

## ***ABSTRACT***

Soybean (*Glycine max* L. Merr.) Is the main commodity in Indonesia besides rice and maize. The increasing of national consumption of soybean becomes a challenge for soybean breeders. The success of breeding programs depends on availability of genetic diversity. The aim of this research was to identify the genetic diversity of USDA introduction soybean varieties by using *simple sequence repeats* (SSR) markers and morphological. PCR analysis was scored as biner data and the collected data was analyzed using NTSYS and PowerMarker. The results showed that the overall marks used in this research as many as 15 markers are polymorphic. As many as 158 alleles with the size of 100-368 bp were identified by a range of 4-18 alleles per locus. The polymorphism level was 0.92 with the highest value 0.96 (SATT463), (SATT249) and (SATT063) while the lowest value 0.87 (SATT038). Result also showed the average of major allele frequency was 14.29% with the lowest value of 3.84% (SATT249) and the highest value of 29.16% (SATT083). A total of 15 markers used in this study have a value of  $PIC > 0.5$  could be used to detect genetic diversity of USDA introduction soybean. The average of genetic diversity index was 0.93. Cluster analysis showed that 27 accessions of soybean were split in two groups coefficient 0.75. The first group consisted of 26 accessions, and the second groups consist of 1 accessions was D76-8070. The information of genetic diversity could be used as a preliminary basis for choosing crossing parents in soybean breeding of USDA introduction. Morphological analysis results indicating accession with the same morphological characteristics in the same quadrant would not necessarily have the same genetic because morphology influenced environmental factors

**Keywords:** Soybean (*Glycine max* L. Merr.), SSR, Genetic diversity, morphological