

Abstract

Grapevine (*Vitis vinifera* L.) is a perennial liana that possesses characteristics of both herbaceous and woody plants. With the development of molecular biology, an increasing number of tools have been invented and exploited in order to cope with the growing repertoire of grapevine genes. These tools provide evidence in studies on the evolutionary relationships of grapevine genes. In this study, 20 grapevine genes and 80 homologous genes were used for a multi-type structural analysis using bioinformatics software. These analyses included sequence alignments and the construction of phylogenetic trees, predictions of subcellular localisation, protein primary structure analysis, secondary structure prediction, and tertiary protein structure model construction. From an analysis of all these data, only ten genes (50%) showed clear clustering, with only six genes keeping their clustering during translation into proteins. According to these results, most protein sequences from grapevine genes did not have characteristics that distinguished them from genes in other woody plants. This study revealed that grapevine genes have co-evolved with genes in herbaceous and woody plants, and not as separate events. This agrees with the taxonomy of grapevine, a perennial liana plant which displays characteristics of both herbaceous and woody plants.