9th International Wheat Conference

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Program and Abstracts

The Wheat Initiative (WI) was created to provide a framework to establish strategic research and organization priorities for wheat research at the international level in both developed and developing countries. Under WI, Expert Working Groups (EWG) for diverse wheat topics are established where there would be benefit from bringing together experts with a focus on topics of relevance to the WI's objectives. This year, an EWG on improving wheat quality and safety was developed and approved by the WI Research Committee. This EWG is aimed at maintaining and improving wheat quality and safety under varying environmental conditions. Our expert group will focus on wheat quality and safety in the broad sense including seed proteins, allergens, carbohydrates, nutrition, processing and food safety. We will also work to share genetic resources and unify gene nomenclature to support these topics. The international research group as an EWG under the WI aims to play a vital role in the advancement of this field and in applying scientific knowledge to the development of improved varieties. The EWG will include some of the best experts available worldwide in the different aspects of wheat quality under study. The following outputs are expected to be delivered: 1. High yield potential and sustainable quality while withstanding climate change effects; 2. High milling efficiency in producing functional and safe products; 3. Meeting demands of food industries and consumers; 4. Improved lines for human health and special health-related and safety requirements; 5. Unified nomenclature of alleles related to wheat quality; 6. Unified methods to analyze substances related to wheat quality; 7. Selecting and sharing standard sets representing quality related alleles. For this last activity, the literature will be reviewed to reevaluate and update the Catalogue of Gene Symbols for Wheat, thereby collating all known diversity for the topics described above.

PO60

Modeling relations on wheat quality using self-organized maps and advanced biometric methods

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Wheat quality is mainly determined by genetic (genotypic) composition but significantly influenced by environment and their interactions. The large diversity and complexity of factors defining wheat quality makes it difficult to understand the interaction between them and to predict functional quality parameters during the wheat breeding process. To tackle this problem, we used the classification capacities of the Self-Organized Maps (SOM), a kind of Artificial Neural Network (ANN) to obtain an insight into the topographic relationships of quality-related data.

Quality tests were applied to 117 recombinant inbred lines (RIL's) generated from various crosses with the 'Avocet" variety used as common maternal parent with other six wheat varieties showing contrasting quality. Each line was analyzed by SDS-PAGE to determine high (HMW-G) and low (LMW-G) molecular weight glutenin subunit composition. Grain samples of the RIL's were analyzed for grain hardness, protein content, SDS-Sedimentation, dough development time in the Mixograph, and dough strength (W) and tenacity/extensibility (P/L) in the Alveograph.

Genomic profiles (based on HMW-G and LMW-G) were coded in a binary format, building one SOM, and "train" according to genomic profile, to obtain information on the influence of these variables on wheat quality determination.

Neural model, SOM, classified automatically the 117 lines in 5 different clusters. Each of this clusters showed contrasting quality features. The quality-related clustering was validated by comparison against wheat end- use quality parameters, resulting consistent with wheat quality evaluation obtained by advanced statistical methods.

The results suggest that SOM, in combination with a careful standardization and structuration, shows potential as a new wheat quality selection tool in breeding programs, and warrants the examination of testing perceptron networks, another kind of ANN, for prediction in wheat quality.

PO61

Progress in breeding and stability of winter wheat grain quality in Serbia in the last 60 years

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Wheat grain quality has in the focus of wheat breeders worldwide, besides breeding for yield, aiming at production of the best possible input for the processing industry.

Twenty-five winter wheat varieties were studied to assess the progress of breeding for wheat quality in the last 60 years. The study included varieties released in different years representing all the various periods in Serbian wheat breeding. Only varieties that played a major role in Serbian wheat production were selected for this four-year trial (2010-2013) carried out at the Rimski Sancevi site near the city of Novi Sad, Serbia.

Two quality parameters were analysed: protein content

– PC (%) and sedimentation value – SV (ml). Changes of wheat quality indicators and their stability, occurring in the varieties from the different breeding periods, were analysed by linear regression. The most stable genotype in the analysed period was determined by multivariate analysis and ranking 10 different stability parameters.

The highest PC average for the four-year study period was found in the varieties Bankut 1205 and Banatka (15.7%) and the lowest in Sava and Simonida (12.4%). There have been no significant changes in protein content for 60 years, and it decreased by only 0.02% per year; simultaneously the stability of this parameter was kept at the same level. SV significantly increased by 0.17 ml per year, and the stability of this parameter also significantly increased. Depending on the analysed trait, the genotypes differed in expressed stability. According to the analysed parameters, variety Jugoslavija was the most stable for PC, and variety Dragana for SV. The most stable variety for both traits was NS 40S (from the last breeding cycle).

The previous 60 years of intensive breeding process resulted in a gradual increase of wheat quality parameters and their stability, which significantly influenced improvement of wheat production in Serbia.

PO62

Heritability of bread-making quality traits in segregating generations of two winter wheat crosses

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Modern wheat breeding programs aim to create cultivars with high genetic potential for yield and high bread-making quality. The effectiveness of selection in segregating generations depends on the heritability of the traits under selection and on the correlations among traits. The aim of this study was to assess phenotypic correlations between grain yield and indirect bread-making quality traits (protein content, wet gluten content, gluten index, Zeleny sedimentation value and Hagberg falling number) in segregating generations (F4 to F6) of two biparental crosses and to estimate realized heritability for these traits between successive generations. Fifty progenies per cross (Golubica x Emesse and Verbunkos x Soissons) were grown in each of the three segregation generations and realized heritability was calculated as parent-offspring regression using standardized values. Results showed that the cross Golubica x Emesse has greater potential for simultaneous selection for yield and quality due to less negative correlations between them as well as due to higher average values of bread making quality traits and stronger positive correlations among them. Realized

heritability between successive generations was not significant for grain yield, whereas for all indirect bread-making quality traits it was significant with values ranging from 0.25 do 0.56. In both crosses, realized heritability for wet gluten content and gluten index were considerably higher in comparison with other traits, suggesting that the two traits should be preferred as selection criteria for improving bread-making quality.

Key words: winter wheat, yield, quality, heritability

PO63

Deciphering the regulatory logic of wheat *Glu-1* genes

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Promoter regions of HMW-GS genes are highly conserved, yet their motif compositions, polymorphisms and motif occurrences are specific to genes rather than to alleles. Promoter analysis of wheat HMW-GS genes and their different alleles are correlated to their respective expression data. Expressions of transcription factors involved in the regulation of *Glu-1* genes were computationally analyzed. Differences in the promoter regions were reflecting the differences in expression dynamics. The most distinct promoters belong to *Glu-1Bx* genes that are always highly expressed and miss a few binding sites present in all other HMW-GS genes. Interesting finding that HMW-GS promoters can be divided into 1-200 bp long *cis* regulatory modules (CRMs) that may hold the key to the underlying regulatory logic of *Glu-1* genes. In order to inspect which of these modules are responsible for tissue specificity, this modular promoter architecture was functionally characterized by a biolistic transient expression system. The experiments were carried out on leaves and endosperm tissue of two species, bread wheat (*Triticum aestivum* cv. Chinese Spring) and *Brachypodium distachyon*. Bombardment with a construct containing a constitutive promoter-driven *uidA* reporter gene resulted in numerous blue spots after histochemical staining. The wild type promoter of *Glu-1Bx* promoter showed signs of leakage. This indicates an epigenetically active but otherwise suppressed transcription. Results of various promoter mutants suggest that tissue specificity is maintained via inhibition. While some part of the promoter would drive transcription in all tissues, a complex in the CRM1 region inhibits it. Interesting, this putative complex also plays a role in transcription in the target tissues