GRAPHICAL ABSTRACT

Leaf architecture and genome size variation of *Durio zibethinus* L. from Jelebu, Negeri Sembilan, Malaysia

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INTRODUCTION

*Durio zibethinus* L. is known as the 'king of fruit' in Malaysia. Meanwhile, Jelebu, Negeri Sembilan has always become the top choice district to visit for durian lover for its Durian Keninga Jelebu.

However, there is still lacking in taxonomic data of *D. zibethinus* especially from Jelebu.

OBJECTIVES

The aim of this study is to examine leaf architecture and genome size variations between selected *D. zibethinus* accessions from Jelebu.

METHODOLOGY

Leaves samples collection were done in December 2021 from durian orchards in Jelebu, Negeri Sembilan. Five accessions of *D. zibethinus* accessions were selected in this study: Jel-4, Jel-15, Jel-34, Jel-45 and Jel-54 including DD79 Musang King as control.

Data collection for leaf architecture analysis were divided into two parts which are (1) gross morphological characteristics and (2) leaf venation variations.

Genome size variations was analyzed by using flow cytometry machine.

RESULTS

1. 37 parameters of leaf architecture were observed and recorded including four main characteristics which are leaf attachment, leaf structure, leaf surface and leaf venation.
2. FCM DNA histogram analysis was successfully analyzed the genome size of *D. zibethinus* by using Eupice max cv. Poleniko as external standard.
3. This study found that *D. zibethinus* genome size ranging between 2,733 to 4,900 pg.

DISCUSSION

Seven parameters of *D. zibethinus* accessions from Jelebu have been recorded which are petiole length, petiole features, leaf size, leaf shape, leaf base shape, lower leaf surface color, and annotation could be used in differentiating between accessions.

In this study, interspecific genome size variations were examined among all 37 collected *D. zibethinus* accessions and it is found that interspecific genome size variation was higher than intraspecific variation study (Hohn & Memel 2010).

CONCLUSION

This study highlights the significant value of leaf architecture and genome size data in taxonomic study of *D. zibethinus* accessions from Jelebu and serve as additional information to avoid confusion for *D. zibethinus* growers as well as researchers in identifying and classifying *D. zibethinus* accessions.

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