LOB-domain (LATERAL ORGAN BOUNDARIES DOMAIN) genes are among typical genes expressed prominently by these boundary-forming cells. They encode a family of plant specific transcription factors characterized by the 100 amino acid long conserved LOB-domain structure being responsible for DNA-binding and protein-protein interactions (Matsumura et al. 2009). Although their exact function is mostly unknown, observations up to now suggest that LOB-domain proteins are involved in almost all aspects of plant development from germination to seed production (Majer and Hochholdinger 2011). Their importance on organogenesis has been studied so far mostly in *Arabidopsis thaliana*, notwithstanding that revealing their role in monocots might be at least so relevant and interesting both for scientific and agronomical considerations, too. Therefore, we aimed to get to know in detail the processes controlled by LOB-domain protein coding genes (LBDs) in *Brachypodium distachyon*, a recently accepted and widely used model plant for cereals with high agronomical importance (Draper et al. 2001).

In current *Brachypodium* genome database we identified 28 LOB-domain protein coding genes. The encoded proteins are clustered into two major classes and some minor subclasses can be distinguished on the basis of their amino acid sequence homology. At first we characterized the relative expression levels of *Brachypodium*- LBDs by quantitative-real-time PCR in dozens of plant parts from root tip to shoot apex, both in vegetative and generative organs. According to our uniquely detailed analysis, LBD genes show variety of tissue specific expression: some of them are definitely active in flowers, in developing seeds and different parts of the floret, some of them have high activity in green plant parts while some others can be described as root specific genes, supporting the extremely diverse function of LBD gene family. Moreover, we got several expression patterns which have a good correlation to the transcriptional activity of their homologues from other species (e.g. *Arabidopsis thaliana* or *Oryza sativa*) that strongly suggests evolutionary conserved function of LBDs.

Aside from few exceptions, the closely related genes clustering into same subgroup showed overlapping expression pattern suggesting potential functional redundancy among them. However, one of the most interesting examples for exceptions are the Bd2g3450 and Bd2g53690 genes which have significantly divergent transcript profile from each other despite of their very close phylogenetic relationship (expression of Bd2g34520 is restricted to root tips while activity of Bd2g53690 is especially high in generative organs). For further exploration of possible functions we have selected these two LBD genes, with special regard on their presumable direct connection with the cell cycle regulating machinery.

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Birds of a feather - comparative gene expression analysis of Ada3 - a meta-analytic review with experimental flavors

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In eukaryotes, alterations of the chromatin structure have an important role in silencing and activation of particular genomic regions. The epigenetic processes are involved in changing the genes expression patterns, therefore the cell is capable of responding to different environmental impacts. Posttranslational modifications of histone proteins are crucial in structural changes of the chromatin. One of the most frequent covalent histone modifications is the acetylation of lysine side chains. The GNAT (GCN5-related N- acetyltransferase) complexes (which contain GCN5 protein as a catalytic component) have a common subunit called ADA3 (alteration/deficiency in activation 3). The homologues of this protein can be found all over in eukaryotes, from yeast to humans.

Lots of experimental data bits can be found which show that ADA3 protein is a lot more than a simple adaptor subunit: although it doesn't have any catalytic activity, it may have a sophisticated role in the function of the multiprotein machineries it is involved in. ADA3

protein may have a direct contact with various nuclear receptors (e. g. T3, glucocorticoid receptors, retinoid receptors, ER (estrogen receptor)), with some signaling pathways (by the interaction of IL-1, and beta-catenin), also with other proteins such as p53 and p300. ADA3 protein was even found to be a target of HPV E6 oncoprotein. Presumably, ADA3 protein is a pivotal contributory partner in many gene expression regulatory processes and abnormal function and regulation of ADA3 may cause severe impairments, such as developmental disorders, or oncogenesis. Since our group's main area of interest is to gain insight into the relationship between histone modifications and tumors, ADA3 is a promising object of investigation.

Previously, the promoter sequence of the *Ada3* gene has been identified in *Drosophila melanogaster* (*dAda3*). On the basis of *in silico* analysis, some truncated promoter variants were produced. The functionality of these promoter fragments were comparatively examined in luciferase reporter gene expression assays, applied in S2 *Drosophila* embryonic cell culture. Using this approach, promoter segments were shown to affect the transcription of the reporter gene, both positively and negatively. Within these segments predicted binding sites were identified, which are dedicated to three well-known transcription factors, namely the *Hunchback*, *Hairy* and *Deformed*.

To describe the ontogenetic expression pattern of the *dAda3* in details, the mRNA level of this gene was measured by qPCR in 15 different developmental stages. The results show that the initial (maternal) amount of the Ada3 transcript is fairly decreased by the time of hatching. Both at the beginning and the end of the prepupa stage, definite increasing was observed, which both coincide with "ecdysone peaks" well-known from developmental biology of fruit fly.

Querying various databases, genes with spatiotemporal expression similar to *dAda3* were identified. According to high-throughput ChIP assays, within the upstream regions of these genes there are resembling TF binding patterns. Meta-analysis of public transcriptome datasets from NCBI GEO revealed numerous additional genes with *dAda3*-related expression. All these genes were used as a core of a predictive interaction network. Strikingly, beside physical and genetic relationships, the representation of GO terms clearly emphasize novel potential functions.

Our experimental results and the analysis of related bibliographic data suggest that *dAda3* has important roles in some fundamental mechanisms like cell cycle, gametogenesis, neuronal differentiation, oxidative stress response and ecdysone pathway. Although the exact mechanism of these interactions is not known, these predicted functions are expected to be conserved in a wide range of eukaryotic organisms. Thus, our subsequent research is planned to focus on a specific area of this subtle commitment.

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No evidence that bacterial gene regulation has adapted to mitigate the accumulation of toxic metabolites

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It has often been suggested that removal of toxic small molecules from the cell is necessary to the survival of the organism. In case of toxic intermediate metabolites, prevention of accumulation helps averting cellular damage. One potential strategy to achieve this is the tight regulation of producing and consuming enzymes around the damaging metabolite. In yeast, it has previously been suggested that toxic intermediate metabolites have their enzymatic genes clustered on the chromosome to promote such coregulation. However, a direct link between coregulation and metabolite toxicity remains unestablished. Here we focused on Escherichia coli to systematically test this theory by making use of a unique toxicity prediction algorithm that has been specifically designed for this organism. We tested two possible strategies to achieve tight coregulation for metabolic genes around toxic intermediates: co-regulation via shared regulators and allocation of genes within the same operon, a bacteria-specific mechanism of strong co-regulation. We show that while toxic intermediates have their neighbouring genes more often in the same operon than expected by chance, this effect is not general bur rather confined to few metabolic pathways. Furthermore, coregulation or mRNA-level coexpression of neighboring enzymes occur with similar frequency in case of both toxic and non-toxic intermediates. Taken together, even in an organism with huge population size, we failed to find any general signature of adaptation to specifically enhance co-regulation of genes participating in the production or consumption of toxic intermediate metabolites. These negative results could indicate that most potentially harmful metabolites do not reach toxic concentrations under physiological conditions. Alternatively, the lack of regulatory mechanisms to avoid toxic metabolite accumulation might be owing to suboptimal gene regulation, which appears to be widespread in bacteria.

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