



SDI Review Form 1.6

Journal Name:	American Journal of Experimental Agriculture
Manuscript Number:	2013_AJEA_8682
Title of the Manuscript:	Assessment of Genetic variability within the genus <i>Citrus</i> in Syria
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:

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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	The paper deals with the molecular characterization of Syrian <i>Citrus</i> cultivars it is an interesting subject, nevertheless some major flaws are present that prevents the publication in the present form. 1) SSR detection through PAGE is a pretty old methodology that does not allow a precise identification of polymorphic pattern. Genotyping through sequencing is cheap and quick and provides high quality data. 2) Methods are poorly described: in Table 2 is not clearly reported the origin of primers and the indication of the forward and reverse sequence; in data analysis it is not reported the function of genetic distance utilized (NTSYS software includes several procedures to estimate distances); the formula of Nei's GD or expected heterozygosity is misspelled. 3) Results: the genetic diversity (GD) for each primer locus is reported in Table 2: These data are appropriate when they are estimated within a population in which the expectation of Hardy-Weimberg equilibrium is possible. 4) Dendrogram reported in Figure 2 represents the clustering of the single plants (114 samples) and not species as indicated in the legend. The choice to cluster single plants is not comprehensible because it makes the tree unreadable without adding any useful information, moreover a bootstrapping of the tree should be convenient for discussing the results.	1-.Although PAGE is an old detection method, but was precise enough to detect the polymorphism between samples, as the difference between alleles size was high (an example is shown in fig. 1). I fully agree that it's not precise enough to estimate the molecular weight in bp, which it was not done in this paper. 2- All requested info were added on the text. 4) the justification of using single plants was to show the similarity or the difference between plants from same cultivar. New figure more readable was provided.



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<u>Minor</u> REVISION comments	Terminology is quite rough: samples are indicates sometimes as species, genotypes, cultivars which are not synonymous. I suggest the use of the general term "accession"	- We adapt the term accession, but we use cultivar when we talk about accessions belonging to the same cultivar.
<u>Optional/General</u> comments		