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CHARACTERIZATION AND PHYLOGENY ANALYSIS OF AZERBAIJAN TEA (*CAMELLIA SINENSIS* L.) GENOTYPES BY MOLECULAR MARKERS

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The tea is one of the most important products in the southern region of Azerbaijan Republic and plays an essential role in the region's economy. Assessing and describing genetic diversity in crop plants is a crucial first step toward their improvement. In this study the tea genotypes from the southern region of Azerbaijan were studied using 10 random amplified polymorphic DNA in order to estimate their genetic diversity and to identify the relationships among their genotypes. The RAPD primers generated 132 amplification products, 113 of which were polymorphic. The polymorphic banding patterns with the number of amplified fragments varied from 4 (OPA-19) to 19 (OPAB-18). Percent polymorphism ranged from 50 to 95 % with an average of 83.94 %. The genetic similarity among the genotypes tested ranged 0.445 to 0.819 with an average of 0.512. The cluster analysis based on UPGMA and Jaccard similarity index revealed 5 main clusters for the RAPD data and the principal coordinate analysis (PCoA) supported the clustering result. According to our results, there is a relatively high genetic distance across tea genotypes in the south of Azerbaijan Republic. Furthermore, it could be inferred that RAPD markers are suitable tools for the evaluation of genetic diversity and relationships within Camellia sinensis.

Key words: *Camellia sinensis, RAPD marker, genetic variation, PCoA, polymorphism.*

ХАРАКТЕРИСТИКА І ФІЛОГЕНЕТИЧНИЙ АНАЛІЗ ГЕНОТИПІВ АЗЕРБАЙДЖАНСЬКОГО ЧАЮ (*CAMELLIA SINENSIS* L.) ЗА ВИКОРИСТАННЯ МОЛЕКУЛЯРНИХ МАРКЕРІВ

Чай – один з найважливіших продуктів у південному регіоні Республіки Азербайджан, який відіграє значну роль в економіці регіону. Оцінка та опис генетичного різноманіття рослин цього виду є значимим першим кроком до їхнього вдосконалення. У цьому дослідженні генотипи чаю з південного регіону Азербайджану досліджували за використання 10 випадково ампліфікованих поліморфних ДНК для того, щоб оцінити їхнє генетичне різноманіття і встановити відносини між їхніми генотипами. Праймери RAPD згенерували 132 продуктів ампліфікації і 113 з них були поліморфними. Поліморфні паттерни смугастості з певною кількістю ампліфікованих фрагментів були у діапазоні від 4 (OPA-19) до 19 (OPAB-18). Діапазон відсотків поліморфізму складав від 50 до 95 % з середнім значенням в 83,94 %. Генетична подібність між генотипами, які тестували, перебувала у діапазоні від 0,445 до 0,819 при середньому значенні в 0,512. Кластерний аналіз на основі UPGMA та індексу подібності Жаккара виявили 5 основних кластерів для даних RAPD, а аналіз головних координат (PCoA) підтвердив результат кластерингу. Згідно з нашими результатами, між генотипами чаю на півдні Республіки Азербайджан існує відносно велика генетична відстань. Крім того, можна зробити висновок, що маркери RAPD – це прийнятні інструменти для оцінки генетичного різноманіття і відносин у межах *Camellia sinensis.*

Ключові слова: *Camellia sinensis*, маркер RAPD, генетична мутація, PCoA, поліморфізм.

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