



Development of SCAR makers for longan (*Dimocarpus longan* L.) authentication in Vietnam

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Abstract

Longan (*Dimocarpus longan* L.) is an important fruit plant in Vietnam and therefore the demand of genetic conservation and variety authentication is of high importance. Due to the limitations of chemical and morphological longan characterization approaches, it is necessary to develop more precise DNA-based methods. In this study, we focused on developing SCAR (Sequence Characterized Amplified Region) markers for longan identification. The total of 11 longan accessions collected from different provinces in Vietnam were genetically characterized by using 20 RAPD (Random Amplified Polymorphic DNA) primers to identify polymorphic RAPD fragments. Twenty two polymorphic RAPD fragments were obtained and 2 of them were further sequenced and developed into SCAR markers. The sequences of specific RAPD fragments were used to design primers. Totally, 2 pairs of SCAR primers were archived. These primers showed significant effectiveness for cultivar identification of 2 favourite longan cultivars of Vietnam namely “Duong phen Hung Yen” and “Chin muon Hung Yen”.

Key words: Longan, molecular markers, RAPD, SCAR

Table S1. List of extended RAPD primers used to directly sequence chosen RAPD fragments (the underlined letters present the nucleotides added to the original RAPD primer)

Primer name	Original RAPD Primer sequence (5'– 3')	Extended RAPD Primer sequence (5'– 3')
D29	GACCCGGAACGA	GACCCGGAACGAG GACCCGGAACGAC GACCCGGAACGAT GACCCGGAACGAA
C59a	CGCGTTCGTGGA	CGCGTTCGTGGAG CGCGTTCGTGGAC CGCGTTCGTGGAT CGCGTTCGTGGAA

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Table S2. SCAR primers designed by using Primer3plus tool used to distinguish between different longan cultivars grown in Vietnam

SCAR primer name	Sequence (5' – 3')	Product size [bp]	T _m [°C]
DHY1	Fw – GTCTTCCAACCTCCCACTCA Rv – ACCCGGAACGATTGTATGA	241	60
DHY2	Fw – AGAAGAACTAGCCCGGGAAC Rv – TGAGTGGGAGGTTGGAAGAC	225	60
DHY3	Fw – GTCTTCCAACCTCCCACTCA Rv – CCGGAACGATTGTATGAGG	239	60
DHY4	Fw – TCTTCCAACCTCCCACTCAG Rv – ACCCGGAACGATTGTATGA	240	60
DHY5	Fw – AGAAGAACTAGCCCGGGAAC Rv – AACGGTCTGAACCTGAGTGG	238	60
CHY1	Fw – TTCCTGCCTTTAGGGTGATG Rv – TGGAAGCAAAGTCGAGAACA	211	60
CHY2	Fw – ATTGGTGAATGGCTTTCCTG Rv – TGGAAGCAAAGTCGAGAACA	225	60
CHY3	Fw – CATTGGTGAATGGCTTTCCT Rv – TGGAAGCAAAGTCGAGAACA	226	60
CHY4	Fw – TGTTCCTCGACTTTGCTTCCA Rv – GACATGCAAAAAGCCCCTAA	216	60
CHY5	Fw – TGTTCCTCGACTTTGCTTCCA Rv – AGACATGCAAAAAGCCCCTA	217	60