

Reviewer's comments:

I have read the last version of the paper that confirmed once again that the authors have not any familiarity with the numerical and multivariate analysis of molecular data. This throws serious doubts about the reliability of the results. As known, SIMINT of NTSYS computes a variety of similarity and dissimilarity coefficients for interval measure (quantitative) data. The presence and absence of SSR bands (1 or 0) or the average of three data cannot be considered as interval measure. SANH is a category of clustering methods and UPGMA is one of these methods.

Author's Feedback:-

Thanks for your comments. For the dendrogram of genetic distance, we used the matrix data 1,0 to estimate the similarity between the different cultivars. The obtained results were used to establish the dendrogram (the tree). In the first version, we used the SimGen with the coefficient of NEI72 to calculate the level of similarity and dissimilarity between all samples. Then, the obtained values of dissimilarity were used for clustering. The comment we obtained in the first time, suggested not to compare all samples but to take the means of 3 samples/same cultivar, and to use them in the analysis. We did that and I would like to mention that the clusters obtained with the analysis of 3 accessions/cultivar and with 1 representative sample/cultivar were identical.

Currently: We produced another table of data where the tree samples (accessions) of a cultivar were presented by one sample. These data were used in 2 ways:

- 1- To calculate the similarity and dissimilarity with SimGen with NEI72 coefficient.
- 2- To calculate the similarity and dissimilarity with Simint with Dist coefficient.

The dendrograms obtained in the 2 ways had the same clusters. (Pls see figures below)

I share the reviewer his opinion that SIMINT is not appropriate for our data, and I think SIMGEN (What we used first) is suitable and more appropriate, and I would like to use it in the last version if the reviewer approve it (it's in the actual revised version #3). Otherwise, I would be thankful if the reviewer suggest another analysis or to use another PC-program for our analysis.

I will present below the dendrograms obtained using the results of SIMGEN and SIMINT. (Both Dendrograms display the same clusters); and to exclude all doubts about our results I am ready to send to the reviewer the excel file of 1,0 used in the analysis and all the documents he wants to check by himself, If he desires that.

Thanking you and all the reviewers for the valuable comments which are very positive for our paper.

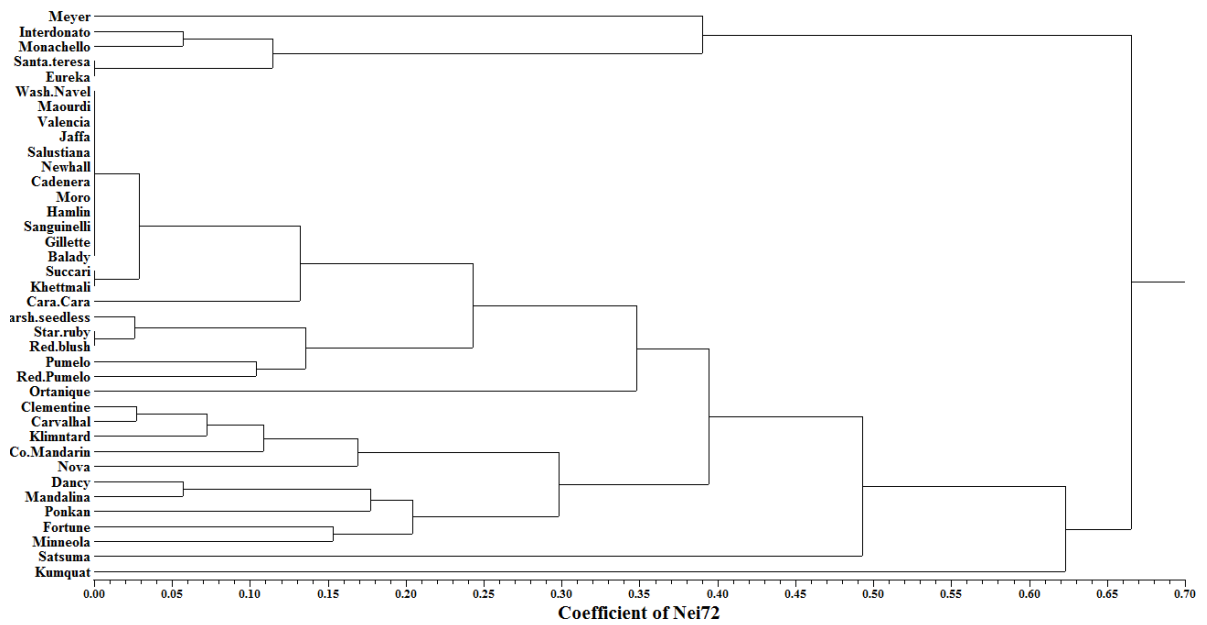


Fig. 1: Clustering based on SIMGEN/ NEI72/ SAHN/ UPGMA

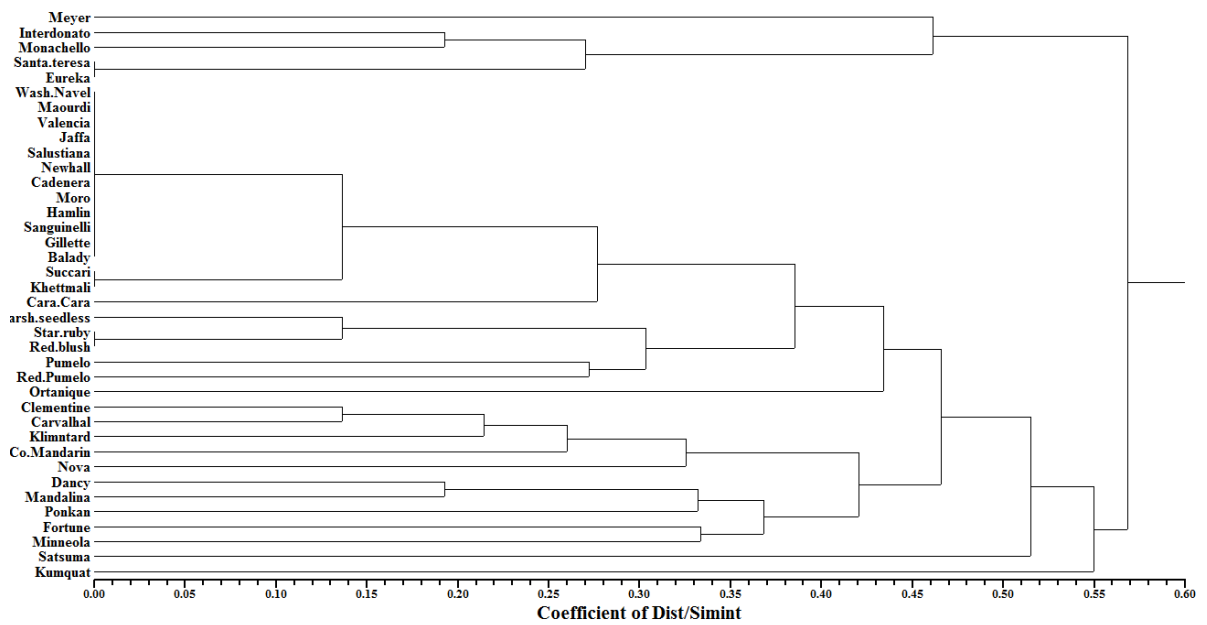


Fig. 2: Clustering based on SIMINT/ DIST/ SAHN/ UPGMA