Review Form 3

Journal Name:	**Journal of Experimental Agriculture International**
Manuscript Number:	**Ms_JEAI_123449**
Title of the Manuscript:	**Advancements in Lentil Genomics for Enhanced Crop Breeding: A Review**
Type of the Article	**Review Article**

Review Form 3

PART 1: Review Comments

Compulsory REVISION comments	**Reviewer's comment**	**Author's Feedback** *(Please correct the manuscript and highlight that part in the manuscript. It is mandatory that authors should write his/her feedback here)*
Please write a few sentences regarding the importance of this manuscript for the scientific community. Why do you like (or dislike) this manuscript? A minimum of 3-4 sentences may be required for this part.		
Is the title of the article suitable? (If not please suggest an alternative title)		
Is the abstract of the article comprehensive? Do you suggest the addition (or deletion) of some points in this section? Please write your suggestions here.		
Are subsections and structure of the manuscript appropriate?		
Please write a few sentences regarding the scientific correctness of this manuscript. Why do you think that this manuscript is scientifically robust and technically sound? A minimum of 3-4 sentences may be required for this part.		
Are the references sufficient and recent? If you have suggestions of additional references, please mention them in the review form.		

Review Form 3

Minor REVISION comments **Is the language/English quality of the article suitable for scholarly communications?**		
Optional/General comments	The manuscript reports the author's work on Lentil Genomics for Enhanced Crop Breeding through contemporary genomic techniques like molecular markers, marker-assisted selection (MAS), and next-generation sequencing (NGS) technology has sped up the discovery of quantitative trait loci (QTLs) and the production of novel cultivars with superior agronomic characteristics. Overall, I believe the manuscript would be a suitable candidate for publication in the Journal of Experimental Agriculture International, but still, many gaps in this review need to be addressed, without these major revisions this review will not be considered for publication in the Journal of Experimental Agriculture International. **Major revision** 1. The abstract is simple and describes only a few molecular tools, which are not recent and are already used a lot. It is important to describe modern tools such as TALENS, CRISPR-Cas9, RNAi, and cisgenesis. Moreover, some important genes, signaling molecules, transcriptional factors, etc. for improving crop breeding also need to be mentioned. 2. The introduction is not rigorous enough. Most information is too superficial. For instance, the molecular mechanism of lentil breeding is lacking. Additionally, the molecular breeding approaches were not mentioned in the introduction. Moreover, the introduction concluding paragraph lacks of purpose hypothesis. Need to revise as a whole and follow the suitable mechanism by reading the related literature. 3. Again the section**.** LENTIL GENOMICS: AN OVERVIEW lack of more advanced molecular techniques and their possible mechanism in improving the crop breeding. If the authors are comparing conventional techniques with molecular techniques, then it is important to write the research gap of conventional methods of improving crop breeding. Following this it is important to draw a figure which demonstrates the complete mechanism of molecular techniques to improve crop breeding. 4. Tables 1 and 2 are drawn well but authors need to cite the information if possible to make it clearer. 5. Most of the information lacks references such as subsections; 3.1 DATABASES FOR GENES AND GENOMIC SEQUENCES IN LENTIL, 3.2 SEQUENCING PLATFORM FOR LENTIL GENOMICS, 3.3 LENTIL GENOME ASSEMBLY. Include the specific references. 6. MARKER TRAIT ASSOCIATION ANALYSIS is well written but due to global climate change it is a burning issue to solve the biotic and abiotic stress, the traits related to biotic and abiotic stresses need to be addressed by marker-trait association analysis. 7. MARKER-ASSISTED BREEDING has many limitations as the authors described the MAS is the most effective method to improve breeding but The development of genomic resources for lentils is slower than for other legume crops, such as soybean, chickpea, and pigeon pea. This limits the ability of lentil breeding programs to implement MAS. Secondly, Recombination between the marker and the gene of interest can lead to false positives. Thirdly, Imprecise estimates of QTL locations and effects can result in slower progress than expected. Like this MAS has many limitations on how to address these problems. Instead, use effective molecular approaches. 8. It is crucial to draw a model for genome selection for lentils to make it informal and tranquil for readers.	

Review Form 3

	9. The clear mechanism is not well written related to genome editing or genetic engineering of lentils, such as Genome editing can help identify genes that control traits like disease resistance, drought tolerance, taste, and size…..Genome editing can help analyze the function of genes….Genome editing can be an efficient way to generate favorable mutants…..A popular repair mechanism for DNA damage in plants, including legumes, that randomly inserts or deletes a DNA strand within a coding region……A method that uses a pegRNA, nickase, and a template to create a new DNA strand that can be inserted into a nicked site in the genome. This method can be used for insertions, deletions, and point mutations……. Make it more concise and dynamic. 10. Rewrite the conclusion accordingly, as mentioned in the above comments. 11. The grammar of the review has many glitches, authors are advised to read the manuscript carefully and make it professional as to scientific writing.	

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)*	

Reviewer Details:

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