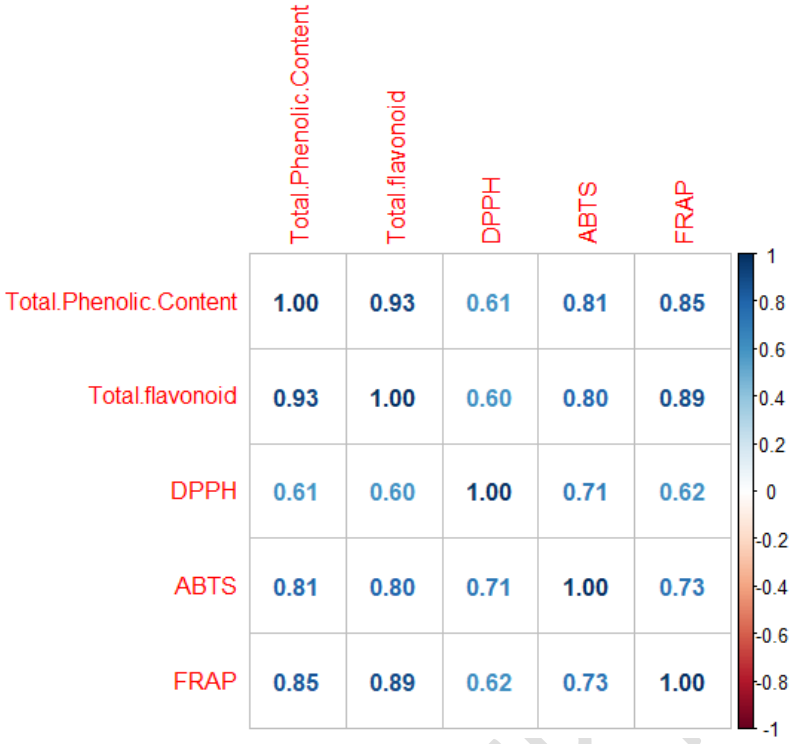

Fig. 2. Correlation coefficient between total phenol (TP), total flavonoid (TF), diphenyl-2-picrylhydrazyl (DPPH), azinobisethylbenzothiazoline-6-sulphonic acid (ABTS) and ferric reducing antioxidant power (FRAP

Conclusion

The present study concludes that chilli genotypes collected from different agro-ecological zones of India displayed high content of total phenols, flavonoids and antioxidant activities. Three genotypes viz. IC-561635, CITH-HP-22 and IC-561731 exhibited highest values for all the antioxidant assays. Utilizing cluster analysis, it was discovered that different genotypes of capsicum showed a variety of antioxidant ranges. In this sense, the genotype of the chilli could be a significant raw material source for developing Nutra pharmaceutical companies and the development of new Capsicum varieties with strong antioxidant levels.

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Competing interests

Authors have declared that no competing interests exist.

Author's contribution

All the authors contribute equally

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