



**TÜRKTOB**  
TÜRKİYE TOHUMCULAR BİRLİĞİ

**TAGEM**  
AR-GE & İNOVASYON



# IV.

## **INTERNATIONAL PLANT BREEDING CONGRESS**

*Plant Breeding for the Future: From Local to Global*  
21-25 November 2022 | Porto Bello Hotel, Antalya, Türkiye

### **CONGRESS BOOK**

[www.intpbc2022.org](http://www.intpbc2022.org)



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23 November, Wednesday		Hall B
14:00-16:00	<b>Resistance to Biotic and Abiotic Stresses II</b> <b>Chair: Gönül Cömertpay</b>	
14:00-14:30	<b>Keynote Speaker</b> Breeding Challenges for Wheat, the Cornerstone for Global Food Security	<i>Hans Braun</i>
14:30-14:45	<b>OP-48</b> Evaluation of Wheat ( <i>T. aestivum</i> L.) Germplasm Under Temperate Conditions and Identification of Sources of Yellow Rust Resistance Genes ( <i>yr</i> ) Using Molecular Markers	<i>Shabir Hussain Wani</i>
14:45-15:00	<b>OP-49</b> Screening of Some Durum Wheat Genotypes to (Warrior) Race of Yellow Rust	<i>Merve Nur Ertaş Öz</i>
15:00-15:15	<b>OP-50</b> Comparison of Yield Potentials of Some Triticale Lines and Cultivars Under Different Climatic Conditions	<i>Emel Özer</i>
15:15-15:30	<b>OP-51</b> Determination of the Reactions of Some Advanced Yield Trials-Durum Wheat Genotypes to Rust	<i>Nilüfer Akcı</i>
15:30-15:45	<b>OP-52</b> Identification of SNP Markers for Grain Quality Traits in A Barley Collection ( <i>Hordeum Vulgare</i> L.) Harvested in Kazakhstan	<i>Yuliya Genievskaya</i>
15:45-16:00	Discussion	
16:00-16:30	<b>Coffee Break</b>	
16:30-17:45	<b>New Breeding Methods for Future Challenges II</b> <b>Chair: Nedim Mutlu</b>	
16:30-16:45	<b>OP-53</b> Effects on the Wheat ( <i>Triticum Aestivum</i> L.) Genome From Five Rapid Genomic Selection (GS) Cycles	<i>Lenin Rodriguez</i>
16:45-17:00	<b>OP-54</b> Colored Wheat: A Source of Nutrition	<i>Om Parkash Bishnoi</i>
17:00-17:15	<b>OP-55</b> Two Different Vernalization Methods Applied in Winter/Facultative Wheat and Their Effects on the Speed Breeding Process	<i>Emrah Koç</i>
17:15-17:30	<b>OP-56</b> Genotyping by Sequencing Based SNP Analysis for Discriminating the Heterotic Patterns of Maize Germplasm From Public and Private Sector of Türkiye	<i>Gönül Cömertpay</i>
17:30-17:45	Discussion	
17:45-19:00	Poster Session - 2	Foyer Area



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### [OP-52]

#### Identification of SNP Markers for Grain Quality Traits in a Barley Collection (*Hordeum vulgare* L.) Harvested in Kazakhstan

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Barley (*Hordeum vulgare* L.) is a cereal crop grown all over the world and used for animal feed, malting, brewing, and food production. In Kazakhstan, barley is the second most cultivated cereal grain, after wheat. Barley grain quality traits are highly variable and the requirements for their level depend on the breeding directions. For example, the raw protein content in malting barley grain should be less than 11.5 %, while in the grain for animal feed this component should exceed 13.0 %. In order to assess grain quality and identify genetic markers associated with them, a collection of barley consisting of 658 barley accessions from the USA and Kazakhstan was analyzed using key quality traits: raw protein content (GPC) and raw starch content (GSC) in the grain, total extractivity (EX), and grain test weight per liter (TWL). These complex traits are quantitative and controlled by many genetic factors, as well as by environmental conditions. In this study, we applied a genome-wide association study (GWAS) that was used for the identification of quantitative trait loci (QTLs) associated with GPC, GSC, EX, and TWL. This collection was grown at three breeding organizations in Kazakhstan (Karabalyk Agricultural Experimental Station (north), Karaganda Agricultural Experimental Station (center), and Kazakh Research Institute of Rice Growing (south)) in 2010 and 2011 and genotyped using the 9K SNP Illumina chip. As a result, 18 marker-trait associations (MTAs) for GPC, 19 MTAs for GSC, 12 MTAs for EX, and 27 MTAs for TWL were detected, resulting in 30 identified QTLs. The genetic positions of 25 out of these 30 QTLs were close to the QTLs and genes previously reported in the scientific literature, suggesting that the 5 remaining QTLs are novel putative loci for studied grain quality traits. Five of the most significant SNP markers ( $P < 2.6E-5$ ) identified in the GWAS were used for the development of informative kompetitive allele-specific PCR (KASP) genotyping assays. The effectiveness of two assays (*ipbb\_hv\_6* and *ipbb\_hv\_128*) was confirmed in a separate barley breeding lines collection

grown in northern Kazakhstan. The genotype "A:A" of *ipbb\_hv\_6* provided an average 1.88% increase in GSC ( $P < 1.2E-05$ ), a 1.02% increase in EX ( $P < 2.9E-04$ ), and a 1.87% decrease in GPC ( $P < 3.5E-04$ ). The genotype "T:T" of *ipbb\_hv\_128* increased the GSC and decreased the GPC values by 1.26 % ( $P < 0.05$ ) and 0.89 % ( $P < 0.01$ ), respectively. Thus, MTAs and KASP assays identified in this study can be efficiently used in breeding barley for malting, food production, and animal feed. The study was supported by grants AP08052804 (2020-2022) and AP14871383 (2022-2024) from the Ministry of Education and Science of the Republic of Kazakhstan.

**Keywords:** GWAS, KASP, grain quality, marker-assisted selection

### [OP-53]

#### Effects on the Wheat (*Triticum aestivum* L.) Genome from Five Rapid Genomic Selection (GS) Cycles

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The Ohio State University, Department of Horticulture and Crop Science, Wooster, OH, USA

Genomic selection (GS) is a molecular breeding tool that models and predicts the genomic estimated breeding value (GEBV) of an individual. The predicted GEBV is then used to select parents for the subsequent breeding cycle. Wheat breeders can use GS to reduce the duration of the breeding cycle to 1 year, as opposed to 7 years when using the traditional phenotypic selection method. The shortening of the cycle is known as "rapid cycling". The wheat genome changes resulting from rapid cycling have not been characterized. The OSU (Ohio State University) soft red winter wheat breeding program has completed five cycles of GS in five years. The OSU program initiated GS from a training population (TP) of 470 wheat varieties that were phenotyped for grain yield. Our objective was to assess the effect of this molecular breeding selection method on the wheat genome, using marker information in the TP as the initial and reference genome (We define genome as the collection of markers used for selection). We genotyped the TP and individuals from the five cycles with 3927 single nucleotide polymorphism markers to assess the dynamics of allele frequencies, genetic diversity (simple matching coefficient, SMC), population structure (Fst), and linkage disequilibrium (LD). We quantified a reduction in genetic diversity, an increase