SUMMARY

Peanut (*Arachis hypogea*) is a typical plant species of tropical regions that has high economic value. The plantation is widely spread over many areas and the production is being pushed to meet the increasing demand. Peanut breeding program is aimed to improve genetic quality, mainly with respect of production and thus information on genetic diversity is necessary as a basis for consideration in breeding, management and sustainable utilization. One approach to analyze the genetic diversity of peanut is by using molecular markers. Random Amplified Polymorphic DNA (RAPD) is a widely used molecular marker for genetic diversity analysis. Therefore, the aim of this study was to assess genetic diversity of peanut cultivars, i.e. Jerapah, Kancil, and Hypoma 2, based on RAPD markers. The study was conducted in a survey method, in which three individuals of each cultivar were analyzed using PCR-RAPD technique employing twelve primers, i.e. OPA-1, OPA-2, OPA-9, OPA-13, OPB-2, OPB-3, OPB-4, OPB-5, OPB-7, OPB-11, OPB-12 and OPJ-07. Data analysis based on morphological data is also included. Molecular analysis revealed that only 7.55% polymorphic band was obtained, while most of the bands were monomorphic, indicating very low variation among the cultivars. The phenogram that constructed based on literature showed that Kancil was closer to Jerapah cultivar, while RAPD-based dendogram showed that Hypoma 2 was closer to Kancil cultivar.

Keywords: peanut cultivars, genetic diversity, RAPD