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## Functional Genomic and Breeding

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### CYTOKININ DEHYDROGENASE ACTIVITY AND WHEAT YIELD

*Maja Boczkowska*<sup>1,@</sup>, *Izabela Rajchel*<sup>1</sup>, *Agnieszka Onyśk*<sup>1</sup>, *Wacław Orczyk*<sup>2</sup>,  
*Barbara Zmijewska*<sup>3</sup>, *Anna Nadolska Orczyk*<sup>1</sup>

<sup>1</sup> Department of Functional Genomics, Plant Breeding and Acclimatization Institute – National Research Institute, 05-870 Radzików, Poland

<sup>2</sup> Department of Genetic Engineering, Plant Breeding and Acclimatization Institute – National Research Institute, 05-870 Radzików, Poland

<sup>3</sup> Plant Breeding Strzelce Ltd., Co. – IHAR-PIB Group, 99-307 Strzelce, ul. Główna 20, Poland

@ e-mail: m.boczkowska@ihar.edu.pl

CKX (cytokinin dehydrogenase) enzymes control local concentrations of cytokinins, thereby affecting the processes regulated by these phytohormones. They catalyse reaction of irreversible degradation of cytokinins by isopentenyl side chain cleavage. CKX are encoded by multigene families, in wheat and barley ten genes have been identified.

The main objective of this study was to verify correlation between *TaCKX* expression level, CKX enzyme activity and yield components in selected wheat genotypes.

The hypothesis of this work: “decreased *CKX* genes expression, lowered CKX enzyme activity correlates with increased plant productivity” was verified in our previous study on barley.

Ten breeding stocks and two modern wheat cultivars were tested. The genotypes were selected based on the differences in yielding. In this study we profiled the expression patterns of all known *TaCKX* genes in seedlings’ roots, young leaves, immature inflorescences and developing spikes collected 0, 7 and 14 days after pollination (DAP). CKX activity was measured in seedlings’ roots and 7 DAP spikes. Another set of plants of selected lines, grown to maturity in containers, were characterized for their aboveground height and weight, grain yield, thousand kernels weight, number of kernels per container and the number of fertile tillers.

The direct comparison of cumulative expression of nine *TaCKX* genes in developing spikes with yield components supported the assumed hypothesis (i.e. lower *TaCKX* expression = higher yield and thousand kernels weight) in the majority of the tested lines. The expression level of all *TaCKX* genes was also consistent with CKX activity in 7DAP spikes. Based on qPCR results of all tested *TaCKX* genes the expression of *TaCKX1* was the highest indicating that it is the key gene involved in cytokinin degradation in developing wheat spikes. Its expression was negatively correlated with yield, thousand kernels weight and number of kernels per container.

The cumulative expression of nine *TaCKX* genes in roots was inversely proportional to the aboveground weight as well as the yield and thousand kernels weight. In roots an equal expression of all genes was observed (except not expressed *TaCKX2*).

In case of leaves positive correlations were found between *TaCKX* genes expression and plant height, weight of aboveground part and the number of fertile tillers. The expression of *TaCKX10* was the highest among all tested genes in all examined tissues indicating that it is the major gene involved in cytokinin degradation in leaves.

Based on these results it can be presumed that the activity of CKX or expression of *TaCKX1* in 7DAP spike may be helpful in selecting high yielding materials.

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## Quality and Utilization

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### QUALITY PARAMETERS OF TRITICALE VARIETIES IN LONG-TERM FERTILIZATION TRIALS

*Erika Ács*<sup>1</sup>, *István M. Petróczi*<sup>1</sup>, *Zsuzsa Kovács*<sup>1</sup>, *Bernadett Langó*<sup>1</sup>, *Antal Véha*<sup>2</sup>,  
*Katalin Ács*<sup>3</sup>, *Lajos Bona*<sup>1</sup>

<sup>1</sup> Cereal Research Non-Profit Ltd., Szeged, Hungary

<sup>2</sup> University of Szeged, Szeged, Hungary

<sup>3</sup> Diabet Trade Ltd., Szeged, Hungary

Hexaploid triticales (*X Triticosecale* spp.) are man-made cereal species from crossing of wheats (*Triticum* spp.) and rye (*Secale cereale*). Acreage of this species has been spectacular as it is grown on more than 4 million ha across the world to date, with 120–140 thousand ha in Hungary. Generally, its quality traits are in-between wheat and rye, even exceeds the ancestors in some characteristics. Triticale pronounces a specific combination of protein- and pentosan-components sourcing from parental species. Pentosans (mainly arabinoxylans) improve the water absorption capacity and the nutritional quality, and extend the shelf-life of the bakery products. Less favorable protein characteristics compared to wheat (special composition of rye- and wheat-origin high molecular weight glutenins, weak gluten, high viscosity and high alpha amylase activity) in triticales may deteriorate the rheological traits limiting its use in the milling and baking industry. For that reason, the use of triticales for bakery industry is suggested in blends wheat flour above all. The quality of the flour blends is influenced not only by the applied ratio but also by the quality of the flours to be mixed. This work focused on the assessment of the qualitative and rheological potential of the triticales varieties as influenced by fertilizer rates in a long term trial.

Grain samples of two triticales varieties were analyzed in this study for milling and baking characteristics. Cultivars *GK Rege* and *GK Szemes* were grown on calciferous meadow soil in Fülöpszállás, Hungary, in a long-term fertilizer trial in 2013 and 2014. The microanalysis of whole and crushed grains were done by PERTEN SKCS 4100 and MININFRA – 5 NIR instruments: the grain hardness, 1000 kernel weight, protein content were measured. White flour was produced by Brabender Senior mill and whole-meal samples were ground by Fluormill A500MSM stone mill. Falling number, Zeleny sedimentation, farinographic (water absorption, quality number) and extensographic properties (stability =  $R_{\max}$  and extensibility = Ext.) were calculated by the standard methods. Sixteen nitrogen (N), phosphorus (P) and potassium (K) fertilizer level were applied in various, elevating combinations.