# DIFFERENTIATION OF TWO TAXA OF *CAULERPA* BASED ON *TUF*A MARKER

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**FACULTY OF SCIENCE**

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Field of Study: Seaweed Biotechnology

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# ABSTRACT

The *Caulerpa* is an economical important genus among chlorophyta, which was initially described by Lamouroux in 1809, since then some 70 species of *Caulerpa* have been identified. The *Caulerpa* species have complex morphology that provides some characters that can be used in taxonomy, but extensive plasticity makes species boundaries difficult to be defined. With advancement in the field of molecular biology, it provides some alternatives for better understanding of taxonomy. In this study, PCR-based molecular techniques were used in an attempt to differentiate two taxa of *Caulerpa* based on *tuf*A marker.

In this research work, specimens were collected from Pulau Redang, Terengganu, Malaysia. Based on the morphology of the assimilators, specimens were identified into two species namely *Caulerpa serrulata* var. *serrulata* and *Caulerpa serrulata* var. *boryana*.

*Caulerpa* DNA was extracted using DNeasy Plant Mini Kit followed by Polymerase Chain Reaction (PCR), with amplification parameters optimized to obtain reproducible results for gene sequencing.

Based on phylogenetic analyses, it is inferred that *Caulerpa serrulata* var. *serrulata* and *Caulerpa serrulata* var. *boryana* are the same species although different morphological characteristics were observed. Both the Maximum Parsimony (MP) and Bayesian Inference (BI) analyses have shown the two varieties are monophyletic and supported with high bootstrap values.

From this study, *tuf*A marker is suitable in resolving the genetic relationship between *Caulerpa serrulata* var. *serrulata* and *Caulerpa serrulata* var. *boryana*.

# ABSTRAK

*Caulerpa* ialah diantara genus kumpulan alga hijau yang penting dari segi ekonomi, yang asalnya digambarkan oleh Lamouroux dalam tahun 1809, sejak dari itu, 70 spesis *Caulerpa* telah dikenalpasti. Spesis *Caulerpa* mempunyai morfologi kompleks yang mempunyai ciri-ciri yang boleh digunakan dalam taksonomi tetapi ciri-ciri yang hampir sama menjadikan spesis ini sukar dibezakan dan dikenali. Dengan kemajuan bidang biologi molekular, ia memberi pelbagai alternatif untuk lebih memahami taksonomi. Dalam kajian ini, berdasarkan teknik molecular PCR, ia digunakan dalam percubaan untuk membezakan dua taksa *Caulerpa* berdasarkan petunjuk *tuf*A.

Dalam kajian ini, specimen-spesimen dikutip dari Pulau Redang,Terengganu, Malaysia. Berdasarkan morfologi penyerapan, specimen-spesimen ini dikenali sebagai dua spesis iaitu dinamakan *Caulerpa serrulata* variasi *serrulata* dan *Caulerpa serrulata* variasi *boryana.*

DNA *Caulerpa* diekstrak menggunakan Kit Mini Tumbuhan DNeasy diikuti dengan Reaksi Rantaian Polimerase (PCR) dengan parameter amplikasi dioptimumkan bagi mendapatkan keputusan yang boleh diulang untuk turutan gen.

Berdasarkan analisis philogenetik, ia menunjukkan bahawa *Caulerpa serrulata* variasi *serrulata* dan *Caulerpa serrulata* variasi *boryana* adalah sama spesis walaupun berlainan ciri-ciri morfologi diperhatikan. Kedua-dua analisis Parasimoni Maksimum (MP) dan ‘Inference Bayesian’menunjukkan terdapat dua variati adalah monophiletik dan disokong oleh nilai ‘bootstrap’ yang tinggi. Daripada kajian ini, petunjuk *tuf*A adalah sesuai untuk menyelesaikan hubungan genetic diantara *Caulerpa serrulata* variasi *serrulata* dan *Caulerpa serrulata* variasi *boryana.*

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| | |
|---|---|
| AFLP | Amplified fragment length polymorphism |
| AP-PCR | Arbitrary Primed PCR |
| BI | Bayesian Inference |
| BP | Bootstrap percentage |
| cDNA | Complementary DNA |
| CI | Consistency Index |
| Cm | Centimeter |
| DNA | Deoxyribonucleic acid |
| dNTP | Deoxynucleotide triphosphate |
| DW | Dry weight |
| ITS | Internal transcribed spacer |
| kb | Kilobase |
| µ | Micro |
| M | Meter |
| m | Milli |
| $MgCl_2$ | Magnesium chloride |
| ML | Maximum-likelihood |
| MP | Maximum-parsimony |
| NCBI | National Centre for Biotechnology Information |
| PCR | Polymerase chain reaction |
| ppm | Parts per million |
| QTL | Quantitative trait locus |
| RAPD | Random amplification of polymorphic DNA |
| rDNA | ribosomal DNA |

| | |
|---|---|
| RFLP | Restriction fragment length polymorphism |
| RI | Retention Index |
| RNA | Ribonucleic acid |
| rpm | revolution per minute |
| RUBISCO, *rbc*L | ribulose-1, 5-bisphosphate carboxylase/oxygenase |
| sp. | Species |
| spp | Multiple species |
| TAE | Tris-acetate-EDTA |
| TBR | Tree bisection reconnection |
| tRNA | Transfer RNA |
| *tuf*A | Elongation factor TU |