

A USER FRIENDLY SOFTWARE TO ANALYZE THE BINARY DATA OF DNA FINGER PRINTING

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DNA polymorphism is widely used to classify living organisms at various levels such as families, species, varieties, breeds and strains. The elucidation of DNA polymorphism is done by using many techniques like RAPD, RFLP, AFLP and microsatellites. In all of these techniques, either presence or absence of bands with respect to the classification group is the fundamental data to be analyzed. Polymorphic bands are selected in such a manner so that they could be taken for the analysis. Calculation of dissimilarity coefficients, and based on them, the drawing of tree diagrams are the frequent procedures of analysis. There are different algorithms established to calculate these parameters and drawings. Manual calculation and drawing are not easy when the number of variables is high. Thus, computer aided programming is necessary. Certain software packages have been used for this purpose but all of them share two basic problems. They require a considerable knowledge to use the software and also to interpret the output. The other problem is that the available software are costly and thus difficult to purchase. Therefore, the objective of this study was to develop a simple software package to analyze the data of DNA finger printing to elucidate relationships.

A software program in Visual Basic was developed including forms, and modules, which contained codes for defined algorithms. Input of presence and absence of bands was done as Boolean integers after specifying the number of bands and varieties. The required dissimilarity algorithm can be selected and hence the data matrix and dissimilarity matrix are displayed as outputs subsequently.

The calculated dissimilarity coefficients are important to draw the hierarchical tree diagrams to elucidate phylogenetic relationships, which are very important in germplasm conservation to avoid the varietal duplications. The program developed is very efficient in calculating dissimilarity coefficients. However, it needs a few improvements. A graphical user interphase should be developed for the easy use of the program and a sub module should be included to draw the tree diagrams.