

Pattern of genetic diversity of the Dothistroma fungus implies a potential biosecurity risk to NZ



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Workshop

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S Carson - *background*

Study:

- BS U Michigan, Natural Resource Ecology, Forestry, Wildlife Mgt
- MS U Michigan, Forest Pathology
- PhD study (2 yrs), U Minnesota, Plant Pathology
- PhD, NC State U, Forest Genetics and Plant Pathology

Employment:

- Plant Pathologist (5 yrs), USDA Forest Service, Asheville NC



Breeding for Disease Resistance

- Each disease is different
- Each disease must be considered as a separate trait
- The genetic parameters of both host and pathogen must be defined



Typical plant disease (Vertical resistance):

- Typically many “races” of the pathogen with virulence to specific varieties of the host
- Typically many resistance mechanisms in host
- Typically single gene control of virulence and resistance
- High variation of both host and pathogen in native range (*thought to confer durability*)
- Breeding gains are often large



Typical plant disease (Vertical resistance):

- Big problems can arise with genetically uniform crops
- Problems when new race develops which overcomes resistance of the genetically uniform crop
- Opportunity for “pyramiding” resistance mechanisms to obtain durable resistance
- Examples: fusiform rust, white pine blister rust, white pine weevil on Sitka spruce (?)



Less studied plant disease (Horizontal resistance)

- Little or no difference in virulence of pathogen
- Host resistance controlled by many genes (quantitative inheritance)
- Breeding gains smaller
- Genetic resistance durable
- Example: Dothistroma in New Zealand



Dothistroma in New Zealand: the classic quantitative trait (Horizontal resistance)

- Normal distribution of symptoms
- Moderately highly heritable
- Clones behave the same as seedlings (no C effects)
- Very little genotype by environment interaction
- Very little specific combining ability
- 1st generation of selection reduced ave % of needles infected by 15%
- Estimated to have saved CHH over \$1M per annum in spraying costs (A.M.P Dick 1989)



What makes a disease Vertical or Horizontal?

- Not a fixed characteristic of a host or a pathogen
- Depends on the geographic pattern of genetic variation of
 - ▶ virulence of pathogen populations
 - ▶ resistance mechanisms in the host populations
- If the patterns change, the type of resistance can change
- *Understanding geographic patterns of variation is crucial to predicting biosecurity outcomes!*



Variation in the Dothistroma pathogen is low in NZ (Hirst et al. 1999)

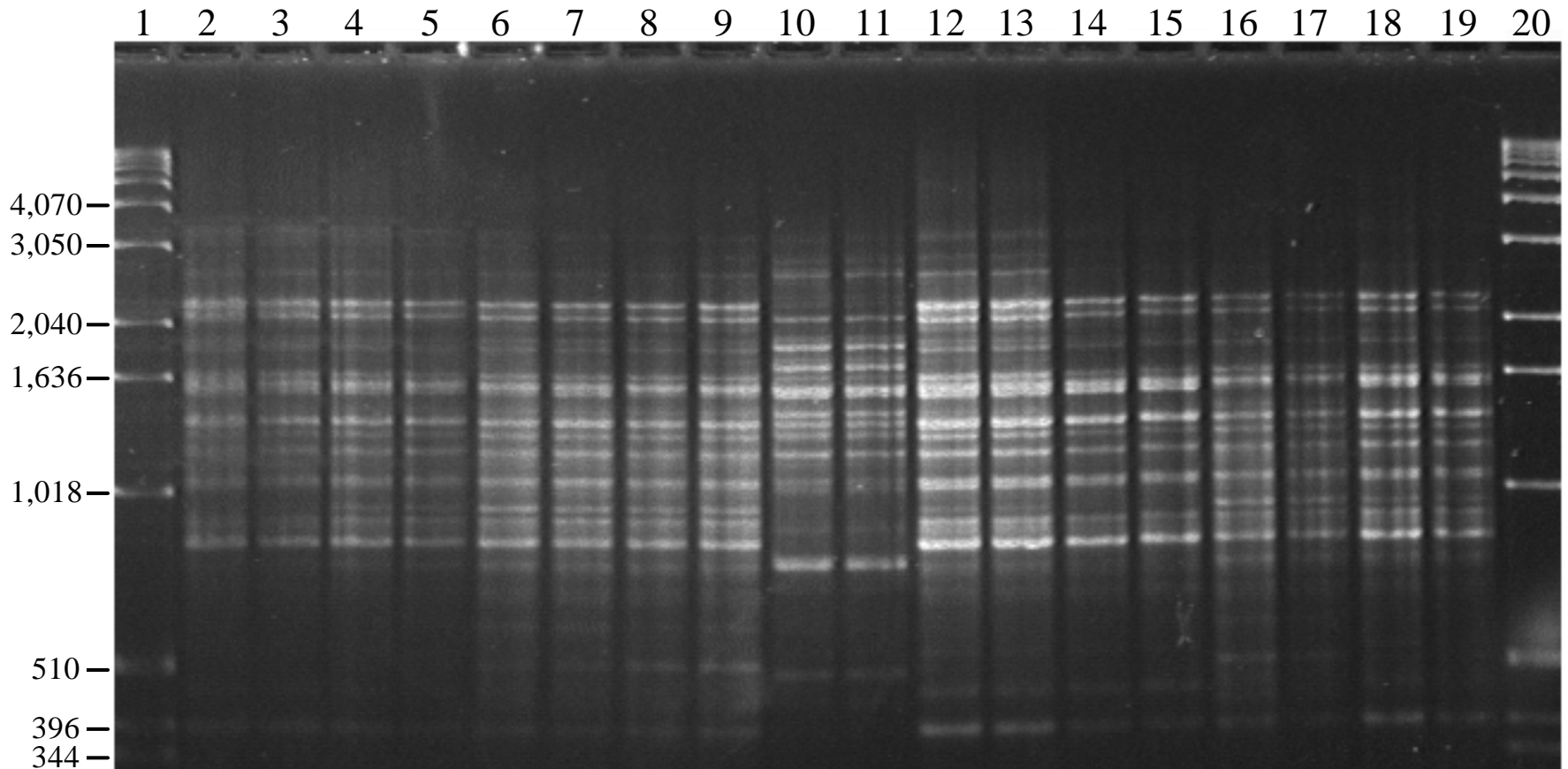
- No variation observed in extensive survey across NZ
 - ▶ Standardized seedlot around NZ
 - ▶ Isolates from resistant and susceptible clones
- The one isolate examined from Australia was different



Dothistroma genetic diversity is low in NZ

1960s (NZ)

1995 (NZ)



1983 (Guatemala) IMI 281626

RAPD reactions carried out in duplicate [NZ J For Sci (1999) 29:459]

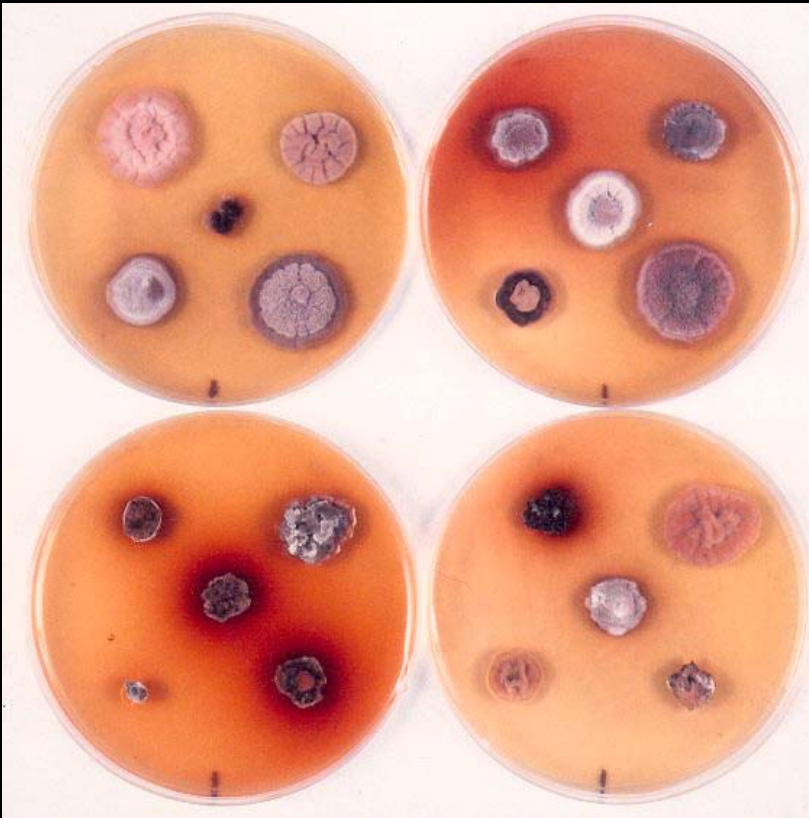
Variation in the Dothistroma pathogen is much higher around the world

- Species definition recently revised based on spore length and DNA markers
- Known differences in dothistromin production
- Tools have been developed to examine pattern of geographic variation around the world
 - ▶ DNA markers
 - ▶ Markers for mating types
- No information on differences in virulence



Global Distribution

NEB1-5



NEB6-10

ALP3-6
SLV

GUA NZE
MIN
FRA ORE

ITS sequence groups

'Group 1'

Europe: FRA, ALP, SLV

Australasia: NZE

North America: CAN, ORE

South America: GUA

NOW *D. septosporum*

'Group 2'

North America: NEB, MIN

NOW *D. pini*

[Bradshaw et al (2000) Mycol. Res. 104: 325]

[Barnes et al (2004) Studies in Mycology 50:551]

Large variations in dothistromin production



ALP3 - German Alps

ORE12 - Oregon

PDA cultures of *D. septosporum*

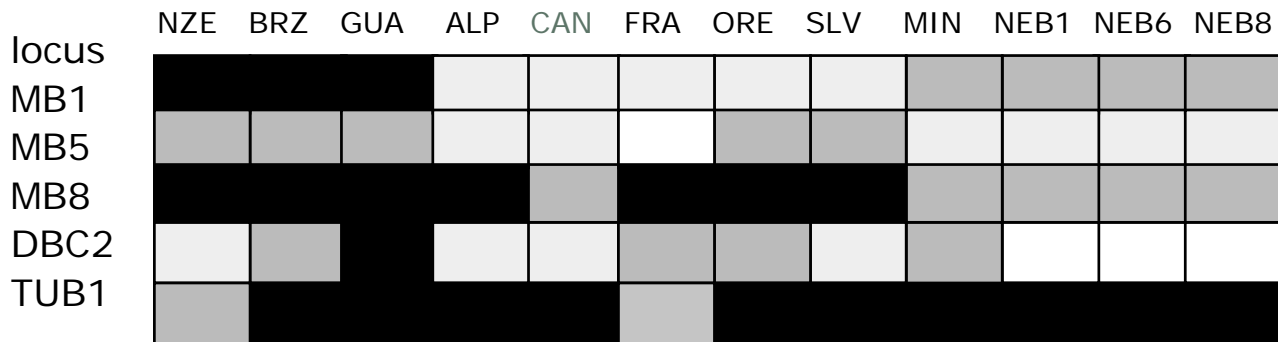
Typing of *Dothistroma* isolates

Microsatellite
Locus MB1

ALP3 BRZ1 CAN3 FRA1 GUA1 MIN11 NEB1 NEB6 NEB8 NZE1 ORE12 SLV1

200 bp

Alleles at five microsatellite loci in:



Alleles 1 2 3 4



New Zealand
Brazil
Guatemala
German Alps
Canada
France
Oregon USA
Slovakia
Minnesota USA
Nebraska USA

Taxonomic Study – Barnes et al. 2004

- 32 isolates from 13 counties
- Reported in context of reviewing taxonomy
- Observed some variation among isolates similar to NZ



Current research - genetic variability

- Canada - Kathy Lewis
 - UK - Anna Brown
 - South Africa - Mike Wingfield & Irene Barnes
 - New Zealand - Rosie Bradshaw
-
- genetic variability (ITS sequence, microsatellites..)
 - mating types?



Bio-Protection



Massey University



IMBS
Institute of Molecular BioSciences

Dothistroma in NZ Today:

- Data suggests no pathogen variation
- Durable quantitative resistance

Dothistroma in NZ Tomorrow:

- There is a biosecurity threat if:
 - ▶ There are genotypes of the fungus in other countries which are different to those in NZ
 - ▶ These genotypes are new “races” which are more virulent than those already in NZ
- Entry of more virulent races could mean more disease in NZ forests



Is importation of new strains of *D. pini* a biosecurity risk?

Recommendation

- Carry out a study of geographic variation around the world using molecular markers
 - ▶ How much of a potential threat is there, ie is NZ population truly uniform?
 - ▶ Where does the potential threat come from, ie how different is the rest of the world from NZ?



Conclusion

Importation of new strains of *D. pini* should be considered as a potential biosecurity risk until further information about geographic variation in the fungus is obtained

