

## 5S rDNA of Rosaceae: Potential for Phylogeny Reconstruction

National Yu. Fedkovich University of Chernivtsi, Ukraine  
E-mail: <sup>1</sup>yurijtynkevich@gmail.com, <sup>2</sup>ra.volkov@gmail.com

The family Rosaceae is one of the largest among flowering plants and contains numerous cultivated species. Further improvement of the existing cultivars involves application of molecular methods. Especially, creation of novel interspecific hybrids requires clear knowledge about genetic distances between parental forms. This goal can be reached by molecular taxonomy methods. Sequencing of selected genome regions and subsequent analysis of the obtained genetic texts using minimal distance, parsimony or likelihood methods allow generation of dendrograms, which reflect relatedness among studied species. However, success in phylogeny reconstruction depends on proper selection of genomic region for the comparative analysis. We have analyzed intergenic spacer region of the 5S rDNA in genera *Rosa*, *Prunus*, *Malus* and *Cydonia*, which represent subfamilies Rosoideae and Amigdaloidae and found that the level of similarity between the species of the same genus ranges from 80 to 99%. In contrast, for representatives of different subfamilies significantly lower similarity - from 20 to 40% - was demonstrated. Hence, the spacer region can be successfully applied for the reconstruction of phylogeny of Rosaceae within genera, but not between subfamilies.