Review Form 1.7

Journal Name:	**Biotechnology Journal International**
Manuscript Number:	**Ms_BJI_104711**
Title of the Manuscript:	**Genotyping by sequencing reveals genetic relatedness and duplicates amongst local cassava (Manihot esculenta Crantz) landraces and improved genotypes in Kenya**
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.
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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)**	=Future demand for cassava is expected to increase in order to mitigate climatic changes, sustain food security and provide raw materials for industry. To meet these demands, adoption of modern omics methods ensures reliability, precision and timely delivery of more productive and resilient varieties. =A total of 112 mix of duplicate clones, diverse local cassava landraces (LARs) and improved genotypes (IMGs) were genotyped using single nucleotide polymorphisms (SNPs) generated through genotyping by sequencing (GBS) approach. =About 17% (5808) of the 33672 SNPs were used for hierarchical clustering and *ADMIXTURE* analysis for ancestries. =Approximately 48 and 52% of the germplasms respectively formed 17 independent clusters (identical clones or duplicates) and admixtures (unique or non-duplicated clones). Of the duplicates, 10 clusters were formed from LARs, four from IMGs and three from a mix of both LARs and IMGs, revealing their genetic relatedness. =About 71 and 29% of clusters contained accessions from the same and different geographical regions respectively, with the geographical restriction of clusters adduced to the minimal movement of planting materials across the country, perhaps linked to either inefficient seed distribution system or disease-driven quarantine measures. =Duplication of LARs was attributed to historical sharing or exchange of planting materials by farmers while duplicates of IMGs could be attributed to convergent evolution, selection, or sharing of common parentage. =The high number of admixtures or unique clones implied minimal loss of genetic diversity. =These findings can aid designing efficient and effective cassava improvement programs through development of a core set of diagnostic markers 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	
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	=The present study, therefore, applied the GBS approach to generate SNPs that revealed genetic relatedness amongst local landraces and improved cassava genotypes sampled from various cassava growing regions in Kenya. This is a preliminary step toward the acceleration of the cassava breeding process in the country =In conclusion, molecular markers have an important role to play as farmers frequently give different names to the same cultivar or landraces, making identification difficult, particularly as	

	cassava varieties are not easy to distinguish morphologically [45]. This enables the correct assessment of adoption rates, which in turn, influences breeding priorities and agricultural policies [56]. =Knowledge on the extent of genetic diversity among cassava landraces and improved genotypes in Kenya using GBS-derived SNP markers may promote their conservation and/or efficient selection and utilization as parental lines for breeding for biotic and abiotic stress tolerance. Although local landraces may be low-yielding, they may have high genetic diversity that could promote gene flow through hybridization [27], enabling crop improvement and adaptability of species to changing climatic conditions, new pests, and diseases [57].	

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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