

GENETIC DIVERSITY OF POTATO BASED ON RANDOM AMPLIFIED POLYMORPHIC DNA AND SIMPLE SEQUENCE REPEAT MARKER

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Abstract	<p>Various potato clones are cultivated by farmers in Banjarnegara and Wonosobo, Central Java, Indonesia such as MZ, NH1, NH2, Vega, Gareta, Granola, Bliss, Merah (Red Potato), Ungu (Purple Potato), Klon_17 (K17), Local Dieng, Margahayu, and X. This encourages the importance of genetic diversity and genetic similarities. This study aimed to analyze genetic diversity and genetic similarities between 13 accessions of potatoes based on seven Random Amplified Polymorphic DNA (RAPD) primers and nine pairs of Simple Sequence Repeat Marker (SSR) primers. The results showed that RAPD and SSR primers could be used to analyze genetic diversity and genetic similarities of 13 potatoes accessions from Banjarnegara and Wonosobo. The PLP value was 80.9% in the RAPD primer and 65.41% in the SSR primer. Four RAPD primers were informative based on PIC value: OPG 08, OPM 19, OPP 13, and OPX 04. Three SSR primer were informative: STM 2005, RGH- SSR 8, and StI 035. Genetic similarities presented by Phylogenetic tree analysis resulted in two main clusters. The first cluster consisted of Granola, MZ, Ungu (Purple potato), Merah (Red Potato), Local Dieng, Margahayu, Gareta, Vega, NH2, NH1, Klon_17 (K17), and Bliss. The second cluster consisted of X. Granola and MZ having a high genetic similarity with a genetic distance of 0.07 and 0.132. Meanwhile, K17 and X had a low genetic similarity with a genetic distance of 0.31 and 0.987.</p>
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Author	SAPTO NUGROHO HADI, S.Si, M.Biotek.