Disease Dynamics in Wild Plant-Pathogen Associations

Jeremy Burdon & Pete Thrall

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The ecological & evolutionary triangle

Pathogen

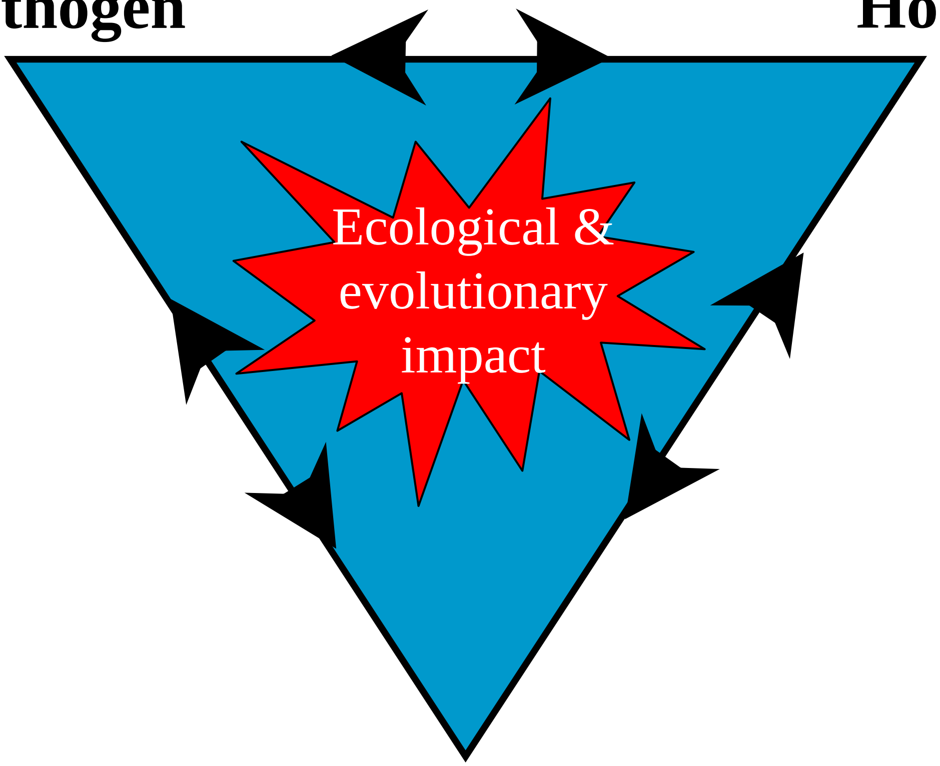
- **Genetics**
- **Phenology**
- **Pathogenicity**
- **Propagule production**
- **Parasitic mode**
- **Target tissue**
- **Dispersal mechanisms**

Etc

Host

- **Genetics**
- **Phenology**
- **Resistance & its distribution**
- **Propagule production**
- **Population size**
- **Dispersal mechanisms**

Etc



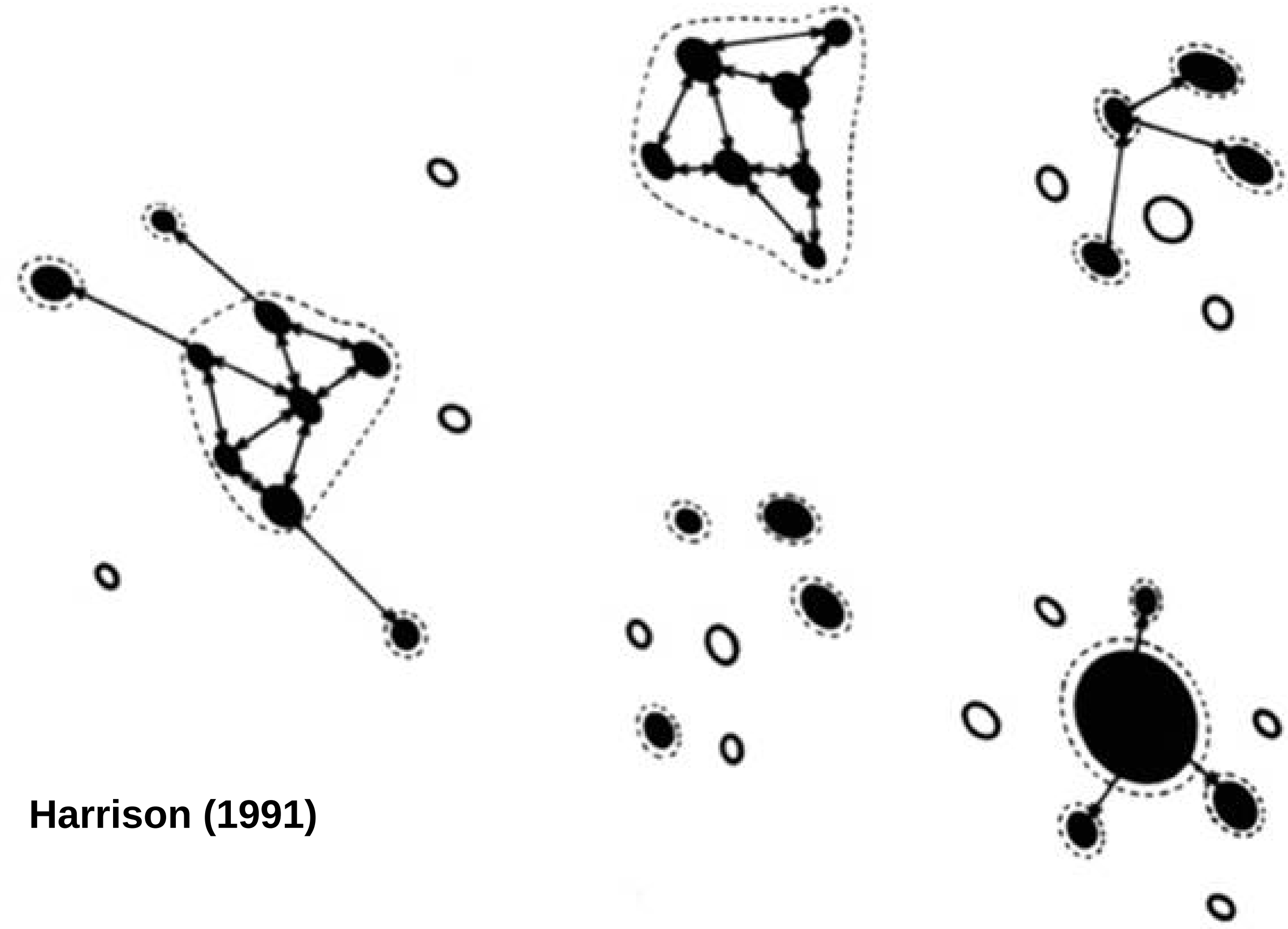
Environment

- **Temperature;** - **Moisture;** - **Season length;** - **Host nutrition; Etc**

Pathogen behaviour in natural ecosystems

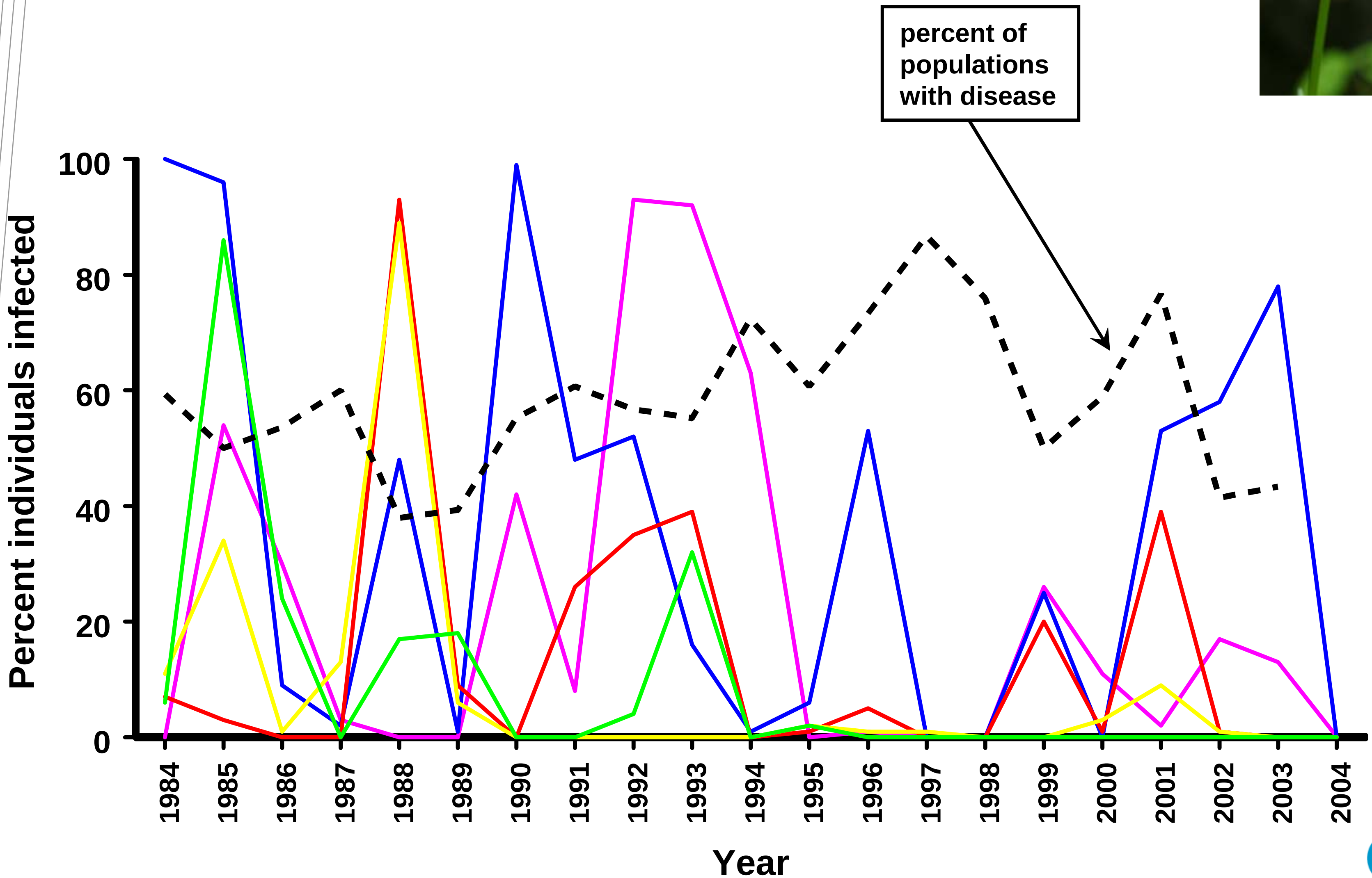
- Wild host-pathogen interactions are genetically and environmentally variable
- Pathogens are much less predictable in natural ecosystems than in agricultural systems.
- Our understanding of host-pathogen interactions in nature comes primarily from two sources: a) long-standing (co-evolved) native associations; and b) invasive situations.
- In native associations, disease typically ‘comes and goes’ (i.e. is unpredictable in space and time) requiring a metapopulation approach.

Metapopulation studies: spatial structure



Harrison (1991)

Local vs. regional persistence in the *Valeriana-Uromyces* interaction



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Life history plays a key role in determining dynamics and disease outcomes

Anthracoidea heterospora

Microbotryum violaceum

- Host range
- Mode of attack and fitness effects (mortality vs. fecundity)
- Transmission mode (e.g. aerial, vector)
- Life cycle (e.g. saprotrophs, necrotrophs, biotrophs)
- Systemic vs. local infection

Life history influences both ecological and evolutionary outcomes

Melampsora medusae

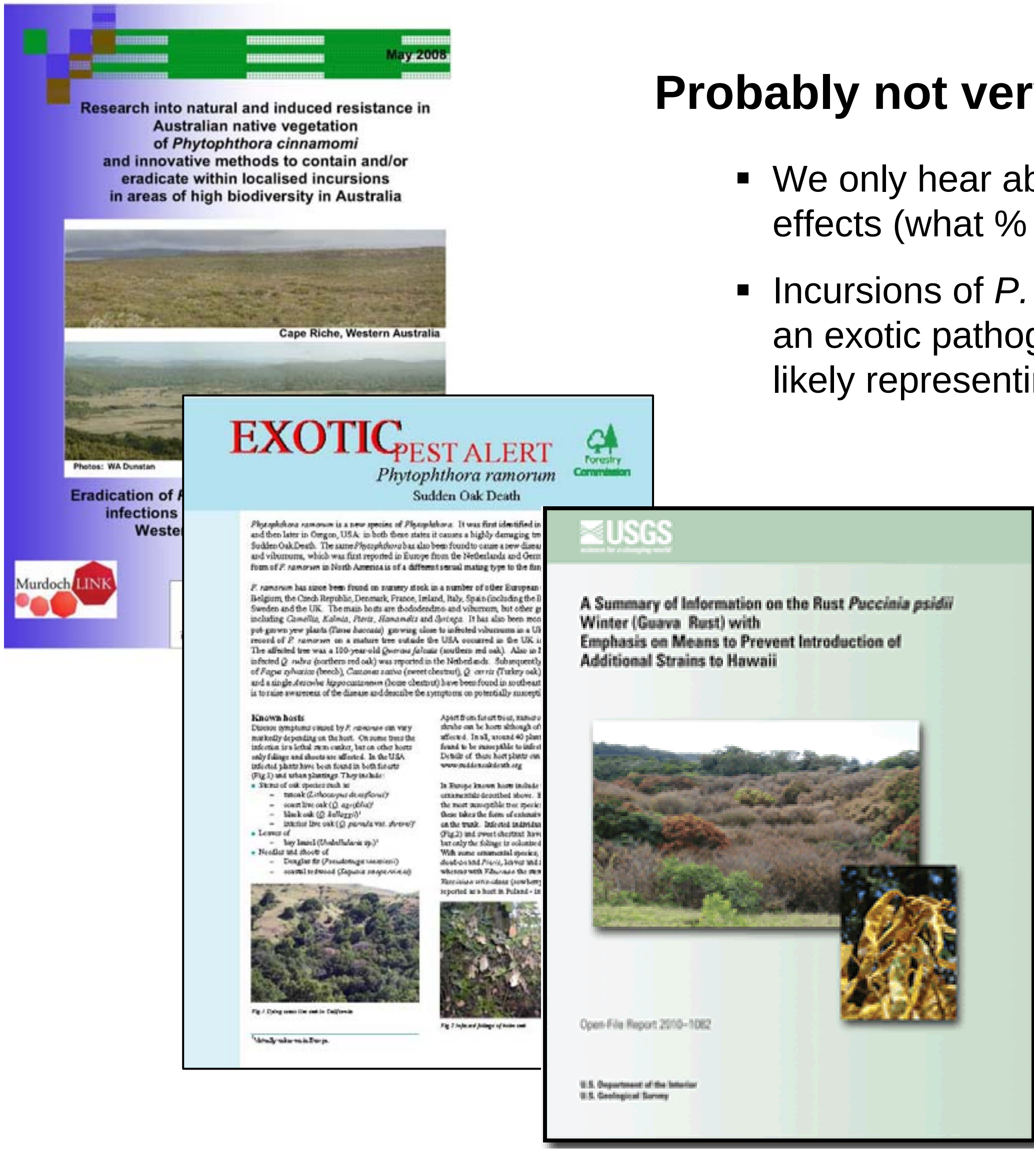
Puccinia psidii

Introduced pathogens: importance of host range

- Pathogens with a narrow host range:
  - Likely to be more predictable in terms of broad geographic distribution and likely ecological impacts…
  - But perhaps less predictably present locally, esp. for those which exhibit epidemic cycles
  - Host-specific pathogens can have major impacts (e.g. chestnut blight in N. America), but often may not (e.g. *Puccinia lagenophora* on *Senecio* sp.)

- Pathogens with a wide host range:
  - Will more likely be buffered from 'boom and bust' dynamics
  - The likelihood of ecosystem and trophic effects is greater but…
  - Perhaps less predictable overall, given potential for spatial variability in host community structure and susceptibility, and variation in fitness effects across environments
  - Will have significant impacts in some, but not all ecosystems

What can we learn from overseas examples?



Probably not very much…

- We only hear about invasive pathogens with dramatic effects (what % of invasions do these represent?)
- Incursions of *P. psidii* in Florida and Hawaii represent an exotic pathogen largely attacking introduced hosts, likely representing low genetic diversity in both.

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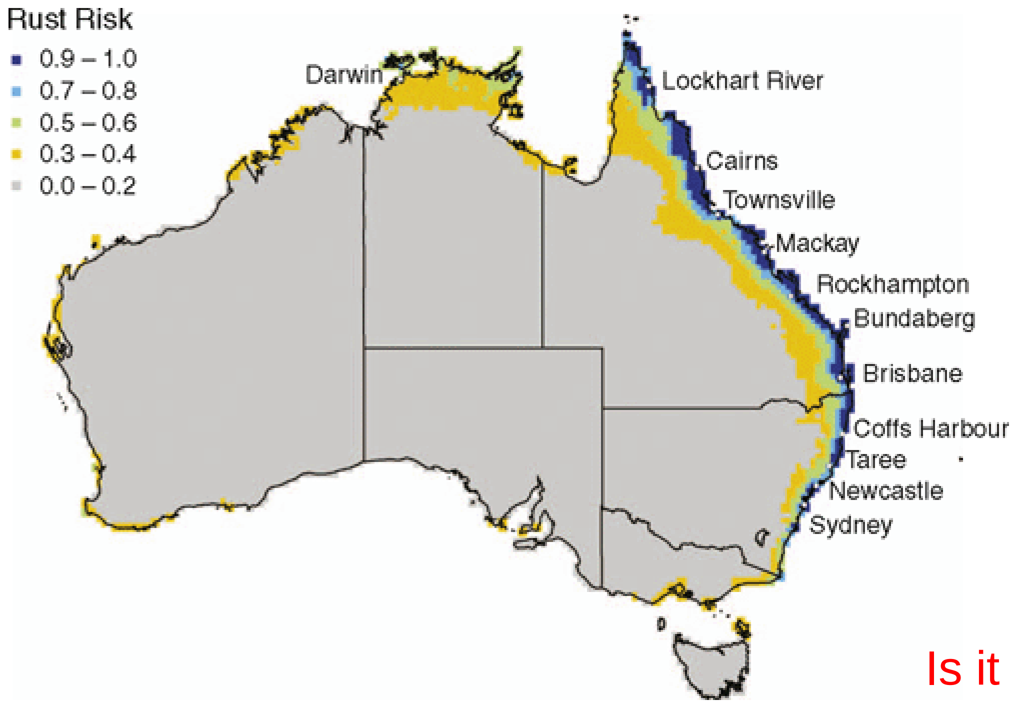
Predicted spatial distribution of myrtle rust in Australia: what's missing?



Glen et al. Aust. Plant Pathol. 2007;36:1-16

- Predicted distribution based on existing knowledge of climatic conditions conducive to rust
- Climatic information was derived from disease occurrence on eucalypts in exotic plantations – how representative?
- Map does not include host susceptibility or variation in myrtaceous community structure in Australia

Is it possible to develop a predictive map for likely disease impacts?

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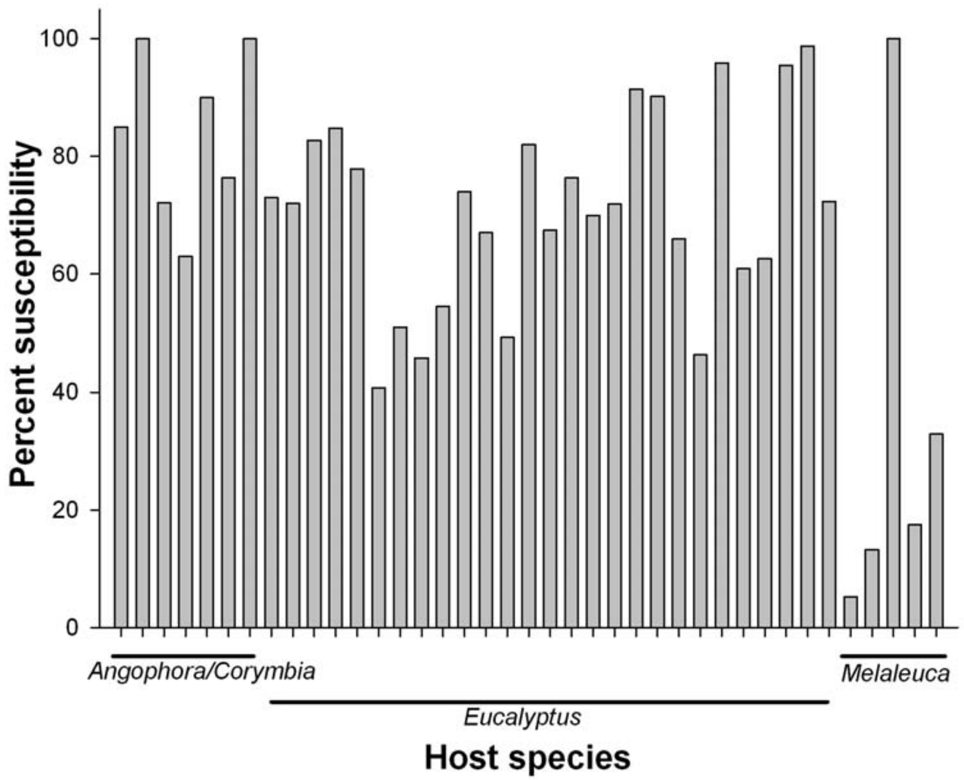
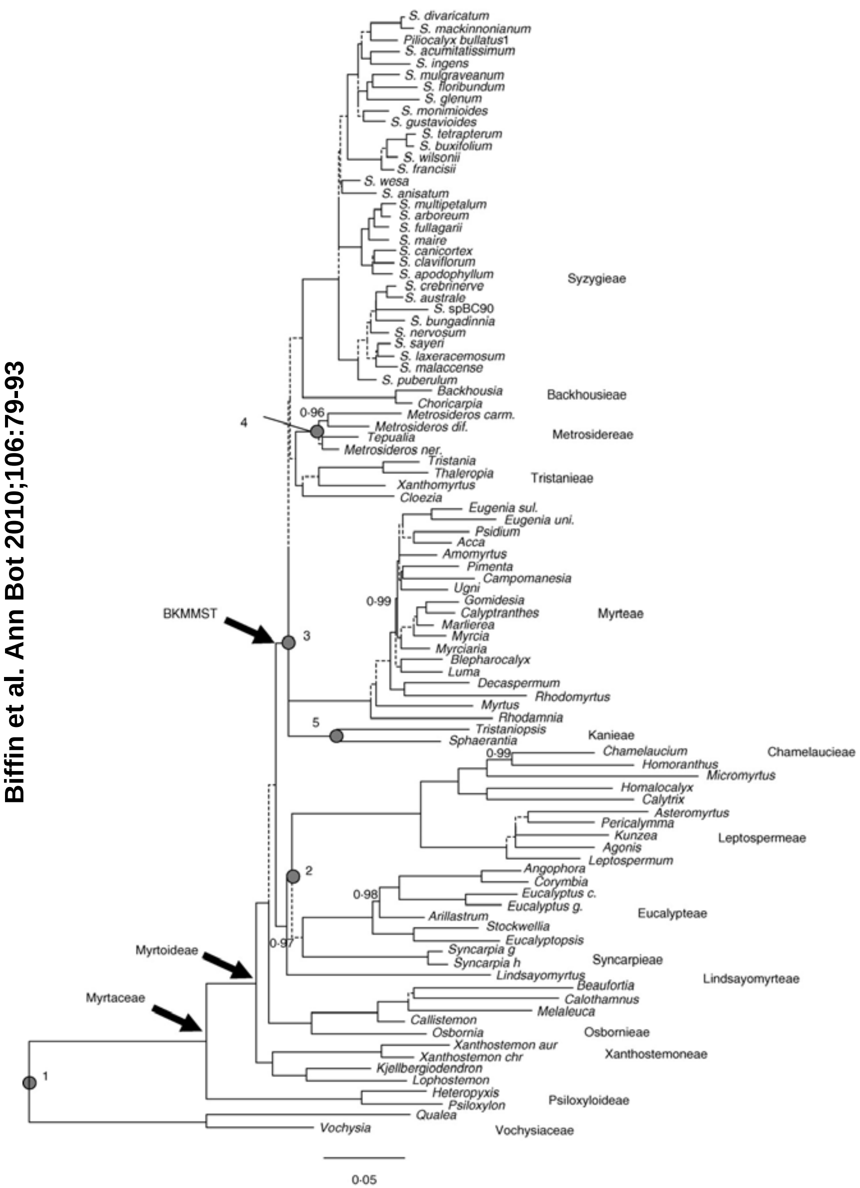
Variation in susceptibility to guava rust in Australian Myrtaceae

- Earlier work suggests susceptibility may vary considerably across the Myrtaceae
- Some evidence for variation within species (but insufficent to draw broad conclusions)
- Preliminary indication of variation in susceptibility in hosts from geographically different regions of Australia



Zauza et al. Aust. Plant Pathol. 2010;39:406-411

What role does host phylogeny play in determining patterns of susceptibility?



Biffin et al. Ann Bot 2010;106:79-93

?

Some major unanswered questions…

- What are the patterns of susceptibility within ecologically and economically important host spp. across geographic ranges?
- How does variation in susceptibility interact with environmental factors to determine host fitness effects?
- Is there heritable genetic variation for resistance and what is the underlying genetic basis of resistance?
- Do evolutionary (phylogenetic) relationships among hosts provide any predictability with regard to likely resistance?
- Is there genetic variation among Australian isolates of myrtle rust and what is the potential for further invasions to: a) increase diversity, and b) facilitate sexual reproduction?
- How does community structure (relative abundance and diversity of Myrtaceae) influence disease incidence and prevalence?
- Are some communities types likely to be more at risk (e.g. in terms of ecosystem impacts, including trophic effects)?

CSIRO Plant Industry
Jeremy J. Burdon

Phone: 02 6246 5546
Email: jeremy.burdon@csiro.au

CSIRO Plant Industry
Peter H. Thrall

Phone: 02 6246 5126
Email: peter.thrall@csiro.au

www.csiro.au

Thank you