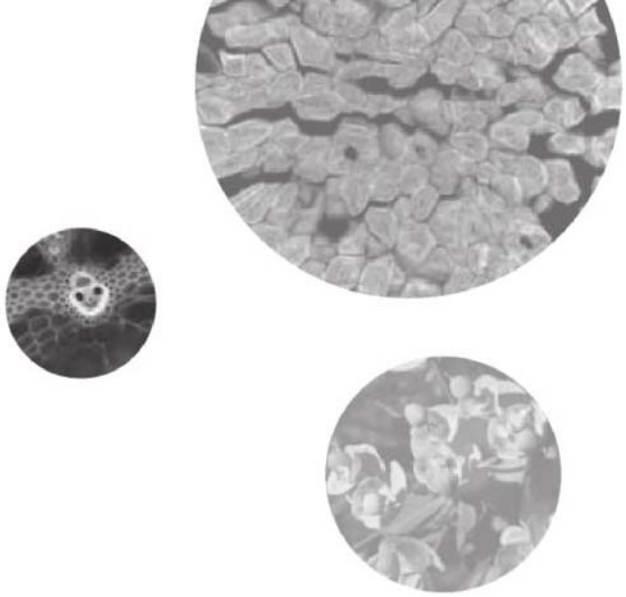

5. SLOVENSKI SIMPOZIJ O RASTLINSKI BIOLOGIJI
z mednarodno udeležbo

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GoMapMan: helping plant scientist fight the omics data

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Background and aims

The aim of systems biology is to bring a novel perspective into understanding of complex interactions in biological systems. By combining public omics databases and ontologies, experimental data can be presented in the biological context and further data exploration, visualization and knowledge discovery is possible. The commonly used Gene Ontology is not well adapted for plant species. Recently, MapMan, a tool for the visualization of transcriptomic and metabolomic data has been developed. It relies on plant specific ontology, available for many plant species, including potato and grapevine (Rotter et al., 2007; Rotter et al., 2009). Our goal was to develop a common database for easier browsing and curation of plant ontologies.

Methods

We have transferred existing MapMan ontology and tabular annotations for *Arabidopsis thaliana*, potato (*Solanum tuberosum*) and grapevine (*Vitis vinifera*) to a common database format. We have designed a centrally maintained database and a web interface for browsing, searching and editing the ontology and gene annotations.

Key results

GoMapMan (www.gomapman.org) is a controlled vocabulary of terms for describing genes of selected plant organisms, organized in an ontology tree. In addition to gene annotations, it provides links to several external resources (e.g. TAIR, Gene Indices, Pfam and Uniprot). The data and ontologies can be exported in the formats suitable for direct use with other tools such as MapMan, GSEA (Subramanian et al., 2005), BioMine (Sevon et al., 2006) and SEGS (Trajkovski et al., 2008).

Conclusions

GoMapMan provides a useful tool for plant scientists as it allows them to use a variety of ontology-based tools for data interpretation and generation of new hypotheses.

References

Rotter A., Camps C., Lohse M., Kappel C., Pilati S., Hren M., Stitt M., Coutos-Thévenot P., Moser C., Usadel B., Delrot S. and Gruden K. (2009) BMC Plant Biology 9, 104.

Rotter A., Usadel B., Baebler S., Stitt M. and Gruden K. (2007) Plant Methods 3, 10.

Sevon P., Eronen L., Hintsanen P., Kulovesi K. and Toivonen H. (2006) Proc. of 3rd International Workshop on Data Integration in the Life Sciences, (DILS'06), July 2006, Springer.

Subramanian A., Tamayo P., Mootha V. K., Mukherjee S., Ebert B. L., Gillette M. A., Paulovich A., Pomeroy S. L., Golub T. R., Lander E. S., Mesirov JP.(2005) Proc Natl Acad Sci U S A, 102(43), 15545-15550.

Trajkovski I., Lavrac N. and Tolar J. (2008) Journal of Biomedical Informatics 41 (4), 588–601.