



Comparative analysis of *Aspergilli* to facilitate novel strategies in fungal biotechnology

JGI – CSP #350



Microbiology
Utrecht University

Fungal Physiology

CBS-KNAW
Fungal Biodiversity Centre



Coordination

- Ronald de Vries
 - CBS-KNAW Fungal Biodiversity Centre, The Netherlands
- Paul Dyer
 - University of Nottingham, UK
- Trish vanKuyk
 - Leiden University, The Netherlands
- Jennifer Wortman
 - Broad Institute, US
- Igor Grigoriev
 - JGI



Aims

- Expand the set of genome sequences of Aspergilli and related fungi
- Detailed comparative genomic analysis of Aspergilli and related fungi
- Support the bioinformatics by comparative experimental studies
- Participation of a large community



Species to sequence

- *Aspergillus tubingensis**
- *Aspergillus brasiliensis**
- *Aspergillus foetidus*
- *Aspergillus sojae*

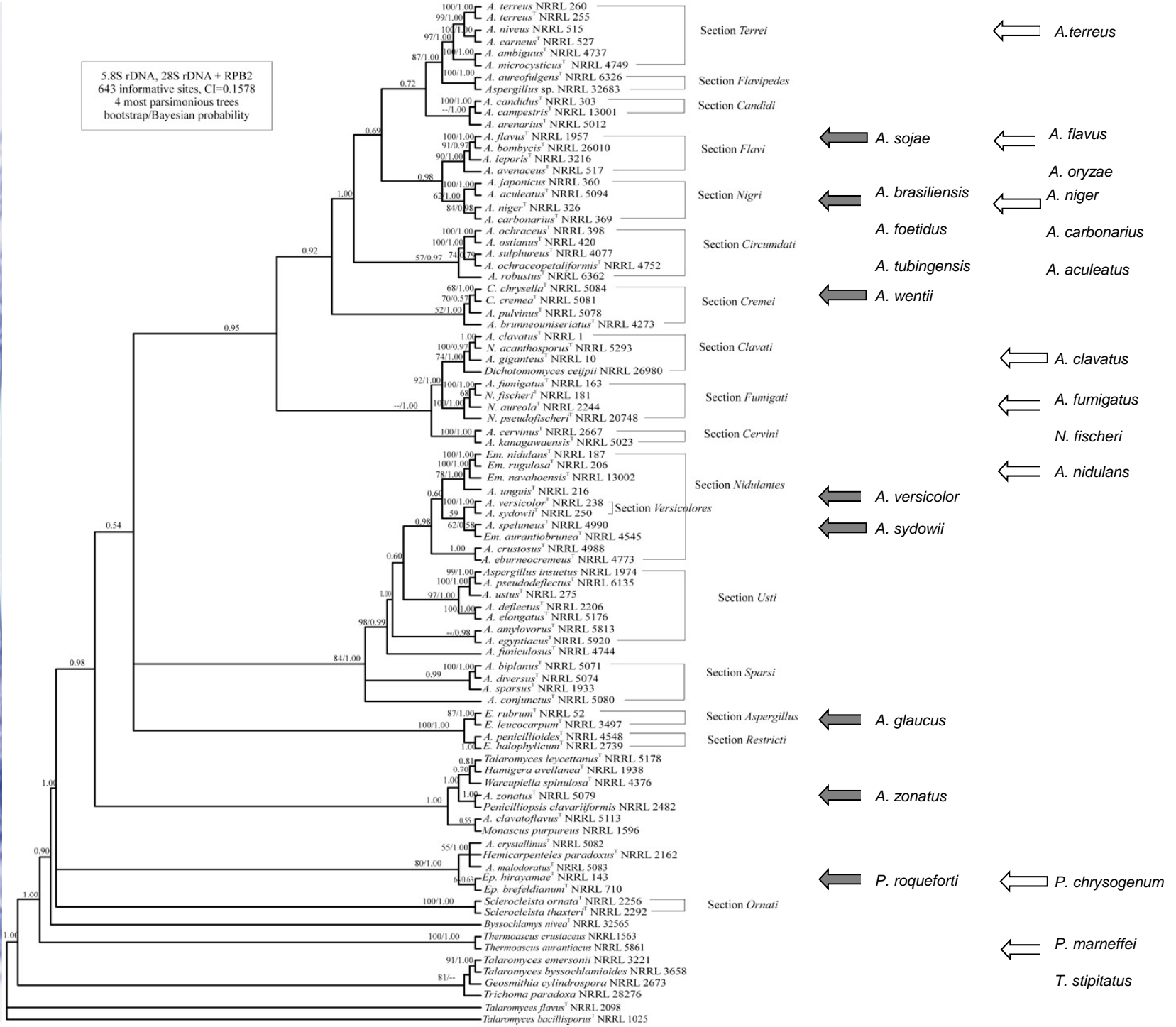
- *Aspergillus versicolor*
- *Aspergillus sydowii*
- *Aspergillus wentii*
- *Aspergillus glaucus*
- *Aspergillus zonatus*

- *Penicillium roquefortii*





5.8S rDNA, 28S rDNA + RPB2
643 informative sites, CI=0.1578
4 most parsimonious trees
bootstrap/Bayesian probability



Approach

- Organisation similar to the *A. niger* genome annotation and the *A. nidulans* re-annotation
- Topic groups with topic group leaders
- Automatic annotation and synteny
- Manual curation
- Supported by biological data



Topics and topic leaders

- General annotation, genome comparison and statistics
 - Jennifer Wortman, Igor Grigoriev
- Nitrogen metabolism
 - Richard Todd, Meriel Jones
- Secondary metabolism and mycotoxins
 - Berl Oakley, Axel Brakhage
- DNA repair, chromatin remodelling, RIP
 - Joseph Strauss, Claudio Scazzocchio



Topics and topic leaders (2)

- Development, Morphology, Sex/Mating, cellular organisation
 - Paul Dyer, Michelle Momany
- Carbon metabolism
 - Bernhard Seiboth, Christian Kubicek
- Plant polysaccharide degradation
 - Ronald de Vries, Bernard Henrissat
- Secondary metabolism and mycotoxins
 - Berl Oakley, Axel Brakhage



Topics and topic leaders (3)

- Transporters
 - Trish vanKuyk, Arnold Driessen
- Secretion, Proteases, UPR
 - David Archer
- Stress response, external environment, pH
 - Reinhard Fischer, Gerhard Braus, Istvan Pocsí
- Lignin degradation
 - Isabelle Benoit



Technical aspects

- Annotation, synteny, genome comparison is largely done by bioinformatic groups
- AspGD will develop a synteny browser for all *Aspergillus*, *Penicillium* and *Talaromyces* genomes
- Focus of the topic groups should therefore be mainly post annotation



Experimental (biological) support

- Crucial to have high impact publication(s)
- The project has no funding outside sequencing
- Should be the minimal needed to support hypotheses/conclusions from genome analysis
- FUNG-GROWTH database



Publication aims

- At least 1 major publication with highlights of comparison of all 20+ genomes
- Followed by Special Issue with topic-specific papers



Open invitation

- If you like to join, e-mail me and topic leader
- Indicate what you can do for the project (including experiments)
- Indicate any data that you'd be willing to contribute to the project

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