



SDI FINAL EVALUATION FORM 1.1

PART 1:

Journal Name:	American Journal of Experimental Agriculture
Manuscript Number:	2014_AJEA_9843
Title of the Manuscript:	EVALUATION OF AFLP MARKERS FOR SCREENING RESISTANCE TO COMMON BEAN ROOT ROT (Pythium spp.)

PART 2:

FINAL EVALUATOR'S comments on revised paper (if any)	Authors' response to final evaluator's comments
Information on the heredity and pathogenicity are still weak. The author should describe from where you referred (or how you scored) resistant or susceptible in Table 1 in Materials and Methods. In addition, You can say nothing about pathogenicity in Fig. 3 without pathogenicity test. I found some mismatches of cluster when we compare those in Fig. 1 and Fig. 3. Cluster 2 in Fig. 1 corresponds with cluster 1 in Fig. 3. Cluster 3 in Fig. 1 corresponds with Cluster 4 in Fig. 3. Cluster1 in Fig. 1 seems to correspond with cluster 5, 7 and 8 in Fig. 3. Mw001 is out of the cluster in Fig. 1 but categorized into cluster 8 in Fig 3. Those clustering may have a linkage with pathogenicity (resistant or susceptible), but we cannot judge this validity because of no information on pathogenicity of the germplasm except some germplasm already evaluated in Table 1.	The bean lines from KARI were donated by one of the co-authors who published the pathogenicity findings of some of the lines in [20] Otsyula R, Buruchara R, Rubaihayo P. Inheritance and Transfer of Root Rot Resistance to Bean Varieties. Biotechnology, breeding and seed systems for African crops conference: Research and product development that reaches farmers. Botanical Beach Hotel in Entebbe, Uganda from 4-7 November 2002; [14] Otsyula RM. Nature of genetic control and inheritance of resistance to <i>Pythium</i> root rot in bean genotypes. Ph.D Dissertation, Makerere University, Kampala, Uganda. 2010. Pathogenicity testing is beyond the scope of this study. This was basically a preliminary screening process. However, we have recommended that pathogenicity be done to validate the findings from the lab work. I think it will be interesting to determine how the findings correlate. This is true – cluster 1 in fig 1 corresponds to cluster 1 in fig 2 and Cluster 2 corresponds to cluster 2a and 2b as indicated on Fig.2. However if you look at the genetic distances there is similarity and this is because dendograms generate magnify many small differences resulting in many clusters in comparison to the clustering in fig 1. Cluster 4 is the small circle while cluster 3 is the big circle. However the labelling of fig 3 have been desegregated for clarity purposes Cluster 1 corresponds to KK, ALULU and SCAM80; KK15 is cluster 7 while ALULU & SCAM80 are in cluster 5 of the dendogram True. There was mis-numbering with cluster umber 6 missing on the figure. This has been rectified and Mw001 stands out alone as cluster 8 This may be or may not be true. However, the point here is that the experiment was a preliminary study conducted to assess the potential of the selected markers for use in delineating susceptible and resistant with regard to pathogenicity tests of the breeder bean lines. The pros and cons of the findings are outlined in the discussion section. Since pathogenicity of the surveyed collections was beyond the scope of this study, what we have done is to highlight this in the discussion and further recommend that there is need to validate pathogenicity of the 35 bean samples and comparisons made with the molecular makers' findings of this specific study.