



Wood decay fungi and tree age in living *Eucalyptus obliqua* in southern Tasmania

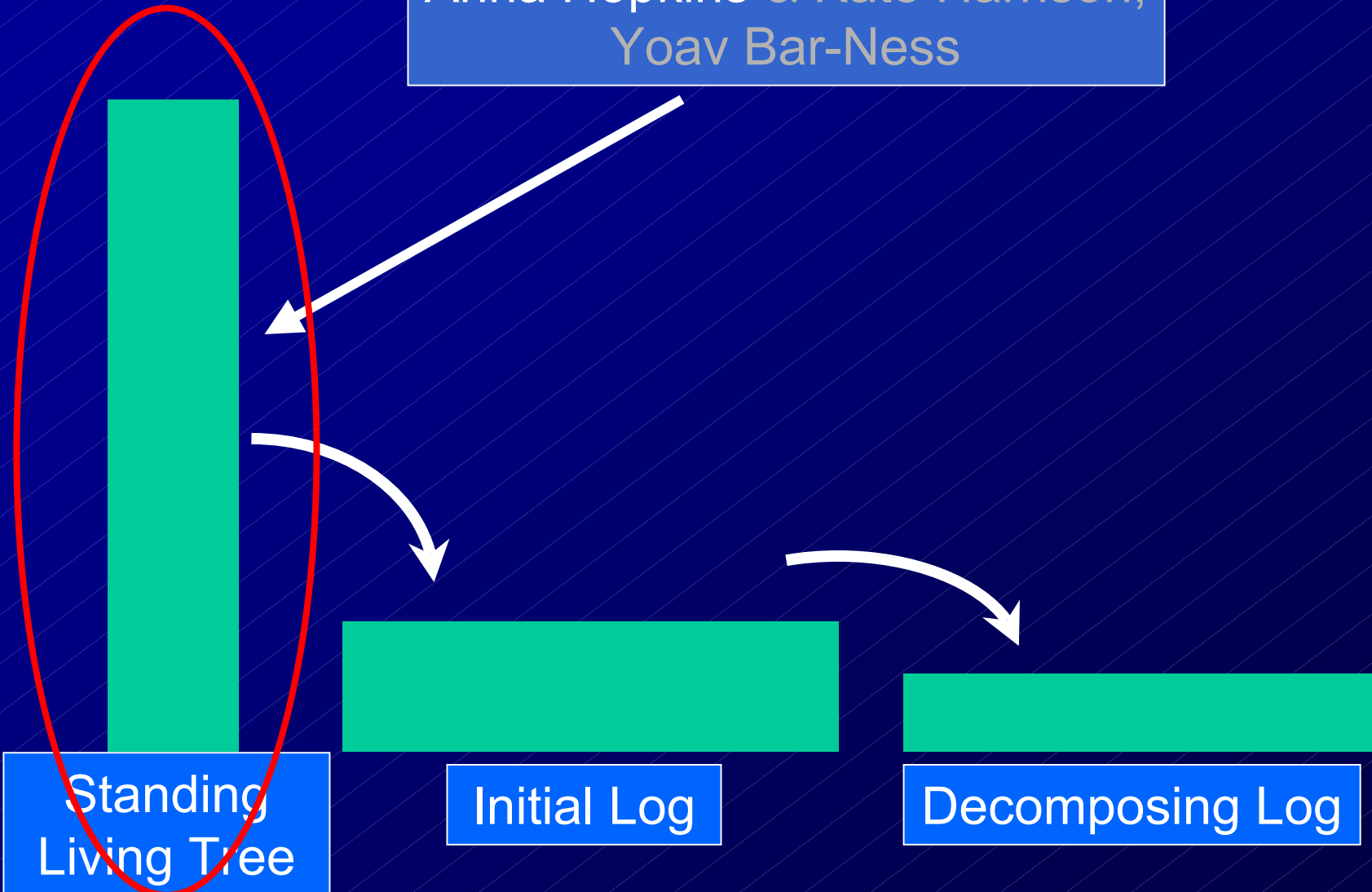
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Project Overview

Anna Hopkins & Kate Harrison,
Yoav Bar-Ness



Forestry in Tasmania

Silvicultural rotation lengths of ~80 years

Reduction of old trees (>150 years old)



Important habitat for mammals, birds..... also invertebrates, fungi & other saproxylic organisms





Aims

Investigate:

- the succession of rotten wood types and;
- the communities of wood decay fungi associated with heart rot formation in *Eucalyptus obliqua* trees of different ages



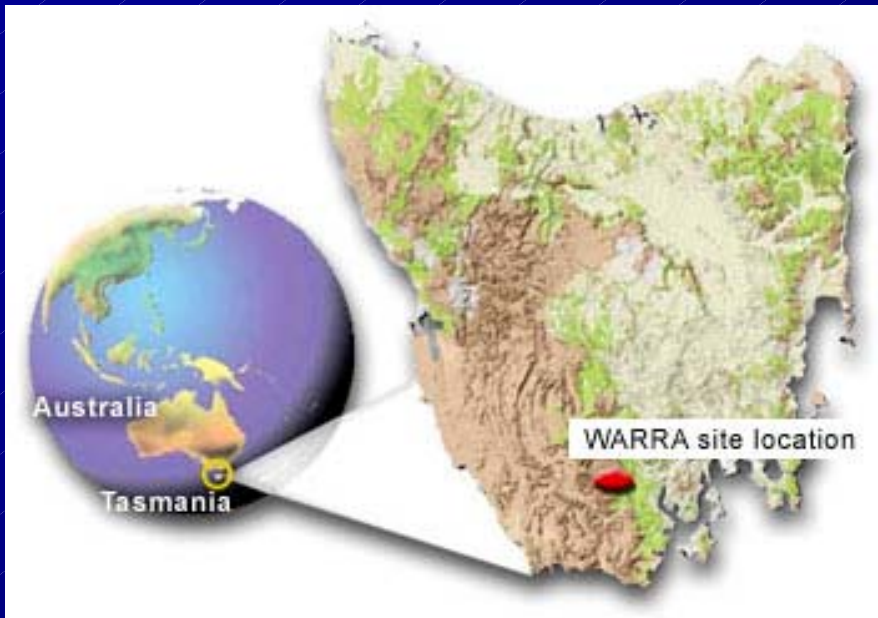
Refine methodologies for the identification of wood decay fungi



Study Site



- At the Warra LTER <http://www.warra.com/>
- In the aggregated retention coupes WR008I and WR001E



Methods



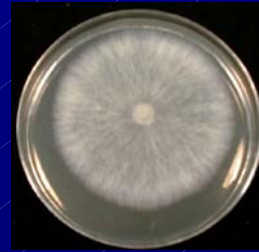
6 trees in each of three age classes: 69, 105, >150 yo.



3 sampling points at 3 heights



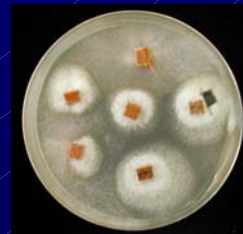
Traced patterns of decay



Cultures of wood decay fungi



Basidiomycete reference library



Incubated decayed wood on specialised media



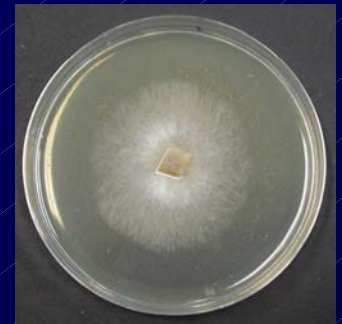
Sampled each decay column

Fungi are poorly studied in Australia

- 5-10% of species described (of 250 000)
- Only ~10 full-time taxonomic mycologists



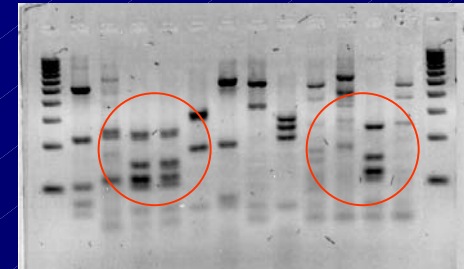
- No taxonomic keys to fungal cultures in Australia
- Use combination of morphology & molecular techniques
- Usually identify to broad morphospecies



Classical Morphology



Molecular Techniques



PCR-RFLP of ITS region & sequencing

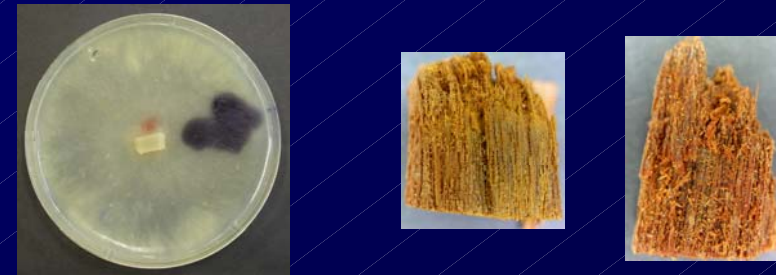


Macro-morphology of cultures



Microscopic characteristics

Ecological Information



Enzyme Reactions & Rotten Wood Type

Results

- 350 individual basidiomycete fungal isolates

Classical Taxonomy

- 16 major morphospecies
- 170 singletons
- No matches to reference library (135 spp.)
- 6 morphospp are old growth specialists
- 10 morphospp are generalists

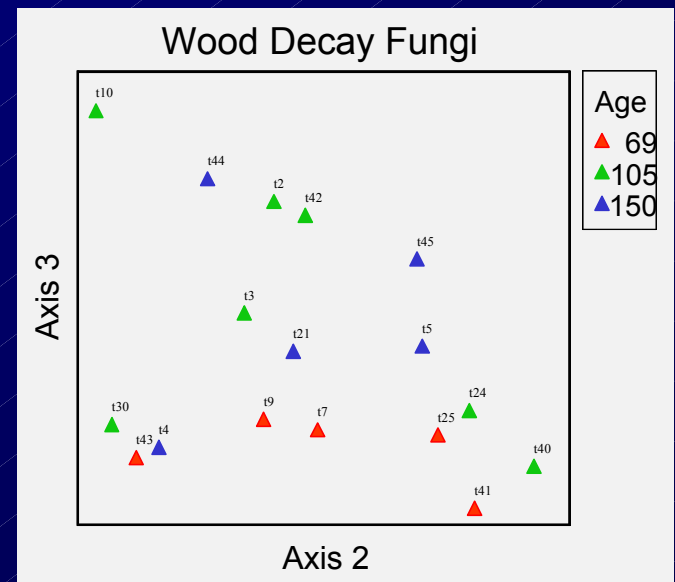


Results: Fungal Abundance

Significantly more morphospecies in old trees

Younger two age classes had similar numbers of morphospecies

Community patterns not clear



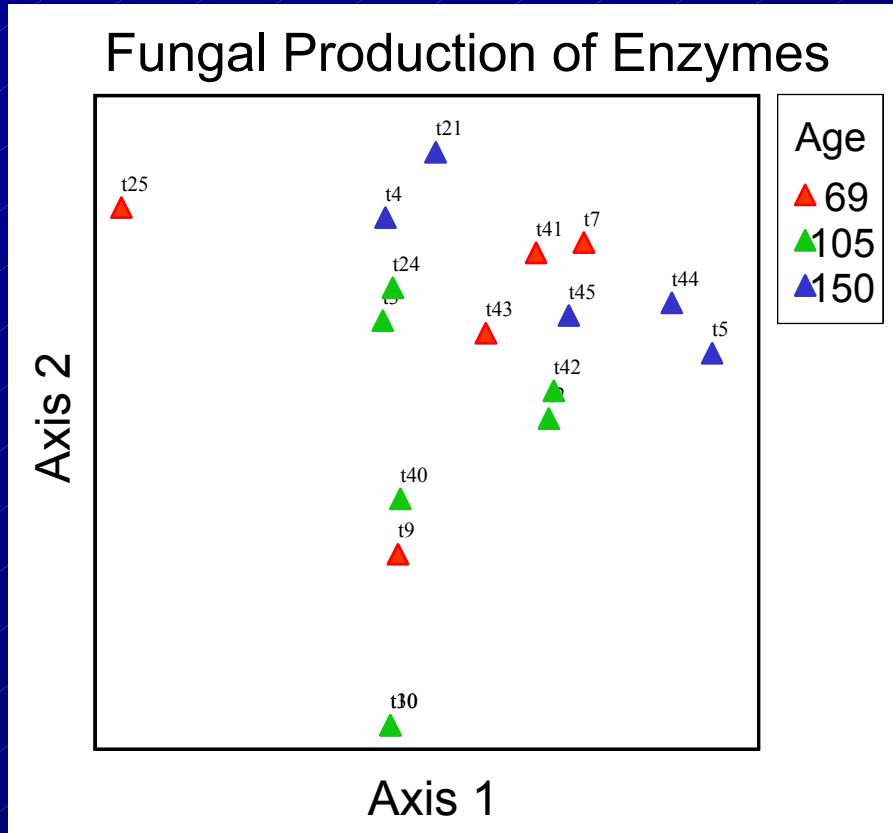
Ordination using NMS

Results: Wood Decay Enzymes

Fungal cultures were tested for 2 enzymes:

White rot (laccase)

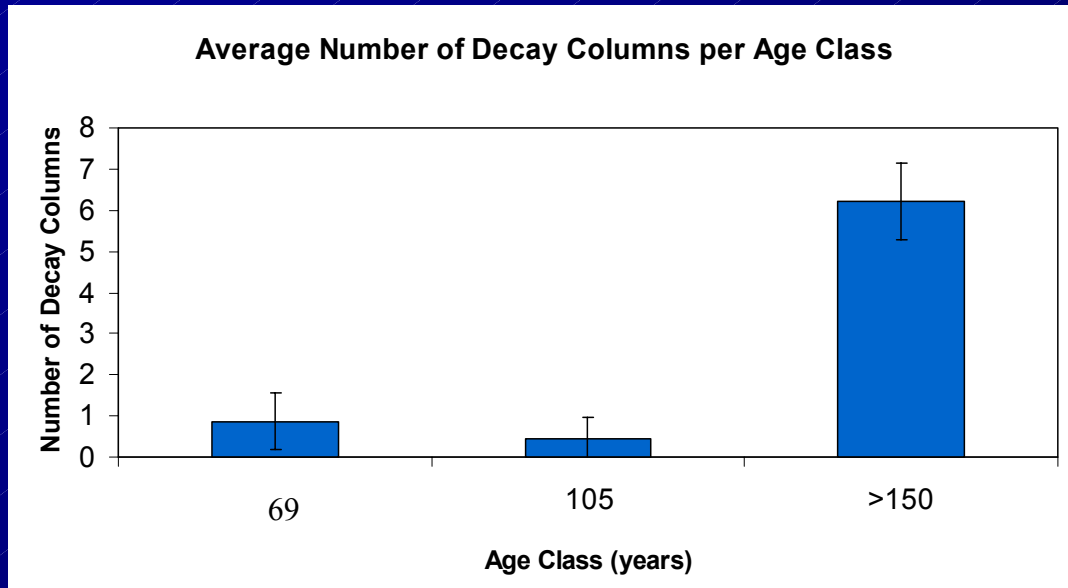
Brown rot (tyrosinase)



Old trees (>150) similar, but also similar to some 69 year old trees

Results: Decay Columns

Measured average number of decay columns in each age



Old trees had more decay than younger trees

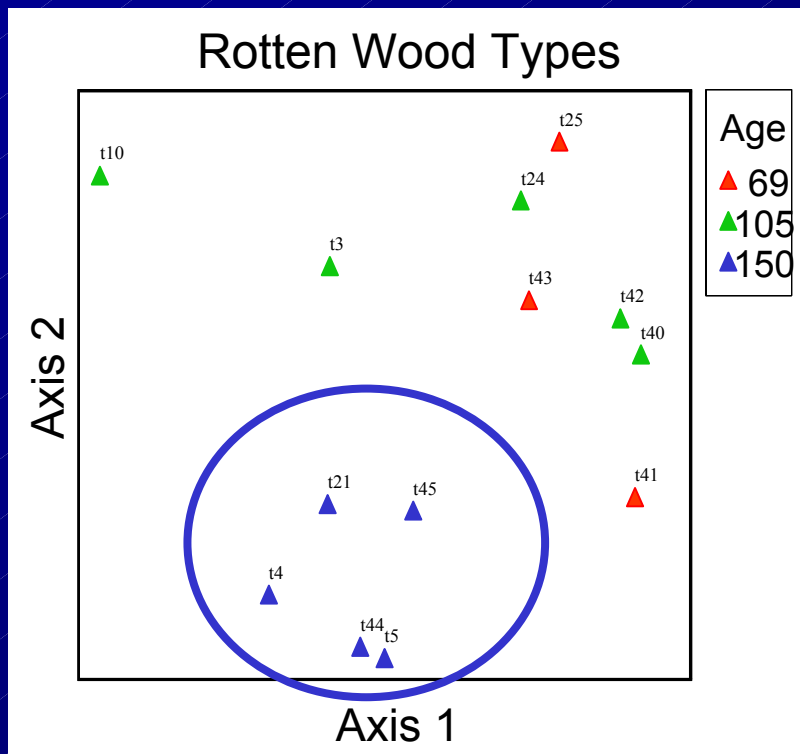
Results: Rotten Wood Types

13 rot types-based on texture and appearance of wood:

White rot (lignin, cellulose & hemicellulose)

Brown rot (cellulose & hemicellulose only)

Selective white rot (lignin only)



Distinctive pattern of rot types found in the old trees

Younger trees all appear to have similar rot types

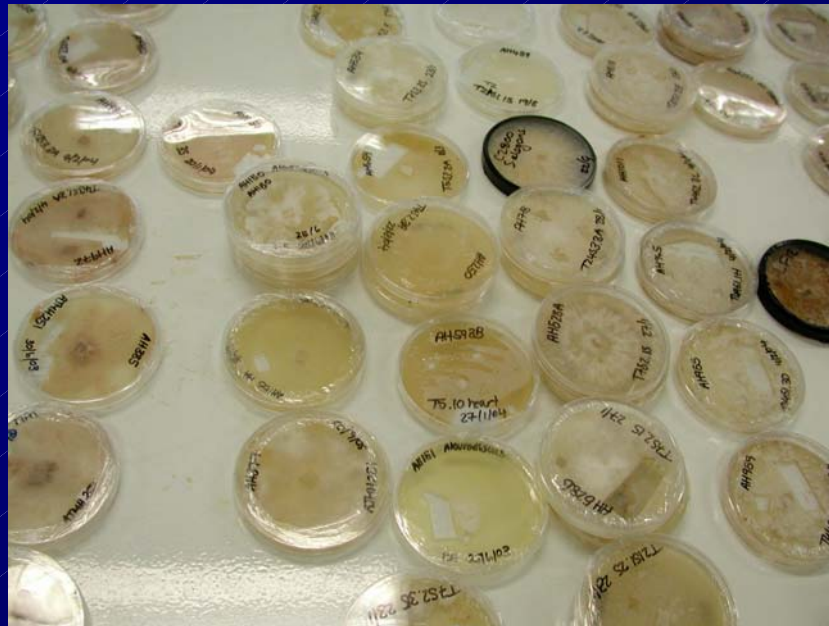
Conclusions: Are old trees special?

YES

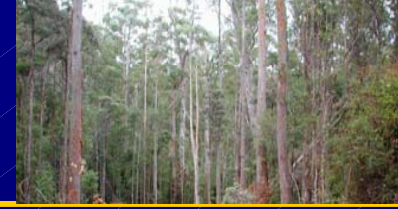


- Patterns of fungal communities not clear but:
 - Old trees (>150 years) have significantly more fungal morphospecies than younger trees
 - Old trees (>150 years) have unique morphospecies of fungi
- Communities of rot types found in old trees (>150 years) are different to younger trees

Begun to develop a database & methods for identification of wood decay fungi in Australia



Future Directions



- Continue to develop molecular methods to identify wood decay fungi
 - Sequence fungi (approx. 350 morphospp.)
- Compare wood decay fungi with saproxylic beetles found in living trees by **Kate Harrison**
- Compare wood decay fungi in living trees with those found in logs by **Zi-Qing Yuan**
- Compare rot types with those found in logs by **Marie Yee** and Zi-Qing Yuan
- Examine fungi associated with hollows in wet forests in collaboration with **Amy Koch**



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