



SDI Review Form 1.6

Journal Name:	Journal of Experimental Agriculture International
Manuscript Number:	Ms_JEAI_31662
Title of the Manuscript:	Application of principal component analysis to access selected rice germplasm phenotypic diversity
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:

(<http://www.sciencedomain.org/page.php?id=sdi-general-editorial-policy#Peer-Review-Guideline>)



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PART 1: Review Comments

	Reviewer's comment	Author's comment <i>(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)</i>
<u>Compulsory</u> REVISION comments	Introduction Even though the paper focused on rice germplasm, the whole introduction section was generic. The introduction should rather focus directly on rice germplasm phenotypic diversity rather than being generic. This helps to justify the gaps in previous studies and provide strong justification for the paper. Also, the introduction should separate the issue of rice germplasm from the methodology approach of PCA justification. It is not clear what the main thesis or problem is about. The research problem should address the question of what is about rice germplasm phenotypic diversity that is of concern to crop breeders? There is strong evidence of the use of multivariate analysis, PCA and cluster analysis on rice germplasm. There is too much justification for using PCA in this study without stating the gaps in other studies that this study seeks to achieve. The introduction should identify the gaps in past studies and state how this study addresses such gaps. Lines 27 to 52 and lines 58 – 65 have been directly lifted from V. Ulaganathan and A. Nirmalakumar (see link in Part 2) Methodology The description of the experimental site should include the type of soil used or acidity state as well as the cultural practices adopted.	This has been revised accordingly



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	Any crop improvement strategy should aim at broadening the genetic base of the breeding stock. This requires wide genetic resources involving qualitative and quantitative agro-morphological properties. However, this paper considers solely the quantitative traits. There should be a strong justification for using only the quantitative traits. How was data on the agro-morphological traits recorded? Which method was used? These questions need to be answered before line 79. Data analysis Provide a table on the eigenvalues and proportion of total variables explained by the principal components and their cumulative variance. This would lay a strong foundation for narrowing down to the two components – PRIN 1 and PRIN 2. In line 92, are you referring to PRIN 1 OR 2? I guess you are referring to PRIN 1. What is the basis for coming to the conclusion in lines 95 to 97 (Table 1)? This should be clearly stated in the work. The number of panicle is 0.40 and should be higher than grain yield, 0.39? In Table 1, which variables are the most strongly correlated with each component? At what level would the correlation be of important? For Table 2, which type of univariate analysis was used – t-test, ANOVA or multiple regression analysis? This needs to be stated in the method section. I am not too sure but which type of univariate analysis provide these statistics? What is the dependent variable involved? These questions need to be analysed in the methodology.	
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	In Figure 2, the box after cluster 3 should be labelled Cluster 4. It is currently empty. Conclusion Lines 174 to 177 seems to a rehab of what the study seeks to achieve. The conclusion should focus on addressing what has the study found out and what is the implication of the findings? Plagiarism issue: A significantly larger part of the introduction was lifted from an already published article by V Ulaganathan: www.sabao.org/journals/.../SABRAO-J-Breed-Genet-47-2-79-88-Ulaganathan.pdf	This has been revised accordingly
<u>Minor</u> REVISION comments	For the cluster analysis, are there any relationships or linkages between/among the clusters?	
<u>Optional/General</u> comments		