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Journal Name:	**International Journal of Plant & Soil Science**
Manuscript Number:	**Ms_IJPSS_106094**
Title of the Manuscript:	**Morphological Variability and Molecular Diversity in Blackgram (Vigna mungo (L.) Hepper) Genotypes Using SSR Markers**
Type of the Article	**Original Research Article**

General guideline for Peer Review process:

This journal's peer review policy states that **NO** manuscript should be rejected only on the basis of '**lack of Novelty'**, provided the manuscript is scientifically robust and technically sound.
To know the complete guideline for Peer Review process, reviewers are requested to visit this link:

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PART 1: Review Comments

	Reviewer's comment	**Author's comment** *(if agreed with reviewer, correct the manuscript and highlight that part in the manuscript. It is mandatory that authors should write his/her feedback here)*
Compulsory REVISION comments **1. Is the manuscript important for scientific community?** (Please write few sentences on this manuscript) **2. Is the title of the article suitable?** (If not please suggest an alternative title) **3. Is the abstract of the article comprehensive?** **4. Are subsections and structure of the manuscript appropriate?** **5. Do you think the manuscript is scientifically correct?** **6. Are the references sufficient and recent? If you have suggestion of additional references, please mention in the review form.** **(Apart from above mentioned 6 points, reviewers are free to provide additional suggestions/comments)**	=A study on the Morphological variability of 25 Blackgram genotypes was carried out in which molecular diversity of 15 genotypes of Blackgram was studied by using 8 SSR markers. =The GCV was lower than PCV for all traits,however, there was narrow difference in PCV and GCV, indicating the effect of environment in lesser frequency. =The high seed yield was recorded in the genotypes PLU-429(8.06gm) followed by PL-416(7.37gm) and VBN-8(7.29gm). =Among all the factors PC 1 to PC 8, the PC 1 (40.610) accounted maximum proportion of variability in the set of all variables. =The Polymorphism information content PIC values of 8 SSR markers valued from 31 percent to 71 percent with mean of 51 percent. BG 18 exhibited highest PIC 71 percent and highest heterozygosity of 62 percent. As per Dissimilarity coefficient, 15 genotypes are grouped into five clusters, Cluster II & V has highest 4 genotypes while in compare with Cluster I, III & IV. SSR marker BG18 has highest number of alleles 5. Shannon's information index(I) ranged from 1.465 for BG18 to 0.611 for BG07. =Fixation index is ranged from 1.000 to -0.111 with mean 0.696. SSRs with high polymorphism information content successfully assisted in the differentiation of genotypes in this study. The title of the article is suitable The abstract of the article is comprehensive Subsections and structure of the manuscript are appropriate The manuscript is scientifically correct The references are sufficient and recent	
Minor REVISION comments **1. Is language/English quality of the article suitable for scholarly communications?**	English quality of the article suitable for scholarly communications	
Optional/General comments	=According to the results of the inquiry, there were substantial differences between the 25 genotypes as shown by the Analysis of Variance, which suggests that it may be possible to choose promising lines from the available germplasm. PLU-429, PL-416, and IPU-99-16 genotypes produced the most amount of seeds. =For the number of primary branches and harvest index, high PCV, GCV, heritability, and genetic progress were recorded as a percentage of the mean. The largest amount of variability in the set of all variables was accounted for by PC 1, the first of all the factors (PCs) (numbered 1 to 8). With a PIC of 71% and a heterozygosity of 62%, BG-18 had the greatest levels of both. Comparatively to Cluster I, III, and IV, Cluster II and V have the highest number of genotypes. =In this work, SSRs with high polymorphism information richness successfully aided in genotype discrimination. The findings of this study indicate that molecular diversity among Blackgram genotypes can be estimated with success using SSR analysis.	

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PART 2:

	Reviewer's comment	**Author's comment** *(if agreed with reviewer, correct the manuscript and highlight that part in the manuscript. It is mandatory that authors should write his/her feedback here)*
Are there ethical issues in this manuscript?	*(If yes, Kindly please write down the ethical issues here in details)*	

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