Genetic diversity and population structure of mongolian wheat based on SSR markers

Narantsetseg Ya¹, Sebastin Raveendar^{2*}, Bayarsukh N¹, Myagmarsuren, Ya¹, Jung-Ro Lee², Kyung-Jun Lee², Myoung-Jae Shin², Yang-Hee Cho², Kyung-Ho Ma², and Gi-An Lee²

 ¹⁾ Institute of Plant and Agriculturel Sciences, P.O.B-908, Darkhan-Uul-45047, Mongolia
²⁾ National Agrobiodiversity Center, National Institute of Agricultural Sciences, RDA, 370 Nonsaengmyeong-Ro, Wansan-Gu, Jeonju-Si, Jeollabuk-Do, 54874, Republic of Korea

Abstract

The production of spring wheat, the major crop in Mongolia, is accounting for 98% of the cultivated area. Collection, conservation and utilization of wheat germplasm resources play an important role in wheat breeding and production in Mongolia. Understanding genetic variability in the existing genebank accessions is important for collection and conservation of wheat germplasms. To determine the genetic diversity and population structure among a representative collection of Mongolian local wheat cultivars and lines, 200 wheat accessions were analyzed with 15 SSR markers distributed throughout the wheat genome. A total of 85 alleles were detected, with 3 to 5 alleles per locus and a mean genetic diversity value of 5.66. The average genetic diversity index was 0.68, with values ranging from 0.37 to 0.80. The 200 Mongolian wheat accessions were divided into two subgroups based on STRUCTURE, un-rooted NJ cluster and principal coordinate analyses. The results from this study will provide important information for future wheat germplasm conservation and improvement programs with Mongolian genebank.

Keywords: Wheat, Genetic diversity, Population structure, SSR marker

Corresponding author* Sebastin Raveendar Address: National Agrobiodiversity Center, NAS, RDA, Jeonju-si, Jeollabuk-do, Republic of Korea Tel: +82 63 239-4863 E-mail address: ravibteri@rediffmail.com