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Journal Name:	American Journal of Experimental Agriculture
Manuscript Number:	Ms_AJEA_20255
Title of the Manuscript:	Assessment of Salinity Tolerance and Analysis of SSR Markers Linked With Saltol QTL in Sri Lankan Rice (<i>Oryza sativa</i>) Genotypes
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.

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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	I contest the assumption of the authors that clustering of genotypes based on markers around the 'Saltol' region can group them according to their salinity tolerance level. The authors would need to test this hypothesis with cultivars with identified level of tolerance first. And according to my understanding of the basis of allelic diversity, their hypothesis would be proven wrong. Clustering of genotypes based on markers spanning 'Saltol' would simply indicate their relatedness with respect to the Pokkali alleles across that region of Chromosome 1-nothing more. Moreover 'Saltol' accounts for ~ 20% of the variance for Na/K ratio (Thomson et al. 2010) and even less for the SES score. The authors need to re-write the paper as 1. Finding suitable donors for salt tolerance traits using physiological parameters that they have used. Clustering based on the 'Saltol' alleles of Pokkali-at best they can find the divergence of their cultivars from Pokkali and nothing more!	We agree with the comment made by the reviewer that if we had done this experiment with known varieties of salinity tolerance we would have tested the hypothesis to prove whether the clustering of genotypes based on markers around the 'Saltol' region can group them according to their salinity tolerance level. Also we understand that salt tolerance is not merely governed by Saltol region as it is governed by other QTLs as well. That is why we have not given such strong conclusions. but we stated that we observed some kind of relationship in the clustering pattern compatible with phenotypic performances. Actually we used an accession of Pokkali (Ac. No. 005556) conserved in PGRC, Sri Lanka and this is not the accession used to investigate Saltol QTL by Thomson et al. 2010. Therefore, whether the Saltol QTL is inherent in this particular accession is not exactly known. However, allelic diversity in-between 10 -15 Mb of Chromosome 1 region may give some clue for the salinity tolerance regardless their phenotypic performance. As the cluster 1V showed tolerant and moderately tolerant cultivars, although their alleles are different from Pokkali, and also susceptible



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		varieties were separately clustered, we think that there may be some relationship between the marker pattern of 10-15Mb region of tested varieties and phenotypic performance of salinity tolerance. That is what we want to say. Please be noted that we have already written this paper with the same meaning as mentioned by the reviewer (The authors need to re-write the paper as 1. Finding suitable donors for salt tolerance traits using physiological parameters that they have used) In our aim and conclusion we have stated the same thing with same meaning but with different words. We have used the term 'selecting parents' rather than 'finding suitable donors' Aim: This research was aimed at assessing Sri Lankan rice varieties for the salinity tolerance using morphological traits and to analyze the SSR markers closer to <i>Saltol</i> QTL of the chromosome 1 to be used in rice breeding and gene mapping studies. Conclusion: Information derived on morphological traits under salinity stress and the polymorphic SSR marker patterns obtained from tolerant and susceptible varieties near <i>Saltol</i> region would be useful in selecting parental lines for rice breeding and gene mapping programs designed for salt tolerance.
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<u>Minor</u> REVISION comments		
<u>Optional/General</u> comments	Please re-check paper for English grammer	English was corrected as instructed by one of the reviewers.