

## **Comparison of cytokinin metabolism kinetics of two distinct *Arabidopsis* ecotypes through experimental and computational techniques**

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Until now, almost 70 cytokinin derivatives have been described in higher plants, suggesting how complex the network of interconversions determining the concentration of particular cytokinin forms have to be. Because of such complexity we have previously used mathematical methods for interactive visualisation and analysis of experimental data obtained after exogenous application of four major cytokinins: trans-zeatin, cis-zeatin, dihydrozeatin, and isopentenyladenin in two-hour time span on *Arabidopsis thaliana* Col-0. The metabolic system was divided into four subsystems according to particular incubations and independent multicompartment mathematical models of these subsystems were then constructed. Multiple Monte Carlo optimization of the models was carried out providing estimates of kinetic parameters of major reactions. Subsequent sensitivity analysis and statistical analysis provided further insight into parameter importance and reliability of the estimates. To reveal whether the metabolic machinery determining the concentration of particular cytokinin forms in A.t. Col-0 is universal for the whole specie or whether the network of reactions is rather specific and might be a subject to adaptational changes, we have analysed distinct *Arabidopsis thaliana* ecotype Van-0 in order to obtain a comparison of kinetic parameter estimates of the major reactions of cytokinin metabolism between Col-0 and Van-0.

Supported by the Czech Science Foundation (16-14649S and 16-19557S).