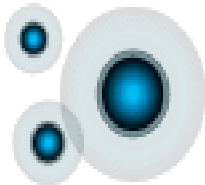


<PHYMYCO-DB>



Tutorial

June 2011 release

This PHYMYCO-DB tutorial aims to help users to use efficiently the database and its tools.

It contains details about how to use the options offered on the left of the main screen (alignments, downloads, selection of fungal sequences, taxonomic browser)

It also refers to a submitted paper that we expect to be published soon.



Content

1-Execute clustalW	3
- > From fasta format file	3
- > From aln format file	4
2. Download sequences	5
3. Download alignment files	6



1. Execute clustalW:

You can execute an alignment on our computer clusters with ClustalW 2.0 and receive the results in your e-mail box.

-> From fasta format file:

First, upload your personal sequences file '.fasta' (1000 sequences max.). Then select the gene of interest (SSU rRNA or EF-1- α gene) and sequences from PHYMYCO-DB using our taxonomic browser.

<PHYMYCO-DB>

Finally, you have the possibility to add an outgroup from a personal file '.fasta' or from our set of outgroup files stored in the database. To launch the application, click on 'Align with ClustalW'.

<PHYMYCO-DB>

	Lineage	NCBI accession number
1	Ascomycota;Pezizomycotina;Sordariomycetes;Sordariales;Lasiosphaeriaceae;Bombardia bombardia	NG_013187.1
2	Ascomycota;Pezizomycotina;Sordariomycetes;Sordariales;undefined;Ascolacicola austriaca	AF242263.1
3	Ascomycota;Pezizomycotina;Sordariomycetes;Sordariales;Chaetomiaceae;Chaetomium sp. KY-52	AB521039.1
4	Ascomycota;Pezizomycotina;Sordariomycetes;Sordariales;undefined;Kionochaeta sp. MK-100	AB521038.1
5	Ascomycota;Pezizomycotina;Sordariomycetes;Sordariales;Lasiosphaeriaceae;Lasiosphaeria ovina	DQ836894.1



Once the job is completed you receive an e-mail containing a link. You can visualize the alignment in HTML format or you can download it as a '.aln' format file.

<PHYMYCO-DB>



The screenshot shows the 'Alignment results' section of the PHYMYCO-DB interface. On the left, there is a sidebar with 'DB Explore' and 'DB Admin' sections. The 'DB Explore' section contains links for 'Execute clustalW', 'Download sequences', 'Download alignment files', and 'Contact the admin'. The 'DB Admin' section contains a 'Login' link. The main content area is titled 'Alignment results' and contains a link 'Click here to visualize your clustalW result file' with an arrow pointing to the right. Below this link is a 'Download result file' button. A dialog box titled 'Ouverture de BDDChampiv25-47976.aln' is open, showing the file name and a question 'Que doit faire Firefox avec ce fichier ?'. The 'Ouvrir avec' dropdown is set to 'Firefox (défaut)'. To the right of the dialog, a preview of the alignment results is shown, titled 'CLUSTAL 2.0.9 multiple sequence alignment'. The alignment consists of 25 sequences, each with a unique ID and the name 'Aschersonia' or 'Hypocrella', followed by a series of dashes representing the alignment.

-> From aln format file:

First, upload your personal sequences file '.aln' (1,500 Ko max.). Then, choose one of our pre-computed alignments - manually cross-checked and stored in the database. They contain up to 400 sequences and are specific to a class or a particular group of fungi.

<PHYMYCO-DB>



The screenshot shows the 'Alignment type' and 'Alignment files' sections of the PHYMYCO-DB interface. The 'Alignment type' section has two radio buttons: 'FASTA format file' (unselected) and 'ALN format file' (selected). The 'Alignment files' section has a text input field for 'Personal sequences file to align (ALN format)' with the value 'C:\Documents and Settings\inviteco\Bureau\sequences(1)' and a 'Parcourir...' button. Below this is a 'Select a file' section with a 'Filter:' text input field and a vertical scrollbar.

To launch the application, click on 'Align with ClustalW'.



2. Download sequences :

All the fungal sequences contained in PHYMYCO-DB are automatically curated and then manually curated (process explained in details in a submitted publication about PHYMYCO-DB). Choose a gene (SSU rRNA or EF-1- α in this PHYMYCO-DB upgrade) and a taxonomic level. The number in brackets corresponds to the total number of sequences for the considered taxonomic level. Click on Envoyer.

<PHYMYCO-DB>

You can download all the sequences from the taxonomic level chosen or only sequences of interest, one by one, by clicking on the button in the download column.

<PHYMYCO-DB>

	Phylum	Subphylum	Class	Order	Family	Genus	Species	NCBI accession number	Download
1	Zygomycota	Zoopagomycotina	undefined	Zoopagales	Piptocephalidaceae	Piptocephalis	Piptocephalis corymbifera	NG_017192.1	RNA_18S_NG_017192.1.fasta
2	Zygomycota	Zoopagomycotina	undefined	Zoopagales	Helicocephalidaceae	Rhopalomyces	Rhopalomyces elegans	NG_017191.1	RNA_18S_NG_017191.1.fasta
3	Zygomycota	Zoopagomycotina	undefined	Zoopagales	Helicocephalidaceae	Rhopalomyces	Rhopalomyces elegans	AY635834.1	RNA_18S_AY635834.1.fasta
4	Zygomycota	Zoopagomycotina	undefined	Zoopagales	Cochlonemataceae	Cochlonema	Cochlonema euryblastum	DQ520640.1	RNA_18S_DQ520640.1.fasta
5	Zygomycota	Zoopagomycotina	undefined	Zoopagales	Piptocephalidaceae	Piptocephalis	Piptocephalis corymbifera	AB016023.1	RNA_18S_AB016023.1.fasta
6	Zygomycota	Zoopagomycotina	undefined	Zoopagales	Sigmoideomycetaceae	Thamnocephalis	Thamnocephalis sphaerospora	AB016013.1	RNA_18S_AB016013.1.fasta
7	Zygomycota	Zoopagomycotina	undefined	Zoopagales	Helicocephalidaceae	Rhopalomyces	Rhopalomyces elegans	AB016012.1	RNA_18S_AB016012.1.fasta
8	Zygomycota	Zoopagomycotina	undefined	Zoopagales	Piptocephalidaceae	Syncephalis	Syncephalis depressa	AB016011.1	RNA_18S_AB016011.1.fasta
9	Zygomycota	Zoopagomycotina	undefined	Zoopagales	Piptocephalidaceae	Kuzuhaea	Kuzuhaea moniliformis	AB016010.1	RNA_18S_AB016010.1.fasta




3. Download alignment files:

You can download one of the pre-computed alignments. They were manually cross-checked and can contain up to 400 sequences of a whole phylum or several classes, families or orders.

Select an alignment using the filter. The name of the taxonomic level is contained in the file name. And click on Download.

<PHYMYCO-DB>



DB Explore

- Execute clustalW
- Download sequences
- Download alignment files**
- Contact the admin

DB Admin


- Login

Download alignment files

Select an alignment file to download
Filter:

- Glomeromycota EF1alpha

<PHYMYCO-DB>



DB Explore

- Execute clustalW
- Download sequences
- Download alignment files
- Contact the admin

DB Admin

- Login

Download alignment files

Select an alignment file to download
Filter:

- Glomeromycota EF1alpha

Ouverture de Glomeromycota_EF1alpha.aln

Vous avez choisi d'ouvrir

- Glomeromycota_EF1alpha.aln
qui est un fichier de type : clustal
à partir de : http://phymycodb.genouest.org

Que doit faire Firefox avec ce fichier ?

Ouvrir avec Firefox (défaut)

Enregistrer le fichier

Toujours effectuer cette action pour ce type de fichier.