



SDI FINAL EVALUATION FORM 1.1

PART 1:

Journal Name:	American Journal of Experimental Agriculture
Manuscript Number:	2015_AJEA_18483
Title of the Manuscript:	Genetic Variability and Association of Traits in (Mid-altitude) Sesame (Sesamum indicum L.) Germplasm of Ethiopia
Type of the Article	Original Research Article

PART 2:

FINAL EVALUATOR'S comments on revised paper (if any)	Authors' response to final evaluator's comments
This is excellent research; however, I still have problems with this being only one year of data collection. Due to changes in environmental conditions from year to year I am not sure you can say that all variables measured will perform the same over a number of years. You are basically saying that the sesame genotypes will perform the same whatever the environmental conditions and I do not believe this is true. I suggest a minimum of 2 years of testing before publication and this agrees with the thoughts of other plant breeders that I have talked to.	I still argue that variability and/or diversity study can be performed with one year data on averagely <u>optimum environment with respect to the natural adaptation of the accessions at which they are thought to express their full potential</u> . This happen mostly when large no. of treatments are considered and when alternative environments are limited. Of course, most breeding works as: yield performance evaluation, genotype x environment interaction analysis, screening of genotypes for specific desirable traits or selection for superiority, variety verification and adaptation test etc. require multi-location and/or multi-season trials. However, our study designed to assess the level of variation among the mid-altitude germplasm collections based on mean values of agro-morphological traits. The expression of these traits can of course vary at different environments, but since the aim is not to select genotypes based on performance, one can determine the relative proportion of variation that exists between the materials under study from the available data by computing mean of morphological traits for different parameters. Moreover, it is not purely a breeding work; but the output of this work may be used as input for breeding program. Such type of works can be done in Botany, Plant Genetics, Biodiversity, so on, for characterization, identification, conservation, etc. purposes.