

Review Form 1.7

Journal Name:	Asian Journal of Biotechnology and Genetic Engineering
Manuscript Number:	Ms_AJBGE_106006
Title of the Manuscript:	Evaluation of Genetic Diversity among CLCuD-Resistant Upland Cotton Varieties Using SSR Markers
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:

<https://www.journalajbge.com/index.php/AJBGE/editorial-policy>)

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) Low scientific value, however may be useful for breeding programs.</p> <p>2. Is the title of the article suitable? (If not please suggest an alternative title) YES</p> <p>3. Is the abstract of the article comprehensive? YES</p> <p>4. Are subsections and structure of the manuscript appropriate? YES</p> <p>5. Do you think the manuscript is scientifically correct? YES</p> <p>6. Are the references sufficient and recent? If you have suggestion of additional references, please mention in the review form. YES (Apart from above mentioned 6 points, reviewers are free to provide additional suggestions/comments)</p>	<p>The paper is devoted to the study of the genetic variability of cotton and has nothing to do with its resistance to CLCuD. Comparison of resistant and susceptible varieties has not been carried out. Therefore, the content of the Introduction should be revised.</p> <p>The Materials and Methods should indicate the URIs of the programs used, manufacturers of reagents and equipment, the PCR conditions, the program for constructing a phylogenetic tree with the parameters used; refine which genetic distances were used. Indicate the origin of the primer sequences, if they have been used in other studies.</p> <p>In Figure 1, I see not 8, but a maximum of 5 polymorphic fragments. Mark polymorphic fragments with arrows. Table 3: What is a meaning of "Allele No."? Figure 4: I see here not 3, but 4 main clusters. One of them with Samaru-72 contains not 2, but 3 subclusters. The clusters should be marked on the tree. Nodes bootstrap support values should be indicated. Species names should be written in Italics.</p> <p>See attached file for other corrections.</p>	
<p>Minor REVISION comments</p> <p>1. Is language/English quality of the article suitable for scholarly communications?</p>	May be improved	
Optional/General comments		

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

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