

Looking for *TaCKX* genes associated with grain yield

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Main question (1): There are at least 10 *TaCKX* genes belonging to the family (Tab. 1). Which ones are responsible for plant productivity?

Our hypothesis: High level of expression of selected *TaCKX* genes in reproductive/generative organs and/or roots might indicate their important role in plant productivity.

Introduction

The *CKX* genes belong to a family that is represented in various plant species. The genes encode cytokinin dehydrogenase enzyme (CKX), which irreversibly degrades cytokinins. Both expression of the genes as well as cytokinin distribution are spatially and temporally regulated during plant development. We documented that RNAi silencing of the selected, barley *HvCKX* genes influenced grain yield [1, 2]. Moreover, expression patterns of these genes might indicate their role in growth and reproductive development [3]. The aim of this research was to prove correlation between the level of expression of some of *TaCKX* genes in selected organs/tissues of breeding lines of wheat and grain yield.

Materials and methods

Experimental material was collected from two mapping populations [4, 5] and two Polish Plant Breeding Seed Companies (PB Strzelce Ltd., PB Danko). The breeding lines were closely related, however differed in their yield. Total RNA was isolated from seedling roots, leaves, inflorescences and kernels: 0 DAP (days after pollination), 7 DAP and 14 DAP. Isolated RNA was transcribed into cDNA and used for quantitative RT-PCR with PCR starters designed for ten known *TaCKX* genes. The CKX enzyme activity was measured in the same plant material.

Tab. 1 The *TaCKX* gene family.

Gene name	Accession No.	Sequence (bp)	CDS
TaCKX	AY831399	260	DNA partial
TaCKX	DQ902563	1598	DNA partial
TaCKX	DQ784574	1634	DNA partial
TaCKX1	DQ784573	2367	DNA complete
TaCKX1	AF362471	413	mRNA partial
TaCKX1	JN128583	1572	mRNA partial
TaCKX1	FJ707293	1356	DNA partial
TaCKX2	HM195292	3906	DNA complete
TaCKX2	HM195293	5000	DNA complete
TaCKX2	HM195294	5159	DNA complete
TaCKX2	JN128584	1854	mRNA complete
TaCKX2.1	FJ648070	1909	mRNA complete
TaCKX2.2	GU084177	1813	mRNA complete
TaCKX2.3	JF293079	1876	mRNA partial
TaCKX2.3	JF292901	161338	DNA complete
TaCKX2.4	JN381555	156678	DNA complete
TaCKX2.5	JN381556	127969	DNA complete
TaCKX3	GQ25404	2555	DNA complete
TaCKX3	JN128585	2035	mRNA partial
TaCKX4	JN128586	989	mRNA partial
TaCKX6-D1b	JQ797673	3748	DNA complete
TaCKX6	JN128587	1838	mRNA partial
TaCKX7	JN128588	1601	mRNA partial
TaCKX8	JN128589	1602	mRNA partial
TaCKX9	JN128590	788	mRNA partial
TaCKX10	JN128591	541	mRNA partial
TaCKX11	JN128592	735	mRNA partial

Results

Looking for the candidate genes (1).

Expression profiles of *TaCKX* genes in different tissues/organs of developing plants (Figs. 1–2).

Fig. 1. Expression profiles of *TaCKX* genes in different tissues/organs of cv. Kontesa (three biological samples).

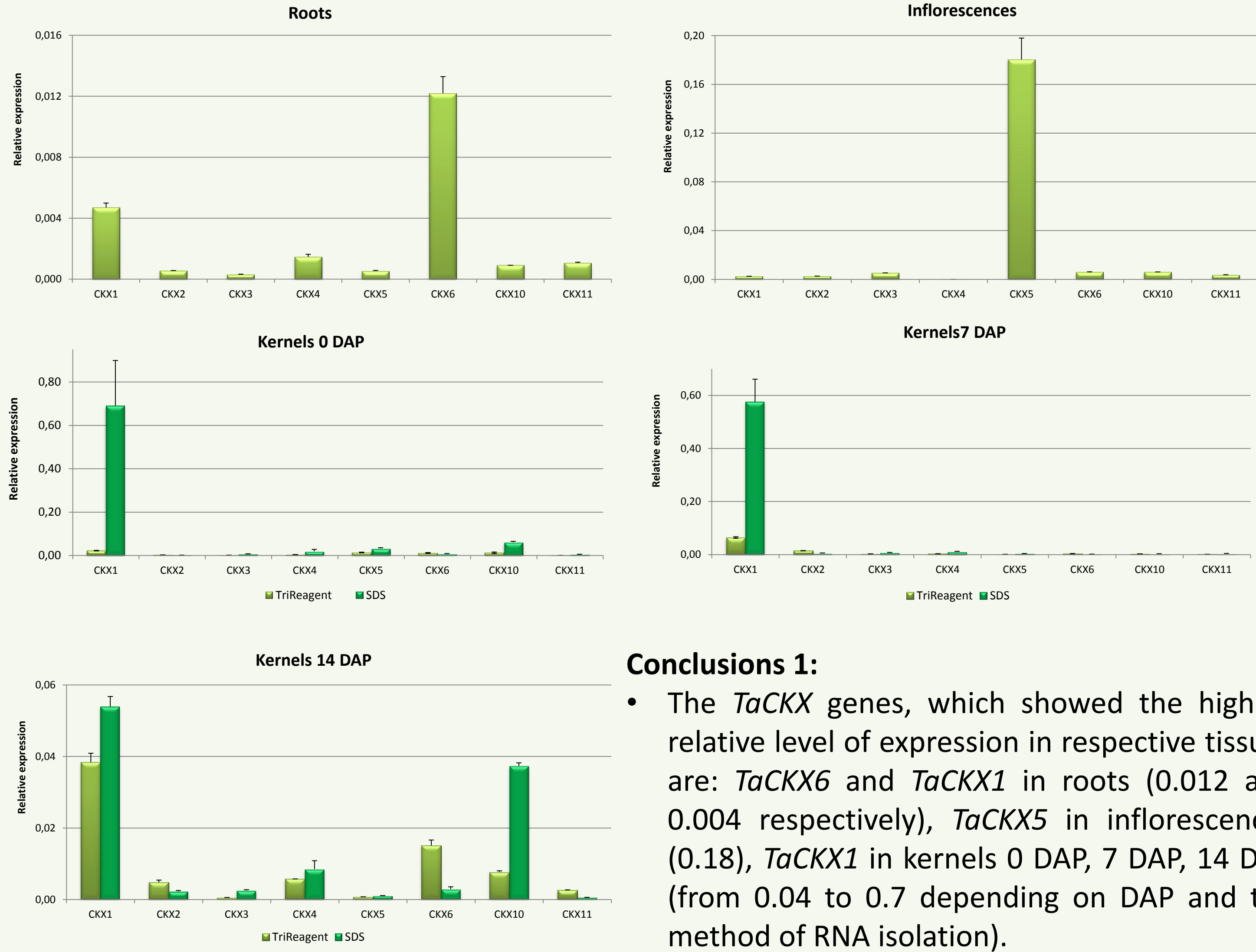
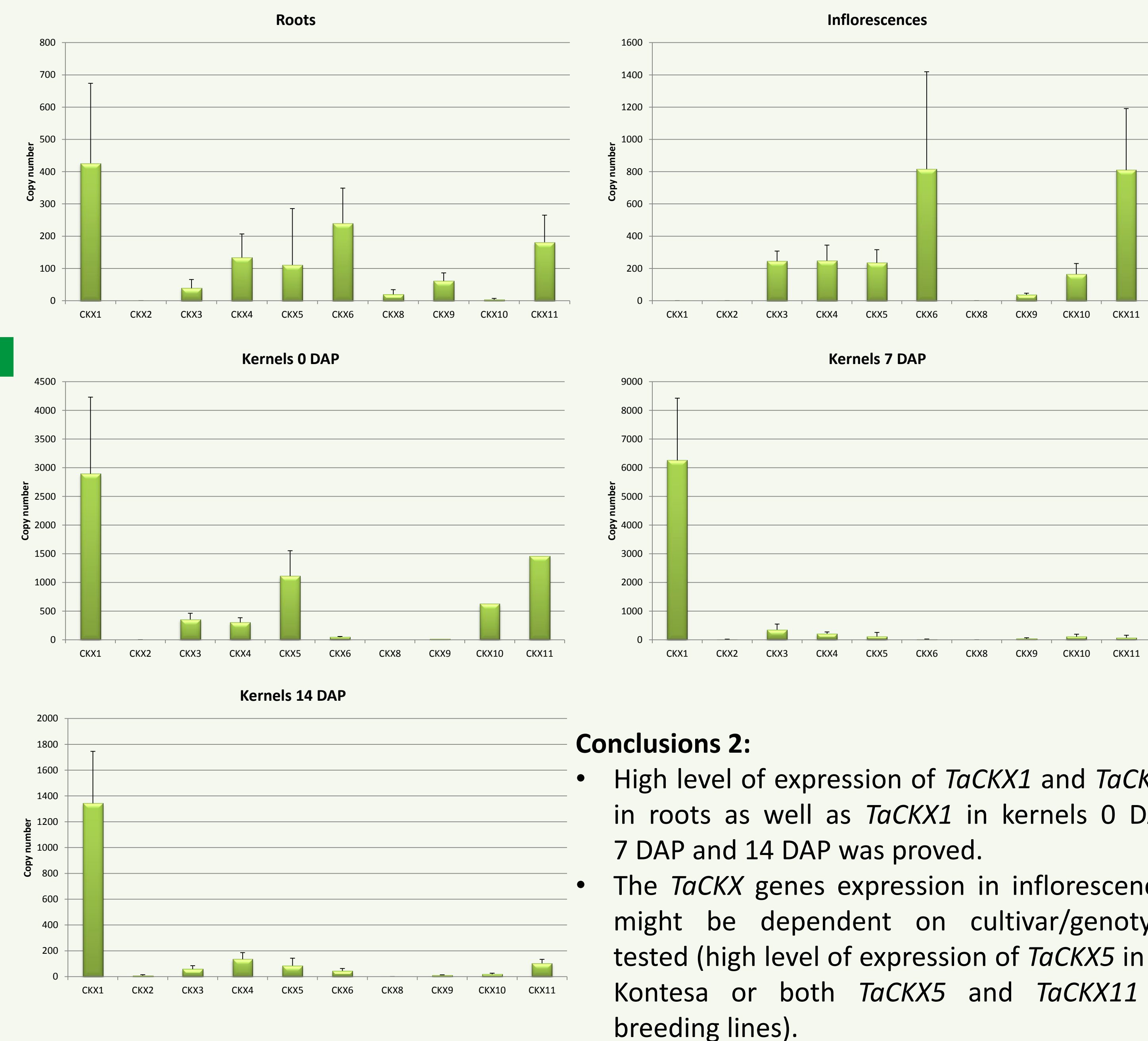


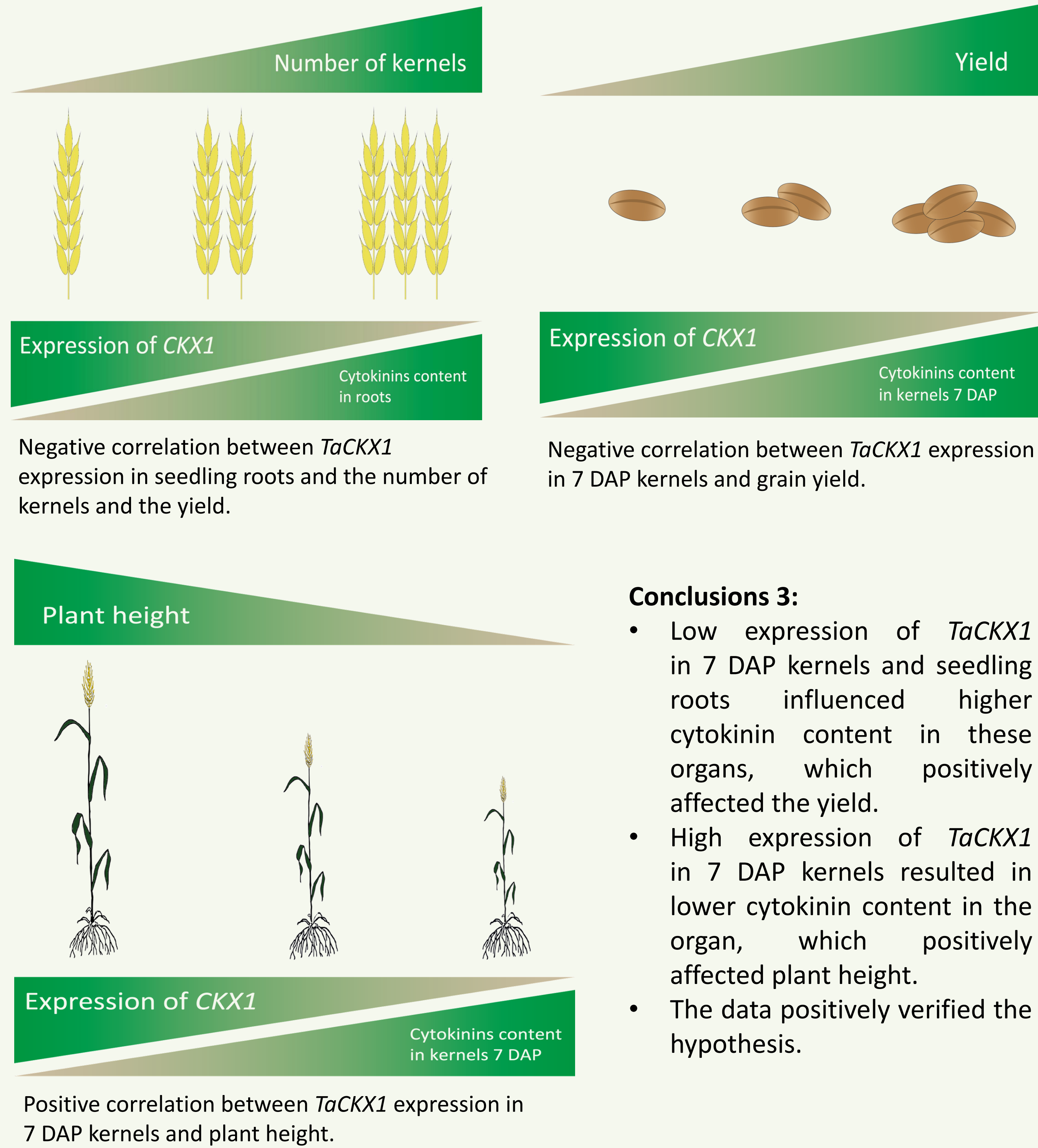
Fig. 2. The mean levels of expression of *TaCKX* genes with standard deviations (SD) in closely related breeding lines of PB Strzelce differing in their yield.



- High level of variability (SD) in expression of selected genes between highly and lowly productive breeding lines proved the possible correlation of expression of selected *TaCKX* genes with productivity.

Looking for the candidate genes (2) – correlation between expression and productivity.

Fig. 3. Correlation between *TaCKX1* expression and yield-related traits (for four populations). The correlation coefficients for the highly expressed *TaCKX1* showed:



Following questions to be resolved:

Question 2: Which allele/haplotype or change in nucleotide sequence of the gene correlates with yield?

Question 3: *TaCKX* genes are present in three diploid genomes of wheat (AABBDD) — alleles of which genome are expressed?

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