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Genetic diversity of conserved potato germplasm using microsatellite markers

Gi-An Lee^{1*}, Kwang-Soo Cho², Myoung-Jae Shin¹, Jung-Ro Lee¹, Yang-Hee Cho¹ and Kyung-Ho Ma¹

Abstract

Potato is important carbohydrate source over the world in that revealing high productivity per the unit area, and their cultivation area is estimated to be increased to cope with a scarcity of food according to the population increase. Major cultivated species of potato is *Solanum tuberosum* (2n = 4x = 48) and regarded as being originated in Andes region of South America. The diverse potato genetic resources has been collected and perserved in Highland Agricultural Research Institute (NICS, RDA), and the genetic materials as DNA stock is conserved in National Agrobiodiversity Center(NAS, RDA). The understanding of genetic constitution of conserved diversity is the basis for the germplam management and further utilization. In this study, we analyzed the genetic diversity of potato germplasm(479 accessions) using 24 microsatellite markers which have been internationally used for fingerprinting of potato accession. The allele number and polymorphic information content (PIC) of total accessions per locus was ranged from 2 to 18 (mean = 8.2) and from 0.214 to 0.771 (mean = 0.595), respectively. Especially, the accession originated from Korea revealed average allele number of 6.0 (2 - 11) and average PIC value of 0.58 (0.193 - 0.763). Three groups were deduced by phylogenic analysis (Group-1, -2, -3); Korean accessions showed close genetic similarity to Japanese and USA accessions, and Korean landraces were mainly included in Group-3. We try to elaborate the genetic diversity analysis of conserved potato germplasm by acquiring more genotypes using applicable molecular markers.

Keywords: Potato, Genetic diversity, Microsatellite

Corresponding author*

Gi-An Lee

Address: National Agrobiodiversity Center, National Institute of Agricultural Sciences, RDA, 370

Nonsaengmyeong-Ro, Wansan-Gu, Jeonju-Si, Jeollabuk-Do, 54874, Republic of Korea

Tel and Fax: +82-63-238-4880/+82-63-238-4859

E-mail address: gkntl1@korea.kr

¹⁾ National Agrobiodiversity Center, National Institute of Agricultural Sciences, RDA, 370 Nonsaengmyeong-Ro, Wansan-Gu, Jeonju-Si, Jeollabuk-Do, 54874, Republic of Korea

²⁾ Highland Agricultural Research Institute, NICS, RDA, 5481, Gyeonggang-ro, Daegwallyeong-myeon, Gangwon-do, 25342, Republic of Korea