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RESEARCH ARTICLE

Genetic diversity and population structure of 288 potato (*Solanum tuberosum* L.) germplasms revealed by SSR and AFLP markers

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Abstract

Potato (*Solanum tuberosum* L.) is an important staple food and economic crop in many countries. China has led world potato production in recent years. To understand the genetic diversity of potato germplasms and to enrich the current gene pool for potato improvement, we made a global collection consisted of 288 potato germplasms from eight countries and the International Potato Center (CIP). Using SSR and AFLP techniques, we evaluated the genetic diversity and population structure of these 288 potato accessions. A total of 190 alleles on 20 SSR loci were detected and all of the SSR alleles were polymorphic among these potato germplasms with an average of 9.5 alleles per SSR locus ranging from 2 to 23. The effective number of alleles per locus (*Ne**), Nei's genetic diversity (*H**), and Shannon's information index (*I**) was from (0.1709±0.3698) to (1.6166±0.3414), (0.076±0.1388) to (0.3812±0.1886), and (0.1324±0.1970) to (0.5347±0.1440), respectively, and the mean polymorphic information content (PIC) value was 0.7312. A total of 988 AFLP alleles were detected by 10 AFLP primer combinations with 983 polymorphic alleles, and 99.49% alleles was polymorphic with an average of 98.3 polymorphic alleles per primer combination ranging from 91 to 116. The values of *Ne**, *H** and *I** were from (1.5162±0.311) to (1.6423±0.3278), (0.3114±0.145) to (0.3675±0.1121), and (0.4761±0.1792) to (0.547±0.1322), respectively, and the average PIC value was 0.9871. Bayesian analysis discriminated the accessions into seven subgroup and an admix group. The majority of accessions from CIP and China were assigned into SG1, SG5, SG6, SG7 and admix group. Accessions in SG3 were mainly from CIP and two small groups SG2 and SG4 were mainly from northeastern China. In general, the results obtained from Bayesian statistical analysis, cluster analysis and principal coordinate analysis consistently revealed the lack of geographical differentiation among country-wide collections, indicating germplasm introduction was common

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for the countries out of potato origin center. The polymorphic markers and the differentiate genetic lineages found in this study provide useful information for potato improvement and conservation programs.

Keywords: potato germplasms, genetic diversity, population structure, SSR, AFLP

1. Introduction

Potato (*Solanum tuberosum* L.) is an important food crop serving as daily food, vegetable or stock feed, and provide major calories for a large population worldwide (Sharma and Nandineni 2014). Potato improvement plays an important role for the food shortage with the increasing population. China has been leading the world in the potato production since 2007, and about 23.9% of world's potatoes were harvested in China in 2013 based on the reports from the Food and Agriculture Organization of the United Nation. Potato-breeding is mainly following the conventional cross and selection method (Duan *et al*. 2009). The identification of potato is based on the morphological characteristics, such as tuber shape, leaf type, flower color, sprout appearance, and so on (Norero *et al*. 2002). These morphological characters are easily affected by environmental factors; furthermore, these characters cannot be measured until the maturity of plants and tubers (Demeke *et al*. 1993). In China, potato improvement is very important because the predominant cultivars were developed using European tetraploid cultivars as parents in 1950 to 1960 (Jin 1999). The close relationship and the low genetic variation make potato improvement very difficult if only through the conventional morphological character to make selection. It is very urgent to evaluate the genetic variation and determine the appropriate combination in breeding programs to improve potato production.

DNA molecular markers have been widely used in germplasm fingerprinting, determining genetic diversity, heterosis analysis and marker-assisted selection in potato breeding (Ritter *et al*. 2005). SSR and AFLP markers have well used in potato germplasm genetic studies. Among various molecular markers, SSR showed many advantages, such as widely distributed over genomes, high polymorphism, good reproducibility, co-dominant inheritance, generally well-conserved within the species, and was used simply *via* PCR (Powell *et al*. 1996). These advantages make SSR become one of important techniques on evaluation of genetic diversity and variation (McGregor *et al*. 2000; Barandalla *et al*. 2006; Ispizúa *et al*. 2007).

AFLP markers were developed by Vos *et al*. (1995). It can generate many random DNA markers in a single PCR amplification and has become a good approach to measure genetic diversity. Milbourne *et al*. (1997) used AFLPs and SSRs to analyze the genetic relationships among 16 commercial potato cultivars, and found that these molecular markers successfully discriminated the 16 cultivars using a single assay. McGregor *et al*. (2002) used AFLP markers to study the wild potato germplasm of the series *Acaulia*. Their results showed that AFLP technique was an efficient method to verify taxonomic classification and identify redundancies in the wild germplasm of the series *Acaulia*. Bamberg and del Rio (2016) analyzed the AFLP markers among cultivars from three potato species in the US potato GenBank and found the genetic diversity was not proportionally increased with the increase of collection number in GenBank due to the redundant deposits.

To evaluate the genetic diversity and determine the appropriate panel of potato germplasm for use in potato improvement and conservation programs in China, we genotyped a global collection of 288 potato accessions (*Solanum tuberosum* L.) consisting of 140 accessions from International Potato Center (CIP), Peru, 105 from different provinces of China, 27 from other countries, and 16 with unknown resource.

2. Materials and methods

2.1. Plant materials

A total of 288 accessions of potato (*Solanum tuberosum* L.) were collected from eight countries and the International Potato Center (CIP), including 140 accessions from CIP, 105 germplasms in China (Ganshu, 1; Hebei, 7; Qinghai, 12; Sichuan, 4; Yunnan, 3; Fujian, 2; Ningxia, 2; Shaanxi, 1; Heilongjiang, 46; Chinese Academy of Sciences, 6; Northeast of China, 21), 7 from the United Kingdom, 4 from Israel, 3 from the United States of America, 2 from Russian, 2 from Canadian, 1 from the Netherland, 1 from New Zealand, and the sources of 23 potato germplasms were unknown (Appendix A). This global collection was conserved in Qinghai Agricultural Sciences of Academy, Qinghai Province, China.

2.2. DNA Extraction

Genomic DNA was extracted from the leaves of potato test-tube plantlet using the CTAB method (Clarke 2002). DNA quality and quantity were measured using agarose