

Review Form 1.7

Journal Name:	International Journal of Plant & Soil Science
Manuscript Number:	Ms_IJPSS_102437
Title of the Manuscript:	Quantitative traits loci associated for biotic and abiotic resistance in maize (Zea Mays L.)
Type of the Article	Review

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> <ol style="list-style-type: none"> Is the manuscript important for scientific community? (Please write few sentences on this manuscript) Is the title of the article suitable? (If not please suggest an alternative title) Is the abstract of the article comprehensive? Are subsections and structure of the manuscript appropriate? Do you think the manuscript is scientifically correct? Are the references sufficient and recent? If you have suggestion of additional references, please mention in the review form. <p>(Apart from above mentioned 6 points, reviewers are free to provide additional suggestions/comments)</p>	<p>The manuscript is important for scientific community. In ancient times, landraces were more popular due to presence of more genetic variability, resistant to biotic and abiotic factors and have heterogeneous nature but it was replaced by improved and uniform cultivars with a higher yield. However, modern maize has more homogeneity which is vulnerable to any dangerous pathogen strain. In the current era of molecular markers, DNA markers play an important role to identify diverse germplasm and/or quantitative trait locus. The review focused on how much work on genome mapping has been done in maize and what is its prospect. Authors describe the types of mapping populations and introduce some concepts of QTL mapping.</p> <p>The title of the article is suitable.</p> <p>The abstract of the article is comprehensive, although needs some work.</p> <p>Subsections and structure of the manuscript appropriate, but the text need to be worked out.</p> <p>The manuscript is scientifically correct.</p> <p>References are sufficient and but not all are recent. For example. ... A review is written by Tanksley <i>et al.</i> [18]. I recommend: Miles, C. & Wayne, M. (2008) Quantitative trait locus (QTL) analysis. <i>Nature Education</i> 1(1):208</p> <p>This technique reveals the significance QTL among individuals with trait of interest [19]. I recommend: Daware A, Parida, Swarup K, Tyagi, Akhilesh K. (2020), "Integrated Genomic Strategies for Cereal Genetic Enhancement: Combining QTL and Association Mapping", in Vaschetto, Luis M. (ed.), <i>Cereal Genomics: Methods and Protocols, Methods in Molecular Biology, Springer US, vol. 2072, pp. 15–25.</i></p>	
<p>Minor REVISION comments</p> <ol style="list-style-type: none"> Is language/English quality of the article suitable for scholarly communications? 	<p>English quality of the article needs to be improved.</p>	
<p>Optional/General comments</p>	<p>Citation style is reference number in brackets, I think it is more convenient to remove the year when using the author's name e.g. Choi <i>et al.</i>, 2019-used DH lines that were developed from normal corn parents (HF1 and 11S6169) [14]. or Wang <i>et al</i> 2019-study genome wide association mapping using 43,958 high-quality SNPs in 359 inbred lines and an IBM Syn 10 population of 273 doubled haploid under three environments (59). Besides the reference number is between parentheses.</p> <p>2.1. MORATAL POPULATION ??</p>	

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	<p>...as as their parents are differing differ from each other.</p> <p>...mapping population is very easy as it required only two generations.</p> <p>. Xie et al., 2019 [12]evaluated genetic map using 7613 SNPs in F2 population and found 14 QTLs for tassel branch number (TBN), spike length (CSL), and meristem length (ML).</p> <p>tassel weight(TW), central (add space)</p> <p>Several other quantitative trait loci ... double haploid population [14]. Text is in Bold.</p> <p>Other corrections:</p> <p>The list of QTLs was identified by different researchers after 2010 is mentioned in Table 1</p> <p>...polygenic characteristics that were involved in the expression of gene at particular time QTL mapping involve the testing of the whole genome with DNA markers to know likelihood chance present of QTLs.</p> <p>...significance QTL among individuals with traits of interest [19].</p> <p>Near isogenic line (NILs) are developed through backcrossing [reference?].</p> <p>Practically, NILs is are different for the single gene and genomic region of...</p> <p>Single seed descent lines also called the RIL lines as each RIL is developed from each single seed of every line.</p> <p>...till 6-8 generations and hence, it becomes completely homozygous.</p> <p>In studied ??, RILs were found better and gives more appropriate results than a F2 population [15]. Disease resistance has been detected with the help of genome-wide association study associated with disease the resistance.</p> <p>Many literatures works have been described to kernel and cob.</p> <p>NLB resistance respectively in maize (add space) [68].</p>	
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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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