



SDI FINAL EVALUATION FORM 1.1

PART 1:

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

PART 2:

FINAL EVALUATOR’S comments on revised paper (if any)	Authors’ response to final evaluator’s comments
The paper in the revised form still presents flaws that make it not acceptable for publication. Even an effort has been made in improving the text; serious concerns still exist related particularly to numerical analysis as previously remarked. The procedure to compute genetic distance, as reported in the text, is incorrect. <i>“The amplification products were scored as 1 and 0 for present and absent alleles, respectively. The data matrix was analyzed and genetic distance was estimated using SIMGEND in the Numerical Taxonomy and Multivariate Analysis System (NTSYS) version 3.2 [25]”</i> The dendrogram of figure 2 is obviously based on a genetic distance matrix of dimension 114 corresponding to the number of accessions. Actually, it is not possible to compute genetic distances among single plants using allele frequencies with the SIMGEND procedure of NTSYS, as the authors did, simply because the allele frequencies are non estimable on a single plant !	Text was revise. Calculations were corrected and new dendrogram was produced using means of three accessions for each cultivar.