INTRODUCTION

Heterobasidion annosum is an ecologically and economically important basidiomycete pathogen that infects temperate, coniferous forests worldwide. Previously thought to be genetically and pathogenetically uniform, three separate H. annosum “intersterility groups” (ISGs) were identified in 1978. Designated P, S and F, these groups are characterized, somewhat loosely, by lack of interfertility, host affinity and morphology. Hybrid S/P ISG H. annosum have also been identified and represent one of few fungal pathogen hybrids. Phylogenetic and isozyme studies have shown the three ISGs to be distinct, and in some cases, further separated according to continent. However, the relationships at a finer scale of geographic resolution are less studied.

Specific Aims

• Use a phylogenetic approach to examine genetic relatedness and biogeographical patterns within an H. annosum ISG at the continental level; focus is on the North American P ISG.

• Compare trees constructed from nuclear regions with those from mitochondrial regions. Incongruence between organelle and nuclear sequence trees can indicate possible reticulation.

METHODS

Isolates:

71 isolates from 17 locations:

• 57 P ISG isolates: 56 from North America, 1 from Europe.

• 14 European F and S and North American S ISG isolates (included for purposes of analysis).

• All European isolates from Aymaville (Valle d’Aosta), Italy.

Regions amplified:

1) Elongation Factor 1-α (nuclear) Strict consensus of 24 equally parsimonious trees.

2) ATPase subunit 6 (atp6) Strict consensus of 3 equally parsimonious trees.

3) DNA insertion in the mitochondrial large RNA gene (mitochondrial) Strict consensus of 4 equally parsimonious trees.

Data Analysis:

• Sequences edited and aligned in Sequencher, with manual refinements to alignments performed using Se-Al.

• Trees constructed in PAUP using maximum parsimony methods.

• Gaps coded as missing data, and sequence insertions present in some isolates but not others coded as discrete characters: 0 (insertion absent) and 1 (insertion present).

• As sequences from an appropriate outgroup for all regions have not yet been obtained, all trees are midpoint rooted.

• Consensus trees calculated using “strict consensus” algorithm in PAUP.

RESULTS

• Multiple, equally parsimonious trees for each analysis.

• Strict consensus trees for each region shown below.

• As 1.8 and 2.0 kb inserts into the mitochondrial large RNA gene do not align, two trees shown for this region.

CONCLUSIONS

• There is evidence of geographic structure within the North American P ISG isolates; isolates divide into “East” and “West” North American clades. No consistent evidence of further geographic structure is indicated by these analyses.

• United States Midwest isolates (Missouri) fall into East North American clades.

• A single Canadian isolate ( ) shows evidence of incongruent nuclear and mitochondrial gene trees. It falls into a clade with the East North America isolates for both mitochondrial regions, but into a clade with the West North America isolates in the nuclear region. This isolate will be investigated further for signs of reticulation.

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REFERENCES
