

## RINGKASAN

Tapak dara [*Catharanthus roseus* (L.) G. Don] merupakan tanaman hias dan tanaman obat dari Familia Apocynaceae. Tanaman yang banyak ditemukan di daerah tropis dan subtropis ini memiliki beberapa kultivar dengan berbagai variasi morfologi, terutama dalam hal warna bunga. Seleksi kultivar tapak dara, khususnya terkait dengan pemanfaatannya sebagai tanaman obat, memerlukan landasan karakterisasi molekuler. Hal ini karena selain tidak dipengaruhi oleh faktor lingkungan, karakterisasi molekuler dapat dilakukan pada semua fase pertumbuhan dan perkembangan tanaman. Penelitian ini bertujuan untuk melakukan perbandingan genetik beberapa kultivar *C. roseus* berdasarkan sekuen daerah intergenik atau *intergenic spacer* (IGS) *atpB-rbcL* dan menganalisis hubungan filogenetik di antara kultivar-kultivar tersebut.

Penelitian dilakukan dengan metode eksplorasi dengan pengambilan sampel tanaman *C. roseus* secara acak dari Kota Purwokerto dan sekitarnya. Kultivar *C. roseus* yang digunakan merupakan tipe liar dan mutan. Variabel dependen berupa kultivar *C. roseus*, sedangkan variabel independennya adalah perbedaan genetik di antara kultivar-kultivar tersebut dengan parameter berupa persentase atau jumlah situs polimorfik, baik substitusi basa maupun indel. Analisis molekuler dilaksanakan di Laboratorium Genetika dan Molekuler Fakultas Biologi Universitas Jenderal Soedirman, yang meliputi tahapan ekstraksi DNA menggunakan metode CTAB dan amplifikasi IGS *atpB-rbcL* menggunakan teknik PCR dengan sepasang primer universal. Sekuensing IGS *atpB-rbcL* dilaksanakan dengan mengirimkan produk PCR ke Firstbase Malaysia. Data sekuen yang didapatkan diolah menggunakan perangkat lunak Bioedit versi 7.0.4.1 dan diperiksa secara manual. Verifikasi sekuen dilakukan melalui blasting menggunakan referensi pangkalan data NCBI. Penjajaran sekuen dilakukan menggunakan Program ClustalW di dalam perangkat lunak BioEdit versi 7.0.4.1. Analisis hubungan filogenetik antarkultivar dilakukan menggunakan analisis Neighbor-Joining, UPGMA, dan Maximum Likelihood dalam perangkat lunak MEGA versi 11.

Hasil penelitian menunjukkan bahwa sekuen IGS *atpB-rbcL* yang didapatkan menunjukkan perbedaan, baik antara kultivar *C. roseus* liar dan kultivar mutan maupun di antara sesama kultivar tipe liar. Perbedaan terlihat baik berupa substitusi basa maupun insersi-delesi. Meskipun demikian, hubungan kekerabatan genetik antarkultivar tersebut masih relatif berdekatan.

Kata kunci: IGS *atpB-rbcL*, perbandingan genetik, tapak dara

## SUMMARY

Madagascar periwinkle [*Catharanthus roseus* (L.) G. Don] is an ornamental and medicinal plant species belonging to the Family of Apocynaceae. This plant commonly found in tropical and subtropical areas has several cultivars of various morphological types, especially with respect to flower colour. Cultivar selection, especially in relation to its utilization as a medicinal herb requires a foundation of molecular characterization. This is because apart of not being affected by environmental factors, such characterization can also be implemented at any stages of plant growth and development. The aims of this study are to perform genetic comparison of several *C. roseus* cultivars based on the sequence of *atpB-rbcL* intergenic spacer (IGS) and to analyse the phylogenetic relationship among the cultivars.

This study was conducted using an exploratory method in which *C. roseus* samples were collected randomly from around Purwokerto City. They were of both wild type and mutant cultivars. The dependent variable was *C. roseus* cultivar, while the independent variable was genetic difference using parameters of the percentage or number of polymorphic sites with respect to base substitutions and indels. Molecular analysis was carried out at the Genetics and Molecular Laboratory, the Faculty of Biology, Universitas Jenderal Soedirman, including DNA extraction using CTAB method and *atpB-rbcL* IGS amplification employing PCR technique with a pair of universal primers. Sequencing of *atpB-rbcL* IGS was performed by sending the PCR products to Firstbase, Malaysia. The sequence data obtained were edited using Bioedit software version 7.0.4.1 and checked manually. Sequence verification was performed by blasting to the NCBI database. Sequence alignment was performed using the ClustalW Program implemented in the BioEdit software version 7.0.4.1. The phylogenetic relationships among cultivars was analyzed using Neighbour-Joining, UPGMA and Maximum Likelihood in the MEGA software version 1.1.

The results revealed that differences in the *atpB-rbcL* IGS sequences of both between *C. roseus* wild types and mutant cultivars, and those within wild type cultivars were observed. These were either of base substitutions or insertion-deletions. However, relatively close genetic relationships among cultivars were still present.

Keywords: *atpB-rbcL* IGS, genetic comparison, Madagascar periwinkle