Research Title	Genetic variation analysis of longan using primers designed from nucleotide sequence data of genes responding to flowering induction by potassium chlorate.
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Abstract

Longan is an important economic fruit crop in Thailand. Flowering and fruit setting are crucial factors affecting longan yield. Previous studies comparing differential gene expression between RNA samples extracted from control and potassium chlorate-induced flowering longan samples at different time points used Next Generation Sequencing (NGS) technology to generate nucleotide sequence data of genes associated with the longan flowering pathway. These sequence data can be applied to various aspects of longan research, particularly in developing molecular markers associated with specific traits or studying the genetic diversity of different longan cultivars in Thailand. In this study, four primers consisted of *NAD(P)H dehydrogenase* (NADPH), *Myb transcription factor* (MYB), *Cytochrome P450* (P450), and *UDP-glucosyltransferase* (UGT) were used to analyze PCR product patterns in DNA samples extracted from 32 different longan cultivars. All DNA samples were

tested for their suitability as templates for Polymerase Chain Reaction (PCR) using an actin primer. The experimental results revealed that the UGT and P450 primers produced different PCR bands among longan samples, ranging from 1,000 to 1,500 base pairs and 1,500 to 2,000 base pairs, respectively. However, to improve clarity, further experiments should be conducted using agarose gel electrophoresis with a higher agarose concentration or polyacrylamide gel electrophoresis, which offers higher resolution for DNA band separation. The results from these analyses could be applied to develop UGT and P450 primers as molecular markers for identifying longan cultivars in the future.