The Mitochondrial Protein Import Machinery of Plants (MPIMP) database

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ABSTRACT

The Mitochondrial Protein Import Machinery of Plants database (MPIMP) is an Internet-accessible database containing detailed information on the protein import apparatus of plant mitochondria. The Arabidopsis genome was searched for components of the mitochondrial protein import apparatus using components from the well-characterized model system of Saccharomyces cerevisiae. Twenty six homologues of 34 components could be found, encompassing the essential components for the general and carrier import pathways. The database is available through the Internet at http://millar3.biochem.uwa.edu.au/~lister/index.html.

INTRODUCTION

The thousand or more proteins thought to be present in the mitochondrion must be imported from the complex mixture of all cytosolically synthesised proteins (1). The mitochondrial import apparatus carries out this act of discrimination, which is responsible for the import and correct intraorganelle sorting of nuclear encoded mitochondrial proteins (2,3). Our knowledge of the components and mechanisms of the plant import apparatus is poor compared to the intensively studied and more amenable systems of Saccharomyces cerevisiae and Neurospora crassa. Several hundred million years of diversification has taken place between organisms since the single endosymbiotic event leading to the formation of mitochondria took place (4). In Arabidopsis, gene families encode the two outer membrane receptors and the inner membrane translocase components, suggesting functional diversification between members. Additionally, structural predictions on several components, particularly both inner membrane translocases, indicates that they differ structurally compared to the well characterised yeast components. Yeast as a model system does not reflect the cellular and developmental complexity of higher plants. Therefore, identification of the components of the protein import apparatus in plants is a necessary first step to understand mitochondrial biogenesis in plants. Identification of the import machinery in plants has enabled the generation of a model for the plant mitochondrial protein import pathways (Fig. 1).

DATABASE DESCRIPTION

The Mitochondrial Protein Import Machinery of Plants (MPIMP) database currently contains detailed information on the protein import components identified from the Arabidopsis genome database. Included are putative homologues to import components that have eluded biochemical characterization.

Information is available online at http://millar3.biochem.uwa.edu.au/~lister/index.html, with hyperlinks leading to detailed information, including multiple sequence alignments between yeast and Arabidopsis homologues, hydropathy predictions, Stanford Microarray Data, secondary structure predictions and protein motifs. Also, links to ESTs, coding sequences, genomic sequences and protein sequences through TAIR and NCBI are present. Additional sequence information is presented for each component, including size, EST number, and similarity to the yeast homolog. An image of a subset of the data in MPIMP is shown (Fig. 2).

METHODS

Identification of Arabidopsis homologues of the yeast mitochondrial protein import apparatus

All bioinformatic programs were used with the default settings unless specified otherwise. Sequence information for the yeast import components was obtained from the Saccharomyces Genome Database. The yeast gene and protein sequences were used to search GenBank and TIGR Arabidopsis sequence databases for homologues by BLASTN, BLASTP and TBLASTN alignment (5).

Identification of Arabidopsis ESTs was achieved by searching the TIGR Arabidopsis Gene Index with BLASTN. Genomic clones were identified by searching GenBank with BLASTN. Protein sequences were deduced from nucleic acid sequences.

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using Translate (University of Wisconsin Genetics Computer Group).

**Analysis of *Arabidopsis* mitochondrial import components**

Protein alignments were generated using PileUp (University of Wisconsin Genetics Computer Group). Residue shading was done with PrettyBox (University of Wisconsin Genetics Computer Group). Similarity between yeast and *Arabidopsis* proteins was calculated using Gap (University of Wisconsin Genetics Computer Group). Prediction of transmembrane alpha-helices was performed using the DAS transmembrane prediction server (6). Prediction of protein secondary structure was done with Garnier (7). TPR motifs were identified using REP (8).

**FUTURE ADDITIONS**

In the future, the MPIMP database will be updated with information about the mitochondrial protein import apparatus from other plant species, such as rice. This will allow comparison of the genes present in different species. Additional analysis of the import component genes will be included in the database as it is generated. Links to all research relating to the plant mitochondrial import components will be added as it is published.
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REFERENCES

Figure 2. Image of the MPIMP database, containing functional hypertext links (blue) to information.