DNA Barcoding of Fungi:Assessing the Effect of Barcode Length

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Questions?

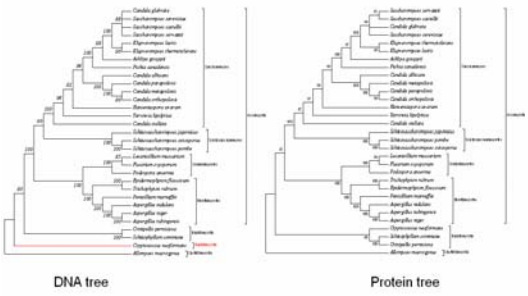
(1) Could standard barcodes (COI with ~650 nt) used in animals work in fungi – for species identification?

(2) Could standard barcodes be used for inferring accurate phylogeny in fungi?

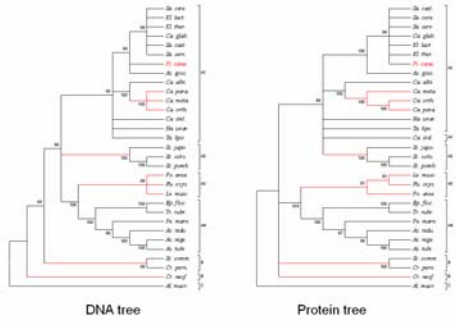
Data collection

31 fungal species: 27 Ascomycota, 3 Basidiomycota, 1 Chytridiomycota
5 protein-coding genes: coding DNA sequences and protein sequences.
COI, COII, COIII, COB, ATP6

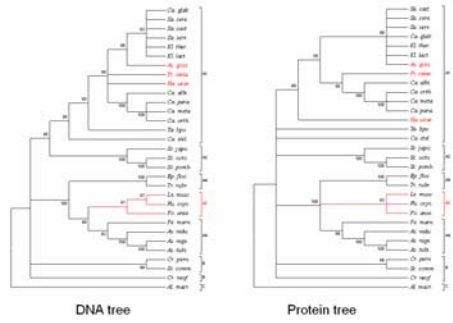
Phylogenetic Trees Based on 5 Genes



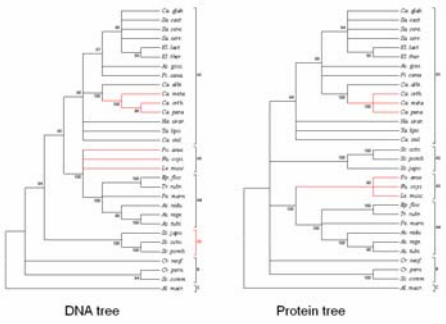
Single-gene Trees (COI)



Single-gene Trees (COB)

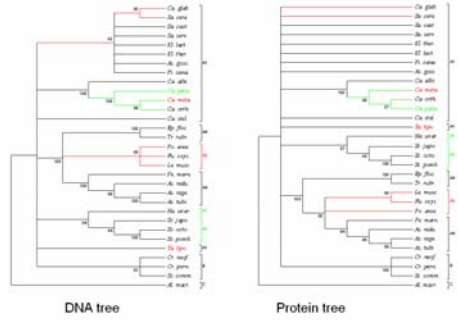


Single-gene Trees (COII)

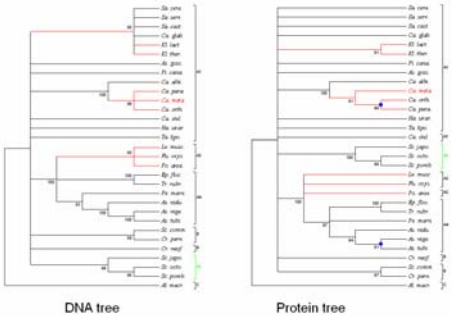


Single-gene Trees (COIII)

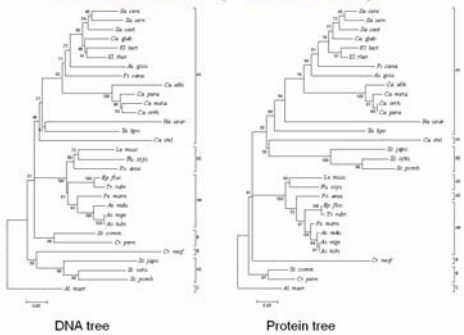
Single-gene Trees (ATP6)



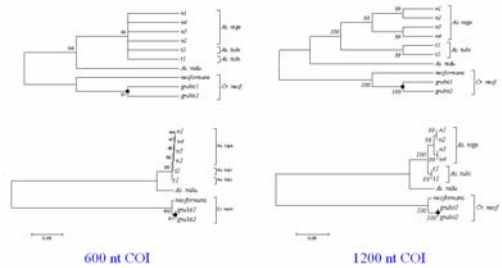
Barcode Trees (~ 600 nt COI)



Barcode Trees (~ 600 nt COI)

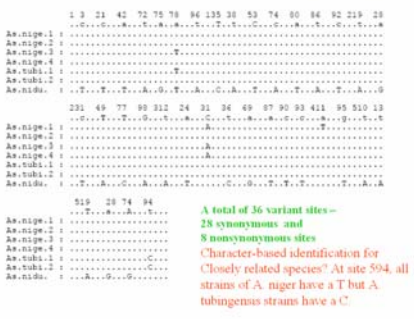


Increasing resolving power by extending barcode length



Clades are labeled as follows: A1, Ascomycota Saccharomyces; A2, Ascomycota Schizosaccharomyces; A3, Ascomycota Sordariomycetes; A4, Ascomycota Eurotiomycetes; B, Basidiomycota; C, Chytridiomycota.

Nucleotide variation within barcode region in Aspergillus species



Summary

➢Standard short barcode sequences are not sufficient for inferring accurate species phylogenetic relationships – though close related species tend to form a correct cluster on a distance-based tree.
➢Based on the publicly available data used in this study, standard barcode region (COI) that is used in animals is suitable (at least promising) for fungal species identification.
➢Extended length of barcode sequences (>= 1.2 kb) are needed for closely related species, i.e., *Aspergillus niger* and *A. tubingensis*. COI has a length of ~1.5 kb – extendable.
➢The suitability of COI still needs to be tested with more intensive sampling – for example, in *Aspergillus* species (there are 200+ species in this genus).

Acknowledgment

This research was supported through funding to the Canadian Barcode of Life Network from Genome Canada through the Ontario Genomics Institute, NSERC and other sponsors listed at www.BOLNET.ca.

The work presented here was published as a full paper of Assessing the effect of varying sequence length on DNA barcoding of fungi. Molecular Ecology Notes. 2007. doi:10.1111/j.1471-8286.2007.01698.x