

Genomic approaches to control fungal diseases of oilseed Brassicas in Australia

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- Fungus has complex arsenal to cause disease: knowledge about disease mechanisms & biology of fungus underpins disease control strategies
- Approaches**
- Genome (DNA) sequencing - list and order of genes, molecular markers for virulence
- Transcript (RNA) sequencing – list of genes activated during plant infection; these are key disease genes (effectors)

Leptosphaeria maculans genome

- French/Australian project completed in 2011; genomes of five Leptosphaeria species and non-Brassica pathogens are now being compared
- Genome 34% larger than *Stagonospora nodorum*
- 34% of *L. maculans* genome is repetitive DNA - copies of 'jumping genes' that have been mutated & inactivated
- Key disease-related (effector avirulence) genes are embedded in repetitive DNA
- Dynamic 'plastic' genome: during crossing genes are readily gained, lost or mutated

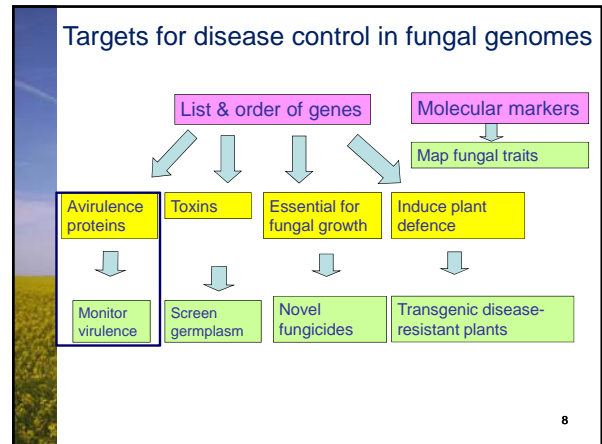
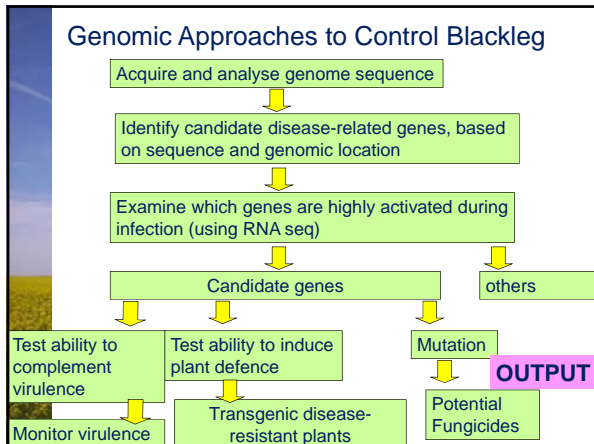
Location of effector genes accounts for ability for fungus to overcome resistance

- Blackleg fungus
 - Sexual reproduction generates large populations of wind-borne recombinant ascospores
 - Prolific asexual crossing
 - High evolutionary potential
- Populations readily adapt to selection pressure from extensive sowing of cultivars with same complement of resistance genes
- Frequency of virulent isolates increases, leading to breakdown of resistance
- We can't beat blackleg but must stay ahead of it: Staying Ahead of Blackleg**

Targets for disease control in fungal genomes

Genomic Approaches to Control Blackleg

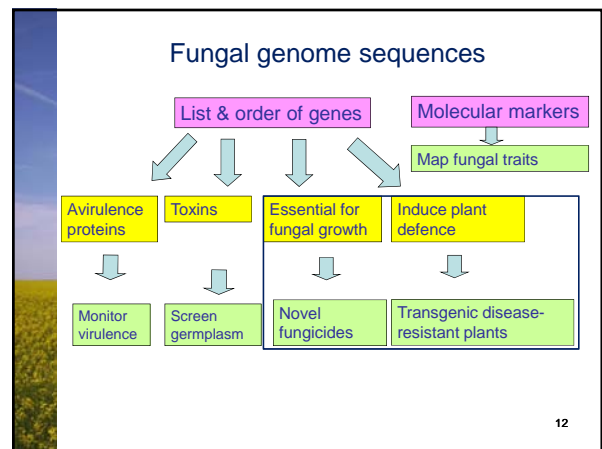
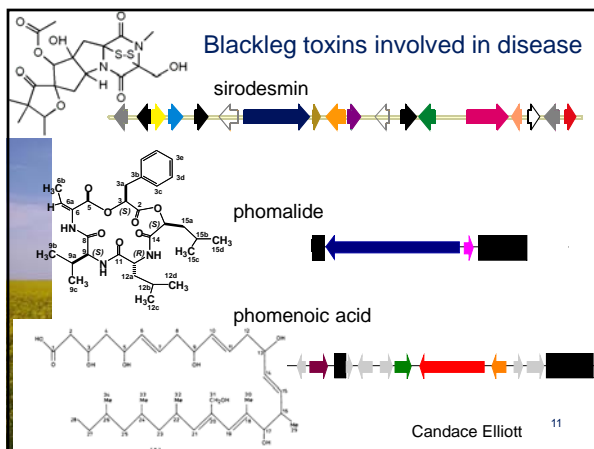
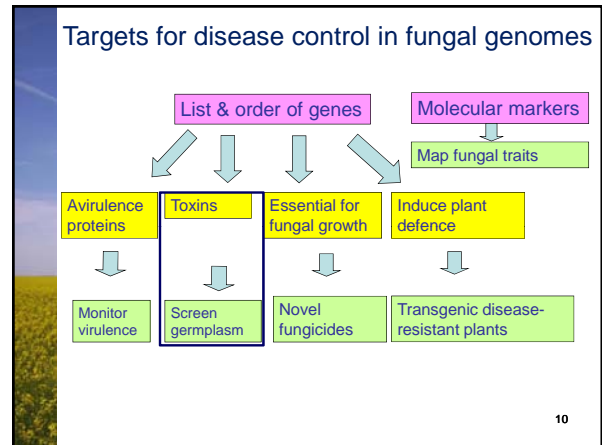
Four groups of candidate disease-related genes



High throughput monitoring of blackleg populations for virulence

- Blackleg-infested stubble collected across Australia
- Ascospores captured on tape, DNA extracted and analysed by q PCR for frequency of
 - Avirulence genes *AvrLm1* & *AvrLm6* (presence/absence of band);
 - AvrLm4* (SNP) pyrosequencing (very sensitive)
- Tens of thousands of spores from many populations (pieces of stubble) can be screened
- In conjunction with disease severity field & glasshouse data (tub screening), risk of resistance breakdown determined

Angela Van de Wouw



Genes: essential for fungal growth

Find fungal gene essential for growth (disease) by mutation
Find inhibitor of fungal protein

Fungal hypha

Fungal growth inhibited

Output: fungicide (multinationals)

Genes: induce plant defence

Find fungal gene that induces defence resistance response by plant

Water

Make transgenic plant with fungal gene; test disease resistance.

Output: transgenic plant (Breeding companies)

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Fungal gene that induces defence responses on canola cultivars

Westar

ZY004

RT108

ZY006

ZhongYo u821

Candace Elliott

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Genomic approaches to control fungal diseases: summary

- *L.maculans* has key disease related genes in unstable regions of the genome, which accounts for ability of fungal populations to rapidly overcome resistance
- Developed and am implementing high throughput molecular assay to monitor virulence of blackleg populations to assess risk of breakdown of resistance
- Characterising role of fungal toxins in disease
- Identifying fungicide targets and anti-fungal genes

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Acknowledgements (when we were young)

Acknowledgements

Robert Lowe
Candace Elliott
Robert van de Wouw
David Dubois
Kylie Chambers
Bethany Clark

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