

PROTIC: A DATABASE AND WEB-BASED APPLICATION TO MANAGE, ANALYSE
AND WEB-PUBLISH PLANT PROTEOME EXPRESSION DATA

Gwenn Houel¹, H el ene Ferry-Dumazet², Luc Moreau¹, Pierre Montalent¹, Christophe
Plomion³, Antoine de Daruvar², Michel Zivy¹, Johann Joets¹

*1-UMR de G en etique V eg etale du Moulon (INRA/CNRS/UPS/INA-PG), Gif-sur-Yvette,
France*

2-Centre de Bioinformatique de Bordeaux, Universit e Bordeaux II, France

3-INRA, G en etique et Am elioration des Arbres Forestiers, Bordeaux, France

Large international efforts have provided community with databases and softwares dedicated to transcriptome data mining. However, less effort has been done for proteomics. To our knowledge, databases developed so far for 2-D PAGE and compliant with plant proteomics do not deal with quantitative data or relationships between protein spots. Then new developments are needed to store and analyse proteome data and to compare them with transcriptome data.

We developed the PROTeome bioinformaTICs software Protic; a database and a web-based application, to manage, track, query and web-publish proteomics data. The database is designed to store complete sets of data generated by experiments, from experiment design description to spot identification (MS, Edmann,...) and quantitative variations. We included in the database schema possibilities to aggregate data from several plants, samples or gel. Then data from those groups can be easily extracted whenever needed, for instance to conduct statistical analysis.

Relations between spot, such as "the two spots are the same protein but in different post-translational modification state" may be very important to consider when comparing experiments. We thus managed to store these information in the database. This system can be extended to any type of relation that could exist between two proteins (or spots). The Protic application can automatically build relations network using transitivity. Thus if a non identified spot is related to an identified one by, for example an allelism relationship, then the first one will inherit of the identification result of the second one.

Database feeding may be achieved by automated uploading of formatted files or by using inter-active web forms. Data files are either files from widely used proteomics softwares like Melanie or tabulated files from spreadsheets.

Protic interface provides users with a set of web forms to query the database and a JAVA interactive graphical tool to query 2D-gel, to annotate the spots and to input spot relationships (see fig 1). This interface allows to view up to 4 gel images at a time. Links to other databases (Swiss-prot, Genbank) are present wherever needed.

Protic is based on Oracle or Postgresql DBMS and will be freely available.

Figure 1. The Protic data base graphical images display tool. More than a browsing and a querying tool, this interface allows to annotate spots with comments, and to record relationships between spots. Quantitative data can be exported in tabulated text files.

