

## COMPARATIVE ANALYSIS ON DIVERSITY PATTERN OF PINEAPPLE BASED ON PHENOTYPIC AND RAPD MARKERS

Sobir, Siska Indriajaya Apriyani, Hajrial Aswidinnoor & Yuniarti  
Department of Agronomy and Horticulture, Bogor Agricultural University, Bogor

Sobir, Siska Indriajaya Apriyani, Hajrial Aswidinnoor & Yuniarti. 2006. Analisis Perbandingan Pola Keragaman Nenas Berdasarkan Penanda Fenotipik dan RAPD. *Floribunda* 3(2): 44–51. — Nenas diperbanyak secara vegetatif sehingga keragaman genetiknya cenderung rendah, oleh karena itu dibutuhkan suatu pendekatan yang akurat untuk mendeteksi keragaman genetik koleksi plasma nutfah nenas. Pada penelitian ini dilakukan analisis keragaman genetik 20 aksesori dari Indonesia dan dua aksesori dari Pantai Gading. Pengamatan 27 karakter morfologi fenotipik dan 29 pita hasil amplifikasi analisis RAPD bertujuan untuk mengetahui jarak genetik dan kekerabatan antar aksesori yang diuji. Analisis gerombol dengan berdasarkan karakter morfologi mampu mendeteksi keragaman genetik sebesar 0.36 hingga 0.84 berdasarkan koefisien kesamaan, dan pada tingkat koefisien kesamaan 0.35, aksesori yang diuji dapat dipisahkan menjadi tiga kelompok utama. Selanjutnya berdasarkan 23 pita polimorfis analisis RAPD mampu menduga keragaman genetik sebesar 0.62–1.00 berdasarkan koefisien kesamaan. Pada tingkat koefisien kesamaan 0.67, aksesori yang diuji dapat dipisahkan menjadi tiga kelompok utama dan mampu memisahkan aksesori tipe Queen dan aksesori tipe Smooth Cayenne. Analisis konkurensi menghasilkan nilai korelasi Rohlf yang rendah ( $r=0.0747$ ). Nilai ini menunjukkan bahwa pengelompokan sebaiknya menggunakan data gabungan morfologi dan RAPD, dan analisis gerombol dengan menduga keragaman genetik sebesar 0.49–0.81 berdasarkan koefisien kesamaan, dan pada tingkat koefisien kesamaan 0.56, aksesori yang diuji dapat dipisahkan menjadi empat kelompok utama dan mampu memisahkan aksesori tipe Queen dan aksesori tipe Smooth Cayenne.

Kata kunci: Nenas, keragaman genetik, RAPD, morfologi, korelasi Rohlf.

Sobir, Siska Indriajaya Apriyani, Hajrial Aswidinnoor & Yuniarti. 2006. Comparative Analysis on Diversity Pattern of Pineapple Based on Phenotypic and RAPD Markers. *Floribunda* 3(2): 44–51. — Pineapple is mostly propagated through vegetative mean, and tend to have narrow genetic variability; therefore, powerful method is required to differentiate their genetic variability, and consequently 20 *Ananas comosus* accessions from nine locations in Indonesia and two accessions from Ivory Coast, were subjected to genetic variability analysis. This research utilizes their phenotypic performance and RAPD markers to evaluate the genetic distance and relationship among those accessions. Twenty-seven morphological characters and 29 RAPD bands had been utilized in this study. Cluster analysis revealed that based on morphological markers the accessions were separated accessions from 0.36 to 0.84 of similarity coefficient, and three primary groups could be distinguished at similarity coefficient of 0.35. Subsequently RAPD analysis has been separated the accessions at 0.62–1.00 of coefficient of similarity. From this analysis, three primary groups constructed at 0.67, and it is able to differentiate Queen and Smooth Cayenne type accessions. The concurrence analysis on morphological and RAPD analysis, showed the very weak Rohlf correlation value ( $r=0.0747$ ), which indicated that grouping of pineapple accessions should be combination of morphological characters and RAPD analysis. Combination morphological showed that accessions distributed from 0.49 to 0.81 of similarity coefficient level, and at 0.56 level similarities, the pineapple accessions were clustered into four primary groups and it is able to differentiate Queen and Smooth Cayenne type accessions.

Key words: Pineapple, genetic variability, RAPD, morphology, Rohlf correlation.

Pineapple [*Ananas comosus* (L.) Merr.] reproduction is predominantly asexual and varieties of *A. comosus* are self-incompatible (seedless when self-pollinated), so that it made low variation in pineapple. Seeds may be produced by artificial cross-pollination or assisted by humming bird, but this rarely happen. Under this condition, breeding by human is needed to increase the variation. In a

breeding program, breeders need high variation of introduction or local germplasm. The variation can be increased by hybridization, mutation, somaclonal variation and other techniques (Collins 1968).

According to Bai et al. (2000), germplasm collections are useful in characterizing individual accessions and cultivars, in detecting duplications of genetic materials, as a general guide in selecting