

Genotyping-by-Sequencing (GBS) Revealed Genetic Diversity of crested wheatgrass (*Agropyron cristatum* (L.) Gaert.)

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With the advent of next generation sequencing technology genotyping-by-sequencing has emerged as a potential tool for molecular characterization of non-model plants with complex and no prior sequence information. Maiden effort with GBS technology was used to sample genome-wide genetic variants of crested wheatgrass [*Agropyron cristatum* (L.) Gaertn.] plants and to assess the genetic diversity present in 192 samples from 12 accessions. Bioinformatic analysis identified 45507 SNP markers for this outcrossing tetraploid grass species. The Bayesian analysis identified four major clusters in the studied samples. The diversity analysis revealed 15.8% of SNP variation residing among 12 crested wheatgrass accessions and 12.1% SNP variation present between four genetic clusters of the samples. These results serve as valuable resource for understanding genetic variability and genetic improvement of this introduced outcrossing polyploid grass species for forage production and land reclamation, and also illustrates the application of GBS in the characterization of non-model polyploidy plants with complex genomes.