Data in Brief 8 (2016) 1438–1442

Contents lists available at ScienceDirect

Data in Brief

journal homepage: www.elsevier.com/locate/dib

Data Article

Dataset of SSR markers for ISSR-Suppression-PCR to detect genetic variation in *Garcinia mangostana* L. in Peninsular Malaysia

Sri A'jilah Samsir [a], Hamidun Bunawan [a], Choong Chee Yen [b], Normah Mohd Noor [a,*]

[a] *Institute of Systems Biology, Universiti Kebangsaan Malaysia, 43600 Bangi, Selangor, Malaysia*
[b] *School of Environment and Nature Resource Science, Faculty Science and Technology, Universiti Kebangsaan Malaysia, 43600 Bangi, Selangor, Malaysia*

ARTICLE INFO

Article history:
Received 16 June 2016
Received in revised form
7 July 2016
Accepted 8 August 2016
Available online 16 August 2016

Keywords:
Garcinia mangostana L.
Genetic variation
DNA markers
Peninsular Malaysia

ABSTRACT

In this dataset, we present 15 Simple Sequence Repeat (SSR) markers with the motifs (AC)n, (GA)n, and (AC)n(AG)n using a ISSR-Suppression-PCR technique in order to discriminate *Garcinia mangostana* from diverse geographical origins in Peninsular Malaysia. A few loci showed differences between 3 and 6 bp in allele size, indicating that there are some polymorphisms between individuals correlating to the number of SSR repeats that may be useful for differentiate of genotypes. Collectively, these data show that the ISSR-Suppression-PCR is a valuable method to illustrate genetic variation of selected *G. mangostana* in Malaysia.

Specifications Table

Subject area	*Biology*
More specific subject area	*Plant sciences*

* Corresponding author.
E-mail addresses: sriajilah.samsir@gmail.com (S.A. Samsir), hamidun.bunawan@ukm.edu.my (H. Bunawan), cychoong@ukm.edu.my (C.C. Yen), normah@ukm.edu.my (N.M. Noor).

http://dx.doi.org/10.1016/j.dib.2016.08.016

Type of data	*Table, figure*
How data was acquired	*Development of molecular markers using ISSR-Suppression-PCR*
Data format	*Analyzed*
Experimental factors	*Three SSR motifs: (AC)n, (GA)n, and (AC)n(AG)n were targeted. PCR amplification was conducted on genomic DNA of Garcinia mangostana to obtain DNA fragments with the SSR motifs at both ends. With this approach, we have developed 15 SSR markers to be used in screening of genetic variation of G. mangostana collected throughout Peninsular Malaysia.*
Experimental features	*Each of the 15 SSR markers was tested on selected G. mangostana accessions. A few loci showed differences of approximately 3–6 bp in allele size. These differences showed that there are some polymorphisms between individuals according to the number of SSR repeats.*
Data source location	*Peninsular Malaysia*
Data accessibility	*The data is available with this article.*

Value of the data

- These data suggest that ISSR-Suppression-PCR is a useful method to provide information on the genetic variation of selected *G. mangostana* genotypes in Peninsular Malaysia.
- These SSR markers can assist researchers to differentiate between accessions of *G. mangostana*.
- Seven out of 15 SSR markers tested on several accessions of *G. mangostana* showed differences between 3 and 6 bp in allele size revealing genetic variation in this apomictic plant and suggesting the usefulness of these accessions as potential resources for future breeding programs.

1. Data

15 SSR markers were developed and tested on selected *Garcinia mangostana* accessions (Table 1) [1]. The data presented here shows that the ISSR-Suppression-PCR technique was very applicable in designing SSR primers and was able to reveal variation of selected germplasm collections [2,3]. These SSR markers can be used to assess genetic variation of *G. mangostana*.

Table 1
List of IP2 and IP3 primers. Each primer pairs was assigned as one SSR locus.

Primer name	Sequence of IP2 primer (3′–5′)	Sequence of IP3 primer (3′–5′)
GM-01	ACGTGGAGAGCCATCCGAAGT	ATAGATAACGTGAGGGTGGAA
GM-02	TTGAGGAAAAGAAGGTAAACTCTC	ATATTTTGGAATGAAACCTCG
GM-03	TGCCTTTCGGGTGGTGTGTTGTGT	CGCGTGGTGAGCTAAGAAAGT
GM-04	TTCATCTCCTCCTCTTTGACTACT	AACAATTTGAATTGGTTGCCT
GM-05	CTGAAGCCCTCAATTTTCATCTCC	CGACCACTATAGGGACACG
GM-06	GGTGGAGGAAATCCCAACAGTCAG	ATAAAATGATACCCACCTC
GM-07	ATTGGGTACCGGTGGAGAAAA	GAAGCCTATGGGCAACTA
GM-08	TAAATGCCCAAGAAAAGAAGG	TTGGTGAATGAGGGAGCA
GM-09	GTTTAGAAAGTGCTGTGTGAC	GATGTATGGGACCTAATG
GM-10	GACATACAGGAAACGGTGGAG	ATTGTAAATGACCATCAACTA
GM-11	GTCACAACCCAATCTAGGTCG	AGCTAATGGTTTGTAGGGAAA
GM-12	GTAACAACCCAATCTAGGTCG	GCGTGGTGACGGCCACACATT
GM-13	CAGACCATAAGCATGATATGT	AAGGTAAGGACATTATGTG
GM-14	ACCAACTGAGCCTCTGGGCTA	CGAGTTCGCCAACACCTA
GM-15	TTATAAATCAATCGAGCCTTT	TAGAAGCCTACGGGCAAT