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Association and multivariate analysis of chromatic and antioxidant attributes in Cape gooseberry (*Physalis peruviana* L.) grown under temperate climate

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Abstract
The present study was carried out to detect genetic diversity for chromatic and antioxidant characteristics and to quantify fruit skin colour and antioxidant contents among twenty Cape gooseberry genotypes. The association and multivariate analysis was performed and among the chromatic traits the L* value was recorded lowest (23.63) in genotypes CITH-CGB-20 while the highest (67.58) in genotypes (CITH-CGB-17) with the standard deviation (10.54) and coefficient of variation (19.56) whereas a* value was minimum (0.127) in CITH-CGB-1 and maximum (23.4) in CITH-CGB-20 with standard deviation and coefficient of variation (5.05 & 236.29). The b* and chroma value found minimum (39.20, 39.21) for the genotype CITH-CGB-19 and maximum (69.6, 79.54) for CITH-CGB-14 respectively however standard deviation (7.59, 8.85) and coefficient of variation (14.02, 16.22) respectively. Cluster analysis revealed that CITH-CGB-20 is generally the most diverged genotype from others with higher mean Euclidean distance of 31.87 while CITH-CB-16 was the least with mean Euclidean distance of 5. The PCA analyses showed that % of variability were explained by only first five principal component (PC) axes. Out of five the first and the second explained 29.51 %, 19.85 % of the variation respectively. Phenotypic correlation revealed positive significant association between chlorophyll a and chlorophyll b (0.537), total phenol content and DPPH (0.960) and these are important traits in differentiating the genotypes. The present findings could be utilized in cape gooseberry breeding programms for the development of cultivars with attractive skin colour fruits and high levels of antioxidant activity.

Keywords: Genetic diversity, multivariate analysis, chromatic, antioxidant, Cape gooseberry

Introduction
The cape gooseberry or goldenberry (*Physalis peruviana* Linn syn. *P. edulis*) is a native of South America which is yellow-orange berry fruit enclosed in an inflated, bladder-like calyx or husk, and can be eaten fresh when ripe or in a variety of processed forms (Klinac, 1986) [18]. It is usually cultivated as short cycle (3-4 months) annual crop but in absence of frost it can be perennial as well. In its region of origin it is grown in a wide altitude range from sea level to 3200 m, with an intense solar radiation to humid and cloudy environment. The fruit can be eaten raw, as a dessert, as an appetizer or as dish decorator. It can also be prepared in elaborated dishes in cakes or used in making jams etc. (Majumdar, 1979) [22]. Moreover, cape gooseberry have been widely used in folk medicine as anticancer, antimycobacterial, antileukemic, antipyretic, immunomodulatory and for treating diseases such as malaria, asthma, hepatitis, dermatitis, diuretic and rheumatism (Ismail and Alam, 2001 [15]; Soares *et al*., 2003) [34]. In recent years there is an increasing interest in finding antioxidant phytochemicals to protect the human body from ROS related diseases (Kumar *et al*., 2013) [20]. Several studies revealed that the pulp of *P. peruviana* fruit is nutritious, containing particularly high levels of carotenoids, vitamin C and minerals beside this many chemical compounds *viz.* 28-hydroxywithanolide, withanolides, phygrine, kaempferol, and quercetin di- and tri-glycosides are reported to be present in *P. peruviana* (Dinan *et al*., 1997 [9]; Elliger *et al*.,) [10]. India has a great diversity in terms of genotypes or species in temperate as well as tropical regions (Singh *et al*., 2014) [32] and the commercial interest in this fruit have grown due to its nutritional properties related to high vitamins content, minerals and antioxidants as well as its anti-inflammatory, anticancer and other medicinal properties. It has high antioxidant capacity

which will be a promising raw material and can be used for human nutrition (Hassanien, 2011 [14]; Wu *et al*., 2005) [37]. At present many genotypes have been developed by various research institutes of India and having different fruit colours and are available in Indian market even though consumption of the Cape gooseberry is very limited. Besides that information on the functional and nutritional properties and the awareness of the consumers regarding the level of beneficial phytochemicals present in this nutritious fruit is also very limited. Keeping this view in mind the present study was undertaken with the objective to screen the 20 capegooseberry genotypes on the basis of fruit skin colour and antioxidant properties and to quantify level of antioxidant contents and fruit color. The information generated will serve as a reference material to breeder to develop nutraceutical rich cape gooseberry genotypes and consumer will get attractive and healthy fruit.

Material and Methods

The present investigation was carried out at Research Farm of the Central Institute of Temperate Horticulture during 2011 and 2012. The Research farm is situated at a latitude of 34° 05'N and longitude of 74° 50'E and at an altitude of 1640 m above mean sea level. The average maximum temperature 19.90°C, minimum 6.09 °C, rainfall 170.70 cm and relative humidity 60.35 %, evaporation 2.15/day and soil characteristics viz. pH= 6.81, EC = 0.36 dSm−1 were recorded in during the growing seasons. The experimental materials comprised of a total twenty genotypes of Cape gooseberry *viz*. CITH CGB-1, CITH CGB-2, CITH CGB-3, CITH CGB-4, CITH CGB-5, CITH CGB-6, CITH CGB-7, CITH CGB-8, CITH CGB-9, CITH CGB-10, CITH CGB-11, CITH CGB-12, CITH CGB-13, CITH CGB-14, CITH CGB-15, CITH CGB-16, CITH CGB-17, CITH CGB-18, CITH CGB-19 & CITH CGB-20 which were collected and introduced from various parts of the country. The experiment was conducted under randomized block design replicated six times and pooled data of two years were analyzed as per the method suggested by Gomez and Gomez (1984) [12]. Plants from nursery were transplanted during first week of May at a spacing of 30 x 30 cm and no training and pruning was done. All the recommended cultural practices were adopted for raising the crop successfully. Randomly collected fruits of Cape gooseberry were brought to labs at temperature of 18± 2 and relative humidity of 95%. The fruits skin colour CIELAB parameters were determined using Hunter colour lab and the results were expressed in accordance with the CIELAB system with reference to CIE 10° Standard observer and CIE Standard Illuminant D65. The measured parameters were L* (lightness), a* (redness) and b* (yellowness). Hue and chroma was calculated by the standard equations. The hue angle [H° = arctan (b*/ a*)] describes the relative amounts of redness and yellowness where 0 °/360 ° is defined for red/magenta, 90 ° for yellow, 180 ° for green and 270° for blue color. Chroma (C* = (a*2 + b*2)1/2) gives further information on the saturation or intensity of color (McGuire, 1992 [23]; Voss, 1992) [36]. The yellowness index (YI) was adapted from CIRG index based on the CIELAB values (Carreno *et al*., 1995) [7]. The chlorophylls estimated as described by Anderson and Boardman (1964) [2] however, carotene by AOAC (1974) [3]. The total phenol was measured by the Folin- Ciocalteau reagent (Aaby *et al*., 2005 [1], Singleton and Rossi, 1965) [33] using gallic acid as standard whereas total antioxidant potential measures in terms of 2, 2-diphenyl-1-picrylhydrazyl (DPPH) percent inhibition determined according to the method described by (Benzie and Strain, 1996) [5] with some modifications. The total flavonoids content was determined using a colorimetric method (Kim *et al*., 2003) [17] however, ascorbic acid as suggested by Robinson *et al*., (1945) [27]. To find out significance level, ANOVA performed using SPSS version 17, and the mean value of traits were used for further analysis. PAST 3 (Palaeontological Statistics; Hammer *et al*., 2001) [13] computer software was used for phenotypic correlation, cluster and principal component analysis.

Result and Discussion

The univariate ANOVA showed significant ($p<0.05$) variation among the selected Cape gooseberry genotypes for all the chromatic and antioxidant traits considered except hue value (Table 1). The significance signifies the possibility of using all traits for further analysis. The color of the fruit skin is the first quality parameter evaluated by consumers and is critical in product acceptance, even before it is tasted. Therefore fruit skin colour of all the genotypes has been measured and from the results it was observed that among the chromatic traits the L* value was recorded lowest (23.63) in genotypes CITH-CGB-20 while the highest (67.58) in genotypes (CITH-CGB-17) with the standard deviation (10.54) and coefficient of variation (19.56) whereas a*value was minimum (0.127) in CITH-CGB-1 and maximum (23.4) in CITH-CGB-20 with standard deviation and coefficient of variation (5.05 & 236.29). The b* and chroma value found minimum (39.20, 39.21) for the genotype CITH-CGB-19 and maximum (69.6, 79.54) for CITH-CGB-14 respectively however standard deviation (7.59, 8.85) and coefficient of variation (14.02, 16.22) respectively. The hue value showed non -significance whereas yellow index was recorded minimum (86.12) for CITH-CGB-19 and maximum (362.64) for CITH-CGB-20 with standard deviation (58.68) and coefficient of variation (38.28). Maximum standard deviation and coefficient of variation was recorded for yellowness index and a* value however lowest for hue trait. These fruit skin color variations among genotypes were likely due to the difference in geographical and genetic makeup of each individual genotype. Similarly chromatic diversity also reported by Ruth *et al*., (2013) [28] in Cape gooseberry genotypes during evaluation for physicochemical, physical and sensory properties. The results can be utilized for selection of attractive fruit color skin genotypes for better consumer preferences.

Besides fruit skin color properties, the antioxidant compounds were also quantified among the selected genotypes (Table 1). Among antioxidant traits total chlorophyll was observed minimum for CITH-CGB-7 (2.04 863mg/100gm) and maximum for CITH-CGB-8 (5.23 863mg/100gm) however, β-Carotene was recorded lowest in CITH-CGB-1 (0.233 mg/100gm)) and highest in CITH-CGB-15 (0.863mg/100gm) with standard deviation (0.88, 0.20) and coefficient of variation (25.96, 48.22) respectively. Similarly ascorbic acid and total flavonol was observed minimum in CITH-CGB-3 & CITH-CGB-8 and maximum in CITH-CGB-15 & CITH-CGB-7 with standard deviation 2.01, 7.50 and coefficient of variation 12.19, 21.62 respectively. These finding are in accordance with Otakar *et al*., (2012) [26]. Further the total phenols and total antioxidant potential (DPPH % inhibition) was measured minimum (33.10, 45.55) in CITH-CGB-15 and maximum (77.42, 94.10) in CITH-CGB-10 with standard deviation (10.74, 14.58) and coefficient of variation (19.45, 20.84). Results showed that genotypes CITH-CGB-8, CITH-CGB-15, CITH-CGB-15 &

CITH-CGB-7 and CITH-CGB-10 could be use as a nutritive food and can select as a parent for breeding programme for enhancing antioxidant contents of cape gooseberry. The present study results are found in simmilar to (Brazantin and Monaresi, 1980; Sarangi *et al*., 1989) [6, 29] whose reported that cape goosebery is rich in vitamin. A, B, B_2, C and polyphenols. Similarly (Chandi, 2000 [8]; Singh *et al*., 2011) [30] also reported genetic diversity among the physico-chemical traits in cape gooseberry genotypes and could be exploits directly as healthy fruit as fresh and processed. To further analyse the genetic divergence among genotypes Skewness and Kurtosis were also calculated. The skewness describes the symmetrical distribution pattern with respect to its dispersion from the mean. The positive skewness was recorded for the traits like a*, chroma, yellowness index, chlorophyll a (mg/100gm), chlorophyll b (mg/100gm), total chlorophyll (mg/100gm), β-Carotene (mg/100gm), Total phenol, ascorbic acid (mg/100g), total flavonoides and DPPH% inhibition however negative skewness for L*, b*and hue. These results showed the distribution of quantitative traits which provides information about nature of gene action and number of genes controlling the traits respectively. The skewed distribution of a trait in general suggests that the trait is under the control of non-additive gene action and is influenced by environmental variables. Positive skewness is associated with complementary gene interactions while negative skewness is associated with duplicate (additive x additive) gene interactions. The genes controlling the trait with skewed distribution tend to be predominantly dominant irrespective of whether they have increasing or decreasing effect on the trait.

Kurtosis tells the weight of the tails of a distribution. In the present set of data it was recorded that platykurtic distribution pattern for the traits like L*, a*, chroma, hue, yellowness index, chlorophyll a, chlorophyll b, total chlorophyll, β-Carotene, total phenol and total flavonoides however leptokurtic distribution for the traits like b*, total chlorophyll, ascorbic acid and DPPH % inhibition. Kurtosis is negative or close to zero in the absence of gene interaction and is positive in the presence of gene interactions. The traits with leptokurtic and platykurtic distribution are controlled by fewer and large number of genes, respectively. Similarly Márquez *et al*. (2009) [21] also found significant variations in the quality of fruits from 10 accessions of commercial cape gooseberry, which apparently were related to physiological and metabolic differences of each genotype likewise Swapna *et al*. (2012) [30] also indicated sizable variability in the minor berry fruits in terms of antioxidant compounds.

In order to assess traits association, phenotypic correlation analysis was done and the results are presented in Table 2. Only few traits showed high order of correlation under the study. Among chromatic traits L*value was highly negatively and significantly correlated with a*value (-0.688). Similarly chroma value was found highly positively and significantly correlated with b*value (0.955). The yellowness index showed positive highly and significantly association with L*, a*,b*& chroma. Chlorophyll a and chlorophyll b was positively associated with each other however the total chlorophyll content was positive and highly significantly related to chlorophyll a and chlorophyll b. This may be due to the similar intracellular pathways for these antioxidant compounds. Total antioxidant potential (DPPH % inhibition) was highly and positively correlated with total phenol content. The Otawar *et al*., 2012 [26] also reported correlation coefficients between the measured chemical parameters expressing antioxidant properties of cape gooseberry are high as compared to other fruit crops which supports the present results that cape gooseberry is a good source of antioxidant Similar scavenging cycles could be a possible reason for the positive correlation between these characteristics. Thus, it may be inferred that the plant selection should be based on chlorophyll a, chlorophyll b and total phenol content for developing cultivars with high antioxidant contents furthermore the cape gooseberry breeders have given little attentions to the phenolics content of cape gooseberry fruit but our study suggest that genetic improvement to increase total phenolics content is a worthy objective. (Novoa *et al*., 2006 [25]; Ávila *et al*., 2006) [4] also reported linear relationship among various fruit quality traits of cape gooseberry and high positive correlation between total phenols and total antioxidant activity (DPPH, FRAP) reported in blueberries (Giovanelli and Buratti, 2009) [11] and in strawberry by Lal *et al.* (2013) [19].

Euclidean distance matrix was produced by assuming 190 total possible pairwaise combinations of the 20 Cape gooseberry genotypes Table 3. The distance coefficient ranged from 0.02 for CITH-CGB-14 and CITH-CGB-7 to 43.95 for CITH-CGB-20 and CITH-CGB-17. Also 0.03 for CITH-CGB-4 and 0.04 for CITH-CGB- 9. The distance coefficient 0.12 for CITH-CGB-16 and CITH-CGB-12, CITH-CGB-19 and CITH-CGB-1, 0.15 for CITH-CGB-11 and CITH-CGB-5, 0.19 for CITH-CGB-11 and CITH-CGB-5, 0.88 for CITH-CGB-15 & CITH-CGB-3, 0.96 for CITH-CGB-6 & CITH-CGB-3, CITH-CGB-15 & CITH-CGB-5 were the next smaller pair wise Euclidean distances. Similarly the next higher distance value were that 41.48 for CITH-CGB-20 & CITH-CGB- 19 (41.48), CITH-CGB-20 with CITH-CGB-1 (41.61) and CITH-CGB-20 with CITH-CGB-18 (39.6). CITH-CGB-20 is generally the most diverged genotype from others with higher mean Euclidean distance of 31.87 while CITH-CB-16 was the least with mean Euclidean distance of 5.78. The results clearly stated the genetic diversity among the genotypes and the most diverse genotypes could be exploited for enhancement of antioxidant of cape gooseberry genotypes.

Hierarchical clustering was attempted by using paired group algorithm with different distance measures like Gowar, Euclidean, Mahalanobis and Manhattan. The result showed that Gower, Euclidean and Manhattan distance measures yielded similar dendrogarm topology and similar cluster membership of the Cape gooseberry genotypes; however Mahalanobis distance measure yielded different dendrogram topology which was characterised by chaining of genotypes. The dendrogram of chromatic and antioxidant traits grouped (Fig. 1) the genotypes in to two group with additional subgroup in each groups. Group I composed of only one genotype and group II composed of 19 genotypes. Group I was composed of distinct genotype CITH-CGB-20, this variety was characterised by distinct fruit skin color traits (*i.e*. L*,a*,Yellowness, hue). Second group contained genotypes CITH-CGB-1 to CITH-CGB-19 which was further sub grouped in to two; subgroup I contained two genotypes CITH-CGB-14 and CITH-CGB-2 which have low a*value and higher b* and chroma however in second sub group consisted 17 miscellaneous genotypes having variable traits. The second sub group further sub divided sub sub group I&II. The sub sub group I contained three genotypes *i.e*. CITH-CGB-17, CITH-CGB-18 & CITH-CGB-19. The sub sub group II consisted 14 genotypes. The second sub sub group further sub divided in to three clusters; cluster I included four

genotypes i.e. CITH-CGB- 7, CITH-CGB-8, CITH-CGB-12, CITH-CGB-13 and there genotypes were characterised by high flavonols and chlorophyll content where as cluster II consist of 7 genotypes and characterized by high total phenols and DPPH% inhibition and cluster III contained 3 genotypes and characterised by high beta carotene and ascorbic acid content. Results of this study indicate that the Cape gooseberry genotypes showed biochemical and chromatic traits that distinguish them from each other, which may be the result of the intense artificial selection for the purpose of agronomic cultivation and fruit quality-related traits (Singh *et al.*, 2013) [31].

The result of the principal component analysis is given in fig. 2 and Table 4. The objective of principal component analysis was the reduction of dimensionality of a data set with a large number of correlated variables or traits (Jolliffe, 2002) [16]. PCs are orthogonal and independent of each other (Mohammadi and Prasanna, 2003 [24]); they explained the variability which was not explained by the others. PCA was carried out by using 20 genotypes and 14 traits. In the analysis a total of 14 PCs, equal to the number of traits were extracted however, the first five PCs with eigen value greater than 1 were retained. The results showed that % of variability were explained by only first five principal component (PC) axes. Out of five the first and the second explained 29.51 %, 19.85 % of the variation respectively. The a* value, yellowness index, chlorophyll a, chlorophyll b, total chlorophyll were the important traits contributing the first PC. In the second PC, however L* value total phenols and DPPH % inhibition were important. Similarly b* value, chroma, ascorbic acid and total flavanols were important in third axes. While only hue and β-Carotene were important trait in the fourth axes and fifth axes respectively (Table 5). The first axis differentiated genotypes which were CITH-CGB-1, CITH-CGB-2, CITH-CGB-11, CITH-CGB-12, CITH-CGB-13, CITH-CGB-14, CITH-CGB-10 and CITH-CGB- 8 with lower a*, low beta carotene, low flavonols and high b*, chroma, chlorophyll a and b, total phenols and DPPH % inhibition however, second axes differentiated genotypes with high beta carotene, high a*, high flavanols and low in total phenols and DPPH % inhibition and total chlorophyll. The PC analysis broadly grouped the genotypes in to two categories based on the traits i.e high chromatic and low antioxidant and low chromatic and high antioxidant except genotypes CITH-CGB-20 (Fig 2). In the present study the first and second PCs explained % of variability, the first being most important. Accordingly, the traits included in the first PC especially those with comparatively high loading are important in separating the genotypes. Thus for the controlled crosses accessions should be selected that performed consistently different by the two clustering methods, as well as in the dispersion of the first five principal components, associated with higher values for the traits of colour and antioxidant interest.

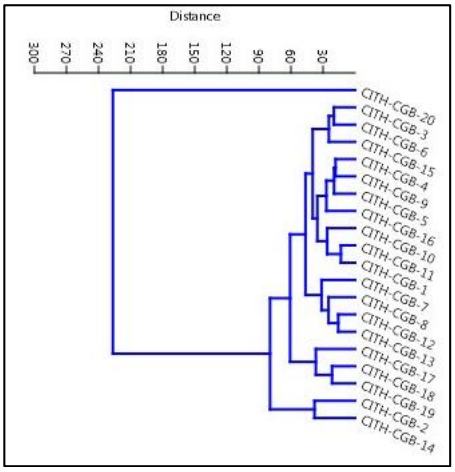

Fig 1: Dendrogram of 20 Cape gooseberry genotypes based on 14 chromatic and antioxidant traits constructed by means of paired group algorithm and Euclidean distance

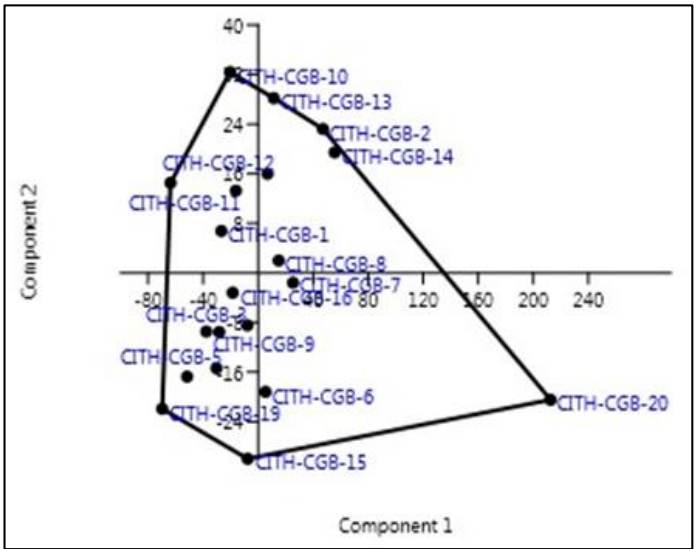

Fig 2: Scattered distribution of the 20 cape gooseberry genotypes by using 14 chromatic and antioxidant traits on the first two principal component axes

Table 1: Maximum and minimum mean values and overall mean, standard error, standard deviation and coefficient of variation of 14 chromatic and antioxidant traits of 20 Cape gooseberry genotypes

Traits	MS (df=19)	Minimum		Maximum		Mean ± SE	Standard Deviation	Skewness	Kurtosis	CV%
		Value	Genotype	Value	Genotype					
L*	333.56**	23.633	CITH-CGB-20	67.58	CITH-CGB-17	53.91 ± 2.35	10.54	-1.34	2.39	19.56
a*	76.43**	0.127	CITH-CGB-1	23.4	CITH-CGB-20	2.13 ± 1.12	5.05	4.35	19.24	236.29
b*	172.65**	39.2	CITH-CGB-19	69.6	CITH-CGB-14	54.09 ± 1.69	7.59	-0.16	-0.24	14.02
Chroma	235.05 **	39.21	CITH-CGB-19	79.54	CITH-CGB-14	54.57 ± 1.97	8.85	0.79	2.25	16.22
Hue	0.0	1.54	CITH-CGB-4	1.55	CITH-CGB-5	1.54 ± 0.007	0.01	-0.54	20.00	0.23
Yellowness index	10328**	86.12	CITH-CGB-19	362.64	CITH-CGB-20	153.28 ± 13.12	58.68	2.50	8.52	38.28
Chlorophyll a (mg/100gm)	1.02**	1.00	CITH-CGB-15	3.41	CITH-CGB-8	1.66 ± 0.13	0.58	1.35	2.95	35.13
Chlorophyll b (mg/100gm)	0.52**	1.033	CITH-CGB-4	2.68	CITH-CGB-2	1.72 ± 0.093	0.42	0.89	1.09	24.23
Total Chlorophyll (mg/100gm)	407.05**	2.047	CITH-CGB-7	5.23	CITH-CGB-8	3.41 ± 0.197	0.88	0.27	-0.78	25.96
β-Carotene (mg/100gm)	1387.45**	0.233	CITH-CGB-1	0.863	CITH-CGB-15	0.42 ± 0.04	0.20	1.10	0.35	48.22
Total phenol (mg GA equivalents/100 g)	272.99**	33.107	CITH-CGB-15	77.42	CITH-CGB-10	55.21 ± 2.40	10.74	0.24	0.04	19.45
Ascorbic acid (mg/100g)	265.78**	13.23	CITH-CGB-3	19.84	CITH-CGB-15	16.48 ± 0.45	2.01	0.11	-1.03	12.19
Total flavonoides (mg catechin equivalents /100 g)	168.66**	25.633	CITH-CGB-8	52.62	CITH-CGB-7	34.68 ± 1.67	7.50	1.09	0.70	21.62
DPPH % inhibition	637.39**	45.553	CITH-CGB-15	94.1	CITH-CGB-10	69.94± 3.25	14.58	0.10	-1.17	20.84

**Significant at the 0.01 level

Table 2: Phenotypic correlation between 14 chromatic and antioxidant traits in 20 Cape gooseberry genotypes

Traits	L*	a*	b*	Chroma	Hue	Yellow index	Chlorophylle a	Chlorophyll b	Total chlorophyll	β-Carotene ((µg/100gm)	Total phenol	Ascorbic acid	Total flavonols	DPPH% inhibition
L*	1													
a*	-.688**	1												
b*	-.344	.213	1											
Chroma	-.294	.172	.935**	1										
Hue	-.041	.026	.117	.229	1									
Yellowness index	-.875**	.838**	.526*	.535*	.201	1								
Chlorophyll a (mg/100gm)	-.128	.076	.210	.256	.176	.213	1							
Chlorophyll b (mg/100gm)	-.190	.132	.184	.254	.169	.289	.537*	1						
Total Chlorophyll (mg/100gm)	-.156	.116	.222	.292	.196	.271	.926**	.810**	1					
β-Carotene (mg/100gm)	-.046	.066	-.115	-.041	-.174	.025	-.292	-.062	-.224	1				
Total phenol (mg GA equivalents/100 g)	-.070	-.092	.241	.211	-.240	.058	.319	.325	.367	-.413	1			
Ascorbic acid (mg/100g)	.027	-.292	.205	.220	-.041	-.140	.038	-.113	-.057	.335	-.013	1		
Total flavonoides (mg catechin equivalents /100 g)	.096	-.242	-.007	-.001	.086	-.153	-.215	-.330	-.300	.085	-.224	.349	1	
DPPH % inhibition	.051	-.292	.267	.258	-.184	-.074	.344	.325	.382	-.372	.960*	.151	-.098	1

**Correlation is significant at the 0.01 level

*Correlation is significant at the 0.05 level

Table 3: Pair wise euclidean distance coefficient for all possible combination of the 20 Cape gooseberry genotypes using 14 chromatic and antioxidant traits

Parameters	CITH-SEL-1	CITH-SEL-2	CITH-SEL-3	CITH-SEL-4	CITH-SEL-5	CITH-SEL-6	CITH-SEL-7	CITH-SEL-8	CITH-SEL-9	CITH-SEL-10	CITH-SEL-11	CITH-SEL-12	CITH-SEL-13	CITH-SEL-14	CITH-SEL-15	CITH-SEL-16	CITH-SEL-17	CITH-SEL-18	CITH-SEL-19	CITH-SEL-20
CITH-SEL-1	0																			
CITH-SEL-2	28.00	0																		
CITH-SEL-3	7.02	21.00	0																	
CITH-SEL-4	15.15	12.9	8.12	0																
CITH-SEL-5	5.14	22.9	1.88	10.00	0															
CITH-SEL-6	7.98	20.00	0.96	7.16	2.84	0														
CITH-SEL-7	22.17	5.86	15.12	6.99	17.00	14.16	0													
CITH-SEL-8	17.00	11.00	9.98	1.85	11.86	9.02	5.14	0												
CITH-SEL-9	15.19	12.80	8.16	0.04	10.04	7.207	6.95	1.81	0											
CITH-SEL-10	4.95	23.10	2.07	10.20	0.19	3.03	17.19	12.05	10.24	0										
CITH-SEL-11	4.99	23.00	2.03	10.16	0.15	2.99	17.15	12.01	10.20	0.04	0									
CITH-SEL-12	12.12	15.90	5.09	3.03	6.97	4.13	10.02	4.88	3.07	7.16	7.12	0								
CITH-SEL-13	10.14	17.90	3.11	5.01	4.99	2.15	12.00	6.86	5.05	5.18	5.14	1.98	0							
CITH-SEL-14	17.02	11.00	10.00	1.87	11.88	9.04	5.12	0.02	1.83	12.07	12.03	4.90	6.88	0						
CITH-SEL-15	6.14	21.90	0.88	9.01	0.99	1.84	16.00	10.86	9.05	1.186	1.14	5.98	4.00	10.88	0					
CITH-SEL-16	12.14	15.90	5.12	3.00	7.00	4.16	10.00	4.86	3.04	7.19	7.15	0.03	2.00	4.88	6.01	0				
CITH-SEL-17	2.34	30.30	9.36	17.49	7.48	10.32	24.48	19.34	17.53	7.29	7.33	14.46	12.48	19.36	8.48	14.48	0			
CITH-SEL-18	2.01	26.00	5.01	13.14	3.13	5.97	20.13	14.99	13.18	2.94	2.98	10.10	8.126	15.01	4.126	10.13	4.35	0		
CITH-SEL-19	0.12	27.90	6.90	15.02	5.02	7.86	22.02	16.88	15.06	4.827	4.86	11.99	10.01	16.9	6.013	12.02	2.46	1.88	0	
CITH-SEL-20	41.61	13.60	34.59	26.46	36.46	33.62	19.46	24.60	26.42	36.66	36.62	29.49	31.47	24.58	35.47	29.46	43.95	39.6	41.48	0

Table 4: Eigen value, total variance, cumulative variance and Eigen vectors for 14 chromatic and antioxidant traits in the 20 cape gooseberry genotypes

Traits	Axis 1	Axis 2	Axis 3	Axis 4	Axis 5
L*	-0.266	0.375	0.0058	0.210	-0.09
a*	0.209	-0.438	-0.212	-0.196	0.041
b*	0.314	-0.117	0.435	-0.046	-0.168
Chroma	0.323	-0.110	0.430	0.0660	-0.141
Hue	0.0937	-0.106	-0.012	0.545	-0.465
Yellowness index	0.340	-0.410	-0.001	-0.1146	-0.017
Chlorophyll a (mg/100gm)	0.341	0.190	-0.130	0.320	0.115
Chlorophyll b (mg/100gm)	0.338	0.120	-0.198	0.233	0.25
Total Chlorophyll (mg/100gm)	0.384	0.186	-0.188	0.321	0.185
β-Carotene (mg/100gm)	-0.147	-0.234	0.139	0.122	0.662
Total phenol (mg GA equivalents/100 g)	0.264	0.364	0.0676	-0.417	-0.005
Ascorbic acid (mg/100g)	-0.034	0.0579	0.527	0.186	0.384
Total flavonoides (mg catechin equivalents /100 g)	-0.169	-0.035	0.392	0.176	-0.147
DPPH % inhibition	0.237	0.428	0.179	-0.291	0.0128
Eigenvalue	4.132	2.779	1.920	1.49	1.204
% variance	29.51	19.85	13.71	10.70	8.60
Cumulative variance	29.51	49.36	63.07	73.77	82.37

Conclusion

The present study findings showed wide diversity among the selected cape gooseberry genotypes and can be used as a reference in breeding programms for the development of cultivars with better fruit color and enhancement of high concentration of antioxidant activity. The knowledge will further help to growers to select attractive genotypes with attractive fruit color and high antioxidant content to get more prices for their produce.

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