

Transcriptomics as an effective tool to study plant cell wall formation and function

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Motivation and Aim: Plant cell wall is the most abundant organic matter on our planet and the major renewable recourse. Together with that, this compartment largely determines the peculiarities of plant biology. All that warms up the interest to this complex supramolecular structure and demands for the approaches for its purposeful design. However, plant cell walls are mainly composed of polysaccharides – complex polysaccharides, most of which have branched irregular structure with numerous types of linkages and are extremely difficult to analyze. Moreover, polysaccharides are synthesized by non-template mechanism with participation of large membrane-bound enzymatic complexes, many participants of which have not been fully identified yet. Besides, the *in muro* modifications of cell wall polysaccharides are performed by the enzymes encoded by huge multigene families. The effective tool to figure out the general picture of cell wall dynamics and the important molecular players is transcriptomics.

Methods and Algorithms: We have developed several plant models that permit to study tissue- and stage-specific processes occurring in cell walls of various tissues and performed corresponding transcriptomic analysis followed by the complementary bioinformatics [1, 2].

Results: The results will be presented on the example of flax phloem fibers – the crucial elements of plant biomechanical system – that in the course of cell development consequently deposit three different cell wall types performing corresponding changes in cell wall machinery. The analysis of transcriptomic data was considerably facilitated by the developed online platform FIBexDB [3] that also helped to characterize individual genes and reveal their coexpression. Though the transcript amount of a certain gene is not always proportional to the amount of corresponding protein and especially to its activity, the changes in transcriptome patterns are very informative to realize the peculiarities of general cell metabolism and to detect the key molecular players, with various cell wall related enzymes and the involved transcription factors among them. Of special interest are proteins with lectin domains that interact with specific cell wall polysaccharides and help to trace the cell wall state [4].

Conclusion: Transcriptome analysis, especially if combined with immunocytochemistry and atomic force microscopy, helps to considerably advance the understanding of the cell wall polysaccharide fine-tuning in everyday life of a plant cell, its importance and possibilities to regulate.

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References

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