MATHEMATICAL MODEL OF AUXIN METABOLISM IN SHOOTS OF *ARABIDOPSIS THALIANA L*

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Motivation and Aim: Auxin participates in regulation of cell differentiation in development of embryo, leaves, vascular tissue, fruit, primary and lateral root and in controlling apical dominance and tropisms. Indole-3-acetic acid (IAA) is physiologically active in the form of the free acid, but can also be found in conjugated forms in plant tissues. IAA can be degraded and redundant pathways lead to its synthesis. The regulation of the IAA metabolism (synthesis, conjugation and degradations) is enough complex and may explain in some aspects how this simple substance is able to influence such diverse processes. Mathematical modeling of IAA metabolic gene network can help reveal the main factors governing this complex process;

Methods and Algorithms: To reach this aim, we first reconstructed a gene network of auxin biosynthesis, conjugation degradation by annotating experimental data from 105 published papers into GeneNet computer system [1]. This gene network after reduction was input into converter [2] to generate the mathematical model of auxin metabolism;

Results: The gene network for the auxin metabolism contains 62 genes and 44 proteins. Different molecular genetic processes within IAA metabolism network take place in 7 compartments. Within this network one regulatory contour with positive feedback and one regulatory contour with negative feedback were identified. For model generation the main regulatory factors in this gene network were selected according to consequences of their disruption for the network maintenance and plant organism functioning. By this way the whole complex network was reduced to core gene network. Based on the mathematical model of the core gene network, we followed the dynamics of the developed gene network and analyzed the key regulatory patterns. We reproduce the experimental data on IAA content in arabidopsis seeds [3].

Conclusion: We have reconstructed the gene network and develop the mathematical model of auxin metabolism in arabidopsis shoots. The model allows to reproduce some phenomenological and molecular-genetic aspects of the auxin role in the plant development.

References:
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3. Park S. et al. (2001) Partial characterization of major amide-linked conjugates of IAA in Arabidopsis seed (Abstract #321). Final Program July 2001, American Society of Plant Biologists/ Canadian Society of Plant Physiologists meeting, Providence, Rhode Island: 81-82.