Genetic diversity and Population Structure of F3:6 Nebraska Winter Wheat Genotypes Using Genotyping-By-Sequencing


Abstract:

The availability of information on the genetic diversity and population structure in wheat (Triticum aestivum L.) breeding lines will help wheat breeders to better use their genetic resources and manage genetic variation in their breeding program. The recent advances in sequencing technology provide the opportunity to identify tens or hundreds of thousands of single nucleotide polymorphism (SNPs) in large genome species (e.g., wheat). These SNPs can be utilized for understanding genetic diversity and performing genome wide association studies (GWAS) for complex traits. In this study, the genetic diversity and population structure were investigated in a set of 230 genotypes (F3:6) derived from various crosses as a prerequisite for GWAS and genomic selection. Genotyping-by-sequencing provided 25,566 high-quality SNPs. The polymorphism information content (PIC) across chromosomes ranged from 0.09 to 0.37 with an average of 0.23. The distribution of SNPs markers on the 21 chromosomes ranged from 319 on chromosome 3D to 2,370 on chromosome 3B. The analysis of population structure revealed three subpopulations (G1, G2, and G3). Analysis of molecular variance identified 8% variance among and 92% within subpopulations. Of the three subpopulations, G2 had the highest level of genetic diversity based on three genetic diversity indices: Shannon's information index (I) = 0.494, diversity index (h) = 0.328 and unbiased diversity index (uh) = 0.331, while G3 had lowest level of genetic diversity (I = 0.348, h = 0.226 and uh = 0.236). This high genetic diversity identified among the subpopulations can be used to develop new wheat cultivars.

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