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CBS

Carleton UNIVERSITY

# Molecular phylogeny, barcoding and ecology of *Pythium* species.

C.A. Lévesque , G. Robideau, N. Désaulniers, K. Bala, W. Chen, J.T. Tambong
Biodiversity / Mycology, Agriculture and Agri-Food Canada,
Central Experimental Farm, Ottawa, ON
Biology Dept., Carleton University

A.W.A.M. de Cock, Centraalbureau voor Schimmelcultures, Utrecht,
The Netherlands

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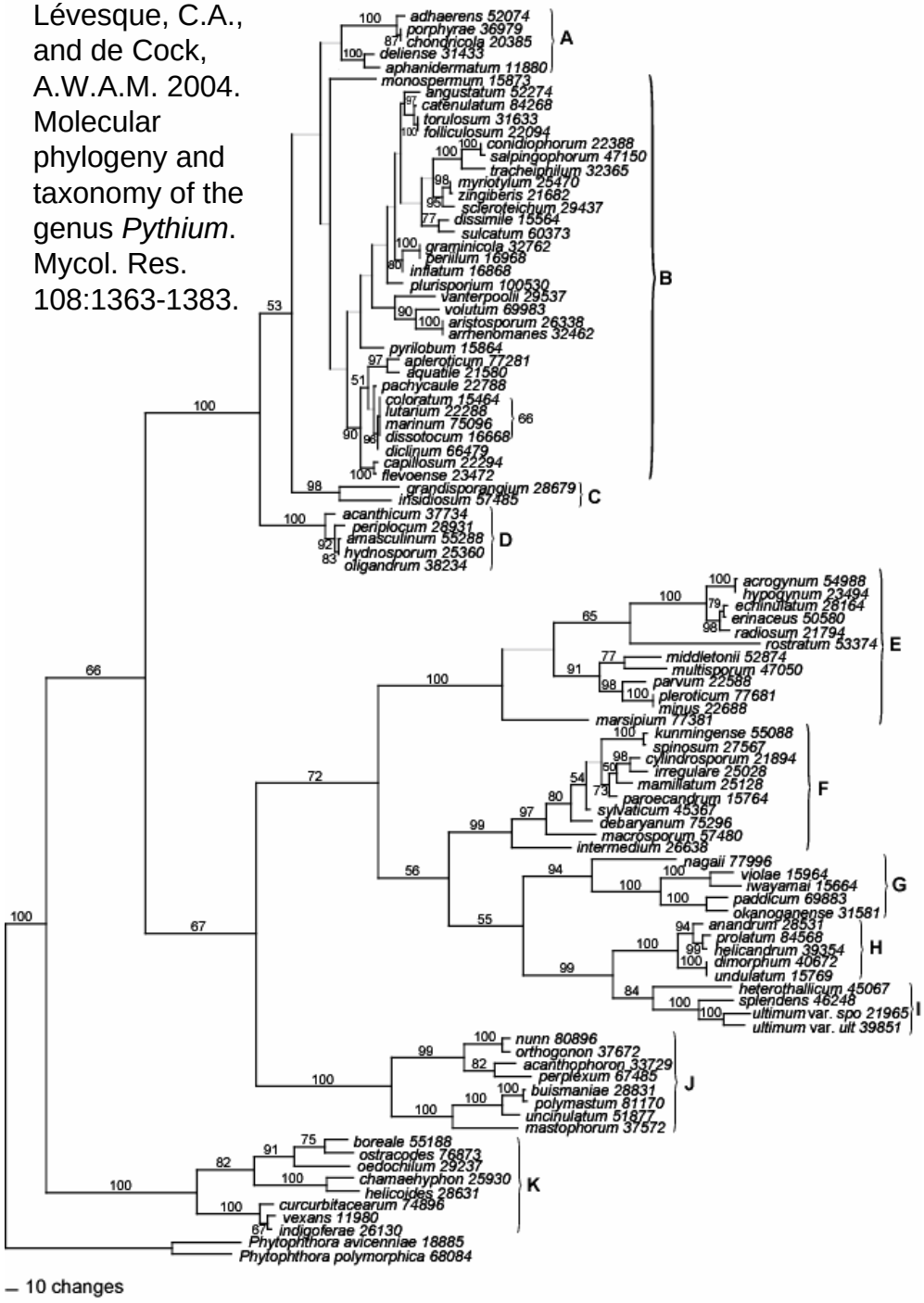
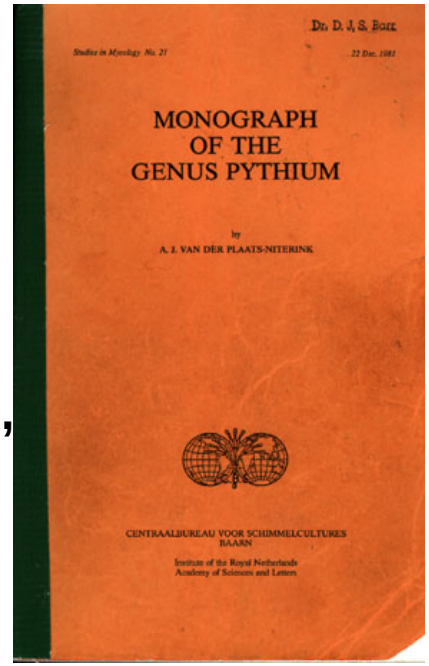
Lévesque, C.A., and de Cock, A.W.A.M. 2004. Molecular phylogeny and taxonomy of the genus *Pythium*. Mycol. Res. 108:1363-1383.

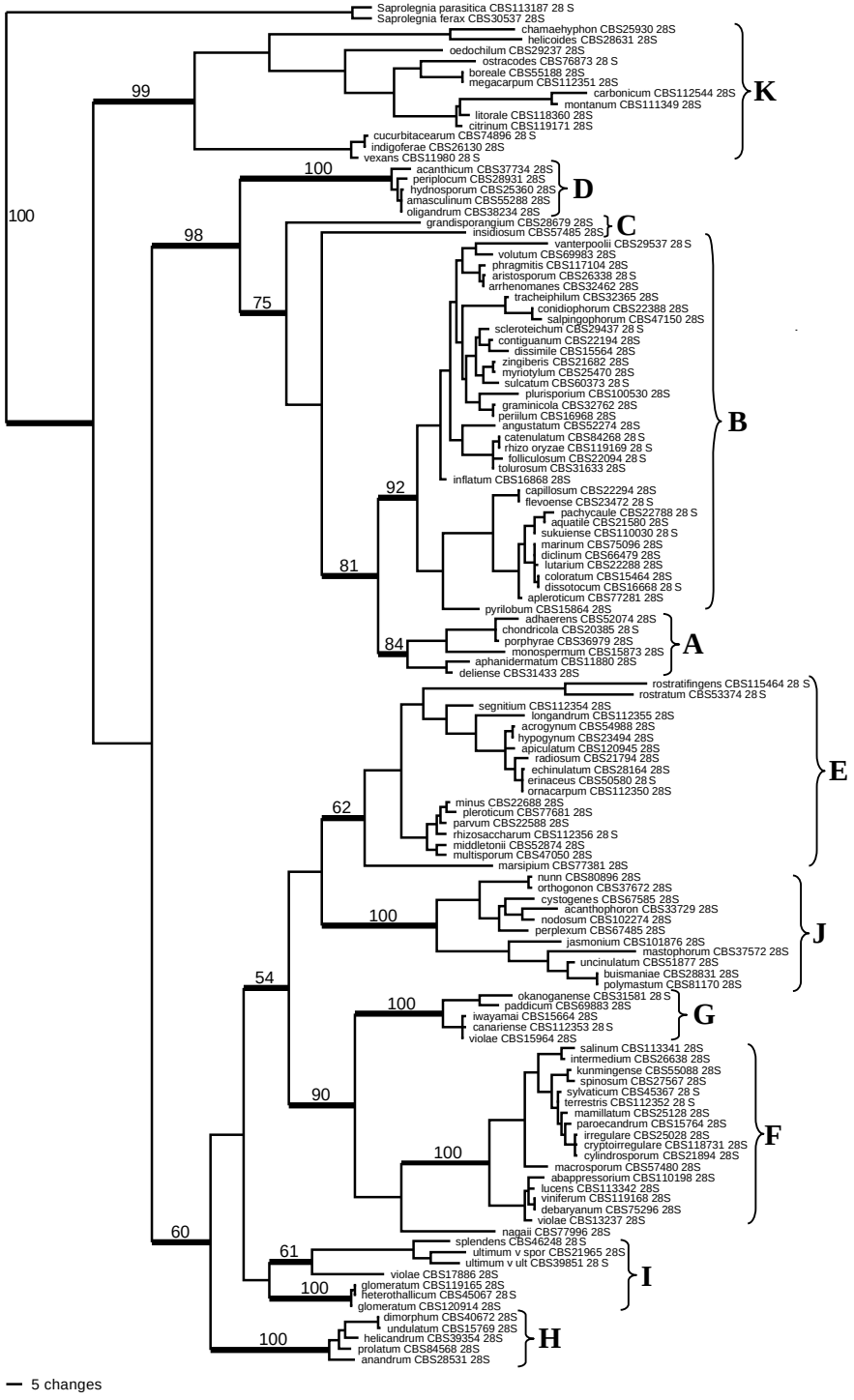



# Evolution of all the species of the genus *Pythium* (ITS and LSU)

**Arthur de Cock, CBS, Netherlands, collection of « ex-type » cultures**



# LSU
# Large Subunit rDNA
# D1 to D3
# (127 species)




Maximum Parsimony

# ITS
# Internal Transcribed Spacer rDNA
# (127 species)


Maximum Parsimony

Global Initiative

# Consortium for the Barcode of Life (CBOL)

CONSORTIUM FOR THE BARCODE OF LIFE

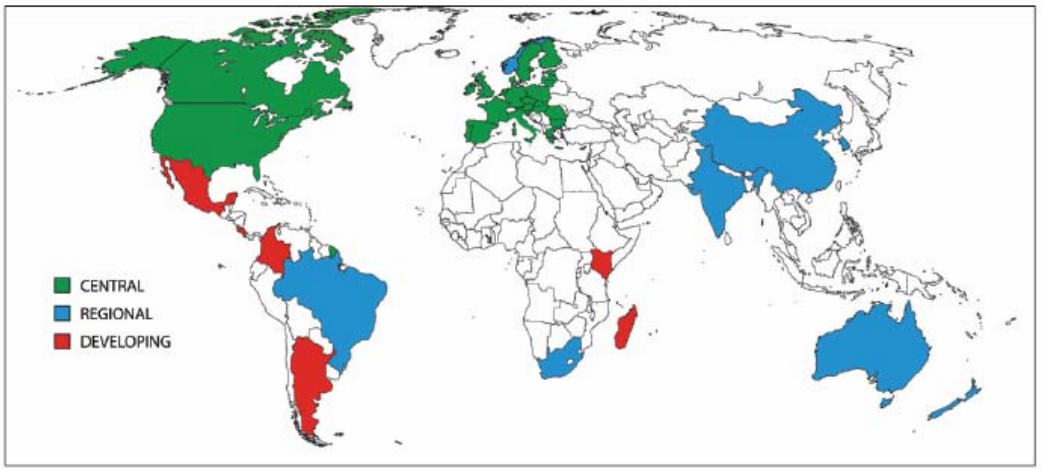
ALFRED P. SLOAN FOUNDATION

From Robert Hanner, Canadian Barcode of Life Network, University of Guelph

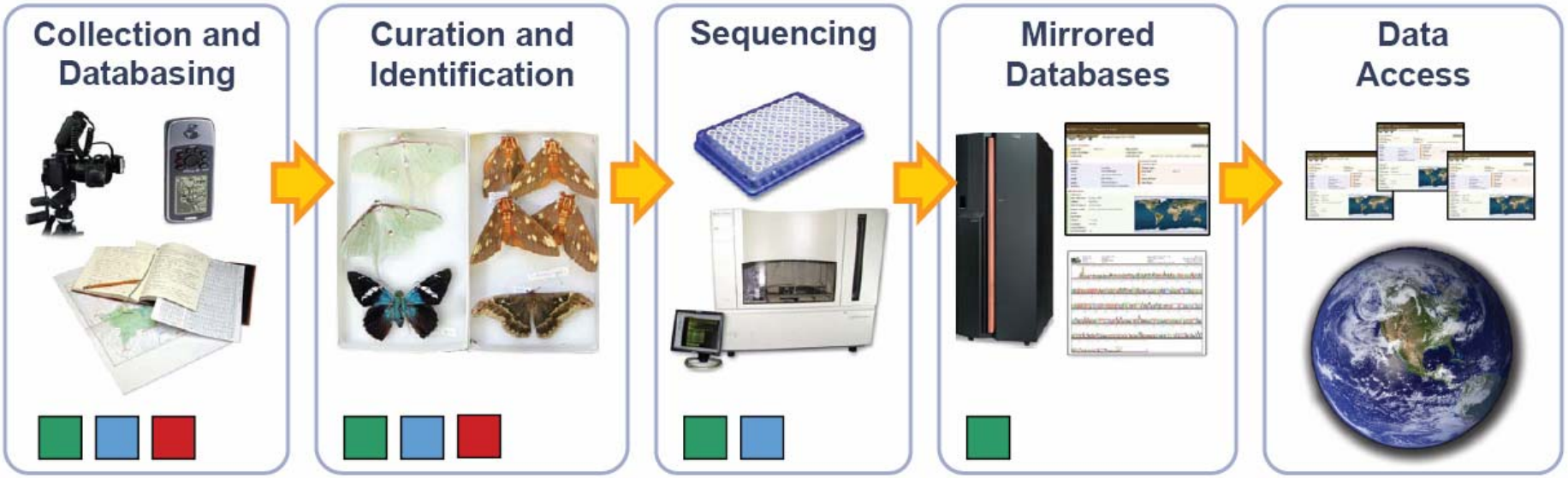
# International Barcode of Life Project

## Research Overview May 2008

# iBOL

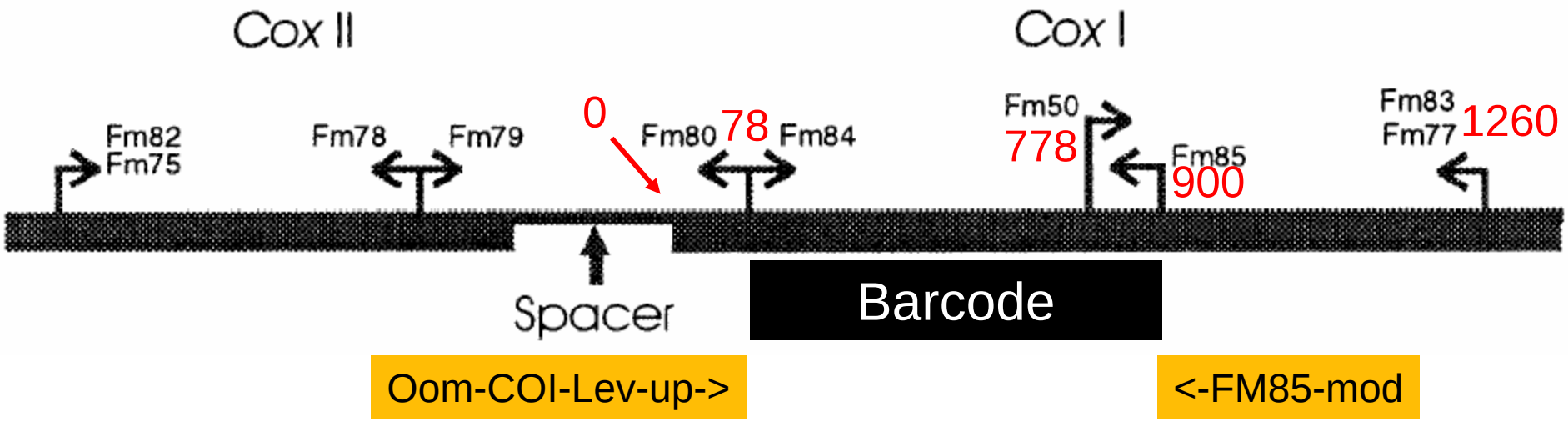



- Central Nodes
- Regional Nodes
- Developing Nodes



# Oomycete barcoding

- Cytochrome Oxidase I *(COI)*
- Good primers designed that amplify a 727bp region of *COI*
- No introns in oomycete *COI* (as opposed to true fungi)




**Martin, F. N., and P. W. Tooley.** 2003. Phylogenetic relationships among *Phytophthora* species inferred from sequence analysis of mitochondrially encoded cytochrome oxidase I and II genes. Mycologia **95:**269-284.


Gregg Robideau
Ph.D. Candidate
(since Feb 2008)
Dept. of Biology
Carleton University

- ~1,000 COI & ITS sequences of oomycetes obtained to date
- Over 100 species of *Pythium*, 70 species of *Phytophthora*, and several other genera such as *Achlya*, *Peronophythora*, and *Saprolegnia*

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# DNA barcoding of oomycetes with the Cytochrome Oxidase I *(COI)* gene

Robideau, Gregg P.[1,2], Smith, Myron L.[2], and Lévesque, C. André[2,1]

1. Carleton University, Ottawa, ON
2. Agriculture and Agri-Food Canada, ECORC, Ottawa, ON

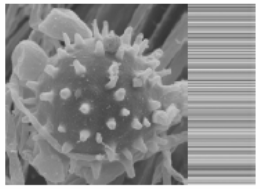
## Introduction

Oomycetes, which include water moulds and downy mildews, are terrestrial and aquatic fungi-like organisms belonging to the kingdom Stramenopila. They include important plant pathogens such as the causal organisms of the potato famine in Ireland (*Phytophthora infestans*), and Sudden Oak Death Syndrome (*Phytophthora ramorum*) devastating California. This group also includes fish pathogens (*Saprolegnia parasitica*) and mammalian pathogens (*Pythium insidiosum*), as well as biological control agents such as *Lagenidium giganteum*, which infects the larvae of mosquitoes, or the mycoparasite *Pythium oligandrum*. Oomycetes are commonly found in fresh water, oceans, soil, and can also be airborne. Our research to date has focussed on the genera *Pythium* and *Phytophthora*.

The current taxonomic groupings of *Pythium* and *Phytophthora* are supplemented significantly by molecular data, specifically from nuclear DNA sequences of the ITS (Internal Transcribed Spacer) and LSU (Large Subunit) regions of rDNA (Lévesque and de Cock 2004). While analyses of these genes and spacers have produced phylogenetic relationships that are generally consistent with morphological species concepts, there are still potential weaknesses in these genes in terms of their usefulness for identification. For example, some species of *Pythium* share the same ITS sequence.

The use of a different gene that may provide resolution to species-level identification is therefore of great interest, especially considering that in *Pythium*, identification to the species level is crucial in determining the ecological role of the organism.

Our research to date has focussed on the validity of *COI* bacode sequencing for oomycete species delimitation.



## Materials and Methods

PCR amplification of *COI* was performed using primers designed to amplify the barcode region of all oomycetes. The forward primer designed was 5'-TCAWCWMGATGGCTTTTTTCAAC-3'. The primary reverse primer used was 5'-RRHWACKTGACTDATRATACCAAA-3' which was modified from Fm85 (Martin and Tooley 2003). In a few cases an internal reverse, 5'-CYTCHGGRTGWCCRAAAAACCAAA-3', was used when the primary reverse did not yield a good PCR product. Sequencing of PCR products was performed with an ABI Prism® 3130XL.

## Results and Discussion

*COI* barcode sequences were easily obtained using the primers designed. The barcode region of the oomycetes sequenced did not contain any introns, and in the vast majority of samples, a 727bp fragment was sequenced as opposed to some samples for which a 680bp fragment was obtained with the internal reverse primer.

The sequences of the barcode region were highly variable, with many species showing intraspecific variation in *COI*. The barcode region still exhibits ability in species identification however, because conspecific barcode sequences clustered together, as seen in Figure 1.

The phylogenetic relationships created with the barcode region did not match the previously established ones that matched morphological characters in the genus *Pythium* (Lévesque and de Cook 2004), but this was not an unexpected result, as short DNA regions do not generally provide enough variable characters to produce accurate phylogenies.

Resolution of *Pythium* species boundary ambiguities that ITS cannot discriminate was not achieved with *COI*. In cases where two *Pythium* species shared identical or similar (≥95%) ITS sequences, they also had similar or identical *COI* sequences. In many cases, the classification of an ambiguous pair as separate species was based on subtle and questionable morphological differences. It is possible that with further study and multi-gene analysis, these species with identical barcodes may be conspecific.

## Conclusions

Although *COI* relationships are not congruent with existing phylogenies, our results have provided unique *COI* sequences for most species of *Pythium* and *Phytophthora* sequenced so far. We have also discovered intraspecific variation of *COI* sequences in some species studied, including the recently defined species of *Pythium attrantheridium*. Although intraspecific variation exists in *COI*, the clustering of conspecific *COI* sequences is reliable for identification. Future investigation will be made into species complexes such as *Pythium irregulare*, and the ability of *COI* to discriminate among members of such complexes.

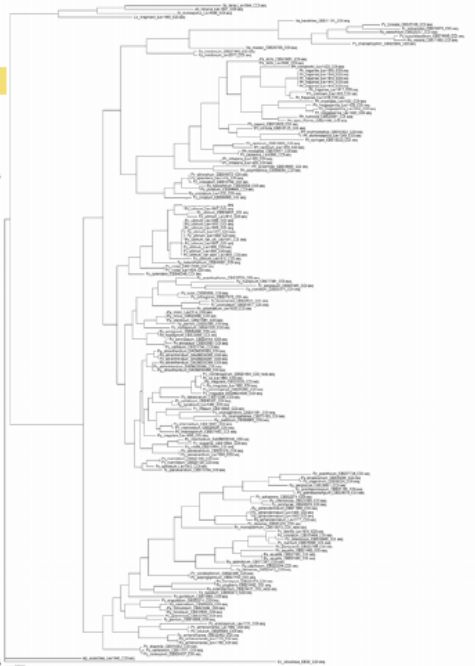


**Figure 1.** Phylogenetic tree of oomycetes based on a 679bp fragment of COI. A heuristic search was performed on 161 representative sequences out of 700 available using parsimony analysis. A brown algae was used as outgroup.

Genus abbreviations:
Ac = *Achlya* Di = *Dictyuchus* Ha = *Halophytophthora* Pe = *Peronophythora* Py = *Pythium*
Ap = *Aphanomyces* Ec = *Ectrogella* Le = *Leptolegnia* Ph = *Phytophthora* Sa = *Saprolegnia*

## Acknowledgements

We wish to thank Rafik Assabgui, Julie Chapados, and Nicole Desaulniers for technical assistance.

## References

Lévesque, C. A., and A. W. de Cock. 2004. Molecular phylogeny and taxonomy of the genus *Pythium*. *Mycological Research* 108:1363-1383.

Martin, F.N., and P.W. Tooley. 2003. Phylogenetic relationships among *Phytophthora* species inferred from sequence analysis of mitochondrially encoded cytochrome oxidase I and II genes. *Mycologia* 95 (2):269-284.



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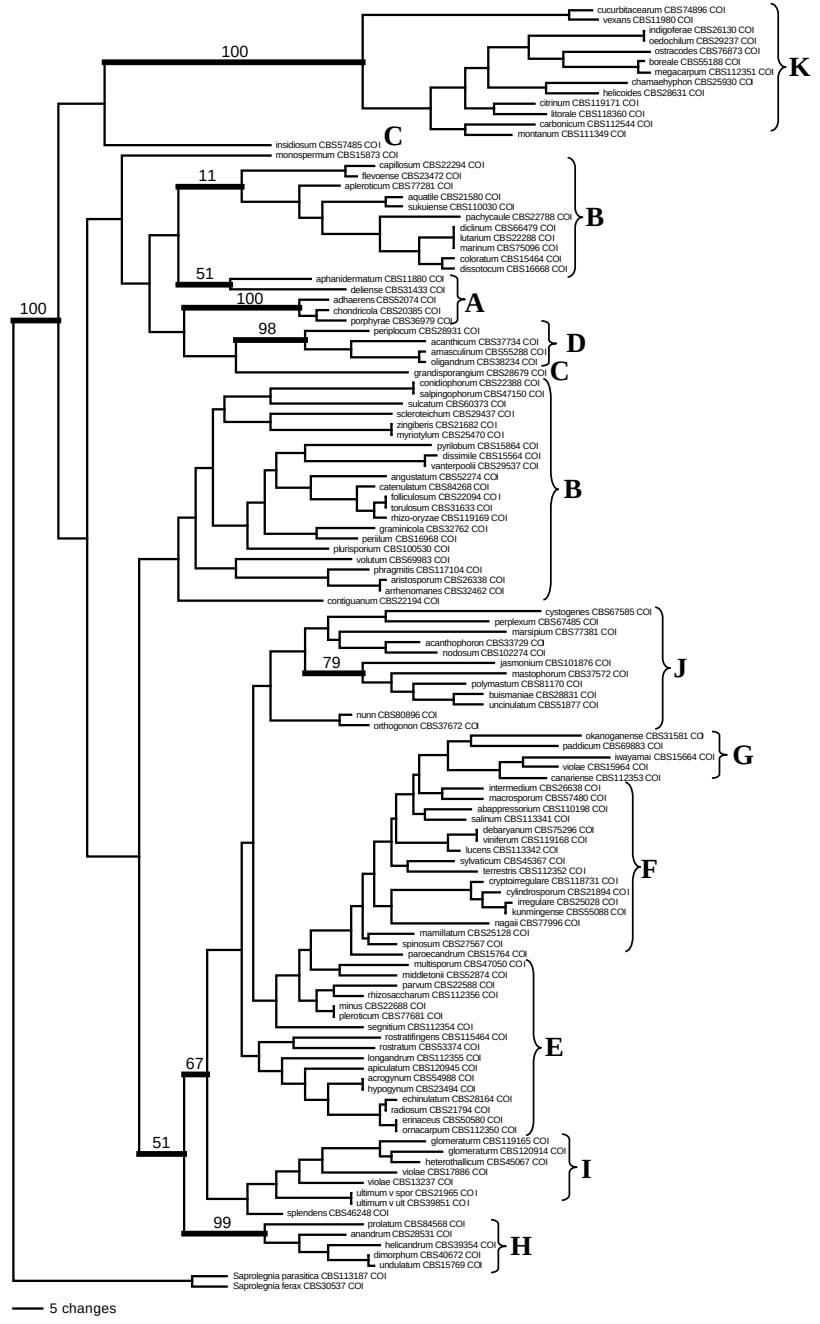
# COI
# 5’ end of
# Cytochrome Oxidase I
# (124 species)




Maximum Parsimony

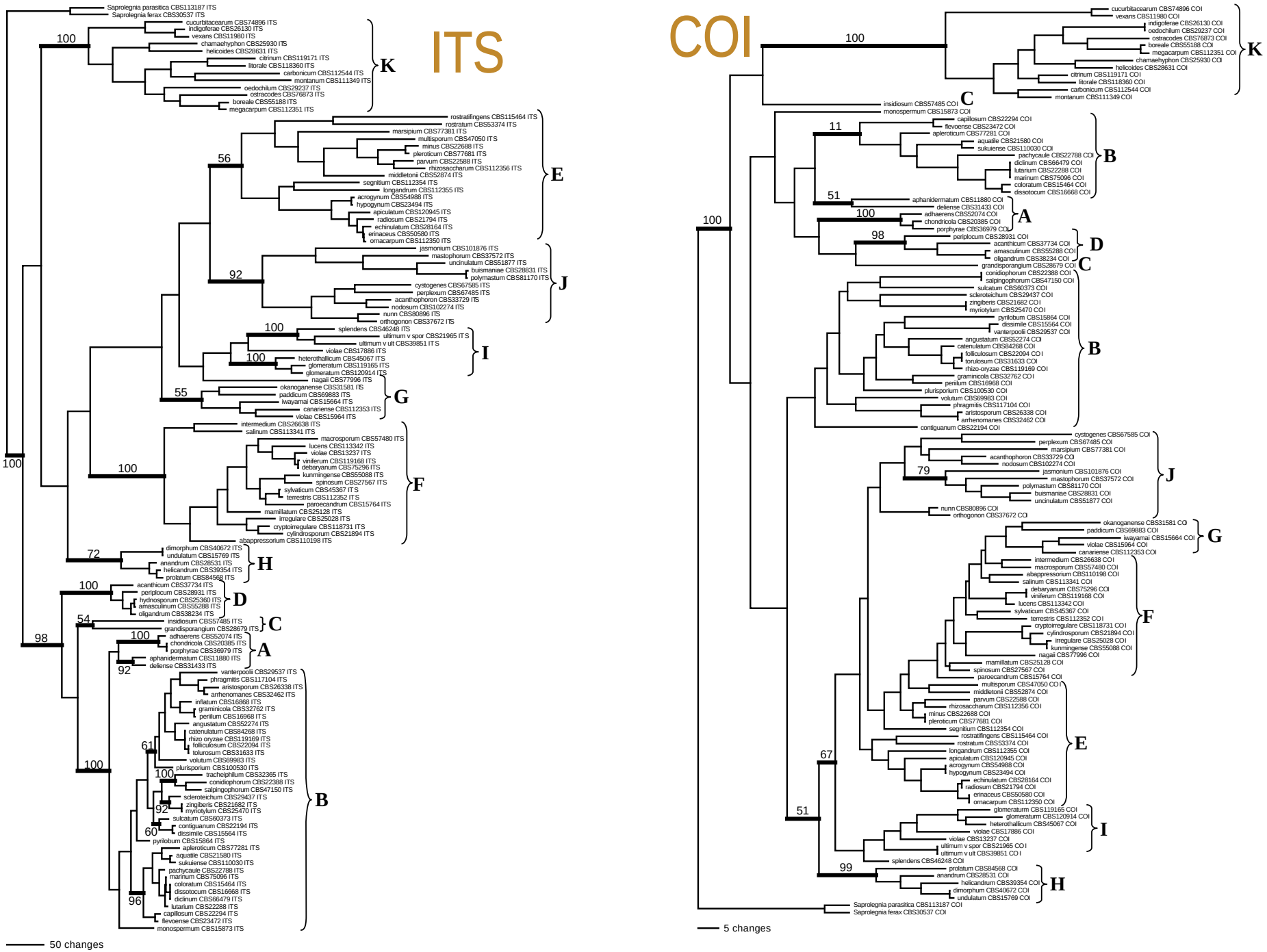
# Interspecific divergence for various markers and clades

**Interspecific Divergence**

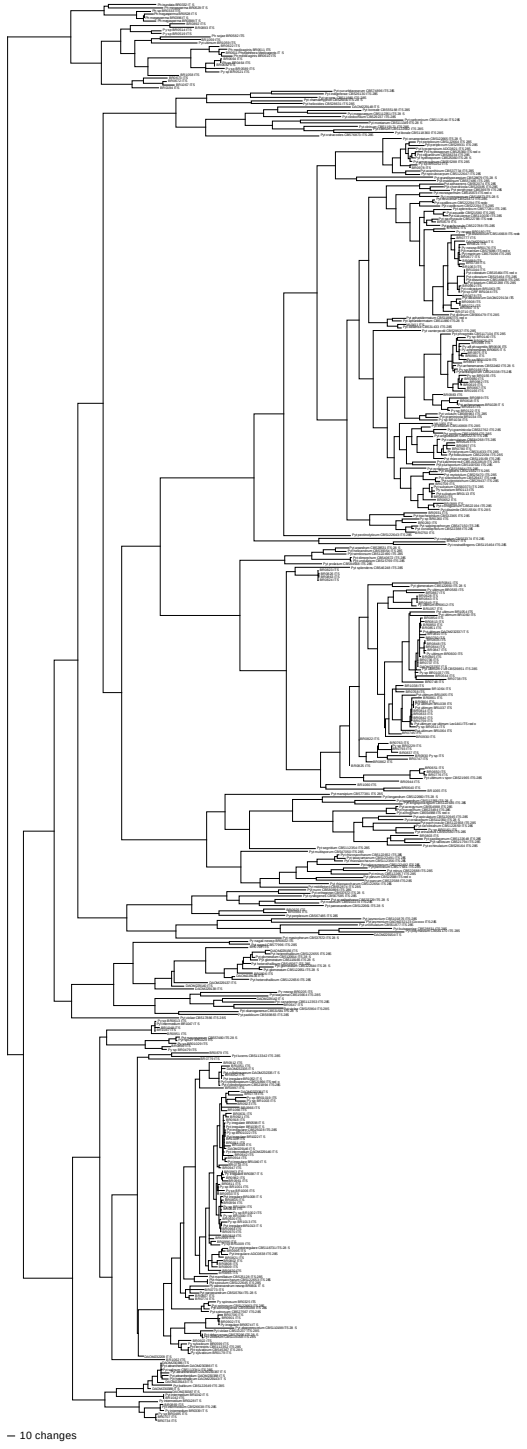
| | | Clades A-D | | | Clades E-J | | | Clade K | | |
|---|---|---|---|---|---|---|---|---|---|---|
| Marker | Average Length | Mean | Min | Max | Mean | Min | Max | Mean | Min | Max |
| LSU | 1452 | 3.8% | 0.0% | 8.1% | 6.0% | 0.0% | 9.9% | 5.8% | 0.0% | 9.3% |
| ITS | 825 | 11.4% | 0.0% | 22.3% | 24.8% | 0.0% | 36.8% | 21.0% | 1.9% | 27.3% |
| COI | 679 | 7.7% | 0.0% | 11.5% | 6.0% | 0.0% | 11.2% | 6.2% | 0.0% | 9.9% |

Mean Interspecific Divergence per Clade

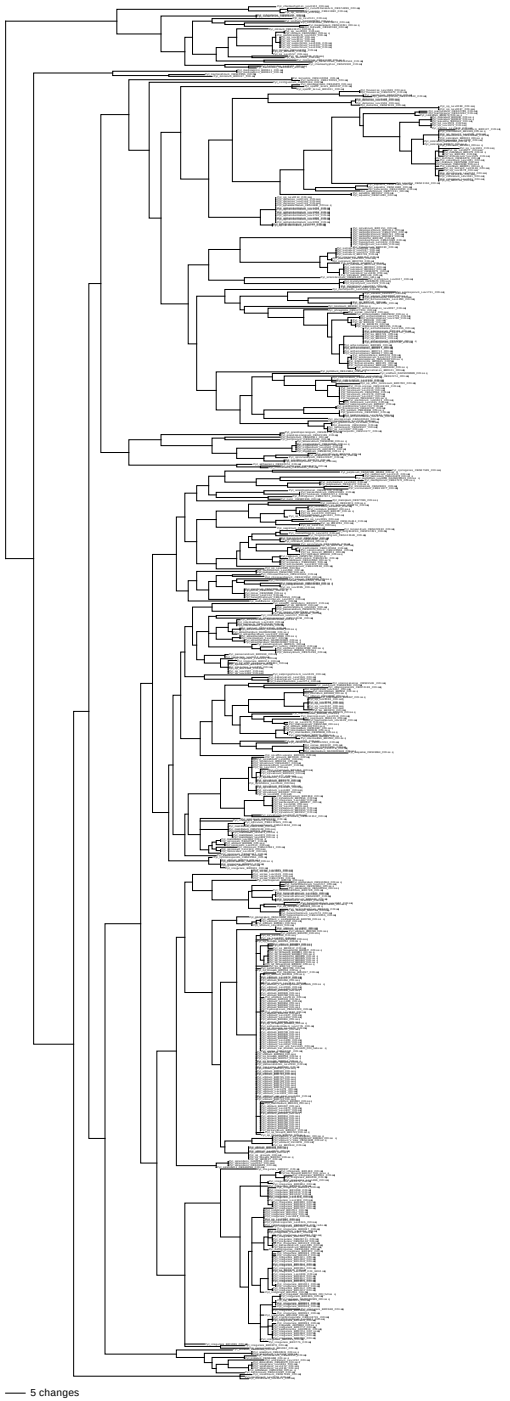
| Marker | A | B | D |
|---|---|---|---|
| LSU | 2.3% | 2.2% | 0.4% |
| ITS | 8.7% | 8.2% | 2.8% |
| COI | 6.2% | 6.9% | 3.4% |

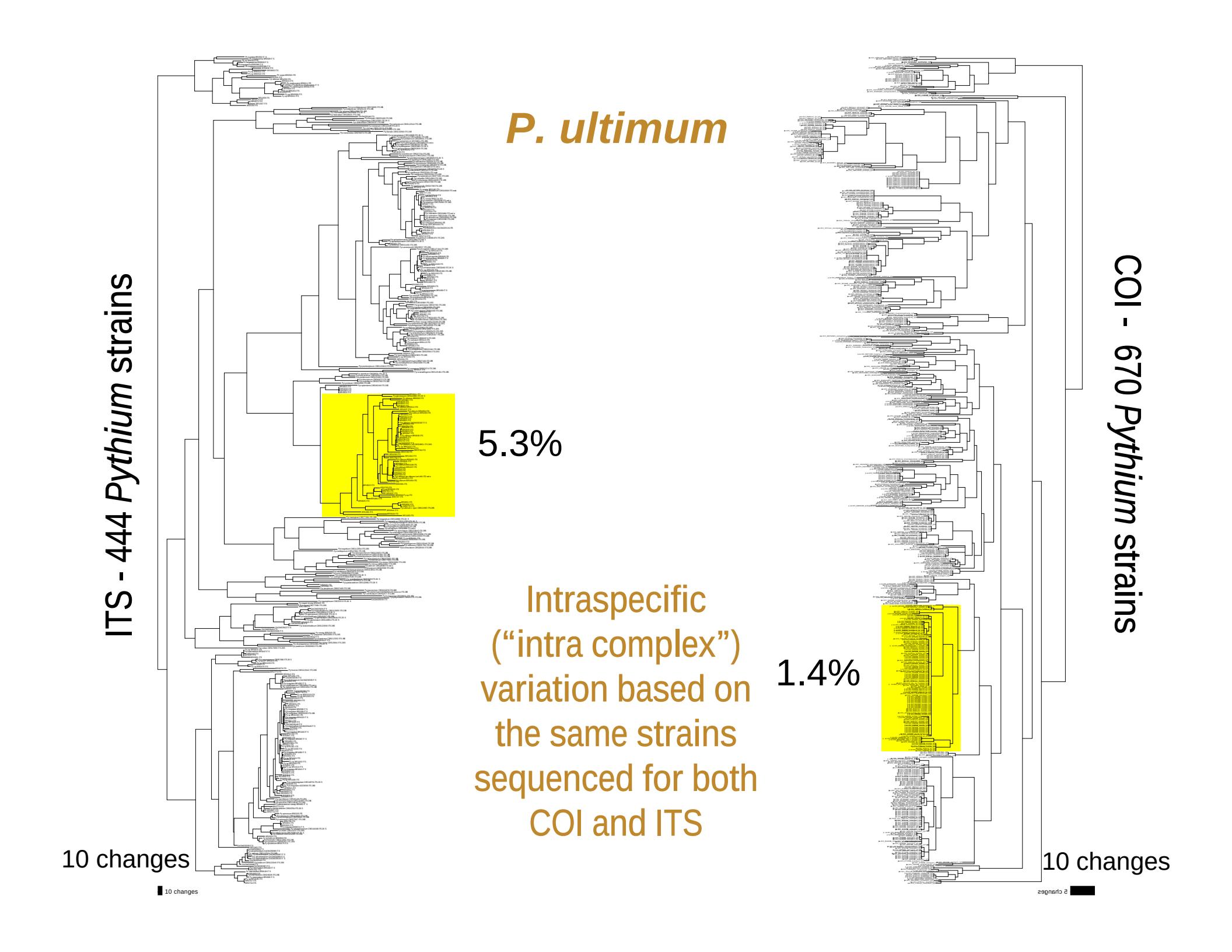

ITS
COI
K
E
J
I
G
F
H
D
C
A
B
50 changes
5 changes

# ITS
# 444 *Pythium* strains
# CBS and DAOM



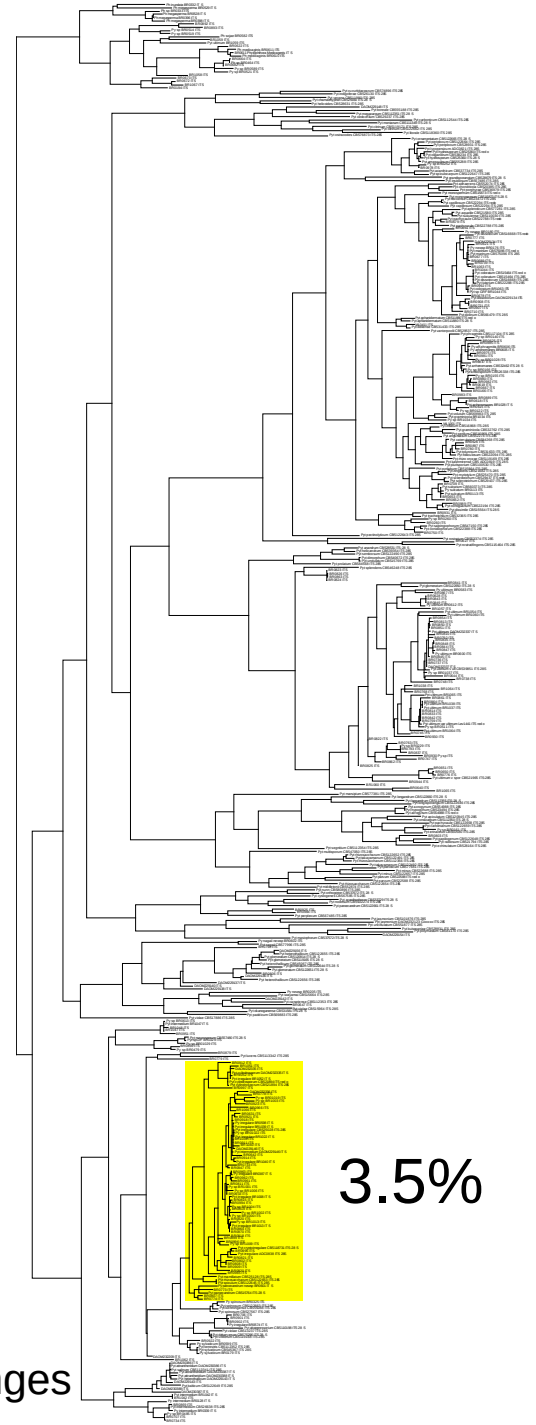
# COI 670 *Pythium* strains CBS and DAOM




ITS - 444 Pythium strains
P. ultimum
5.3%
Intraspecific ("intra complex") variation based on the same strains sequenced for both COI and ITS
1.4%
COI - 670 Pythium strains
10 changes
10 changes
10 changes

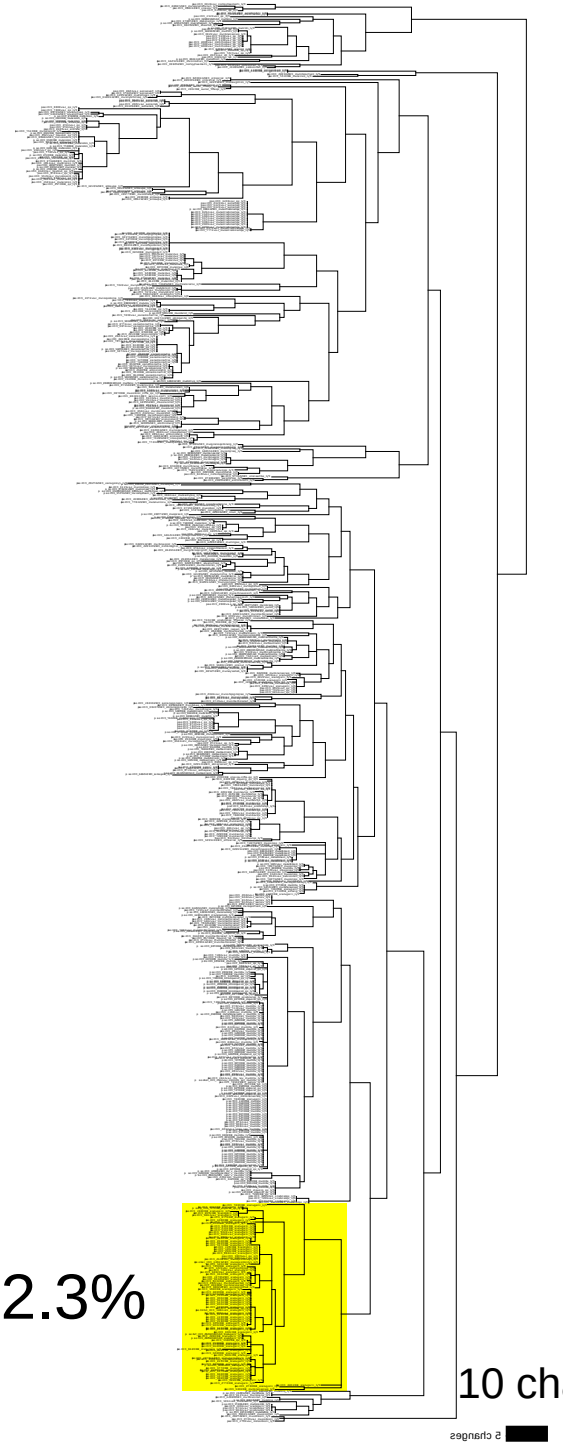
# *P. irregulare*

ITS - 444 *Pythium* strains




Intraspecific ("intra complex") variation based on the same strains sequenced for both COI and ITS

COI - 670 *Pythium* strains



## There are also analogies between functional genomics and molecular diagnostics using phylogenetic databases

- Identify Up and Down regulated genes.

  some techniques:
  EST's
  and arrays
- Quantify most important genes affected

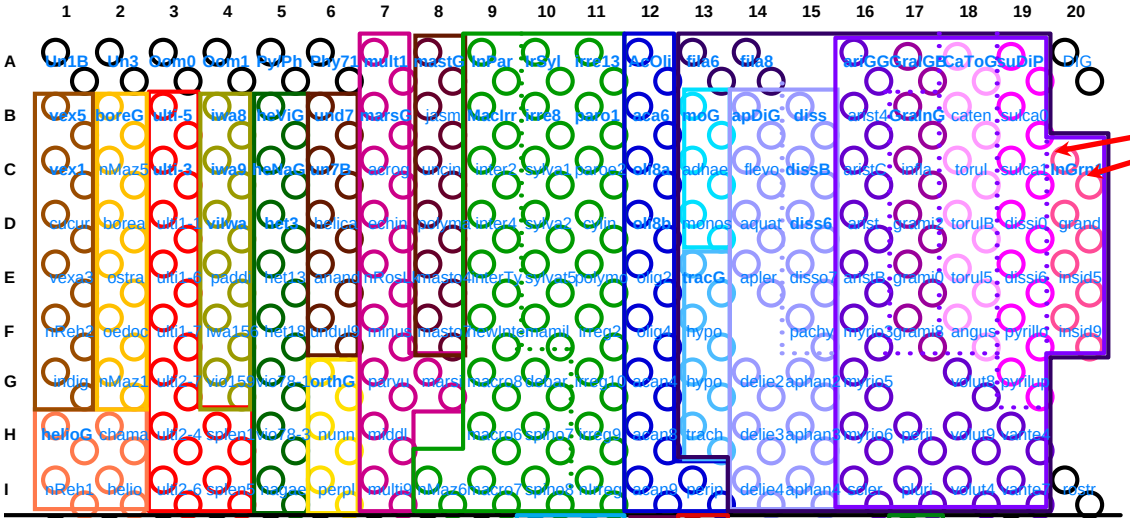
  RT-qPCR

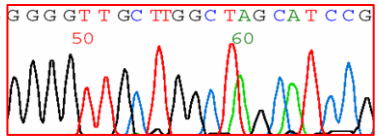
- Identify « Up and Down » regulated species.

  some techniques:
  PCR/cloning/sequencing
  and arrays
- Quantify most important species in pathosystem

  (RT)-qPCR

# Oligo arrray for *Pythium* species




Each pair of dots is a «signature» DNA fragment for a species

*Pythium* species array

# Detection with DNA arrays

extract DNA from sample

↓

PCR: amplify-label barcode using oomycete-specific primers

↓

Hybridization: mix PCR product
and a DNA Array

↓

read results

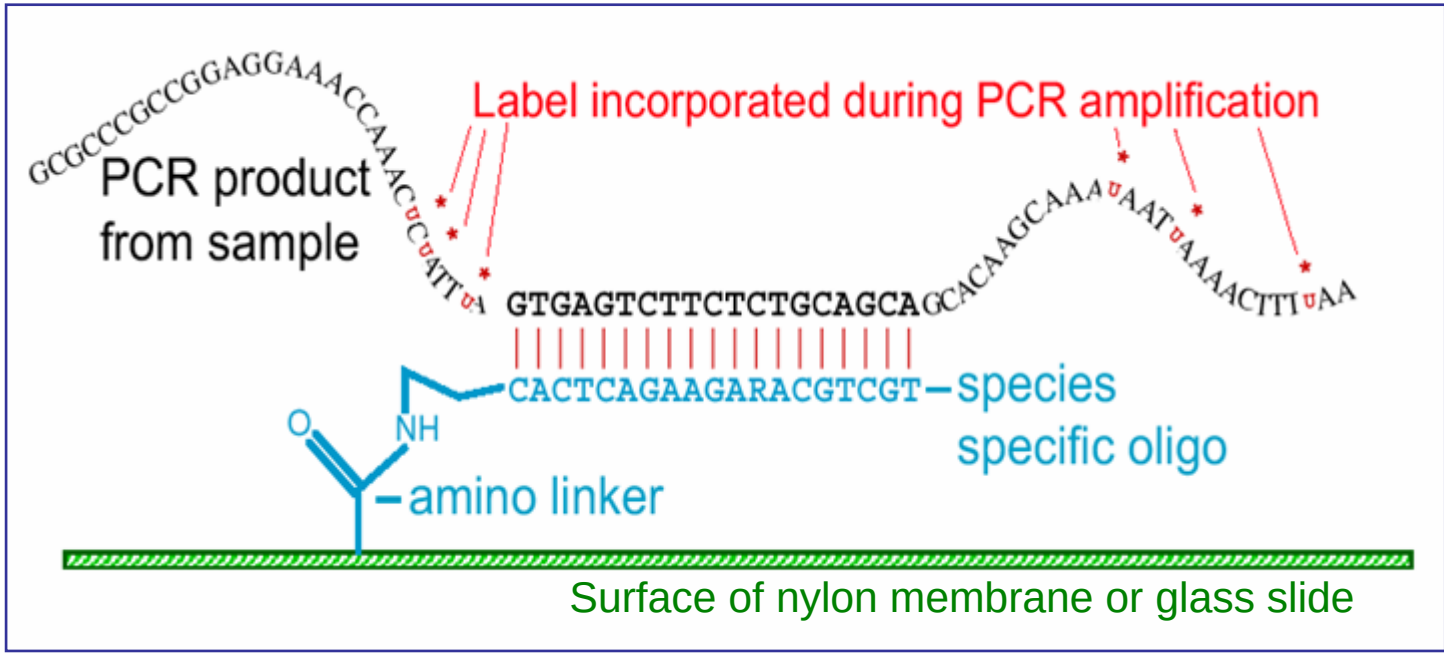


TABLE 1—*Continued*

| Location | Code | Origin(s) of oligonucleotide | Sequence |
|---|---|---|---|
| C16 | ari192 | *aristosporum = arrhenomanes* | AGTTAATTCTGTACGCGTGGT |
| D16 | ari193 | *aristosporum = arrhenomanes* | GTTAATTCTGTACGCGTGG |
| E16 | ari194 | *aristosporum = arrhenomanes* | GTTAATTCTGTACGCGTGGT |
| F16 | myr195 | *myriotylum = zingiberis* | GCTCTGCGCGAGTGGG |
| G16 | myr196 | *myriotylum = zingiberis* | CTGCTGTTATGGCGGAC |
| H16 | myr197 | *myriotylum = zingiberis* | TGCTGTTATGGCGGACT |
| I16 | scler679 | *sclerotеichum* | GTGTAGTAGAACTTTGCTGCTC |
| A17 | GIn210 | *graminicola, inflatum* | CGATGTACTTTTCAAACCCA |
| B17 | GIn211 | *graminicola, inflatum* | CGATGTACTTTTCAAACCCATT |
| C17 | infla | *inflatum* | GGCGCATGTATGTGTGTCTG |
| D17 | gra213 | *graminicola* | TCCACAGACTAATCCCAAATT[b] |
| E17 | gra214 | *graminicola* | CTCTCGAGGGTAAAGGAGG |
| F17 | gra215 | *graminicola* | GGCTGCATGTATGTGTAGTC |
| G17 | | NS | |
| H17 | perii | New species | GGTGGAGCCGTCAGGTTCT |
| I17 | pluri | *plurisporium* | CATTTGTTTGGTTCTGCCGA |
| A18 | CaTo74 | *catenulatum, torulosum* | TACATGCAGCTCTACCTTCGTT[b] |
| B18 | cat222 | *catenulatum* | GGTTTCTGCCGATGTACT |
| C18 | tor223 | *torulosum* | GGTTTTGCCGATGTACTT |
| D18 | tor224 | *torulosum* | GGTTTTGCCGATGTACTTT |
| E18 | tor225 | *torulosum* | CTCTTGGACGCCCTACT |
| F18 | angus | *angustatum* | CATGTATGTGCGGCTTTGC |
| G18 | vol201 | *volutum* | AATGTAGTTTATTCTGTATGCG |
| H18 | vol202 | *volutum* | GTTTATTCTGTATGCGCG |
| I18 | vol203 | *volutum* | GTGTTTGAGAGAAGTGCTGAC |
| A19 | SuDi231 | *sulcatum-dissimile-pyrilobum* | GTGGGCCGCTTTATTGTGG |
| B19 | sul232 | *sulcatum* | AACCGTAATAATCATGTTTTGT |
| C19 | sul233 | *sulcatum* | ACCGTAATAATCATGTTTTGT |
| D19 | dissi234 | *dissimile* | TATTGTGGCTTGCCGATG |
| E19 | dissi235 | *dissimile* | GCTTTATTGTGGCTTGCC |
| F19 | pyril236 | *pyrilobum* | GCAGCAACCTCCTACTACAC[b] |
| G19 | pyri237 | *pyrilobum* | GTGTAGTAGGAGGTTGCTGCT |
| H19 | van204 | *vanterpoolii* | GTGTGACTTGTGAACGCATTG |
| I19 | van205 | *vanterpoolii* | AAGGTGGATAGTGGCGTA |
| A20 | | SD[a] | |
| B20 | | NS | |
| C20 | InGr241 | *insidiosum, grandisporangium* | GCGTTCGAGCATYACACTT[b] |
| D20 | grand | *grandisporangium* | GTGCTTTGCTGCTGCTGAG |
| E20 | Insi243 | *insidiosum* | CGTTGATCTCTCTTGTGTCTTA |
| F20 | Insi244 | *insidiosum* | GGCTTGAGGCTGAACGAAG |
| G20 | | NS[b] | |
| H20 | | NS | |
| I20 | rostr251 | *rostratum* | GAGCAGAGGTGAAGTGTCTC |

[a] Codes are the first few letters of a species or group from which the oligonucleotides were designed. Oligonucleotides were designed from the positive-sense strand of the ITS sequences, including the 5.8S rRNA gene, except for those indicated.
[b] Oligonucleotides designed from the complementary strand of the ITS sequences.

| Sequence |
|---|
| TTCTTAACGGAACAAGCG |
| TGTATGTGTGTTGTGGGCG |
| |
| TGGCGTGCGTTTTGCGT |
| CTTTCGTTCTCACAGTATAATCAGT[b] |
| CGACTACACGGAAGGAAGAA |
| AGGTCGAGTTGCTTTGCT |
| GTCGAGTTGCTTTGCTCT |
| CTGTTGGCTGTATTTGATACTG |
| TGCTGGCTTTGTTGCTGG |
| GAGCTTCATTGTTTGGCG |
| TGCGGGTGCTATTTTGAC |
| CTGCTTTGCATGAATGTG |
| ACACACAACAAATAACGACAG[b] |
| GTTTTTGCATACTTGTGTGTG |
| AGGTCGTGTTGCTGTGTGC |
| GGCTGACTTACTTTTTCAAA |
| TTGGTATATTTGTTTATGCACA |
| GCGGGTGTGCTGTGCG |
| GCGGGTGCTGATGCGAC |
| GAAGGTTGTGTGTTGTTATGTG |
| AAGGTTGTGTGTTGTTATGTG |
| GGTCGTGTGTTGCTGTGTG |
| GGTCGTGTGTTTGCTGTG |
| GGCTGACTTATCTTTTTCAAA |
| TGTGTGTGCAGTTGAGGGC |
| TAGGTCAGCCGCGCAC[b] |
| TGTTGCATGCGCGGCT |
| GAGTGTGTGTGTTGTCGGT |
| CGAGTGTGTGTGTTGTCGGT |
| TGCGTATGCGGATGTCTCT |
| TCAGCAAATCCGCATC[b] |
| CGTTCAGCCTCAAATCTT[b] |
| GAGTCTGCGTCTATTTTGGA |
| TCTGCGTCTATTTTGGATG |
| GCTTCGTCGCAAGACTTG |
| TTCGTCGCAAGACTTGA |
| TGTTCTGTGTCTCGTCTTGT |
| CTGTGTCTCGTCTTGTCAAAA |
| TGTGCCTCGTCTTSTTGAAA |
| GCCTAACATACCGCCAA[b] |
| GAACGAAGGTGAGCTGCT |
| TGAGCTGCTGTTATGGTGG |
| TATTTTTGTATTGTGGCTTGC |
| AGAAGGCACAGAACATAATTTT[b] |
| CTGCCGATGCTTTTTCAA |
| GCGATGCTTTATTGCGT |
| CTGCCGATGTATTTTTCAAAC |
| GAAGACGAAGCACAGAACATA |
| TGCAAMGTCGGGCCGAA[b] |
| ACAATTAAGCAGSCCACCT[b] |
| CGGGAGAGCTGAACGAAG |
| TGTTCTGTGCGATCTCCTC |
| CTGTGCTTTTTCTCCTCGG |
| |
| ACGAAAGTTTCTGGTTTTAAT |
| CGAAAGTTTCTGGTTTTAAT |
| |
| TCTTCTCGGAGAGAGCTG |
| TCTTCTCGGAGAGAGCTGA |
| TGACTGGAGTTGTTTTCTGTT |
| CGCTCTAGCTTCGGTTAGA |
| CGAAACAGAGCGTTCAAGA[b] |
| AACGAAAGTTTATGGTTTTAAT |
| ACGAAAGTTTATGGTTTTAAT |
| TTGCAATTTATTGTGAACAA |
| CAAAAACTTTCGTTCTCGGA[b] |
| GTGTGACCTTCGAATGCGG |

*Continued on following page*

tted on the DNA arrays[a]

| Sequence |
|---|
| TTTCGCTGCGTTCTTCATCG[b] |
| CWAGASATCCRYYGYTGAAAS |
| GTGTGGTAATGATCCTTCCG[b] |
| CGAGCCTAGACATCCACTG[b] |
| CATCCACTGCTGAAAGTTG[b] |
| AATCCTGCAATTCGCA[b] |
| GTGACCTTTGGCGATGG |
| TTGATTGTGCTGGCGG |
| GAGCATGTTTTGGGCTTC |
| GCGTTTTGAGTGTGTGTTC |
| GAATTTGTGTTTTGATACCGTC |
| GAGTGTGCTTGCGCAATT |
| ATGTCACAAACGGTTCACGT[b] |
| CGAGGAAGGCGAGCTATCT |
| AAACAATTCACGTGGAAAG[b] |
| GCCGTTGTCTTGTTCTTTTGT |
| AGGGCGTTTATTGTGTCGT |
| CCCCTTTTTTTTTAACATGAA |
| GCGTGTCGTTGCTTTGTGA |
| CCCCCTTTTTTTTTATTTTGT |
| CGGGGAGGATGAGCTATC |
| GTGCGTGTTCTCTCTGTTTTG |
| ACCGAAGTCGCCAAAA[b] |
| CGCTAGACTTGCTTACAGTT[b] |
| TGCAAGTTATGATGGACTAGCT |
| GTGTTTTCCTATTTTTGGG |
| CATTTTTGGACACTGGAAC |
| GCGAAAATGTCCTACTAAAC[b] |
| AGATGGAAAATGTGCAGATG |
| GGTGTTTTCATTTTTGGAC |
| GTGAACTGTCTTACTTAGTTTTG |
| TGAACTGTCTTACTTAGTTTTGC |
| TGCTTGATTGTATGCGGG |
| CGTGGTGCGCTGTTTATCT |
| GGTGGCGTCTTGTCTTCT |
| GTTGAGTGTGTTGTCTTTTGC |
| GGTTGGTCTCGTAATGTAAATT |
| GATCTGGTGTTTTCGGATAC |
| CCAGTTCAAGCACACAACC[b] |
| GGCGAAAACAGATTCCACA[b] |
| ACTGTCAAACCTGTTCTGTGC |
| GGTTGGTTTTCTTCTTGTGAG |
| GTCTCCTGTTTTATATATGGG |
| CAATGTGTGTGTGCGGGAC |
| AACCGTCAAGTAATAGATTCAGT |
| TACTTGCCTGTGTCGCTCTTT |
| GGTCGGAGTAAAATCTGG |
| GGTCGGAGTAAAATCTGGC |
| ACGCTAGGGGTTAATGCTC |
| TCTATCTTTTTAAACCCATTACT |
| ATCTATTTTTTAAACCCATTCTT |
| ATTCGCCAAAGTCGCCGT[b] |
| TTGTGCCGTTGCTGTTGTC |
| TCTTTCAAACCCATACATTAAA |
| GGCTGATCGAAGGTCG |
| CAAAGACTTTCGTCCTCACA[b] |
| TATCGCACTTTATTGTGTGTGT |
| GTCGCACTTGATTGTGTGTAT |
| GTGGCGTTAGCAAGCATTGTA |
| CGAGAGGATATTGTGATGCA |
| GGAGGATGTGGATGGATGG |
| TGTGCTGTATTTATATCGTGCG |
| TCTTCTTGGAGATGTGTGCG |
| GTACACCTCAAAGCAAACGC[b] |
| GCGAGCGAGGAGGAGAAGA |
| TTTTCTCGATTGCTTTTTAATT |
| CGATTGCCGTTTTTAATGA |
| GGGTGTTTTTTTCATTTTTG |

*Continued on following page*

**James T. Tambong, A.W. de Cock, N.A. Tinker, and C.A. Lévesque.** 2006. Oligonucleotide array for identification and detection of *Pythium* species. Applied & Environmental Microbiology *72*:2691-2706

# Soil processing with *Pythium* ITS array



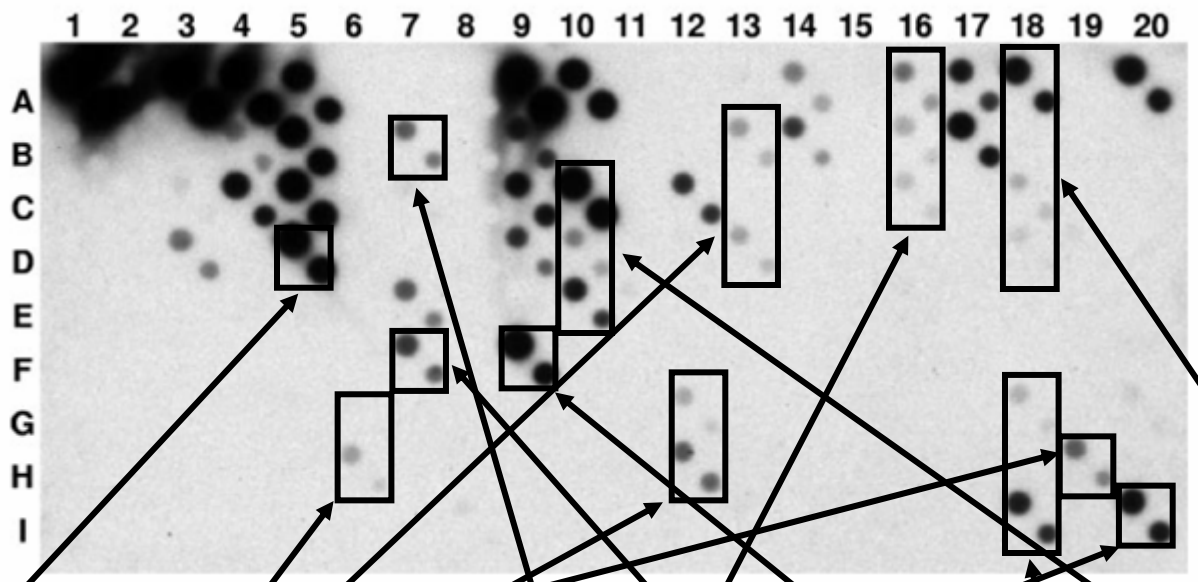
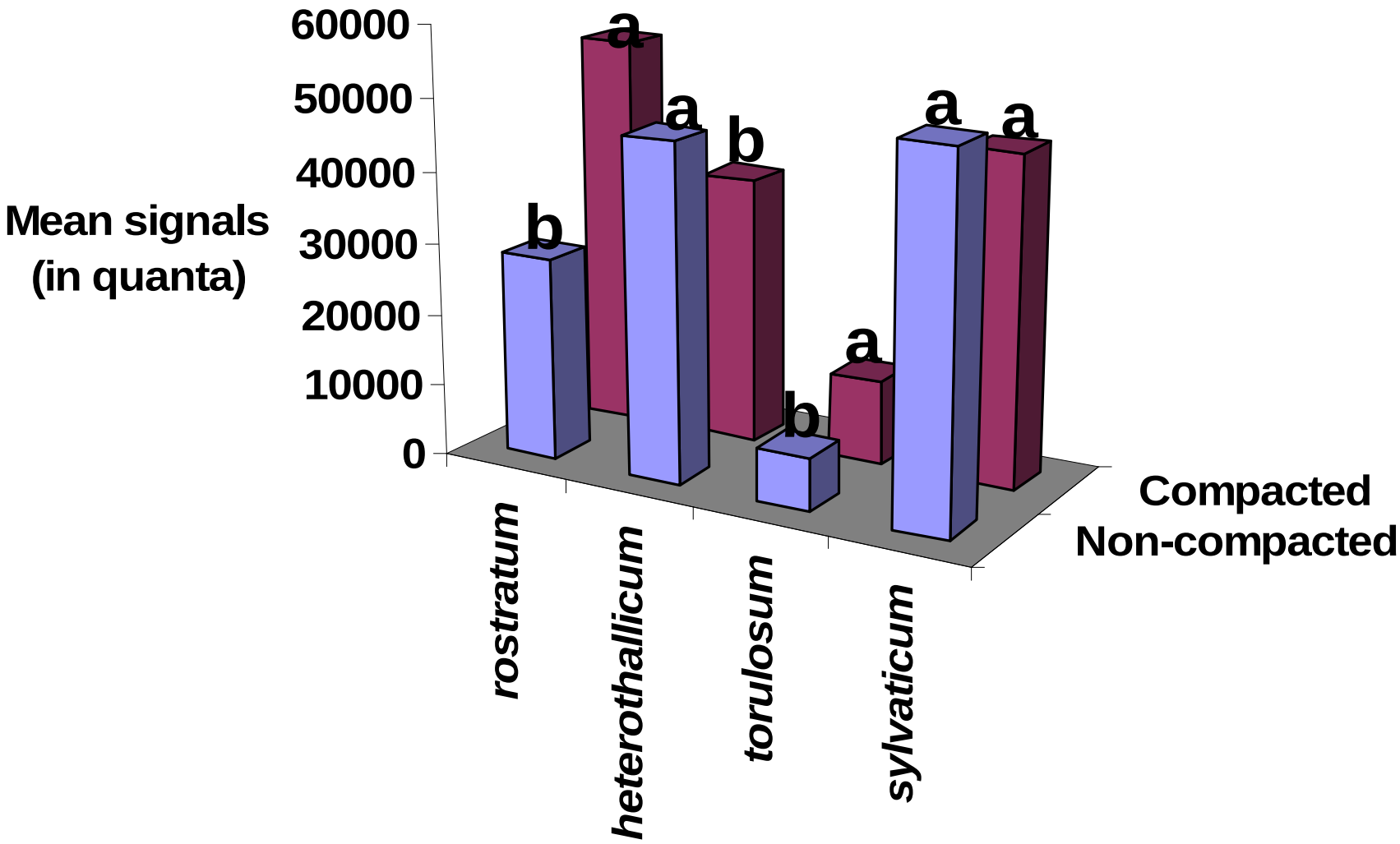



FIG. 3. Hybridization patterns of digoxigenin-labeled PCR amplicons obtained by direct processing of soil. One representative sample out of four replicates that had very similar hybridization patterns and showed the same species complex. Spots A1 to A5 are universal, family- or genus-specific oligonucleotides as described in Table 1. Chemiluminograms were repeated at least twice, and similar patterns were obtained. The species detected in all soil samples were *P. acanthicum* (G12, H12), *P. arrhenomanes* (B16, C16, A16), *P. volutum* (G18, I18), *P. torulosum* (A18, C18, D18), *P. vanterpolii* (H19), *P. monospermum* (B13, D13), *P. acrogynum* (C7), *P. minus* (F7), *P. attrantheridium* (F9), *P. sylvaticum* (C10, D10, E10), *P. heterothallicum* (D5), *P. nunn* (G6, H6), and *P. rostratum* (I20).

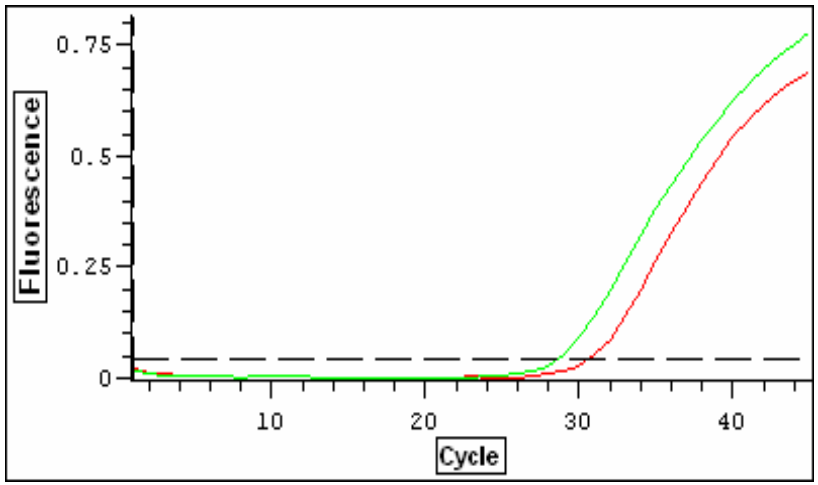
# 13 *Pythium* species found by array hybridization

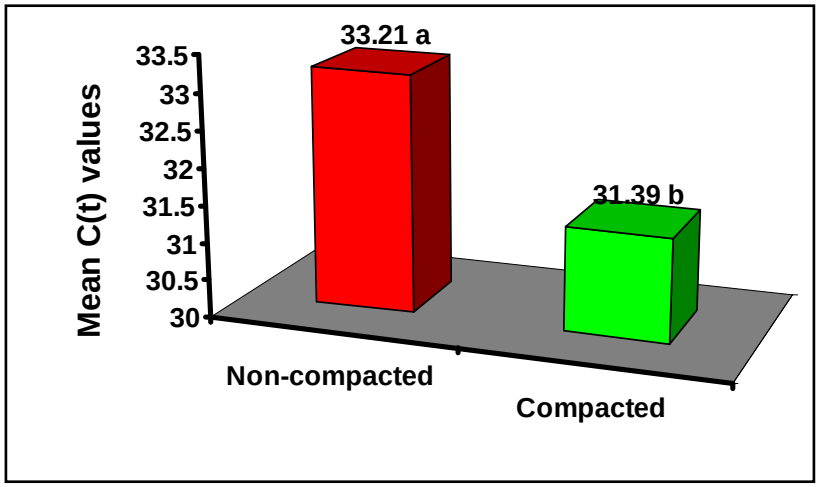
# Effect of soil compaction on populations of different *Pythium* species

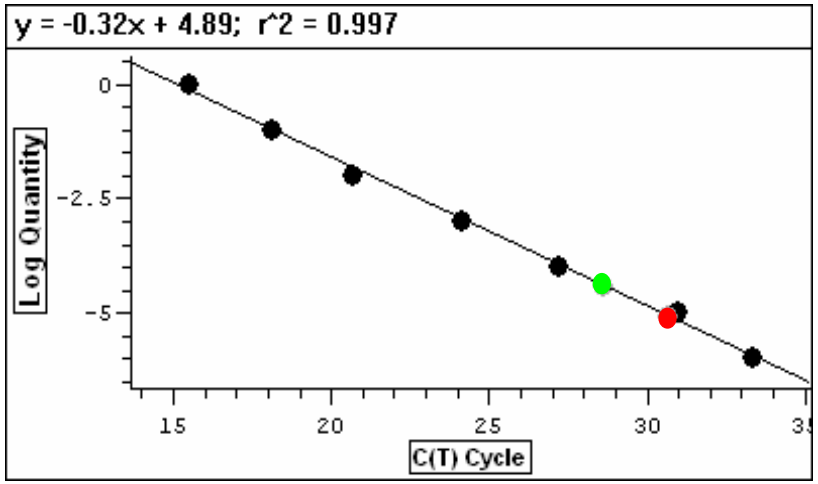
(hybridization signals of species-specific oligonucleotides spotted on DNA array)

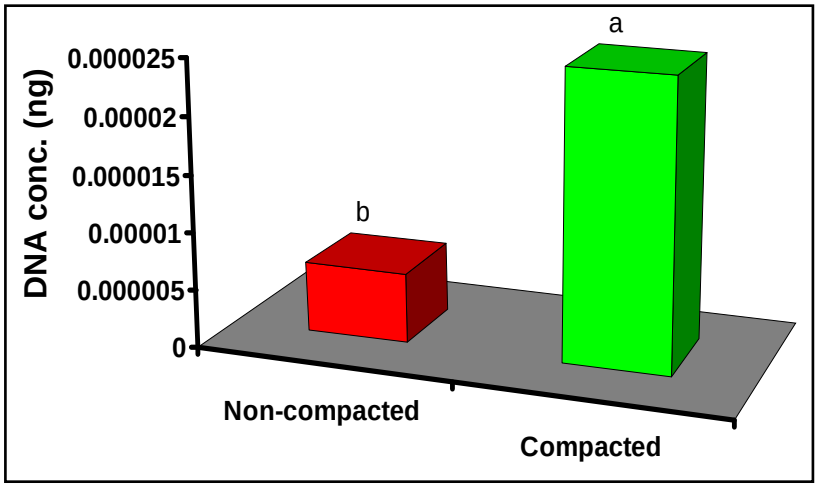


# Validation of DNA array quantitative data by real-time PCR using taqman chemistry: *P. rostratum*



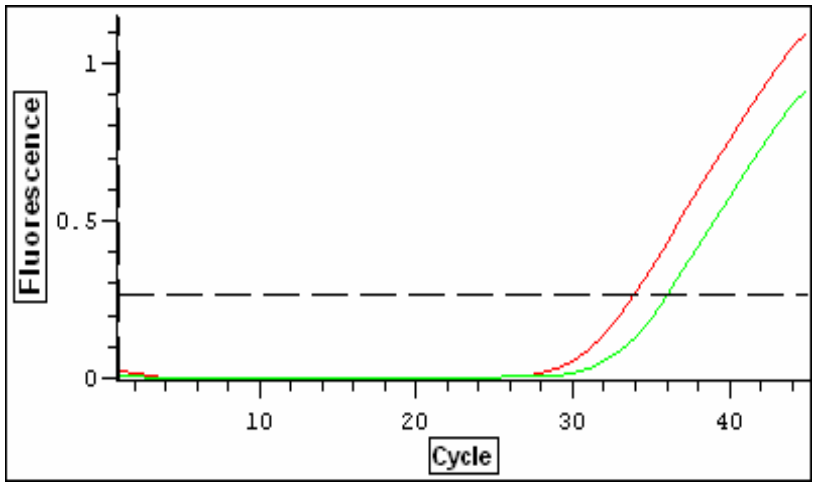



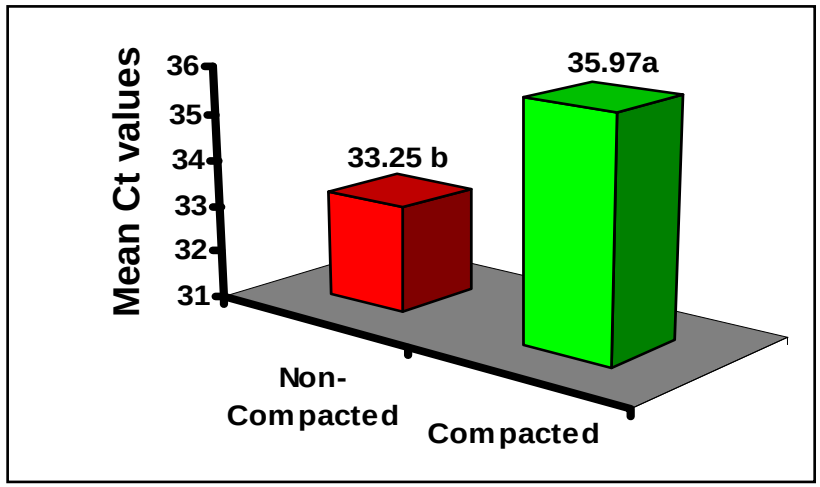



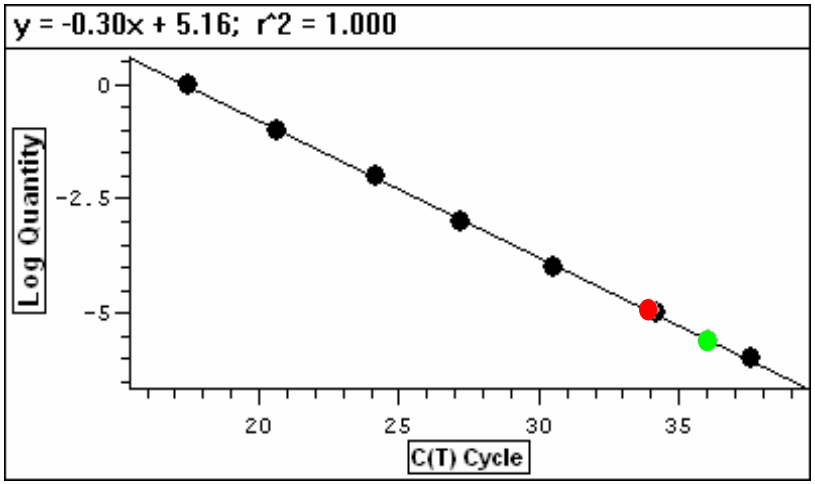



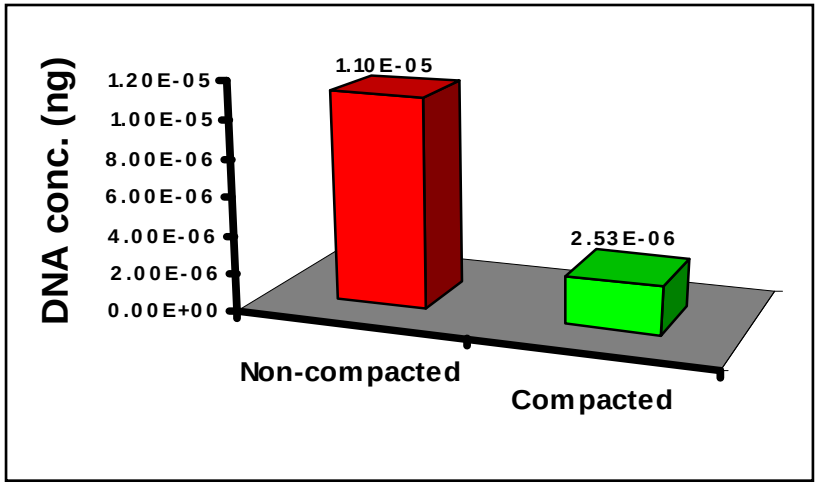

**Standard curve based on known DNA concentration of *P. rostratum***

# Validation of DNA array results for *P. heterothallicum* by Real-time PCR



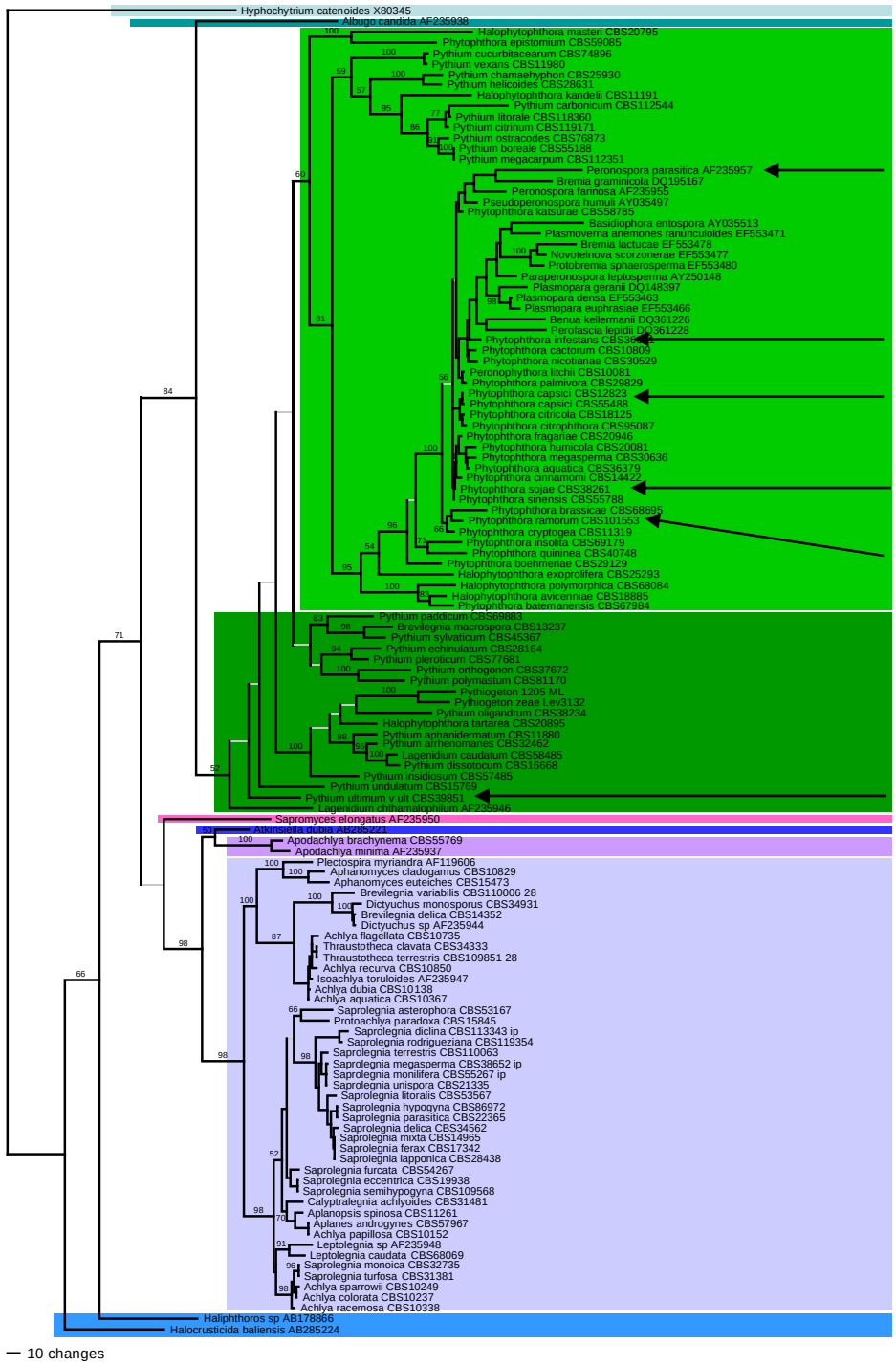




**Standard curve based on known DNA concentration of *P. heterothallicum***

# Phylogenomics

LSU (D1-D3)
Max. Pars. tree
125 sequences
96 CBS
29 GenBank




Hyphochytriales
Albuginales
*Peronospora parasitica*
Peronosporales
*Phytophthora infestans*
*Phytophthora capsici*
*Phytophthora sojae*
*Phytophthora ramorum*
Pythiales
*Pythium ultimum*
Rhipidiales
Atkinsiellales
Leptomitales
Saprolegniales
Haliphthorales

## "Whole Genome Sequencing of *Pythium ultimum*"
## *funded by* US National Science Foundation & USDA

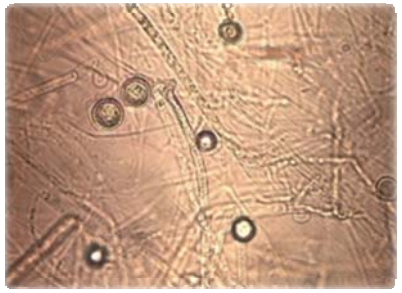
Marcello Zerillo | Ned Tisserat | Jan Leach | Jillian Lang

Colorado State University

John Hamilton

**Collaboration between AAFC and C. Robin Buell, Michigan State University formerly at The Institute for Genomic Research (TIGR)**

# *Pythium ultimum* Transcriptome and Diagnostic Marker Development



*Pythium ultimum*, J. Lang

- EST Library DAOM BR144 = CBS 805.95
  - Starved and nutrient rich media
  - Sequenced using Sanger (9,578 reads) and 454 technologies (90,664 reads); total = ~10Mb
  - 34,495 unique sequences in hybrid assembly
    - Sanger & 454 were complementary
  - 91% of sequences were similar to other oomycetes
- Testing markers to differentiate *Pythium* from *Phytophthora* based on available EST and genomic sequence
  - First set based on EST derived SSRs – variable results, even strain differentiation
    - Some primers amplified a few *Pythium* sp., but not all
  - Second set based on introns, exons or intergenic regions
    - Most primers are specific to *P. ultimum*

# The issue of name (in)consistency

## Google Hits

| | |
|---|---|
| straminipila | 1860 |
| straminopile | 121 |
| straminipile | 87 |
| stramenopile | 8010 |
| stremenopile | 1 |
| stramenipilous | 2 |
| straminipilous | 1760 |
| straminopilous | 16 |
| stramenopilous | 17 |

| | |
|---|---|
| Oomycota | 129,000 |
| oomycetes | 161,000 |
| oomycete | 60,800 |
| oomycetous | 2,810 |
| peronosporomycetes | 5,120 |
| Peronosporomycota | 2,240 |
| peronosporomycete | 498 |
| peronosporomycetous | 9 |

An identity crisis in the oomycetes?

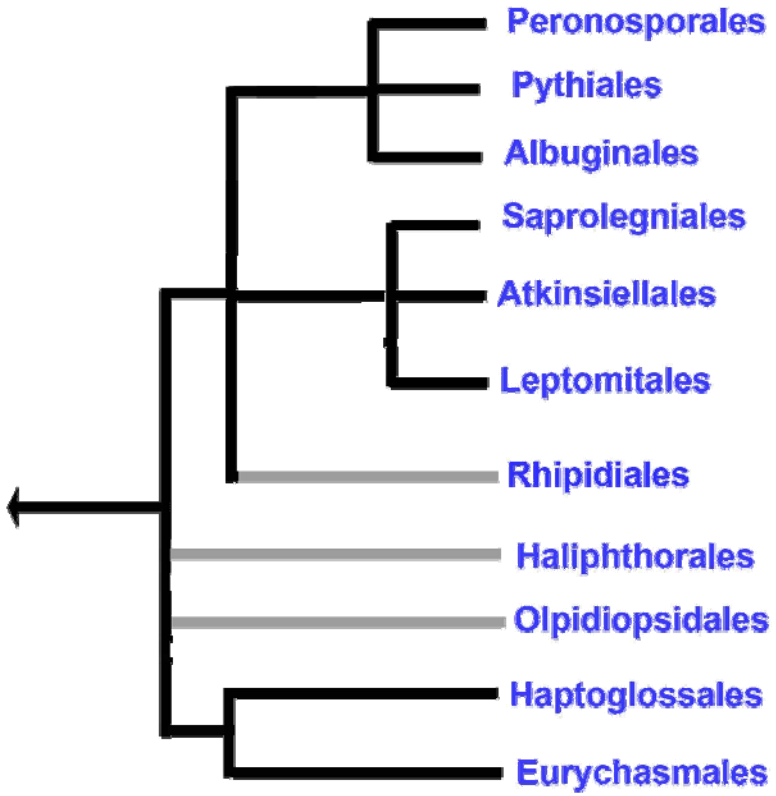
A more coordinated approach for assembling the oomycete tree of life is needed

“AOTOL”?

# Assembling the mycologists of oomycete for the tree of life "AMOOTOL"

**Dr Gordon Beakes**
Mycology
School of Biology and Psychology
Newcastle University

Email: g.w.beakes@ncl.ac.uk




*Draft – Order Tree*

Protists Tree of Life -
Patrick Keeling

These branches may not be monophyletic

# Acknowledgements


- Gordon Beakes
- The Barcode of Life Initiative