

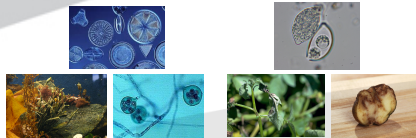
Identification and Evolution of Transcription Factors in Stramenopiles

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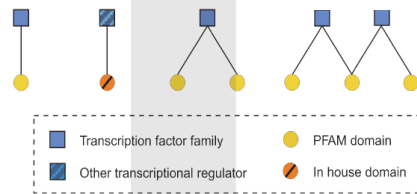
High diversity among Stramenopiles



Mechanisms of diversity?

Stramenopiles is a Protist group that range from large multicellular seaweeds to tiny unicellular species; their members are present in freshwater, marine and terrestrial habitats, and embrace many ecologically important organisms (e.g., diatoms, brown algae) and many species of economically importance such as *Phytophthora infestans*, an important pathogen of potato, or *Saprolegnia parasitica*, a major fish pathogen.

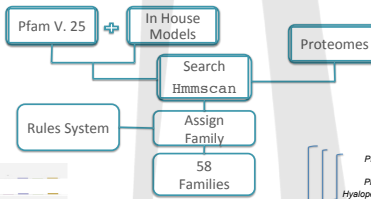
A rules system for classification of TFs and TRs



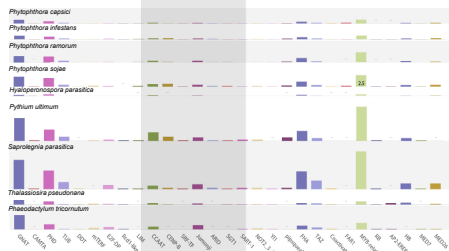
Modified from Riaño-Pachón et al. 2007. BMC Bioinformatics 8:42

Rules for the classification of TFs and TRs depicted as a bipartite graph. Blue squares represent families, TFs are indicated in solid color, TRs are indicated by shaded squares. Yellow circles represent protein domains from the PFAM database (<http://pfam.sanger.ac.uk/>), orange circles represent domains generated in-house. In house domain models were generated based on seed alignments and profile HMMs were built using HMMER 3.0 (<http://hmm.janelia.org/>)

Identification of these mechanisms?

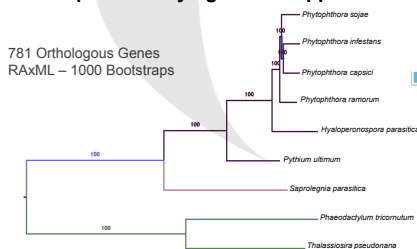


The Relative Importance of TFs and TRs greatly varies among species



Columns represent selected families of TFs and TRs, rows represent the species included in this study and bars represent the relative importance: the proportion of a family over the total number of regulators. This analysis will highlight the importance of different TFs and TRs families. We can see that some families have greater representativity in some organisms. In some species, however, there is a homogeneity among families.

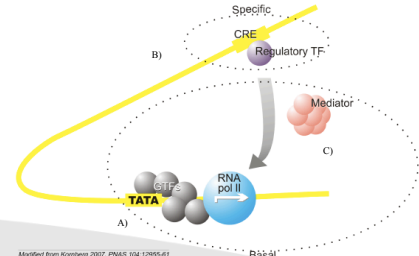
Evolutionary Relationships Among Stramenopiles: A Phylogenomic Approach



First, we recovered orthologous groups using Ortho-MCL (<http://www.orthomcl.org/>), finding 781 genes clusters. The phylogenetic reconstruction was carried out with Maximum Likelihood analysis using RAXML (Stamatakis, 2008) with 1000 bootstraps. In the tree we can see a clear separation between autotrophic organisms (Green), and the heterotrophic organisms (Blue).

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Modified from Komberg 2007. PNAS 104:12955-61

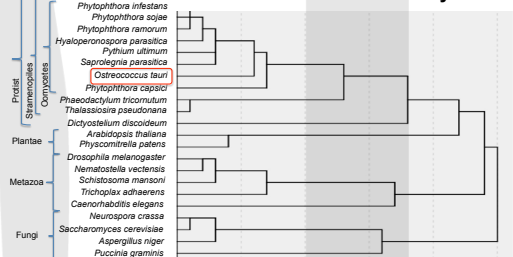
Transcription regulation model A) General transcription factors (GTFs) recruit RNA polymerase II in order to start the transcription of the gene; generally, this type of transcription factors are common among genes transcribed by RNA-Pol II. B) Regulatory transcription factors (TFs) interact with the gene promoter to regulate gene transcription, this transcription factors are usually specific for each gene and have been found to be linked to the generation of diversity in organisms (Komberg, 2007) C) Other transcription regulators (OTRs) as the Mediator complex participate in the process of transcription, but generally do not interact with DNA.

Species included in this study

Organism	Size	Genes	Proteins	Source
<i>Phytophthora infestans</i>	237 Mb	18179	18140	BROAD
<i>Phytophthora ramorum</i>	65 Mb	15743	15066	DOE-JGI
<i>Phytophthora capsici</i>	64 Mb	19805	19919	DOE-JGI
<i>Phytophthora sojae</i>	86 Mb	19027	19276	DOE-JGI
<i>Saprolegnia parasitica</i>	53.09 Mb	20113	20088	BROAD
<i>Hyaloperonospora parasitica</i>	82.05 Mb	14567	14565	BROAD
<i>Pythium ultimum</i>	44.91 Mb	15291	12614	BROAD
<i>Thalassiosira pseudonana</i>	32 Mb	11397	11318	DOE-JGI
<i>Phaeodactylum tricornutum</i>	28 Mb	10489	10389	DOE-JGI

We use all the available genome sequences of Stramenopiles, there are large differences on genome size, number of genes and number of predicted proteins in this group.

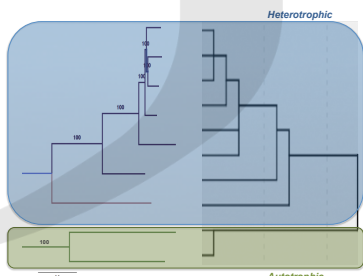
Hierarchical Clustering of Species based on TFs and TRs family size



In addition to Stramenopiles, we also identified and classified families in other organisms from different lineages. We can see that species are clustering according to their evolutionary relationships, as in Oomycetes, Stramenopiles, Protists, Plants, Metazoan and Fungi.

The only exception is *O. tauri*, which belongs to the lineage of plants and is grouped within the Oomycetes, which are heterotrophic, this might arise due to its small genome size, a feature shared with parasitic organisms.

Phylogenetic Signal



A contrast between the species phylogenetic tree and the family size hierarchical clustering shows that both trees have the same topology, implying that TFs and TRs families-sizes carry a strong phylogenetic signal.

Outlook
 Deep Analysis TFs/TRs families
 Phylogenetic independent contrasts (PIC) qPCR
 Inference of gene regulatory networks

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