

Review Form 1.7

Journal Name:	International Journal of Plant & Soil Science
Manuscript Number:	Ms_IJPSS_106594
Title of the Manuscript:	Deciphering Millet Diversity: Proteomic Clusters and Phylogenetic Insights
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)
<p>Compulsory REVISION comments</p> <p>1. Is the manuscript important for scientific community? (Please write few sentences on this manuscript)</p> <p>2. Is the title of the article suitable? (If not please suggest an alternative title)</p> <p>3. Is the abstract of the article comprehensive?</p> <p>4. Are subsections and structure of the manuscript appropriate?</p> <p>5. Do you think the manuscript is scientifically correct?</p> <p>6. Are the references sufficient and recent? If you have suggestion of additional references, please mention in the review form.</p> <p>(Apart from above mentioned 6 points, reviewers are free to provide additional suggestions/comments)</p>	<p>Millet are known for their climatic resilience and high nutritive value, and they are a regular part of the diet in many countries, including India and Africa. Millets are rich in protein sources, dietary fiber, polyphenols, minerals, vitamins, and other nutrients. A recent study examined the proteomic signatures of several millet species, including Fonio, Finger, Proso, Sorghum, and Foxtail millet, to understand their evolutionary and adaptation mechanisms. The study performed orthologous analysis to discover common and distinctive protein clusters among these species using the OrthoFinder algorithm in conjunction with visualization tools. The study found that: A total of 16,247 clusters were shared by all species, offering light on similar evolutionary or adaptation mechanisms. Each species had distinctive clusters, particularly those in Finger millet, highlighting how it differed from other millets. A phylogenetic tree built using the Maximum likelihood approach and the JTT+CAT evolutionary model further clarified the evolutionary links, with Foxtail and Proso millets showing a closer kinship. The research sheds light on the complex genetic network of millets, evolutionary histories, and potential adaptive processes. These results open the avenue for focused genomic studies and millet crop development techniques. In summary, the study provides insights into the proteomic diversity of different millet species and their evolutionary and adaptation mechanisms, which can inform the development of millet varieties with improved stress tolerance and nutritional properties.</p> <p>Understanding Millet Diversity: Phylogenetic Insights and Proteomic Clusters Proteomic Clusters and Phylogenetic Insights in Understanding Millet Diversity</p> <p>Abstract is written in a comprehensive manner. But this section some improvement regarding addition of major findings of the result. Keywords must be accurate</p> <p>They should be set according to the guidelines of journal authors.</p> <p>adding more recent references is recommended</p>	
<p>Minor REVISION comments</p> <p>1. Is language/English quality of the article suitable for scholarly communications?</p>	<p>Need to improve the language</p>	
<p>Optional/General comments</p>	<p>Follow journal guidelines</p>	

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PART 2:

	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>
Are there ethical issues in this manuscript?	<i>(If yes, Kindly please write down the ethical issues here in details)</i>	

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