

MINISTER OF EDUCATION AND TRAINING

CAN THO UNIVERSITY

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INFORMATION ON RESEARCH RESULTS

1. General information

- Project title: Establishing DNA barcodes database of special fruits in Southern area, Vietnam
- Coordinator: PhD. Do Tan Khang
- Implementing institution: Can Tho University
- Duration: from 01/2019 to 6/2021

2. Objective(s)

General objective: Establishing DNA barcodes database of 10 special fruits in Southern of Vietnam.

Detailed objectives:

Evaluating the status of 10 approved special fruit trees in Southern of Vietnam.

Sequencing DNA barcodes and analysing genetic diversity of each DNA barcode of fruits based on bioinformatics softwares for establishing DNA barcodes database which can be applied in authenticating 10 special fruits in Southern of Vietnam.

3. Creativeness and innovativeness

DNA barcoding and metabarcoding have potential in the context of quality control of both well and poorly regulated supply systems. Standardisation of protocols for DNA barcoding and DNA sequence-based identification are necessary before DNA-based biological methods can be implemented as routine analytical approaches and approved by the competent authorities for use in regulated procedures.

4. Research results

- “Da xanh” pomelo: Based on the degree of nucleotide difference, ITS is a potential sequence to identify the green-skinned pomelo variety. The similarity ranging from 0.66-0.95 with a range of 0.07 divided into 3 main groups: group I with Group 2 with similarity coefficient of 0.76, group I, II with similarity coefficient of 0.76. group 3 has the lowest similarity coefficient of 0.66.
- “Mat” orange (*Citrus sinensis* L.): the *ycf1b* gene shows that there are 5 SNPs that can distinguish honey orange varieties from other varieties. The pedigree based on the ISSR marker showed that there were genetic differences between the seedless orange samples and the other orange samples in the study.
- “Nhan” rambutan: The *matK* gene can be used as a barcoded DNA to identify the yellow-fleshed forest rambutan, Java rambutan and Tien Cuong hybrid rambutan from Vietnam. This ISSR primer-based polymorphism analysis divided eight varieties – 14 rambutan samples into four large groups. With similarity coefficients between varieties ranging from 72 to 100%.
- “Ha Chau” Burmese grape: *AtpF-H* sequence showed that the sequence of “Ha Chau” Burmese grape was completely different from the control samples at 11 nucleotide positions. Based on the diagram, it shows that the genetic diversity between 12 strawberry samples is expressed through a similarity coefficient of 74%. “Ha Chau” mulberry samples have a relatively high similarity coefficient, ranging from 0.875 to 1 and are in the same group on the diagram.
- “Xiem” soursop (*Annona* spp.): The analysis results showed that the *rpoC1* gene, the research results gave 7 positions of nucleotide difference. In which, there are 2 positions specific to the species of bowl, 4 positions are capable of identifying the custard apple species. The above results show that the ISSR is suitable for characterization of three *Annona* species and there is a significant difference in genetic diversity between species.
- “Hong Lai Vung” mandarin: The results of sequencing analysis in the ITS region show that there are 14 different positions between “Hong Lai Vung” mandarin and other varieties of mandarin. From the results of ISSR marker, the similarity level of the samples varied from 0.49 to 1.00.
- “Ri-6” durian: Detecting 6 SNPs between sequences of durian samples. Among them, there is a specific SNP for durian variety Ri-6 at position 444, in durian Ri-6 it is G while the rest is C. Analysis results are based on molecular markers ISSR has divided 20 Durian varieties obtained

in four provinces of the Mekong Delta were divided into five groups with similarity coefficients ranging from 0.61 to 0.97.

- “Ruot do” dragon fruit: Red flesh dragon fruit variety was identified by three loci, *atpF-H* + *rbcL* + *matK*.

- “Lo Ren” star apple: Based on the DNA sequence of *atpF-atpH* region, there are differences between five varieties of Lo Ren suckling, pink buttermilk, purple buttermilk, purple breast, and Mica. Genetic diversity analysis using ISSR markers showed that all varieties have similarity from 0.68 to 1.00 in which the Lo Ren suckling varieties were classified into a separated clade.

- “Hoa Loc” mango: Through the analysis of the *matK* sequence region, a variety of variable positions occurred in most of the 16 sequences, of which 27 positions could identify Hoa Loc mango. with the rest of the samples. Based on the ISSR molecular marker, the mango samples were divided into 2 groups with an average similarity coefficient of 0.67.

5. Products

Scientific products:

- 05 international articles

 - + 01 article published in Asian Journal of Plant Sciences 20(3) (2021) – Q3

- + 01 article published in Biodiversitas 2021 – Q3

 - + 01 article published in Asian Journal of Agriculture and Biology 2021(2) (2021) – Q4

 - + 02 article published in International Journal of Agriculture and Biological Sciences 04 (2021)

- 02 national articles

 - + 01 article published in Scientific Journal of Can Tho University

 - + 01 article published in Journal of Sciences and Agricultural Technology of Vietnam

- 01 book: “DNA barcode and genetic diversity of fruits”.

Educational products:

- Supporting for 06 master theses.

Applicable products:

- Library of DNA barcodes of fruit trees.

- Database of DNA barcodes of 10 fruit varieties (<https://dnnavf.ctu.edu.vn/>).

6. Effects, transfer alternatives of research results and applicability

6.1 Effects

- For organizations: storing and maintaining genetic resources of fruit trees in order to use for research and agricultural production.
- The applied institutions: the result brings scientific and practical benefits to researchers and farmers, and it helps farmers in selecting of varieties.
- Evaluating and concluding the feasible of DNA barcode application in agriculture.

6.2 Method of transferring results

DNA barcoding can be used for authenticating products based on single herbal ingredients and DNA metabarcoding for assessment of species diversity in processed products, and both methods should be used in combination with appropriate hyphenated chemical methods for quality control. Standardisation of protocols for DNA barcoding and DNA sequence-based identification are necessary before DNA-based biological methods can be implemented as routine analytical approaches and approved by the competent authorities for use in regulated procedures.