ABSTRACT

Nepenthes plant species (Pitcher plants) are one of the carnivorous plants. These plants are used in the traditional medicines and widely exploited as an ornamental plant. Due to high demand as an ornamental plant, this valued *Nepenthes spp.* population is depleting from the forests. The DNA markers are very helpful in the precise identification of plant species and can be used in identification of individual *Nepenthes spp.* In addition, it is important to study endophytes of *Nepenthes spp.* in order to understand types of endophytes associated with them. Plant endophytes are known to play a significant role in the host plants growth and development. Therefore the main objectives of this study were to isolate bacterial endophytes from eight *Nepenthes spp.*, to identify isolated endophytes based on 16S rDNA sequences, to screen endophytes for cytokinin-like compounds, to screen eight *Nepenthes spp.* using 120 RAPD primers and 11 mirosatellite primers, and to report on the genetic variation in eight *Nepenthes spp.* based on RAPD and microsatellite profiles analysis. Genomic DNA (gDNA) was successfully isolated from eight *Nepenthes spp.*; and 30 ng gDNA was used as template in each RAPD and microsatellite-polymerase chain reaction (PCR). All eight *Nepenthes spp.* were analyzed by using 120 RAPD and 11 microsatellite primers to identify potential DNA markers for their precise identification. Surface-sterilized plant tissues (leaf and stem) were used to isolate bacterial endophytes from 8 *Nepenthes spp.*; and isolates were identified using PCR amplified 16S rDNA sequence based method of bacterial identification. Ethyl acetate extracts from cell-free broth of isolates were screened for cytokinins using cucumber cotyledon greening bioassay (CCGB). The RAPD and microsatellite-PCR analysis showed that 120 RAPD and 11 microsatellite primers produced potentially useful 390 and 16 informative DNA markers, respectively. Ninety three (93) endophytic bacterial isolates were isolated from *Nepenthes spp.* samples that were collected from FRIM and Gunung Jerai. Analyses of 16S rDNA and identification of endophytic bacterial isolates (EBIs) suggest that isolates belong to 17 genera and 46 *spp.* Majority (53.76%) of EBIs were from *Bacillus* genus; and *Bacillus cereus* was the most dominant (13.98%) sp. within EBIs. The CCGB results showed that out of 93 EBIs, only 44 isolates broth extracts do have cytokinin-like activity. RAPD and microsatellite markers reported in this study could be useful in identification of 8 studied *Nepenthes spp.* However, a suitable mechanism of EBIs usage needs to be identified to utilize the leads from CCGB for their applications in agriculture.