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Journal Name:	Journal of Experimental Agriculture International
Manuscript Number:	Ms_JEAI_42266
Title of the Manuscript:	Genetic Variability of Sugarcane Clones as Affected by Endemic Diseases at One-Row Screening Stage in Ferké, Northern Ivory Coast
Type of the Article	

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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	Introduction I see two independent factors: genotypes and plant/ratoon, these should both come out in the objectives and in the analysis Methodology No evidence of the author having inoculated the pathogens or assurance that the area was a hotspot for the three diseases screened against. When screening, u need to be sure of a high disease pressure There was need for more than one check in this experiment, not just a commercial check, but also a susceptible check and/or resistant check Lines 84 to 104 contains literature which should be a reserve of the introduction section if indeed it is necessary, but not the methodology The different scales used to measure disease severity quite misleading if indeed the author wanted to compare these diseases. One scale would have been adopted and used for all diseases. For now, treat each disease independently Analysis ANOVA lacking, this calls for re-running the analysis because there is no evidence of statistical significance despite using RCBD design. Results - Author should report results in comparison to the performance of the commercial check - I find fig 4 not necessary if fig 3 is well done - I wonder why info in Table 1a and Table 2 cannot better be left in cluster analysis figures provided these are clear and informative! It is indeed more of repetition - Failed to understand Table 3. What does CV mean? If it is coefficient of variation? If so, then these are already very high CVs and unacceptable unless a good explanation is given. In any case, this data might have needed transformation. Discussion - 254 to 279 has nothing to do with discussion of results generated from this study. It is just like any other literature review Conclusion - Conclusions based on cluster analysis can be reliable - No conclusion on plant cane vs ratoon in regard to disease severity has been made yet it's necessary. However, with lack of anova, reliable conclusion does not come easy	Ok, corrected. At one-row screening stage, selection of genotypes occurs in first ratoon cane. That's why objective and data analysis are much more related to the first ratoon cane. Ok, corrected. Experiment was conducted under natural infection as pressure of the three endemic diseases is high in the agro-ecology investigated. The check variety is high yielding, susceptible to smut, and resistant to the two other diseases (leaf scald, pokkah boeng). Ok, corrected as suggested. Scales used seemed to be specific to diseases from literature. Comparison of plant cane/ratoon cane was made for each disease. Not between diseases as different scales were used. Analysis Ok. Because of the huge number of genotypes investigated at this breeding stage (863 clones) cane rows were not replicated except for the check variety. Therefore Anova could not be performed. Nevertheless, significance of data is now provided using error bars at 5 % level (Fig 1). Anova is rather performed at advanced breeding stages where much less number of genotypes is involved (up to 30 and then up to 10 for the last one). Therefore with different sizes of plots (20 m² and 80 m², respectively). That's why for the screening stage studied, multivariate statistics were much more used. Results - To select the best performing genotypes based on quantitative and qualitative traits, comparison with commercial check is used. In the current disease study regarding the same experiment, disease ratings were made following symptoms observed on genotypes not necessarily in comparison with the check. - Ok, corrected as suggested (fig 3 deleted). - Tab 1 & 2. Groupings are based on field observations made. They are not generated from cluster analysis. Furthermore, clusters derived from statistics were separately performed. Now, we made definitely a difference between results from observation groupings (G groups) and that from cluster analysis (C clusters). - Tab 3: CV is coefficient of variation. High values determined explain diversity in diseased clones. Another table of Mahalanobis D² statistics is provided to show the significance clusters determined. Discussion Ok. We should explain the reason why the issue of resistance was discussed. In sugarcane breeding, the issue of susceptibility or resistance to diseases is very important. Varieties selected should be not only high yielding but also resistant to major endemic diseases. Across the study, we found that some



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		genotypes were disease-free and the others susceptible. Therefore we have motivated the discussion on this issue in the text. Conclusion - Cluster analysis. Ok - We have included the result related to high infestation in first ratoon in comparison with plant cane. Explanation on the issue and literature are provided in the text (discussion section).
<u>Minor</u> REVISION comments		
<u>Optional/General</u> comments	-Serious grammatical errors right from the abstract, meaning that the manuscript was not given utmost attention. Find my edits in scanned copy attached. -Some sentences unnecessarily too long therefore hard to comprehend	