

Assessment of the genetic diversity of barley landraces maintained in the Vavilov Institute of Plant Genetic Resources (VIR) in the world scale

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The Vavilov Institute of Plant Genetic Resources (VIR) maintains a large barley (*Hordeum vulgare* L.) germplasm collection comprising more than 20,000 accessions from 24 different species. For the accessions “passport” data describing geographical origin, taxonomic status and some phenotypic characters are available. No attempt has yet been made to assess the genetic diversity of the collection with the large number of environmentally neutral, easily scorable molecular markers such as single nucleotide polymorphism (SNP). With the modern technology of Genotyping-by-Sequencing (GBS) available there is a good opportunity to evaluate the genetic diversity of the VIR barley collection for use in crop improvement programs. In the frame of the collaboration between VIR and Leibniz Institute of Plant Genetics and Crop Plant Research (IPK) 501 barley landraces and local cultivars from the VIR collection were assessed using high throughput GBS technique. The 501 barley accessions originated from 46 countries and were randomly selected for the analysis based on their diverse phenotypic traits. Two individuals from each accessions were genotyped. Reference based variant discovery pipeline identified 76,501 SNPs out of which 23,733 SNPs with ≤ 10 % missing data were selected for downstream study. The yielded SNP data were compared with those of the ‘Bridge’ project combining genotyping data of 22,626 barley DNA samples from the National Crop Genebank of China (NCGC), the Institute of Crop Sciences of the Swiss National Genebank of Agroscope and the IPK barley germplasm collection. The results of GBS approach performed allowed to compare the genetic diversity of the barley landraces maintained at VIR with the barley germplasm diversity preserved at world gene banks.