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Genetic Characterization and Comparative Analysis of Korean Potato Germplasm using Genome-wide SNP markers with Global Potato Diversity Panel

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[Introduction]
Characterizing breeding materials regarding genetic diversity and population structure is essential for breeding to improve crop plants. The high-throughput genotyping platforms which provide genome-wide representation of SNPs present in potato germplasm have been developed and applied to investigating genetic diversity and population structure.

[Materials and Methods]
Using the SolCAP 8303 SNP Infinium Array, a 110-line Korean potato germplasm were genotyped. After filtering, 6575 SNPs were used to perform STRUCTURE, DAPC and HC. The global dataset comprising a total of 393 clones were generated using the ClusterCall software. The resulting 3977 SNPs were used to carry out DAPC, HC and KLFDAPC. The percent heterozygosity for clones and informativeness of SNPs were calculated. Selection signatures were analysed using iHS and XPEHH approaches.

[Results and Discussion]
Following tetraploid model, we conducted population structure analysis and revealed three subpopulations represented by two major Korean potatoes groups and one separate foreign potato group within 110 lines. The analysis of 393 global potato clones revealed country/region specific genetic patterns. The Korean potato clones exhibited a higher average percent heterozygosity compared to the ones from Japan, the United States and other landraces. We also identified selection signatures spanning candidate genes that might be associated with biotic and abiotic stress tolerances. Ten of highly informative SNPs discriminating all of 393 potatoes were identified. Our results on molecular characterization of cultivated potato clones could help understand how potato cultivars diversify for distinct market classes depending upon countries' breeding strategies and assist in genomics-facilitated breeding efforts to create new varieties that are better adapted to climate changes and meet market demands.

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