



SDI Review Form 1.6

Journal Name:	European Journal of Medicinal Plants
Manuscript Number:	Ms_EJMP_37036
Title of the Manuscript:	MOLECULAR AND AGRO-MORPHOLOGICAL GENETIC DIVERSITY ASSESSMENT OF GLORIOSA SUPERBA MUTANTS
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:

(<http://www.sciencedomain.org/page.php?id=sdi-general-editorial-policy#Peer-Review-Guideline>)



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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	<ol style="list-style-type: none"> 1. Abstract should not start with statistical terms like analysis of variances, rewrite the whole abstract; a. the first two sentences must be about the plants and its importance b. then two lines about the purpose of research c. No of treatments and name of the treatments d. Effect of treatments d. statistically different or not, analysis of variance RCBD or CRD e. last two lines must be concluding remarks. 2. What is VM2 generation? There may be other generations, must mention all generations. 3. Introduction is very short, You should add three more paragraphs. What is the gloriosa in the last paragraph of introduction? Why ISSR? What gene do you want to study? Any previous work? All must be in introduction? 4. What do you mean by over exploitation of tubers? 5. What is the family of Gloriosa superba L ? Mention and the reference with that family name 6. What do you mean by 12 ISSR primers? 7. You have selected primers based on polymorphism and the distinctness of the bands why? 8. How did you select the primers? Which gene are you interested? 9. Polygenic quantitative traits can be well detected by the estimation of variance, genetic advance and other genetic parameters of mutants? Do you have any proof or any formula by which you estimate the polygenic trait? 	<ol style="list-style-type: none"> 1. Abstract redesigned. 2. VM2 given clearly in materials and methods 3. Detailed information about gloriosa given in introduction 4. Over exploitation means using the crop in large extent leading to extinction of the crop. Now the crop is in endangered list. 5. Family –colchicaceae. given in introduction 6. PCR was performed by means of 12 ISSR primers (as described by University of British Columbia, Canada) synthesized at Sigma - Aldrich (USA), Bangalore, that were selected out of 45 ISSR primers tested. 7. The primer selection was based on the degree of polymorphism and the distinctness of the bands they produced when tested on a sample set. 8. Just interested in creating variation, not targeted on particular gene 9. Estimation method given in detail 10. Discussed in discussion



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	10. Any correlation between GCV and PCV?	
<u>Minor</u> REVISION comments	Grammatical errors	
<u>Optional/General</u> comments	None	