Original Research Article

Performance of French Bean (*Phaseolus vulgaris* L.) under Temperate conditions of Kashmir Himalaya

Comment [I1]: Title Need to modify properly again according to the statement of problem in the study area

ABSTRACT

The extent of diversity in the germplasm can be effectively used to breed desirable cultivars and to challenge the consequences of the biological, physical and chemical stresses in the growing conditions. In the present study, total 30 diverse French bean genotypes collected from different regions of Kashmir and three check varieties *viz.*, Arka Arjun, Arka Sharath and Contender were grown under randomized complete block design with three replications. The genotypes were evaluated for genetic variability using various statistical procedures. The pod yield per hectare correlated positively and significantly with Plant height, Pod length, Number of pods per plant showing a scope for simultaneous improvement of yield and yield related traits. Principal Component biplot revealed that genotypes Arka Arjun, Sel-3, DARS-17, KDR-2019-3, WB-1455, WB- 9596 were the most genetically distinct.

Comment [I2]: In the abstract it is need to include shortly on purpose of the study, research methodology, important findings about correlation and PCA variation studies and originality / value means smart conclusion part.

Key words: French bean, *Phaseolus vulgaris*, Principal Component analysis, Variability

INTRODUCTION

French bean (*Phaseolus vulgaris* L.) is the most important leguminous vegetable grown worldwide for direct human consumption (Gepts, 2001). It is also known as Kidney bean, Common bean, Field bean, Garden bean, Bush bean, Navy bean, Haricot bean, Pinto bean, String bean, Marrow bean & Snap bean etc. It is processed as a frozen vegetable and is mainly grown for fresh pod consumption in many countries. French bean is an important

Comment [I3]: Add some more recet references protein source for human consumption in the developing countries. It is also rich in calcium, iron and different types of vitamin B (Karasu and Oz, 2010).

Comment [I4]: Need to write about botanical description of the crop with references

In Kashmir, French bean is grown over an area of 24360 hectares, with an annual production of 14380 tonnes and with the productivity of 600 kg/ha (Anonymous, 2018). Despite being a vegetable of utmost importance, its production and productivity is still low in Kashmir. Lack of diversity and non-availability of determinate types is a major bottleneck in bean improvement programmes in India (Dikshit *et al*., 1999). The reason for low production of French Beans is the non-availability of high yielding, early and short duration, biotic and abiotic stress tolerant and insect pest and disease resistant varieties. Thus, these factors have led to absolute requisite to select and evaluate high yielding breeding lines of French bean with desirable quality characteristics under temperate conditions of Kashmir. French bean is an important well suited crop of Kashmir, however, its area and production has progressively declined. The yields are disappointingly low and the cultivation is being limited to marginal areas with low input support. French bean is losing ability to compete with other crops and is progressively being eliminated from cultivation. The lack of high yielding varieties that could fit in highly intensive farming systems have resulted in fast shrinkage of area under French bean. Also in order to increase the yield, there is need to identify parents with yield potential that are well adapted under temperate conditions of Kashmir. There is an urgent need to characterize and evaluate the already present variability in French Beans and also to create new combinations that will not only increase the productivity with resilience but also enhance the quality. This requires in depth evaluation of already present variability for morphological and yield traits. For the above mentioned reasons studies similar to the present study, were conducted by Negahi *et al.* (2014) who found high significant differences among genotypes for all studied traits among which 100-seed weight, seed yield, biomass yield, number of pods per plant and number of seeds per plant had high phenotypic coefficients of variations.

Comment [I5]: Add such more recent references to prove the above statement

Comment [I6]: Give the reference for this statement due to above factors yield is lowin the study area

Comment [I7]: Prove with suitable references

Jhanavi *et al.* (2018) also conducted similar experiment on 36 genotypes of French bean showing high heritability coupled with high genetic advance for the plant height, pod width, number of pods/plant, weight of ten pods, yield /plant, number of root nodules /plant, dry matter content of pods, roots and protein content. Characterization at phenotypic level using morphological traits serves as a principle tool in establishing the identity and distinctness of the genotypes in the concerned species for breeding purpose. Such information on characterized genotypes will help in building a strong national gene pool. In view of these facts, the present investigation was designed to document and characterize the existing genotypes of ~~genetic variability in~~ French bean in the research area.

Comment [I8]: Statement of problem has to be improved in the stronger way. Why this research study has dire need in study area.

MATERIALS AND METHODS:

The basic plant material comprised of 33 lines collected from different parts of Kashmir as well as from national gene banks and maintained at SKUAST-K. The checks included Arka Arjun, Arka Sharath and Contender. These genotypes were evaluated for morphological and yield parameters. The experiment was conducted at the research field of Sher-e-Kashmir University of ~~Agricutural~~Agricultural Sciences and Technology of Kashmir, (34°08’56.40’’N, 74°52’22.80’’E; 1500 m.a.s.l) in the *kharief* season. The experimental site has clay loam soil with an average annual rainfall of 720 mm and maximum temperature of 30°C. The experiment was laid in a randomized complete block design with 3 replications. Seeds were sown at a spacing of 45 cm × 15 cm. Two seeds per hill were dibbled at a depth of 2.0 to 2.5 cm. Thinning operation was carried out on 20th day after sowing and one healthy and vigorous plant per hill was retained. The standard cultural practices recommended for growing French bean were followed.

Comment [I9]: It will better to give the detais of checks which are better in the mentioned longitude and latitude they are performing will.

Comment [I10]: Write about year during which year experiment was conducted

Comment [I11]: Need to explain about net plot size and gross plot size with different distance kept in between to net plots as well as two blocks

Comment [I12]: Include table which containing the details of the genotypes, tier collection number or local names etc.

~~DATA COLLECTION:~~

The data was collected on 8 morphological parameters of the bean genotypes *viz*. Plant height, Plant spread, pod length, pod width, No. of seeds/pod, No. of pods/plant, Average pod weight, Yield/ha on five randomly selected plants per plot.

Comment [I13]: The said parameters are not related with plant characterization

~~STATISTICAL ANALYSIS:~~

The baseline data generated was summarised using the descriptive statistics for a clear data overview. Data collected was subjected to analysis of variance (ANOVA) using SAS Software (Inc., USA) and critical difference (cd) was used for post hoc comparisons. The genotypic effect was considered as a fixed factor. Pearson's correlation was used to assess the correlation between the parameters. Principal component analysis (PCA) was done using accession means to evaluate the contribution of the parameters under consideration towards the variability among the bean genotypes. Both correlational analysis and PCA were executed using the R studio statistical software (Version 3.6.3).

Comment [I14]: Need to include formula of PCA and according need to write about bioplot construction and explaination.

Comment [I15]: Different subheading like study area, Planting material and design, data collection, statical analysis, and principal component analysis should include separately and should be explained properly under the heading of Methods and materals

RESULTS AND DISCUSSION:

DESCRIPTIVE STATISTICS: The basic features of the data generated were described using the descriptive statistics as shown in Table 1.

Table 1: Summary of the recorded parameters

Comment [I16]: Table heading should be properly written along with the year

Parameter	N	Minimum	Maximum	Mean	Std. Deviation
Plant Height (cm)	33	35.22	62.71	49.22	6.46
Plant Spread (cm)	33	29.13	48.27	37.14	4.12
Pod Length (cm)	33	8.77	15.31	11.56	1.87
Pod Width (cm)	33	0.76	3.17	1.17	0.39
No of seeds/pod	33	3.40	6.67	5.09	0.78
No. of pods/plant	33	9.20	61.53	19.12	10.51
Avg. Pod weight(g)	33	2.45	7.61	5.45	1.12
Yield/ha(Q)	33	19.63	202.17	68.81	36.39

The maximum plant height was seen to be 62.71 cm in case of the Arka Sharath while minimum height of 35.22 cm was recorded in WB-206, maximum plant spread was found to be 48.27 cm in DARS-17 while minimum of 29.13cm was recorded in KDR-2019-4, maximum pod length of 15.31 cm was seen in WB-429 and minimum of 8.77 cm in KDR-2019-4, maximum pod width of 3.17 cm was found in DARS-10-1, and minimum of 0.76 cm in Sel-3. Also, the No. of pods/plant were highest in Arka Sharath (61.53) and lowest in KDR-2019-4 and FB-7996 (9.20), highest no. of seeds /pod were seen in Arka Arjun (6.67) and the lowest in KDR-2019-4 (3.40). the average pod weight was maximum in WB-923 (7.61g) and minimum in WB-249 (2.45g) and yield per hectare was maximum in Arka Sharath (202.17Q/ha) while the lowest yield/ha was recorded in FB-7996 (19.63 Q/ha).

Comment [I17]: This explanation should be needed after the explanation of ANOVA. Also explanation on this area should be need to write properly with suitable recent references.

ANOVA: The ANOVA showed highly significant ($p \leq 0.01$) differences among the tested genotypes for all agronomic traits, showing high level of phenotypic differences among them (Table 2). Similar results were reported in case of a study on cowpea by (Nwosu *et al*., 2013; Gerrano *et al*., 2015; 2019). Similarly, Kamara *et al*. (2017) observed significant variations in the agronomic characteristics of the cowpea cultivars in Nigeria. Also this work is supported by the research of Junaif *et.al*., (2019) and Junaif *et.al*., (2010b)

Comment [I18]: ??

Comment [I19]: All the references need to arrange chronologically

Comment [I20]: Explanation of this ANOVA needed to keep at the starting of the results and discussion part and also need to include the ANOVA table.

Table2: Table of means for the traits of 33 genotypes.

Comment [I21]: Heading of table should be need to modify

GENOTYPES	Plant height	Plant Spread(cm)	Pod Length(cm)	Pod width(cm)	No of seeds/pod	No. of pods/plnt	Avg Pod wt(g)	Yield/ha(Q)
Contender	49.673	34.1	13.327	0.987	5.533	25.067	6.167	102.197
Arka Arjun	49.333	30.227	15.033	0.833	6.667	28.867	5.873	108.862
Arka Sharath	62.707	44.08	14.467	0.987	5.4	61.533	4.887	202.172
Sel-3	53.447	37.627	14.9	0.76	5.133	43.267	4.76	135.522
DARS-10-1	37.74	34.153	11.873	3.167	5.467	18.733	4.907	66.65
DARS-16	46	37.373	14.853	1.047	5.733	15.467	5.46	53.32
DARS-17	58.787	48.267	11.06	1.073	5.467	26.8	4.853	82.202
KDR-2019-1	43.927	31.78	10.633	1.36	5.267	10.647	5.893	41.835
KDR-2019-3	43.127	36.673	10.287	1.153	4.467	9.393	5.1	31.945
KDR-2019-4	39.28	29.133	8.773	1.227	3.4	9.2	4.967	30.473
KDR-97	53.527	36.493	12.387	1.24	4.4	15.733	7.373	77.398
KDFB-3	45.273	40.393	9.58	1.167	5.067	18	5.24	62.868
KDFB-37	44.98	41.893	9.427	1.193	5.2	19.733	4.967	65.344
WB-6	50.033	42.74	12.733	1.287	4.867	11.693	6.06	47.267
WB-22	52.18	40.333	10.34	1.173	5.333	9.8	4.66	30.523
WB-195	54.473	39.633	12.8	1.16	4.867	18.733	7.307	91.271
WB-206	35.22	31.627	10.147	0.773	4.467	23.067	4.387	67.622
WB-249	49.533	39.273	11.5	0.86	4.333	20	2.453	32.796
WB-429	44.993	36.64	15.313	0.993	6.267	17.667	6.493	76.522
WB-630	41.347	35.307	11.627	1.073	4.467	11.813	5.28	41.625
WB-634	47.607	30.28	11.087	1.02	6.067	16.2	5.18	56.013
WB-651	50.613	38.447	9.347	1.24	5.467	22.667	6.427	97.132
WB-923	61.38	36.273	10.52	1.46	4.467	17.733	7.607	90.009
WB-1129	49.38	35.013	12.533	1.027	5.8	16.667	6.813	75.74
WB-1185	52.167	38.727	10.433	1.26	5.533	9.333	6.327	39.385
WB-1319	46.807	36.52	9.853	1.107	5.067	27.933	5.493	102.376
WB-1446	46.247	37.427	11.36	1.333	5.2	11.8	5.64	44.409
WB-1455	56.493	37.62	13.207	1.173	6.267	18.667	6.06	75.491
WB-1492	55.58	38.28	9.933	1.02	3.667	18.667	3.753	46.861
WB-1643	57.947	40.593	10.493	1.267	6.067	21	6.307	88.353
WB-1644	47.28	35.22	10.793	1.147	4.8	9.6	5.447	34.989
WB-9596	52.153	33.7	12.16	1.227	4.267	16.467	4.72	51.927
FB-7996	45	39.833	8.84	0.773	3.667	9.2	3.2	19.633
CD	**0.061**	**0.068**	**0.031**	**0.007**	**0.013**	**0.202**	**0.164**	**0.207**
SE(d)	**0.031**	**0.034**	**0.015**	**0.003**	**0.006**	**0.101**	**0.082**	**0.103**
SE(m)	**0.022**	**0.024**	**0.011**	**0.002**	**0.005**	**0.071**	**0.058**	**0.073**
CV	**0.076**	**0.111**	**0.161**	**0.339**	**0.152**	**0.399**	**0.221**	**0.444**

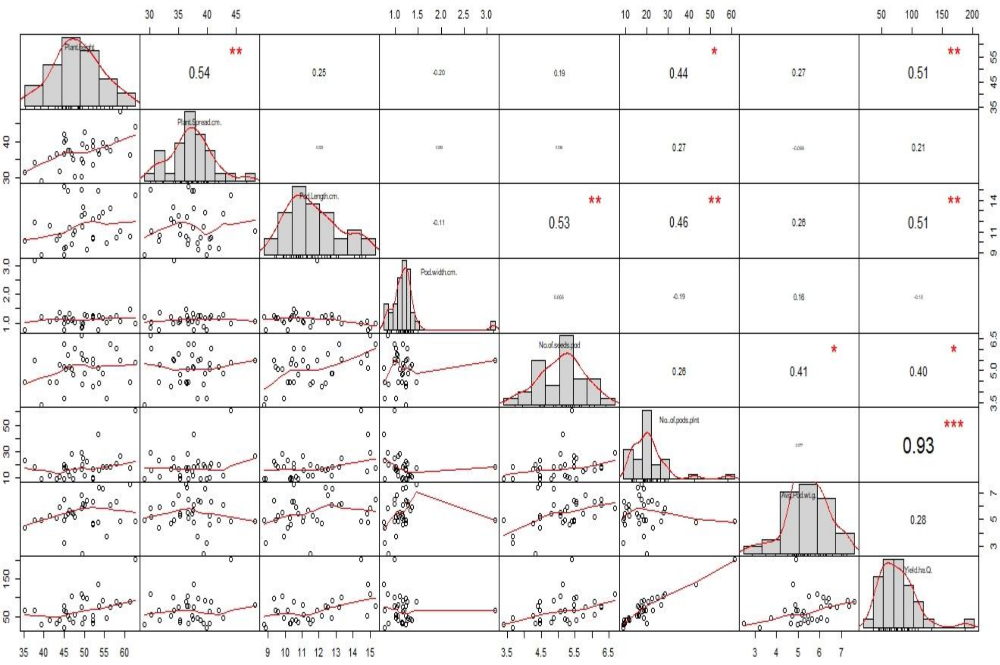
Comment [I22]: All the values of the decimal point should maintained in two digits rather than keeping un evenly

CORRELATION ANALYSIS:

The correlational analysis was executed in the form of chart of a correlation matrix using the package “**Performance Analytics**” of the R Studio software. The analysis revealed highly significant correlations between the parameters as is shown in Figure 1.

Figure 1: Correlation chart

Comment [I23]: Correlation chart for what?, correlation chart is very impressive but need to explain properly and summarized properly



In the above plot the distribution of each parameter is shown on the diagonal and on the bottom of the diagonal, the bivariate scatter plots with a fitted line are displayed. On the top of the diagonal and the value of the correlation plus the significance level as stars are displayed. Plant height revealed highly significant positive correlation with plant spread (r=0.54) and no. of pods per plant (r=0.44). Similarly, highly significant correlations were also observed between pod length and number of seeds/pod (r=0.53), pod length and no. of pods/plant (r=0.46), No. of pods/plant and plant height (r=0.44). The yield/ha was found to have a high significant correlation with plant height (r=0.51), pod length (r=0.51), No. of seeds/pod (r=0.40) and No. of pods/plant (r=0.93). The results are in accordance with the work of Junaif *et.al.*, (2010a)

Comment [I24]: Need to include more recent references and has to be explain properly

Principal component analysis (PCA):

Principal component analysis (PCA) simplifies the complex data by transforming the number of correlated variables into a smaller number of variables called principal components (Ajmal et al. 2013). PCA is interpreted based on the correlations among variables: the further the number from zero in either direction, the greater the positive or negative correlation (Mumtaz *et al.* 2018). PCA provides variable independence and balanced weighting of traits, which leads to an effective contribution of different characters based on respective variation Mohammadi *et al.* 2003).

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The results of the PCA are presented in Table 2 and Figure 2. The first three principal components explain more than 72% of the total variation. All the three PC's had eigen values greater than one and were retained as per the Kaisers criterion. Pod length, no. of pods/plant, yield per hectare were found to have high negative loadings axis 1, indicating that higher values on PC 1 correspond to lower values of these parameters. Average pod weight was found to load on axis 2 and the rest of the parameters were found to have high positive loadings on axis 3 respectively.

Comment [I25]: Need to explain about 1 PC, II PC and positive and negative values and why this so with proper explanation and with references.

Table 3: Eigen Values of the principal components

Comment [I26]: Heading should be neede to write agin

	PC1	**PC2**	**PC3**	**PC4**	**PC5**	**PC6**	**PC7**	**PC8**
Standard deviation	1.7576	1.2556	1.0540	0.9354	0.8064	0.6459	0.5264	0.0639
Proportion of Variance	0.3861	0.1971	0.1389	0.1094	0.0813	0.0521	0.0346	0.0005
Cumulative Proportion	0.3861	0.5832	0.7220	0.8314	0.9127	0.9648	0.9995	1.0000
EigenValues	3.0891	1.5764	1.1108	0.8750	0.6503	0.4172	0.2771	0.0041

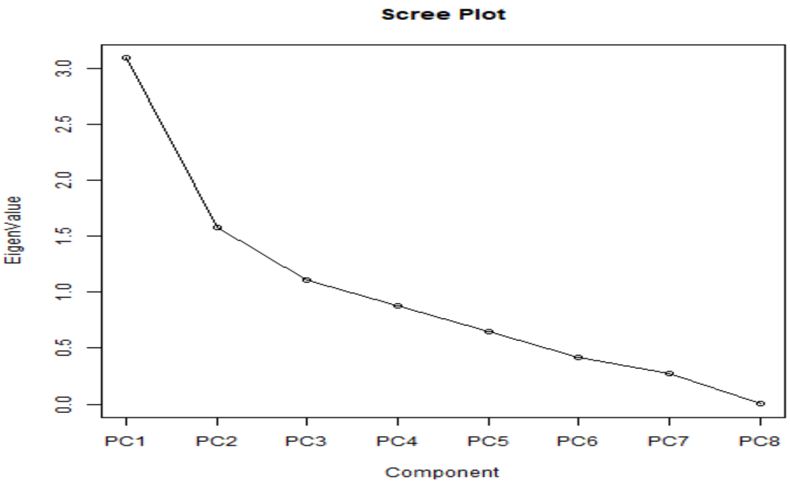
Table 4: Eigen Vectors of the principal components

Variables	**PC1**	**PC2**	**PC3**	**PC4**	**PC5**	**PC6**	**PC7**	**PC8**
Plant height	-0.3925	0.2518	0.4332	-0.2291	0.1712	-0.2469	0.6724	0.0028
Plant Spread	-0.2098	0.4712	0.5309	0.0695	-0.4417	0.0082	-0.5019	0.0132
Pod Length	-0.3903	-0.2700	-0.3058	-0.1048	-0.3264	-0.7347	-0.1523	0.0263
Pod width	0.1067	-0.3726	0.3937	0.7914	-0.0154	-0.2194	0.1413	-0.0111
No of seeds/pod	-0.3322	-0.4320	0.0262	-0.0818	-0.5789	0.5374	0.2678	-0.0087
No. of pods/plant	-0.4695	0.2219	-0.2994	0.3566	0.1726	0.1469	-0.0300	-0.6792
Avg Pod weight	-0.2000	-0.5164	0.4155	-0.3332	0.4341	0.0509	-0.3954	-0.2498
Yield/ha	-0.5170	0.0204	-0.138	0.2459	0.3399	0.1952	-0.1544	0.6894

Comment [I27]: Upto 4th PC values are more suitable rather than taking upto 8th PC. After 4th PC if % contribution of the traits are needed to add and should be explain properly.

The scree plot generated is useful for understanding how variance is distributed among the principal components, and it should be the first step in analysing a PCA. The scree plot is particularly critical for determining how many principal components should be interpreted.

Figure 2: Scree plot

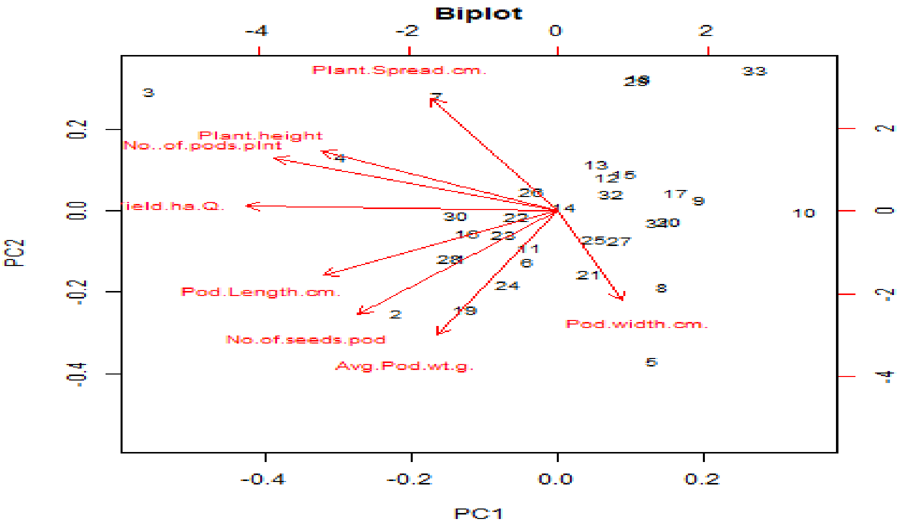


For our data set, two or possibly three principal components should be examined closely. The first three PCs account for almost 72% of the variance, and there is a drop-off in percent variance from the third PC.

Comment [I28]: That's why no need to keep the values of PC after 4th PC in the table 4.

The biplot generated has arrows added to show the loadings, as are labels to identify the loadings. Most of the tested germplasm accessions were concentrated in the biplot (Fig 3) indicating that the genotypes are genetically similar while some of the genotypes were scattered far away from the origin in the plot indicating their diverse nature and importance for future breeding programmes.

Figure 3: Biplot



The PC biplot indicated that the genotypes under study were scattered randomly across the entire biplot, indicating the existence of wide range of genetic variability among them. The genotypes grouped into clusters based on their agronomic trait associations. Arka Sharath, WB-1492, FB-7996, KDR-2019-4, DARS-10-1, KDR-2019-1 were positioned far from the origin, indicating that these genotypes had unique genes/alleles compared to the rest of the genotypes evaluated, while rest of the genotypes had a similar genetic relationship for most of the traits. The genotypes *viz.*, KDFB-3, KDFB-37, WB-22, WB-206, WB-9596, WB-1185, WB-1446, KDR-2019-3 and KDR-2019-1 had the lowest values for all the traits and were located to the top right quadrant of the biplot. The biplot also indicated the relative association of genotypes to traits based on their closeness. Genotypes far from the origin viz. appear to be the most genetically distinct based on the traits evaluated and can serve as potential and candidate parental lines for hybridization for the traits of interest in future French bean breeding.

Comment [I29]: Under the results and discussion part the explanation each and every part like correlation. PCA, PCA, Biplot should be need needed to keep in subheading and needed to explain separately with proper explanation and with suitable references.

CONCLUSION:

The pod yield per hectare correlated positively and significantly with Plant height, Pod length, number of pods per plant showing a scope for simultaneous improvement of yield and yield related traits. The ANOVA revealed a statistically significant difference between the genotypes with respect to the parameters under consideration, thus revealing a diversity and distinctiveness among the studied genotypes. Principal Component biplot revealed that Arka Arjun, Sel-3, DARS-17, KDR-2019-3, WB-1455, WB- 9596 were the most genetically distinct genotypes and can serve as candidate parental lines for hybridization to achieve transgressive segregation population in breeding programmes.

Comment [I30]: Should be very smart and needed to write on variability or diversity properly It should be also needed to explain about PCA values which cause the more percentage of variation and also with biplot which genotypes are more suitable for parental selection for further hybridization programme has to be explined.

COMPETING INTERESTS DISCLAIMER:

Authors have declared that no competing interests exist. The products used for this research are commonly and predominantly use products in our area of research and country. There is absolutely no conflict of interest between the authors and producers of the products because we do not intend to use these products as an avenue for any

litigation but for the advancement of knowledge. Also, the research was not funded by the producing company rather it was funded by personal efforts of the authors.

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Comment [I31]: Should be written according to the style of the journal

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