Analisis Tetua Teh (*Camellia sinensis* (L.) O. Kuntze) Berdasarkan Penanda SSR dan morfologi

Intisari

Indonesia merupakan negara penghasil teh ke lima di dunia, tetapi produktivitas teh di Indonesia dari tahun 2009 hingga 2014 mengalami penurunan karena usia pohon terlalu tua, sehingga perlu dilakukan peremajaan. Dalam peremajaan teh diperlukan pengembangan klon teh unggul berdaya hasil dan bermutu tinggi. Pemuliaan teh di PT Pagilaran dilakukan melalui persilangan bebas karena teh merupakan tanaman menyerbuk silang dan bersifat *self-incompatible*. Penelitian ini bertujuan untuk mengidentifikasi tetua jantan dari individu F1 hasil persilangan bebas klon Assamica berdasarkan penanda SSR dengan metode alel penanda khas dan eksklusi-*likelihood*, kemudian hasil pendugaan tetua jantan berdasarkan penanda SSR dikonfirmasi dengan menggunakan penanda morfologi. Pendugaan tetua jantan menggunakan 72 bibit F1 hasil persilangan bebas dengan 6 klon kandidat tetua jantan (PGL 10, GMB 9, GMB 7, TPS 93, GMB 11, dan TRI 2025) dengan tetua betina PGL15. Penanda SSR dihasilkan dari 13 primer sedangkan penanda morfologi yang diamati meliputi rasio panjang/lebar daun, panjang tangkai, berat segar daun, berat segar tangkai, berat kering daun, dan berat kering tangkai. Pendugaan tetua jantan berdasarkan penanda molekuler dilakukan melalui dua pendekatan yaitu berdasarkan alel penanda khas sementara dan eksklusi-*likelihood* dengan perangkat lunak Cervus 3.0., sedangkan pendugaan tetua jantan berdasarkan penanda morfologi dilakukan dengan metode eksklusi berdasarkan perbandingan rerata penanda khas klon tetua jantan berdasarkan hasil uji Dunnet's dengan perangkat lunak JMP Pro 15. Hasil penelitian menunjukkan bahwa tetua betina (PGL 15) dan enam kandidat tetua jantan memiliki penanda khas SSR dan morfologi sementara yang dapat dikenali di keturunannya (individu F1). Alel penanda khas SSR dapat digunakan untuk menduga tetua jantan dari 25 bibit hasil persilangan bebas. Pendugaan tetua jantan berdasarkan metode eksklusi dan *likelihood* mampu menduga tetua jantan dari 72 bibit hasil persilangan bebas yaitu, 10 pasang tetua jantan-keturunan F1 dengan tingkat kepercayaan 95% Berdasarkan kajian kembali dengan sifat morfologi, dihasilkan 57 individu bibit yang tetua jantan terduganya sesuai antara hasil pendugaan tetua berdasarkan penanda molekuler dan morfologi.

Kata kunci: teh, pendugaan tetua jantan, penanda SSR, penanda morfologi

Paternity Analysis of Tea (*Camellia sinensis* (L.) O. Kuntze) based on SSR and Morphological Markers

Abstract

Indonesia is the fifth tea producing country in the world, but the tea productivity from 2009 to 2014 decreased due to ageing, so replanting is necessary. In case of replanting, developing superior high yield and high quality tea cultivars is needed. Tea breeding in PT Pagilaran was carried out through natural cross-pollination because tea is a cross-pollinated plant and self-incompatible. This study aimed to identify male parents of F1 individuals of natural cross between Assamica accessions based on SSR markers using specific allele and exclusion-likelihood method, then the paternity analysis results based on SSR markers were confirmed using morphological markers. Paternity analysis based on SSR markers was carried out by comparing the allele similarity of 72 F1 progenies from natural cross-pollination and 6 accessions of candidate male parents (PGL 10, GMB 9, GMB 7, TPS 93, GMB 11, and TRI 2025). Paternity analysis based on morphological markers was conducted by observing quantitative characteristics including leaf length/width ratio, stem length, leaf fresh weight, stalk fresh weight, leaf dry weight, and stalk dry weight. Parentage analysis based on morphological markers was carried out by the exclusion method based on the comparison of the mean of specific markers of the male parent accessions based on the Dunnet's test results that was analyzed using JMP Pro 15 software, while the paternity analysis based on molecular markers was carried out through two approaches, based on specific putative alleles and exclusion and likelihood that was analyzed using Cervus 3.0 software. The results showed that the female parent (PGL 15) and six candidate male parents had putative specific SSR and morphological markers that could be recognized in their progeny (F1 individuals). The specific SSR alleles can be used to putatively predict the male parents of 25 progenies. Paternity analysis based on the exclusion and likelihood methods was able to predict the male parents of 72 progenies, where 10 male parent-progeny pairs had a 95% confidence level. Based on the result of the re-assessment using the morphological characteristics, there were 57 individual progenies whose candidate male parents were matched to both results of paternity analysis based on the morphological and molecular markers.

Key words: tea, paternity analysis, SSR markers, morphological markers.