

RINGKASAN

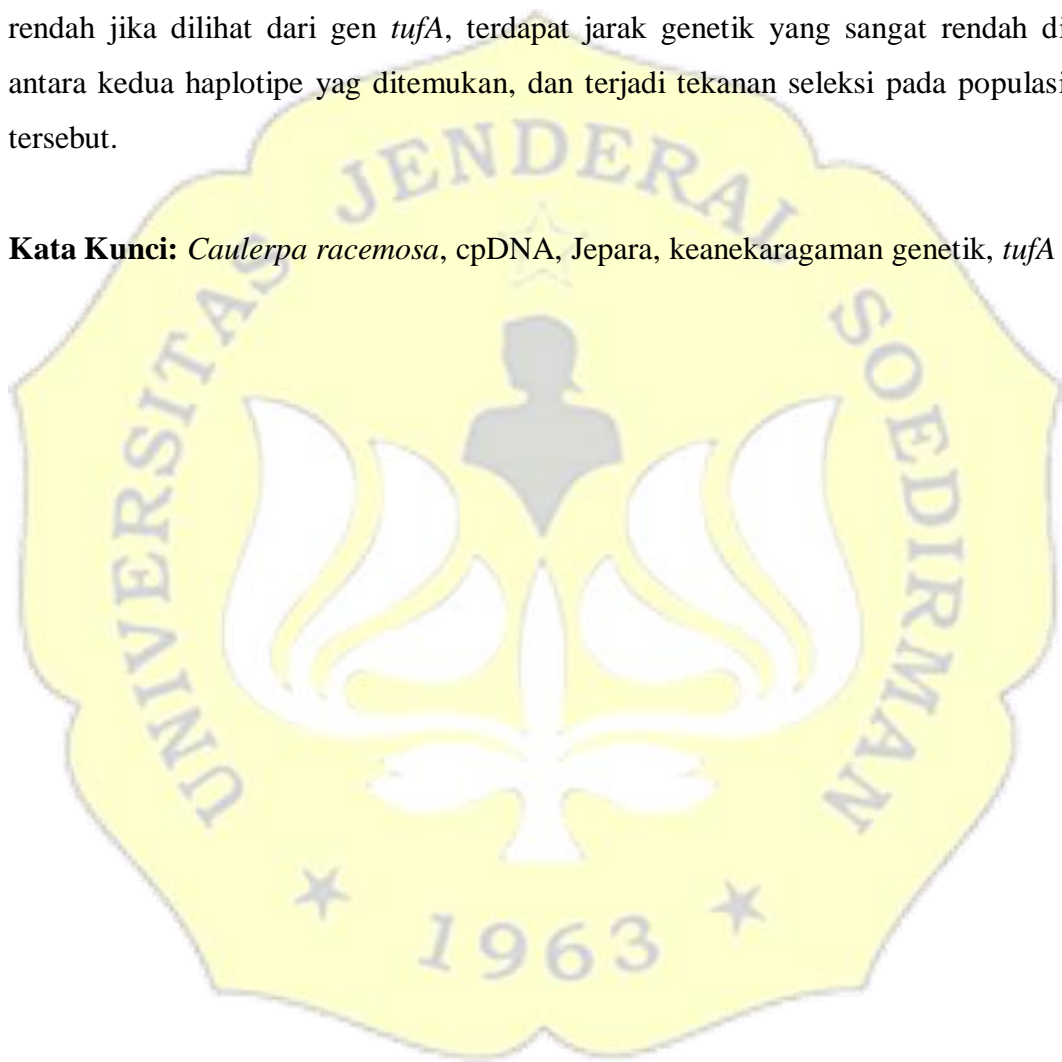
Caulerpa racemosa J. Agardh banyak ditemukan di perairan Laut Jepara, Jawa Tengah. Analisis keanekaragaman genetik spesies rumput laut hijau ini dapat dilakukan menggunakan teknik molekuler. Salah satu marka molekuler yang dapat digunakan adalah sekuen gen *tufA* yang terdapat di dalam genom kloroplas atau cpDNA. Tujuan penelitian ini adalah mengetahui keanekaragaman genetik, jarak genetik di antara haplotipe-haplotipe yang ada, dan pengaruh tekanan seleksi terhadap populasi *C. racemosa* di Perairan Laut Jepara berdasarkan gen *tufA*.

Penelitian ini dilakukan dari bulan Oktober 2022 sampai Januari 2023 di Laboratorium Genetika dan Molekuler Genetika Science, Tangerang. Tahapan penelitian meliputi pengambilan sampel *C. racemosa*, isolasi DNA genomik, amplifikasi gen *tufA*, sekuensing gen *tufA*, dan analisis data. Pengambilan sampel dilakukan pada dua lokasi, yaitu Teluk Awur dan Pulau Panjang Jepara, Jawa Tengah. Isolasi DNA genomik dilakukan dengan kit isolasi Quick-DNA Plant/Seed Miniprep Kit (Zymo Research, D6020), sedangkan amplifikasi gen *tufA* dilakukan menggunakan mesin *thermocycler* advanced primus 25 dengan primer universal 5' -TGAAACAGAAMA WCGTCATTATGC- 3' sebagai *forward primer* dan 5' -CCTTCNCGAATMGCRAAWCGC- 3' sebagai *reverse primer*. Sekuensing gen *tufA* dilakukan dengan metode Sanger yang diautomatisasi di Firstbase Malaysia. Urutan basa hasil sekuensing dianalisis menggunakan Program DNASP untuk mengetahui keanekaragaman haplotipe dan keanekaragaman nukleotida, Program Mega 11 untuk melakukan konstruksi filogenetik, dan Program Arlequin untuk menguji ada tidaknya pengaruh tekanan seleksi terhadap populasi *C. racemosa* berdasarkan uji netralitas *F_s*.

Hasil penelitian menunjukkan adanya dua haplotipe *C. racemosa* di Perairan Laut Jepara. Keanekaragaman genetik populasi *C. racemosa* di Perairan Laut Jepara termasuk rendah, yang diindikasikan dari nilai keanekaragaman haplotipe yang berkisar dari 0,00 hingga 0,22 dan keanekaragaman nukleotida yang berkisar dari 0,000 hingga 0,007. Ditemukan dua haplotipe dengan jarak genetik sebesar

0,000 menunjukkan tidak adanya perbedaan genetik yang signifikan di antara kedua haplotipe. Hasil analisis pohon filogenetik dengan kladogram menggunakan metode neighbor-joining membentuk 3 kelompok *in group* dan 1 *out group*. Uji netralitas D dan *Fu's Fs* menghasilkan nilai $D = -1,97415$ dan $Fu's Fs = 7,82672$. Berdasarkan hasil penelitian tersebut dapat ditarik kesimpulan bahwa keanekaragaman genetik *C. racemosa* di Perairan Laut Jepara sangat rendah jika dilihat dari gen *tufA*, terdapat jarak genetik yang sangat rendah di antara kedua haplotipe yang ditemukan, dan terjadi tekanan seleksi pada populasi tersebut.

Kata Kunci: *Caulerpa racemosa*, cpDNA, Jepara, keanekaragaman genetik, *tufA*



SUMMARY

Caulerpa racemosa can be found in the Jepara Sea, Central Java. Analysis on the genetic diversity of this green seaweed species can be carried out using molecular techniques. One of the molecular markers that can be used is the *tufA* gene sequence contained in the chloroplast genome or cpDNA. The purpose of this study was to determine genetic diversity, the genetic distance among haplotypes found, and the effect of selection pressure on *C. racemosa* populations in the Jepara Sea based on the *tufA* gene.

This study was conducted from October 2022 to January 2023 at the Genetics and Molecular Genetics Science Laboratory, Tangerang. The stages of the study included sampling of *C. racemosa*, isolation of genomic DNA, amplification of the *tufA* gene, sequencing of the *tufA* gene, and data analysis. Sampling was carried out at two locations, namely Teluk Awur and Panjang Island, Jepara, Central Java. Genomic DNA isolation was carried out using the Quick-DNA Plant/Seed Miniprep Kit isolation kit (Zymo Research, D6020), while *tufA* gene amplification was carried out using a thermocycler advanced primus 25 machine employing universal primers 5' - TGAAACAGAAMAWCGTCATTATGC- 3' as forward primers and 5' - CCTTCNCGAATMGCRAAWCGC- 3' as reverse primer. Furthermore, *tufA* gene sequencing was carried out using automated Sanger method at Firstbase Malaysia. The base sequences of the sequenced results were analyzed using the DNASP program to determine haplotype diversity and nucleotide diversity, the Mega 11 program to carry out phylogenetic construction, and the Arlequin program to test whether selection pressure had an effect on *C. racemosa* populations based on the Fs neutrality test.

The results showed that two haplotypes of *C. racemosa* were found in Jepara Sea. Low genetic diversity of *C. racemosa* population in the Jepara Sea was observed, as indicated by the haplotype diversity values ranging from 0.00 to 0.22 and nucleotide diversity ranging from 0.000 to 0.007. Two haplotypes were obtained showing genetic distance of 0.000, which indicated that no significant

genetic difference between the two haplotypes was observed. Phylogenetic tree analysis with cladograms using the neighbor-joining method resulted in 3 in-group groups and 1 out-group. The neutrality test of D and Fu's Fs resulted in a value of $D = -1.97415$ and Fu's $F_s = 7.82672$, indicating that the *C. racemosa* population in the Jepara Sea was subjected to selection pressure. Based on the results, it can be concluded that the genetic diversity of *C. racemosa* in the Jepara Sea is very low when analyzed using the *tufA* gene, no genetic distance between the two haplotypes found was observed, and selection pressure was found working on the population.

Keywords: *Caulerpa racemosa*, cpDNA, genetic diversity, Jepara, *tufA*

