Global diversity in barley landraces

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Introduction

Barley is one of the principal cereal crops in the world cultivated in all temperature areas (Hayes et al., 2003) ranking fourth in world crop production. It’s used for animal feed, brewing malt, and human consumption (Hayes et al., 2002). Considered as a model species for genetic analyses thanks to its widely available genetic information (Hayes et al., 2003), an extensive amount of data was increasingly produced from genetic diversity surveys at microsatellite marker loci in wild and cultivated barleys at national, regional and worldwide levels during the past ten years (Greulich et al. 2007, Malykhova-Otte et al. 2006).

Aim

Investigating the genetic diversity and geographical differentiation of a worldwide barley germplasm of three hundred and five samples from four barley subspecies using twenty microsatellites markers covering the three barley SSR linkage groups.

Abstract

Twenty genic- and genomic SSR markers were used to study genetic diversity and geographical differentiation of barley landraces from 29 countries through analysis of 304 worldwide cultivated barley cultivars. Out of them, 38 landraces were highly polymorphic in the material studied. Based on Nei-distance matrix, Principal Component Analysis (PCA) and cluster analysis using UPGMA associated with AMOVA data revealed countries’ grouping within regions. This data germplasm pools were identified in the landraces. The most of landraces were from Eastern Africa (Ethiopia and Ethiopia) and South America (Ecuador, Peru and Chile) suggesting that barley introduction to South America might have originated from East Africa or that they share a common genetic basis for adaptation. The second was the Caspian (Kazakhstan and Georgia) and the third included the remaining regions of Central Asia, Near East, Northern Africa and Eastern Asia. Genetic diversity of barley subspecies (Hordeum vulgare, Hordeum distichon, H. spontaneum and H. murinum) also discriminated them into three groups: cultivated barley (vulgare and distichon), subspedes H. spontaneum and subspecies H. murinum. Those data demonstrate that H. vulgare and H. spontaneum might be distinct and do not support a hybrid origin for H. vulgare to be further investigated on the basis of more intense sampling of the wild relative H. spontaneum and H. murinum.

Materials & Methods

Obtained from ICARDA’s gene bank, out of the 304 barley samples investigated, 95% of them were landraces of 4 barley subspecies originating from 29 countries in 7 different geographical regions throughout the world (Fig.1). Material from Europe was not included due to its low diversity (Malykhova-Otte et al. 2006). At the Centre of Plant Conservation Genetics Australia (CPCG), DNA samples were extracted using a Qiagen MagAttract 96 Kit on the Tiangen TiMax robotic platform and sequenced on the Illumina HiSeq 2000/2500 platform. Depicted in Figures, twenty labeled SSR markers (out of them 3 genic markers: HVMCA, HVMCFP, HBMAYQ) were used, multiplexed into 3 subsets and run in the capillary electrophoresis (ABI 3730x1). Six PCR conditions were employed using Tsal and GeneMphi (PCR) primers for thermal cycling. Data from the capillary electrophoresis were captured using GeneMapper® 3.7, checked by MicroChecker, converted with Genemapper® and analyzed using PowerMarker. Allele frequency, Nei’s gene diversity, polymorphism information content (PIC) and relatedness were calculated using UPGMA on Nei-1972 distance matrix, Principal Coordinate Analysis (PCoA) and Analyses of Molecular Variance (AMOVA) were calculated.

Results & Discussion

A total of 435 alleles were detected at the 305 SSR with an average of 20.2 alleles per locus in the entire sample. The number of alleles varied from 27 at the 26 (316 loci) to 3 at the 151. Relatively, in the group of genic SSR markers, only HVMCA had a low number of alleles while HVMCFP and HBMAYQ with 22 and 24 alleles respectively revealed high polymorphism (Figures). Private alleles were observed from 0 (Bam399) to 10 (Bam123). As shown in Figure 2 and Table 3 respectively, PIC values were ranging from 39% (HVMCA3, HBMAYQ) to 87% (GMS 2, 16) with an average of 78% while NAF were highly polymorphic (80%) with the lowest PIC value in SAMS (28%). The partitioning of the genotype variances between regions, between countries within regions, among genotypes within countries and between all genotypes was assessed by AMOVA revealing that 30.6% of the genetic variance was between all genotypes, while 26.4% was among genotypes within countries illustrating distinct barley landraces. Small variance was observed both between countries (3.5%) and within regions (3.5%) revealing high material exchanges between them (Table 1). Principal Component Analysis (PCoA) (Figures) explaining 95.9% of the variance and Cluster analysis (UPGMA) for regions (Figure 1) revealed three distinct groups A, B and C (A: SAMS and EAF; B: CAS, NE, NAF and EAS; C: CASU), bootstrapping analysis (100 repetitions) displayed a percentage of replicates supporting the groups (NE and EAF) of about 50%. NAF material showed similarity to EAS material, and these two regions are areas for food barley production. This observation could be the effect of years of natural and human selection for food barley landraces and material exchanges. Similarly, the PCoA (86.7% of the variance) (Figures) and Cluster analysis (UPGMA) depicted in Figures1 discriminate between countries. All Near East countries (SYR, JOR, TUR, QUN, IRQ, PAL, YEM, and UMN) grouped together as well as the Caspian countries (ARM and GECI). From Central Asia, KAZ, KHY and TJK as the first subgroup and AFG and TJK as a second subgroup were clearly distinct. Countries from Eastern Africa (ETH and EBS) were more closely with countries from Southern America (ECU, PER and CHL) barley subspecies were subject to discrimination through PCoA (Figures) and cluster analysis (Figures 1). Three groups were distinct: cultivated barley consisting of six-rowed barley and two-rowed barley, the subspecies H. spontaneum and the subspecies H. murinum. Hence, there was a clear distinction between the landraces of H. spontaneum and the landraces of H. murinum to confirm this distinction and possible independent domestication.