SEQUENTIAL EXTRACTION OF RNA AND DNA FROM THE SAME SAMPLE OF *NEOLAMARCKIA CADAMBA* (ROXB.) BOSSER

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Abstract

Most of the established molecular techniques in plant molecular biology rely on the reliability of extraction methods to obtain nucleic acids from a given environmental source. The development of protocols for isolating both RNA and DNA from the same sample is recently becoming a major concern especially when the sample is small. Despite a number of methods that describe the simultaneous isolation of RNA and DNA from the same sample have been reported, most of these methods have yet to be optimized to deal with the reduced quantity and compromised quality of samples encountered in plant genetics analysis. *Neolamarckia cadamba* (Roxb.) Bosser was chosen in the present study due to its commercial value and fast growing ability. Total RNA was successfully isolated from the leaf tissue with subsequent recovery of DNA from the extraction mixture through alcohol precipitation. Reverse transcriptase-Polymerase Chain Reaction (RT-PCR) was performed and arbitrary primers that produced reproducible, scorable and informative bands were selected for randomly amplified polymorphic DNA (RAPD) analysis. The amplicons of RT-PCR and RAPD were successfully obtained from all isolates, indicating that the extracted nucleic acids were intact and pure enough for quantitative molecular analysis.

INTRODUCTION

Reliability of extraction methods to obtain nucleic acids from a given environmental source is a crucial point for applicability, efficiency and precision of any molecular techniques in plant genetics (Berendzen *et al*. 2005). Recently, the development of protocols for isolating both RNA and DNA from the same sample is becoming a major concern especially when the sample is small.

Sequential extraction of RNA and DNA from the same sample begins by extracting RNA and then re-extracts the DNA from the collected organic phases. One of the major advantages of this method is that it only requires minimal amounts of plant materials to yield sufficient quality of DNA and RNA templates for PCR and RT-PCR reactions (Berendzen *et al*. 2005). Additionally, this new method also require considerably less time compared to other purification methods.