

In silico extraction of a complement of putative PTKs from the Arabidopsis proteome

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Protein tyrosine kinases (PTK) are crucial to the control of human and animal growth and development, as many receptor-like (RTKs) as well as cytoplasmic PTKs are deeply involved in the regulation of cell shaping, migration and responses to extracellular signals. In unicellular eukaryotes such as yeast, reversible tyrosine phosphorylation is mediated only by a few dual-specificity (Ser/Thr and Tyr) kinases and it seems to concern only a limited number of stress proteins. Since a plant PTK has not been identified yet, it has been suggested that also in plants protein tyrosine phosphorylation is limited to a few DSKs and stress proteins. However, tyrosine phosphorylation is particularly important even in multicellular prokaryotes (e.g. *M. xanthus*), and we have recently demonstrated that it concerns a large number of plant proteins and depends on the developmental conditions.

Genome sequencing of *Arabidopsis thaliana* has been completed, hence a whole proteome sequence could be inferred for a model flowering plant. In order to get preliminary evidence on plant PTKs, we have performed an in silico screening of the whole *Arabidopsis* proteome, using canonical or slightly degenerate functional signatures to identify a complement of bona fide PTKs. Then, extracted sequences have been further analysed by bioinformatic tools to unravel conserved or special moieties and to relate them to animal counterparts. A particular attention has been given to a group of putative RTKs, which seem clearly related to developmental control, i.e. showing a possible role reminiscent to animal RTKs.