PRINCIPAL COMPONENT ANALYSIS OF 100 INDIGENOUS & EXOTIC ACCESSIONS OF PIGEONPEA [*Cajanus cajan* (L.) Millsp.] OF INDIAN NATIONAL SEED BANK.

Abstract:

In all, 100 pigeonpea genotypes, including six checks (KRG-33, PT-0012, UPAS-120, CORG-9701, BDN-716, and C.G ARHAR-2), were analyzed using Augmented Block Design. To identify genetic diversity among genotypes, the study used principal component analysis (PCA) on yield and its contributing traits. Principal component analysis found that the first four principal components had an eigen value larger than one, accounting for 66.56% of total variance. Principal component analysis showed that 100 seed weight contributed the most variance in genotypes, followed by number of pods per plant, days to maturity, and pod length. Diversity in plant genotypes allows plant breeders to develop new and improved cultivars with desired features such as earliness and yield contributing attributes

Keywords :Diversity, Germplasm,Pigeonpeaand Principal component analysis.

Introduction:

Pigeon pea is a high-protein crop whose seed is often used in a variety of recipes and can also be served as a substitute for Cowpea. It consists of 62.78 g of carbohydrates, 1.49 g of fat, and 21.7 g of protein in 100 g. Generally, the Protein content ranges from 18-29 % which is about three times the value found in cereals (Techale*et al.*, 2013). It has been acknowledged as an excellent source of vegetarian protein, particularly in underdeveloped nations where the bulk of the population relies on low-cost vegetarian diets. In India, pigeonpea is the second most significant pulse crop after chickpea (Vijayalakshmi *et al.,* 2013). India is the world's largest pigeon pea producer accounting for 90 per cent of the world production (Rangare*et al.*,2013). The world's most significant pigeonpea producing areas include India, Eastern Africa, Central and South America, the Caribbean, and the West Indies(Vijayalakshmi *et al.*,2013).

The polymorphism present in pigeonpea genotypes provides information on the nature and degree of genetic diversity, which is required for any plant breeding project.The backbone of every crop development endeavor is the collection, conservation, and characterization of genotypes, which is dependent on the level of genetic diversity present in the gene pool.Diversity in plant genotypes allows plant breeders to create new and improved cultivars with desired traits.Natural genetic diversity within crop species has been harnessed from the beginning of agriculture to meet subsistence food requirements, and it is currently being concentrated on excess food production to meet the requirements of expanding populations. In this instance, principal component analysis (PCA) may be used to identify patterns and remove duplication in data sets (Mahalingam *et al.,* 2020) as morphological and physiological variations routinely occur in crop species. PCA reduces a huge data series into smaller set of variables without sacrificing any critical information of the original data set by looking for groups that have extremely high inter-correlation with percent variation explained for each component towards the overall variability (Das *et al.,* 2017). Biplot Analysis is an investigative graph approach used in statistics with two-dimensional graphs that represent a multidimensional dataset.The research purpose was designed to determine the diversity by genotype categorization using Principal Component Analysis(PCA).

Material and Method :

100 pigeonpea genotypes, including 6 checks (KRG-33, PT-0012, UPAS-120, CORG-9701, BDN-716, and C.G. ARHAR-2), were examined in Augmented Block Design (Table 1) during*kharif* season 2022-23 at experimental area of pigeonpea, IGKV Research farm and specific traits were again recorded and verified in next *kharif* 2023-24 in the same Augmented block design.9 biometrical traits were recorded for the assessment of variability and diversity present in germplasm.

For assessment of diversity in yield aspect, nine biometrical characteristics were recorded, Which were, 1.plant height (cm). 2. The number of primary branches 3. Number of pods per plant, 4. The pod's length (cm), 5. Seeds per pods. 6. Days until the first flowering, 7. Days to 50% flowering, 8. Days to maturity and 9. 100 seed weight (g). The mean data from the pigeonpea accessions was used to perform Principal Component Analysis (PCA). The study was conducted using the INDOSTAT software package.

Result And Discussion

A thorough understanding of the magnitude of variability present in each character in germplasm would simply contribute to improving traits via selection. Hybridization programs require knowledge of the genetic diversity among germplasm accessions in order to get a diverse range of recombination. The Principal Component Analysis (PCA) resulted in the formation of four principal components with eigen value larger than 1 (Table 2). The eigen values of PC1, PC2, PC3, and PC4 were 2.560, 1.182, 1.195 and 1.054, respectively, and PCA 5 demonstrated discriminating power (0.940). The first four principal components which accounted for 66.56 per cent of total variation which was depicted in Table 2. Hamid *et al.,* (2011) found 76.2% of total variance during the study of hundred germplasm lines for various morphological and agronomic variables.Table 3 depicts a component matrix with latent vectors associated with the first four principle components.PC1 gave the greatest percentage of variation (28.45%) to the overall variance, followed by the third principal component (PC3) (13.272), second principle component (PC2) (13.130%), and fourth principal component (PC4) (11.707).

The first principal component (PC1) provided the most variance to the total variation and had positive loadings for all of the characters investigated. Similar results were obtained by Rekha et al. (2013) and Tharageshwari and Hemavathy (2020) using pigeonpea germplasm accessions. Eigen vector values greater than 0.4 may be considered substantial loadings. The characteristic with eigen vector values larger than 0.4 might be efficiently used for selection, providing more variance to the principle component. In Principle component 1, the plant height had the highest loading value (0.431). The findings were consistent with those of Hemavathy et al. (2017), with PC1 contributing the most to overall variation.The second principal component (PC2) accounted for 13.130 percent of the variation, with high loadings for traits such as number of pods per plant (0.526) and days to 50% flowering (0.631), which contributed the most to the percent of variance.The rest of the traits demonstrated positive loadings in PCA 2. Yohane et al. (2020) showed similar findings for variables such as plant height (positive loading), number of main branches (positive loading), and number of pods per plant (max positive loading).

The third principal component (PC3) explained 13.272% of the overall variance. It demonstrated positive loadings for traits such as plant height (0.377), number of pods per plant (0.147), days to first flowering (0.149), days to maturity (0.155), and 100 seed weight (0.315). In addition, the number of main branches showed the highest positive loading (0.565). On the other hand, negative loading was seen in traits such as pod length (-0.359), seeds per pod (-0.220), and days to 50% flowering (-0.440), indicating that these features contributed negatively to genetic divergence.The results were confirmed by the findings of Zavinon et al. (2019), who discovered that the characteristics days to 50% flowering had a negative contribution to divergence.

The fourth principle component accounted for 11.70 percent of variation. In PCA 4, 100 seed weight had the highest positive loading (0.826), whereas negative loadings were seen for number of primary branches per plant (-0.285), number of pods per plant (-0.375), and days to 50% flowering (-0.002).

PCA Biplot analysis.

The PCA biplot was represented by a two-dimensional graph, which depicts a multidimensional dataset and to determine correlation between traits angle between two vectors is determined(Fig.1). If the angle between two variables was 90 degrees, it indicated that there was no association between them. If the angle was less than 90 degrees, a positive correlation was recognized; if the angle was greater than 90 degrees, a negative correlation existed between the two variables. Vector line length was employed to depict the variable's variation level. The distance between genotypes and variables was utilized to determine the contribution of the variable to the genotype. The value increases as the distance decreases, and vice versa.

Considering the previously mentioned criteria, the PCA biplot (Fig. 1) revealed that the traits days to maturity and days to fifty percent flowering showed a modest positive connection with hundred seed weight, but no association with pods per plant or pod length. Negative correlation was observed between number of seeds per pod and the traits days to maturity and fifty per cent flowering. High positive correlation was observed among the traits *viz*., days to maturity, days to fifty per cent flowering, plant height, pod length and number of branches per plant. The results were in concurrence with the findings of Yohane (2020) while analyzing phenotypic divergence of eighty onepigeonpea genotypes for both quantitative and qualitative traits. In the PCA biplot, the best performing genotypes were concentrated in the right quadrant of the biplot. The genotypes IC-245520 AND IC-245519 which were observed to have minimum value for all the variables was plotted in the negative left quadrant. Likewise, the genotypes IC-28192 and IC-28195 which showed maximum performance of all the variables plotted on the right quadrant.
The percent contribution of traits to diversity is indicated in Table 4 and Figure 3. Hundred seed weight contributed most towards diversiy (19.22%) followed by number of pods per plant (18.55%), days to maturity (13.90%)., pod length (12.32%) and seeds per pod (10.50). Least contribution to diversity was given by days to 50% flowering (1.28%). Similar results were obtained by Dhanushree and Hemavathy (2022) in sixty eightpigeonpea genotypes.

CONCLUSION

PCA is a significant tool for improving breeding programs since it isolates all of the principle components and shows their contribution to overall variability. The PCA biplot demonstrated that the high-performing genotypes, RP-1, IC-28192, and IC-28195, may be efficiently used for crop development programmes.

FUTURE SCOPE

Principal Component Analysis (PCA) speeds up crop improvement by categorizing key elements and their contributions to variance. Genotypes that contribute significantly to yield can be selected and used as parents in future breeding projects.

Table 1. List of pigeonpea accessions used in investigation.

S.No.	Accessions	S.No.	Accessions	S.No.	Accessions	S.No.	Accessions	S.No.	Accessions
1	KRG-33	21	IC-15707	41	IC-22511	61	IC-28194	81	IC-261382
2	PT-0012	22	.IC-16206	42	IC-22531	62	IC-28198	82	IC-267493
3	UPAS-120	23	IC-25053	43	IC-22532	63	IC-28196	83	IC-268203
4	CORG-9701	24	IC-28193	44	IC-22533	64	IC-28195	84	IC-329116
5	BDN-716	25	EC-843234	45	IC-22534	65	IC-28199	85	IC-323307
6	C.G. ARHAR-2	26	EC-843247	46	IC-22535	66	IC-245477	86	IC-347516
7	RPS 2015-49	27	EC-843254	47	IC-22536	67	IC-245478	87	IC-349776
8	RPS 2015-51	28	EC-843277	48	IC-22555	68	IC-245479	88	IC-385887
9	RPS 2015-4	29	EC-843278	49	IC-23672	69	IC-245482	89	IC-393694
10	RPS 2015-40	30	EC-8362	50	IC-23679	70	IC-245519	90	IC-424779
11	RPS 2015-1	31	IC-11011	51	IC-23683	71	IC-245520	91	IC-468174
12	RPS 2014-32	32	IC-14992	52	IC-23685	72	IC-245522	92	IC-468334
13	RPS 2014-34	33	IC-15710	53	IC-25050	73	IC-245525	93	IC-468590
14	RPS 2014- 6	34	IC-16194	54	IC-25054	74	IC-245534	94	IC-468591
15	RPS 2014-21	35	IC-16195	55	IC-25055	75	IC-245539	95	IC-521410
16	RPS 2014- 19	36	IC-16203	56	IC-25056	76	IC-245550	96	IC-523150
17	RP-1	37	IC-16210	57	IC-25059	77	IC-245560	97	IC-634397
18	IPAD-5	38	IC-22501`	58	IC-25060	78	IC-259318	98	IC-634438
19	EC-14995	39	IC-22502	59	IC-26114	79	IC-259319	99	C.G. ARHAR-1
20	IC-15706	40	IC-22510	60	IC-28192	80	IC-261355	100	Rajeevlochan

Table 2. Eigen value and percentage of total variances for different principle components.

Components	Eigen Value	Percentage of variances	Cummulative percentage of variances
PCA 1	2.560	28.45	28.45
PCA 2	1.182	13.13	41.60
PCA 3	1.195	13.27	54.85
PCA 4	1.054	11.707	66.56

Table 3. Component matrix showing positive and negative loadings of traits.

S.No.	Traits	PCA 1	PCA 2	PCA 3	PCA 4
1	Plant height (cm)	0.431	0.192	0.377	0.040
2	Number of primary branches	0.248	0.151	0.565	-0.285
3	Number of pods per plant	-0.018	0.526	0.147	-0.375
4	Pod length (cm)	0.349	0.042	-0.359	0.250
5	Seeds per pod	0.307	0.357	-0.220	0.015
6	Days to 50% flowering	-0.058	0.631	-0.440	-0.002
7	Days to flowering	-0.490	0.282	0.149	0.173
8	Days to maturity	-0.537	0.138	0.155	0.040
9	100 seed weight (g)	0.074	0.195	0.315	0.826

Table 4. Percent Contribution of traits towards diversity.

Sl. No.	Source	Contribution %	Times ranked 1st
1	Plant height (cm)	9.76	488
2	Number of primary branches	9.88	494
3	Number of pods per plant	18.55	928
4	Pod length (cm)	12.32	616
5	Seeds per pod	10.50	525
6	Days to 50% flowering	1.28	64
7	Days to flowering	4.59	230
8	Days to maturity	13.90	695
9	100 seed weight (g)	19.22	961

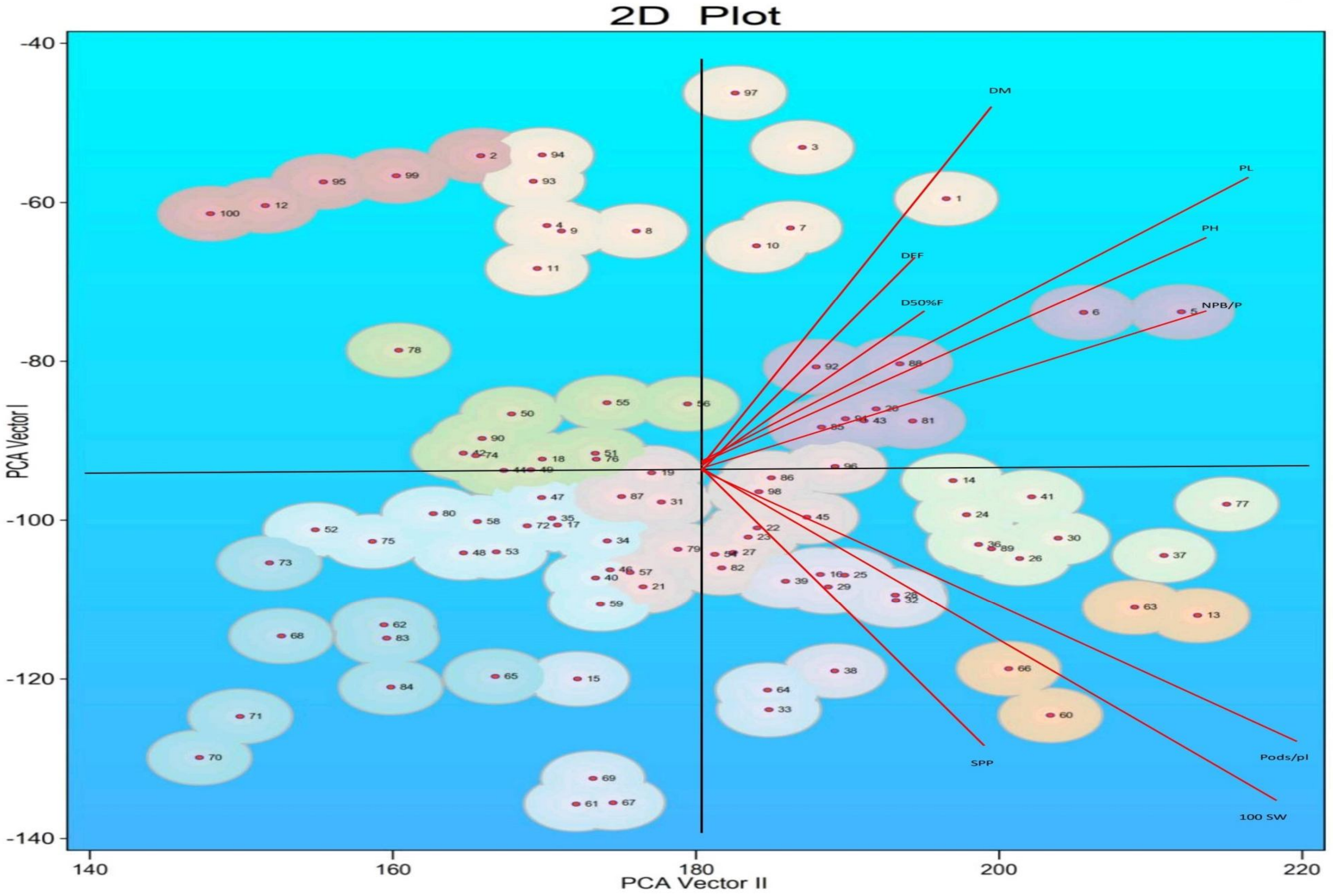

Fig. 1 2D PCA biplot with vectors depicting variance due to traits.

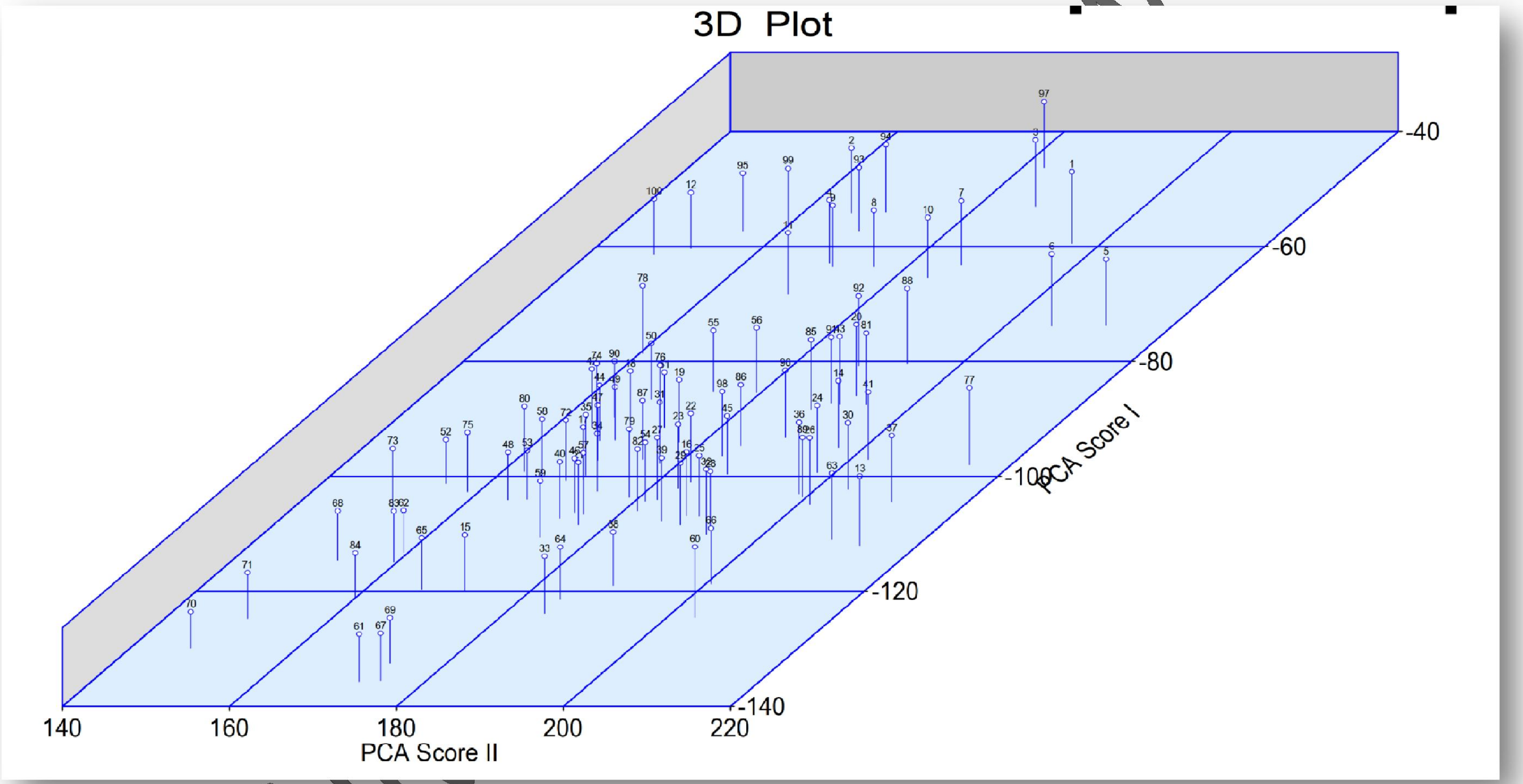

Fig.2. Three dimensional representational of PCA Biplot.

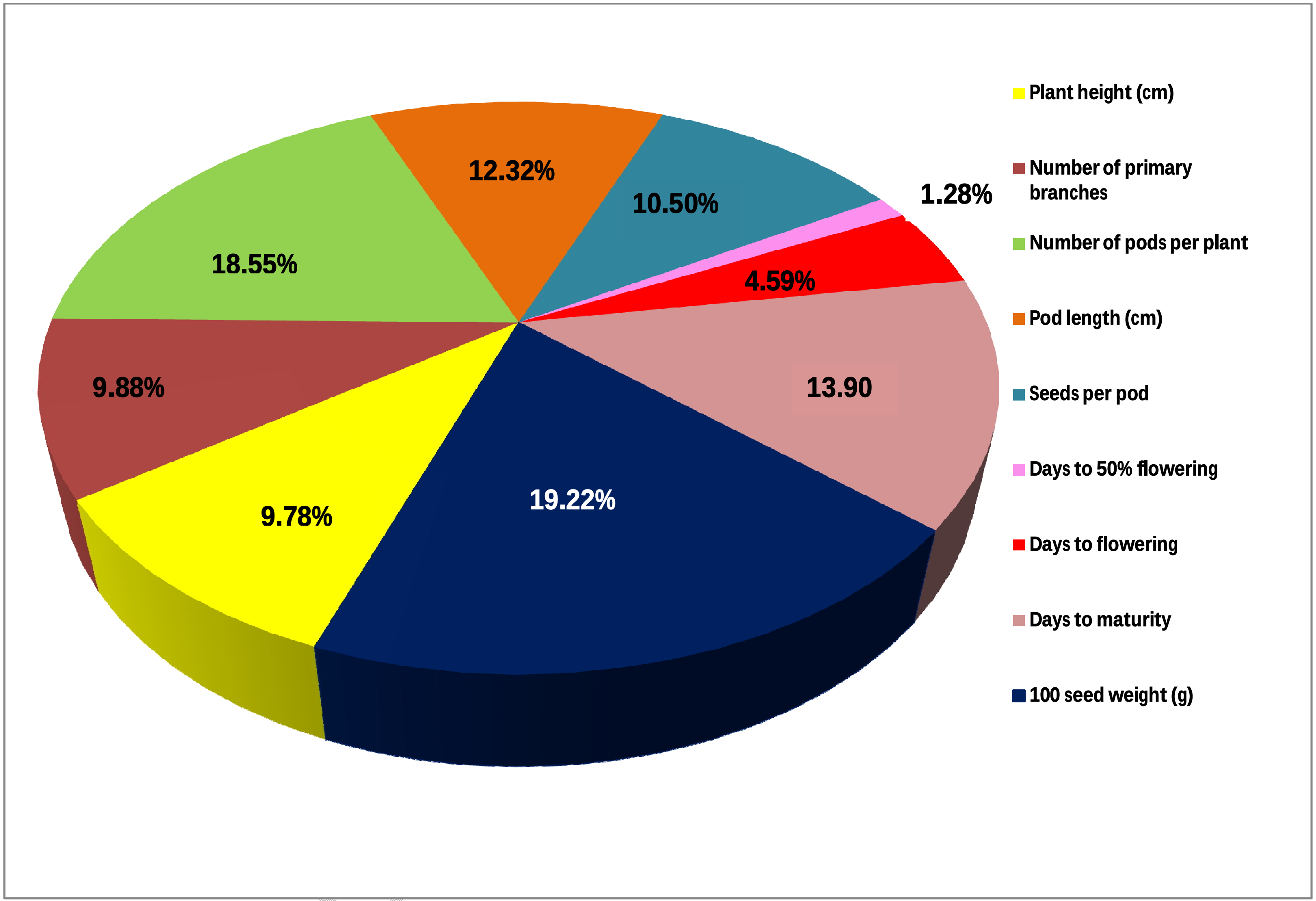

Fig. 3. Percentage (%) contribution of traits towards diversity.

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