Journal of Pharmacognosy and Phytochemistry

Available online at www.phytojournal.com

Kattula Nagaraju
PhD Scholar, Division of
Vegetable Crops, ICAR-IIHR,
Bengaluru, Karnataka, India

Saraswathi Thiruvenkatasamy
Horticultural Research Station,
TNAU, Kodaikanal, Tamil
Nadu, India

Genetic characterisation of ash gourd (*Benincasa hispida* (Thunb.) Moench) germplasm for yield and quality traits through principal component analysis

Kattula Nagaraju and Saraswathi Thiruvenkatasamy

Abstract
The present study was carried out at the College Orchard, Department of Vegetable Crops, Horticultural College and Research Institute, Tamil Nadu Agricultural University, Coimbatore during 2013-2014. The results revealed that more than 75% of the total variability present among all the genotypes of ash gourd is explained by the first thirteen principal components (PC). But out of eighteen, the first six component axes in the principal component analysis had Eigen values up to 1.0 and above, presenting cumulative variance of 75.38%. The first PC explained characters *viz.*, vine length (VL), intermodal length (INL), node at first female flower appearance (NFFA), average fruit weight (AFW), polar diameter (PD), equatorial diameter (ED) and number of seeds per fruits (NSF) which are positively related with yield while total soluble soilds (TSS) observed to have negative effect on yield and it was cleared from the values of PC1. Characters like average fruit weight (AFW) and number of fruits per vine (NFPV) were observed in PC2 whereas traits like days to first female flower appearance (DFFA), hundred-seed weight (HSW) and protein content (PRO); sex ratio (SR) and flesh thickness (FlT); number of primary branches (NPBr) and carbohydrate content (CHO); crude fibre content (CRUDE) were explained by PC3, PC4, PC5 and PC6 respectively. Therefore, the above-mentioned variables might be taken into consideration for effective selection of parents during hybridization program for broadening the genetic base in the population as well as to develop elite lines.

Keywords: principal component analysis, ash gourd, yield, quality, scree plot and bi-plot

Introduction

Ash gourd (*Benincasa hispida* Thunb. Moench (Synonym- *Benincasa cerifera*) commonly known as Boodidagummadikayi, belong to family Cucurbitaceae. It is a rich source of vitamins and dietary fibre, protein, fat, carbohydrate and minerals. It also contain different phytonutrients which have immense value in treatment of disease like urinary dysfunction, summer fever, cough and to cure weak nervousness and debility (Nadhiya *et al*., 2014) [8]. This valuable pharmacological plant shows different activities such as anticonvulsant, anxiolytic, gastroprotective, antinociceptive, antipyretic, antihistaminic, anti-inflammatory(Chandrababu and Umamaheshwari, 2002) [4], analgesic, antioxidant, antidiarrhoeal, anorectic angiogenic, anthelmentic and anti-ulcer (Grover *et al*., 2001) [6]. With the passage of time population has increased manifold and it will continue to increase further. So as to keep up with the rising demand of ash gourd production, good initial breeding material is required in the germplasm which can later be utilized for the development of high yielding quality ash gourd varieties. Selection of the appropriate genotypes for the start of the breeding programme depends largely on the primary identification and grouping of genotypes according to the characteristics relevant to the objectives. Accurate evaluation of these characters is made more difficult by the genotype by environment interaction (Tadesse and Bekele, 2001) [12]. Principal component analysis helps plant breeders to distinguish significant relationship between traits. This is a multivariate analysis method that aims to explain the correlation between a large set of variables in terms of a small number of underlying independent components (Beheshtizadeh *et al*., 2013) [3].

Vast improvement can be made in ash gourd using genetic diversity available. Hence, the present investigation was conducted in order to determine the dependence relationship between yield, yield contributing components and quality characters of tomato cultivars using principal component analysis.

Materials and Methods

The present study was carried out at the College Orchard, Department of Vegetable Crops, Horticultural College and Research Institute, Tamil Nadu Agricultural University, Coimbatore.

Correspondence
Kattula Nagaraju
PhD Scholar, Division of
Vegetable Crops, ICAR-IIHR,
Bengaluru, Karnataka, India

Forty accessions were raised during 2013-14 in randomized block design (RBD) with three replications. Pits of 60 cm diameter and 30 cm depth were taken at a spacing of 1.5 x 1.0 m^2. The forty genotypes (40 treatments) in each replication consist of ten pits and three seeds were sown in each pit. The cultural and management practices were adopted according to the package of practices recommended by Tamil Nadu Agricultural University and standard methods followed for pollination. Eighteen biometrical traits of ash gourd were recorded on five randomly selected plants in each of the accession per replication. Recorded data for all the studied traits were subjected to Principal Component (PC) Analysis using SPSS version 21 and SAS-JMPSW-12 statistical softwares. The principal component was used to determine the extent of genetic variation in the given germplasm. Eigen values obtained from PC were used to determine the relative discriminative power of the axes and their associated characters (Pradhan *et al.,* 2011) [9].

Results and Discussion
Principal Component Analysis (PCA)
It is evident from the Table 1 that more than 95% of the total variability present among the forty genotypes of ash gourd is explained by the first 13 principal components but out of 18, the first six component axes (Table 1) in the principal component analysis had Eigen values up to 1.0 and above, presenting cumulative variance of 75.38%. Principal component one (PC1), with Eigen value of 6.126, contributed 34.03% of the total variability, while PC2, PC3, PC4, PC5 and PC6 with Eigen values of 2.30, 1.56, 1.38, 1.17 and 1.01 accounted for 12.81%, 8.70%, 7.67%, 6.54% and 5.61% of total variability, respectively(Table 1). The first PC explained characters *viz.*, VL, INL, NFFA, AFW, PD, ED and NSF which are positively related with yield while TSS observed to have negative effect on yield and it was cleared from the values of PC1 (Table.2). Characters like AFW and NFPV were observed in PC2 whereas traits like DFFA, HSW and PRO; SR and FlT; NPBr and CHO; CRUDE were explained by PC3, PC4, PC5 and PC6 respectively. Hundred-seed weight was explained by PC3 and had negative effect with yield. Hence, selection towards negative direction should be made for hundred-seed weight.

Although correlation analysis helps in determining the effective traits in order of indirect selection of superior genotypes but on the other hand, principal component analysis is a suitable multivariate technique in identifying and determining of independent principal components that are effective on plant traits separately. Therefore, PCA also helps breeders for genetic improvement of traits such as yield that have low heritability specifically in early generations via indirect selection for traits effective on yield (Golparvar *et al*., 2006) [5].

Principal component Analysis is a technique which identifies plant traits which contributed most to the observed variation within a group of genotypes and it had a practical application in the selection of parental lines for breeding purpose (Ahmadizadeh and Felenji, 2011) [2]. The cumulative variance of 76% by the first five principal components with Eigen values of more than 1.0 indicated that the identified traits within this axes exhibited great influence on the phenotype of the cultivars and could effectively be used for selection

among them. Pradhan *et al.,* 2011 [9] reported from their principal component analysis that the first two components out of twelve trait components had eigen values up to 1.0, presenting cumulative variance of 84.10%.

From the results of the present investigation, it is concluded that the traits *viz.*, vine length (VL), intermodal length (INL), node at first female flower appearance (NFFA), average fruit weight (AFW), polar diameter (PD), equatorial diameter (ED), number of seeds per fruit (NSF), total soluble solids (TSS), number of fruits per vine (NFPV), yield per vine (YPV), days to first female flower opening (DFFA), hundred-seed weight (HSW), protein content (PRO), sex ratio (SR), flesh thickness (FlT), number of primary branches (NPBr), carbohydrate content(CHO) and crude fibre(CRUDE) are important for improving yield and quality traits. Therefore, these traits might be taken into consideration for effective selection of parents for hybridization program for broadening the genetic base in the population as well as to develop elite lines or F$_1$ hybrids. Furthermore, selection of the genotypes with the highest yield per plant and its components should be recommended as one of the best breeding strategy for genetic improvement of ash gourd. The similar results were emphasized by many researchers like Sattar*et al.*, (2011) [10]; Ahmadizadeh and Felenji, (2011) [2] and Lohani *et al*., (2012) [7].

Principal Component scree plot
Scree plot explains the percentage of variance associated with each principal component obtained by drawing a graph between Eigen values and PC and thus it helps to determine the appropriate number of principal components; we look for an 'elbow' in the scree plot. The component number is taken be the point at which the remaining eigenvalues are relatively small (<1) and all about the same size. The scree plot is shown figure 1 exhibited six principal components and showed the highest variation in PC 1 to explain maximum variation in the data set, so the selection of genotypes based on this PC will be useful.

Relationships between variables and between genotypes was reviewed based on bi-plot of first and second components, so that the horizontal axis was related to first component and the vertical axis was related to the second component. Based on the component values, the location of genotypes, variables and their grouping were determined in top of bi-plot. From figure 2, it is explained that the traits *viz.,*vine length (VL), polar diameter (PD), equatorial diameter (ED), average fruit weight (AFW) and flesh thickness (FlT) contributed maximum towards the total variability present in the evaluated germplasm. Thus, selection should be directed towards these traits to have genetic improvement in ash gourd. Based on the component values, the location of genotypes and their grouping were determined in top of bi-plot (figure 3). Therefore, according to bi-plot figures it is clear that there is a lot of variability was present in the studied genotypes and among those Shadnagar local, Chityal local, Debpurna and Coimbatore local were identified as the best genotypes as these genotypes grouped in positive part as well as they can be easily identified as distinct from the rest of the genotype groups of the bi-plot. Bi-plot had been utilized by many researchers such as Ahmadizadeh and Felenji, (2011) [2] in potato, Afuape *et al.*, (2011) [1] in sweet potato to decide the best genotype among the studied ones.

Table 1: Eigen value and contribution of the principal component axes towards variation in tomato germplasm

Principal component	Eigen value	Variability (%)	Cumulative %
PC1	6.126	34.032	34.032
PC2	2.306	12.812	46.844
PC3	1.566	8.701	55.545
PC4	1.382	7.677	63.222
PC5	1.178	6.544	69.767
PC6	1.011	5.614	75.381
PC7	0.761	4.230	79.611
PC8	0.733	4.071	83.681
PC9	0.659	3.664	87.345
PC10	0.507	2.814	90.159
PC11	0.499	2.774	92.933
PC12	0.345	1.914	94.847
PC13	0.287	1.592	96.439
PC14	0.243	1.347	97.786
PC15	0.164	0.913	98.699
PC16	0.144	0.801	99.500
PC17	0.077	0.427	99.927
PC18	0.013	0.073	100.000

Table 2: Contribution of different qualitative and quantitative traits of tomato towards major principal components.

	PC1	PC2	PC3	PC4	PC5	PC6
VL	0.678	0.304	-0.205	0.157	-0.205	0.221
INL	0.827	0.214	-0.065	0.057	-0.113	0.135
NPBr	0.038	0.186	0.058	-0.362	0.558	-0.421
DFFA	-0.281	-0.069	0.790	-0.001	-0.311	0.081
NFFA	0.605	0.384	-0.070	-0.124	-0.112	-0.203
SR	-0.161	-0.019	0.010	0.847	0.117	0.058
AFW	0.616	0.652	0.092	0.061	0.038	0.064
FlT	0.246	-0.001	0.143	0.792	-0.270	-0.025
PD	0.698	0.018	0.204	0.118	0.016	0.433
ED	0.829	0.225	-0.106	0.054	-0.001	0.251
NSF	0.793	-0.176	0.061	-0.083	-0.052	0.018
HSW	0.446	0.090	-0.578	0.192	-0.063	-0.291
NFPV	-0.095	0.864	-0.122	-0.030	-0.099	0.028
CHO	-0.287	-0.146	-0.129	0.034	0.859	0.040
CRUDE	0.259	0.064	0.016	-0.006	-0.048	0.763
PRO	0.211	-0.048	0.749	0.340	0.104	-0.181
TSS	-0.824	-0.096	0.297	0.015	0.123	0.051
YPV	0.449	0.844	-0.047	-0.035	0.066	0.008

Whereas, VL= vine length, INL= internodal length, DTFFA = days to first female flower opening, NFFA = node at first female flower appearance, SR= sex ratio, NPB= number of primary branches, NFPV= number of fruits per vine, AFW= average fruit weight, FlT= flesh thickness, PD= polar diameter, ED= equatorial diameter, NSF= number of seeds per fruit, HSW= hundred-seed weight, YPV= yield per vine, CHO= carbohydrate content, CRUDE= crude fibre content, PRO= protein content, TSS= total soluble solids and PC= principal component.
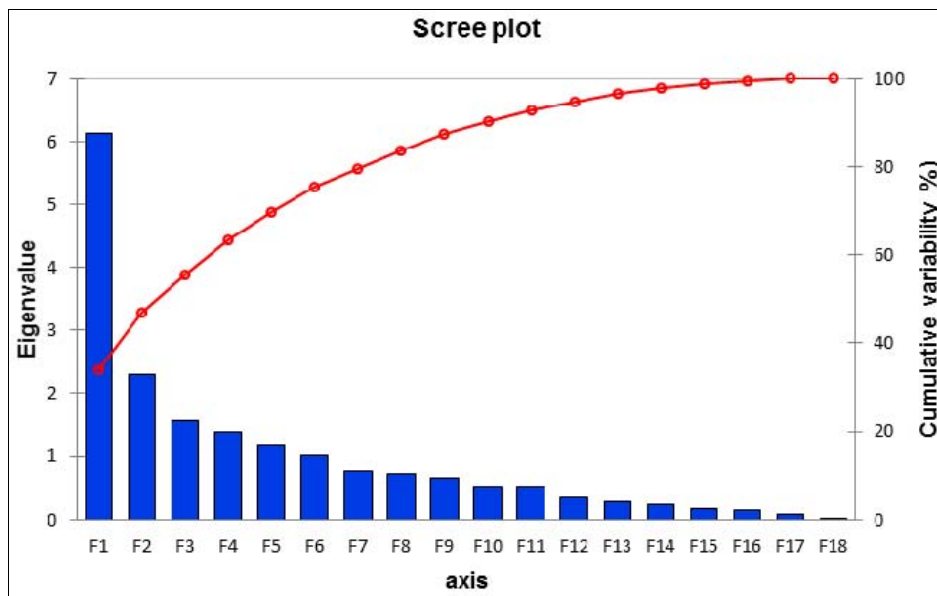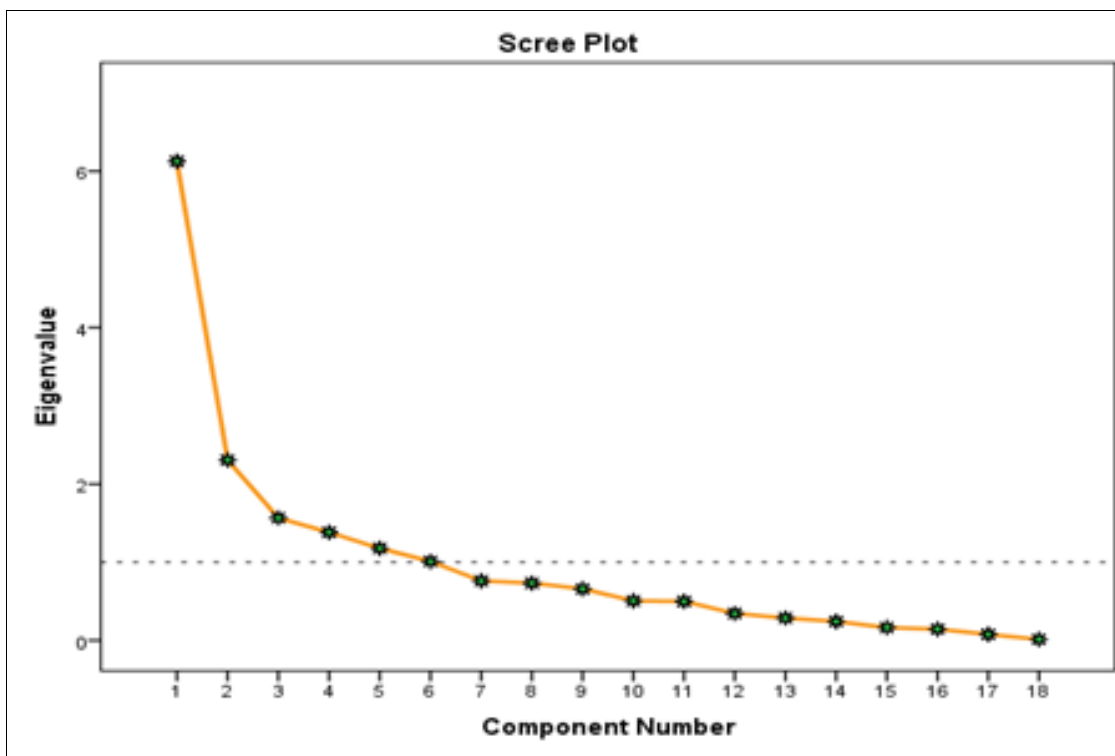
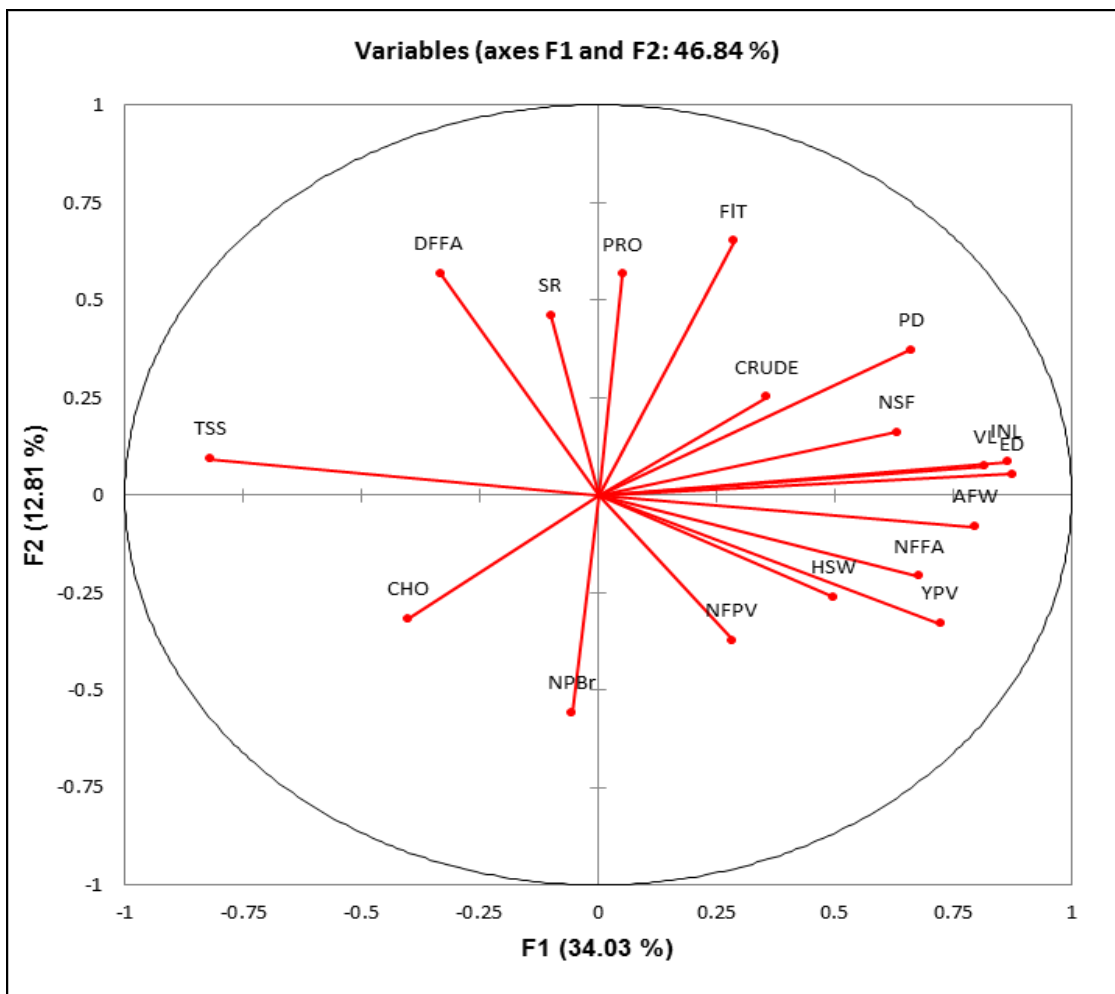**Fig 1.a, b:** Principal scree plot between component number and Eigen values

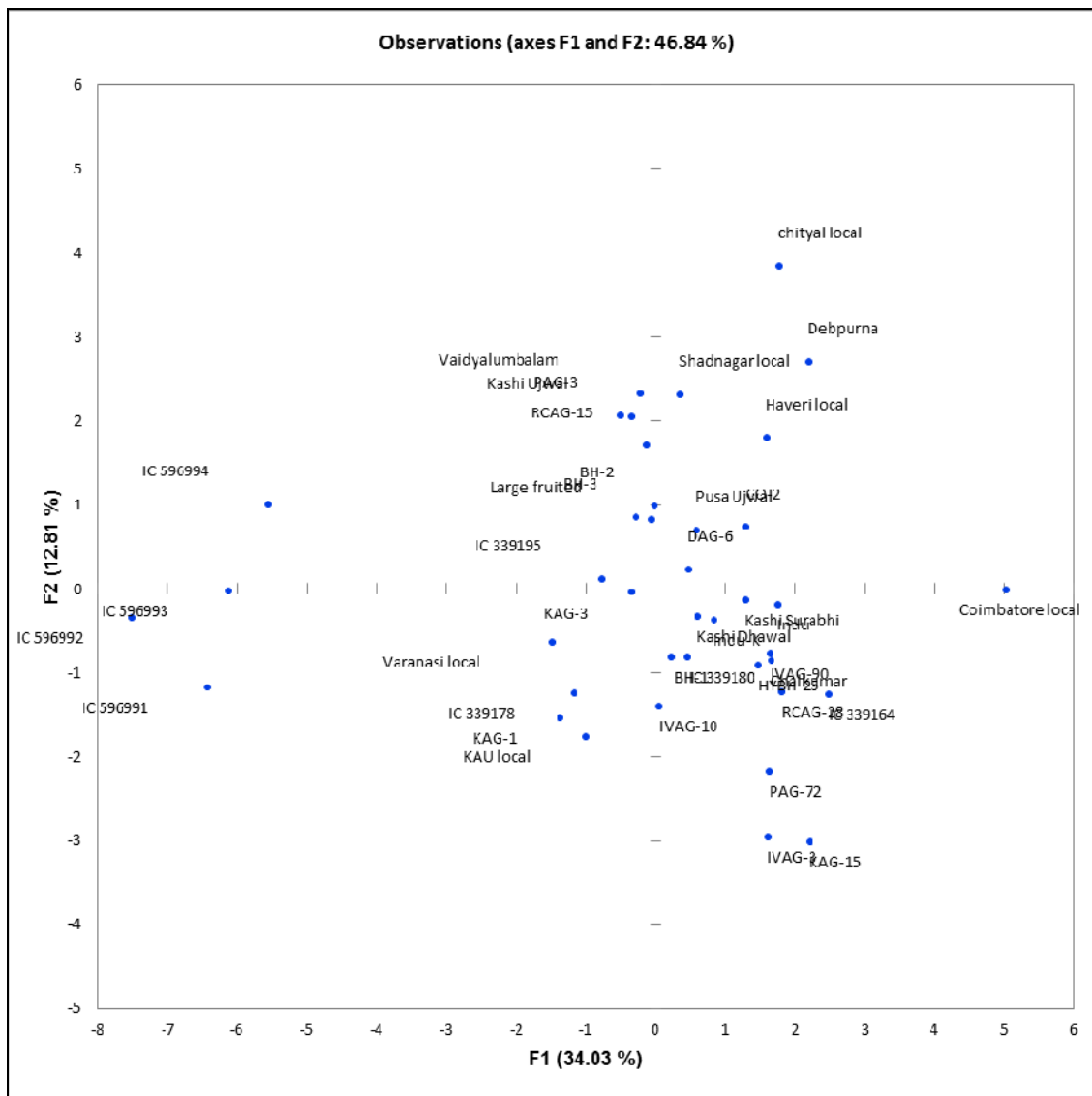**Fig 2:** Principal component bi-plot between 18 morphological characters

Fig 3: Principal component bi-plot of forty ash gourd genotypes

Conclusion
From the above study it can be concluded that vine length (VL), intermodal length (INL), node at first female flower appearance(NFFA), average fruit weight(AFW), polar diameter(PD), equatorial diameter(ED), number of seeds per fruit(NSF), total soluble solids(TSS), number of fruits per vine(NFPV), yield per vine(YPV), days to first female flower opening(DFFA), hundred-seed weight(HSW), protein content (PRO), sex ratio(SR), flesh thickness(FlT), number of primary branches(NPBr), carbohydrate content(CHO) and crude fibre(CRUDE) are important for improving yield and quality traits in ash gourd. Based on the performance of genotypes for above mentioned characters few genotypes have been selected (Coimbatore Local, IC 339164, KAG 15, PAG 72, IVAG 10, Indu, Chalkumar, KAU Local, Shadnagar Local, Chityal local and Debpurna and among the scented genotypes IC 596991, IC 596992 and IC 596994) as parents to be utilized in future breeding programs.

Acknowledgement

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