

Review Form 1.6

Journal Name:	International Journal of Environment and Climate Change
Manuscript Number:	Ms_IJECC_84164
Title of the Manuscript:	Correspondence between phenotypic and genotypic distance matrices of advanced breeding lines from diverse parents using Mantel test.
Type of the 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	<ul style="list-style-type: none">-Report the relationship between distance matrices and diversity generated based on phenotypic data and molecular genotypic data on advanced breeding lines with specific reference to Mantel test results-The authors result correspondence between different distance matrices subjected to correlation based on Mantel test.-An insignificant (p-value > 0.05) correlation was observed between the matrices due to causal factors such as data type, markers used and genetic properties of lines as explained in the text.-Certain promising lines were selected from phenotypic performance as well as molecular fingerprints and grain quality evaluation relative to checks (CAUR1 and Shasarang) with specific context to north eastern hill region.-The present report focused on correspondence between agro-morphological and molecular data based dissimilarity distance matrices evaluated on a set of advanced breeding lines of lowland rice.-Significant Mantel test correlation if observed would be surprising and meant that data was incorrect as limited number of molecular markers were used on the lines that are well structured and related. However, that is not true. <p>Figures were not clear, please improve</p> <p>Especially in figure show correlation between phenotype-genotype</p>	
Minor REVISION comments	<ul style="list-style-type: none">-Evaluation of advanced breeding lines developed from a set of diverse parents involved in different cross combination facilitates selection of promising genotypes, resource management and planning further breeding activities.-A set of 22 advanced breeding lines of lowland rice in F7 were evaluated agro-morphologically and genotyped with molecular markers-Advanced breeding lines in self pollinated crops like rice are the genotype material of later generations developed from crossing a set of favourable parental elite lines or landraces.-The progeny in each generation undergoes selection for favourable trait expression as per breeding objective and harbour promising better genotype with respect to parents.-Such advanced lines are well structured, share ancestry and capable of replacing parental lines in terms of farmer adoption owing to accumulation of favourable alleles after careful within line selections by breeders- Different categorical distance matrices generated from a set of lines under study are compared and related by testing linear independence of its elements by Mantel test (Mantel, 1967) when distance based hypothesis is formulated thus measuring the correlation between the two.	
Optional/General comments	<ul style="list-style-type: none">-Diversity and variation at species and inter/intra population levels are the inevitable yet explorable elements on which plant breeders primarily depend.-They act as tools in designing a breeding program and selection is practiced by identifying diverse lines for many population and line improvement activities such as heterotic grouping (Silva et al. 2020),-Creation of general combining ability based synthetic populations (Goldringer et al., 2017), Donor selections (Allier et al., 2020),-Narrowing down to best lines as promising varieties and creation of mini cores (Zhang et al., 2012) thus enhancing resource management and breeding activities through evaluation of population structure.-Genetic variation is studied from several qualitative and quantitative traits detected from expressed phenotypic variation categorised as morphological technique, in-silico data (Carvalho et al., 2019) and further, from the biochemical and molecular techniques at protein level and DNA sequence level using breeder friendly molecular markers, respectively.	

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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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