

Staying Ahead of Blackleg

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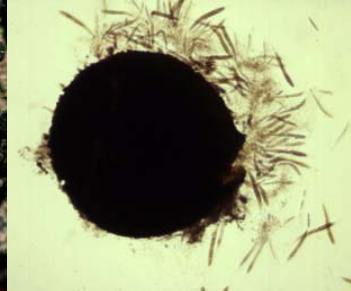
Australian Government
Grains Research and Development Corporation



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Leptosphaeria maculans

- High risk pathogen for overcoming resistance:
 - Sexual (outcrossing) reproduction: generates variation
 - Large populations of wind borne ascospores (inoculum)
 - Many asexual spores
- Populations readily adapt to selection pressure from extensive sowing of varieties with ‘major’ resistance genes.
- Frequency of virulent isolates increases leading to breakdown resistance (eg. sylvestris-derived resistance)



Sylvestris resistance overcome – 2003 Eyre Peninsula



Blackleg & canola: 'Boom and bust' disease cycle

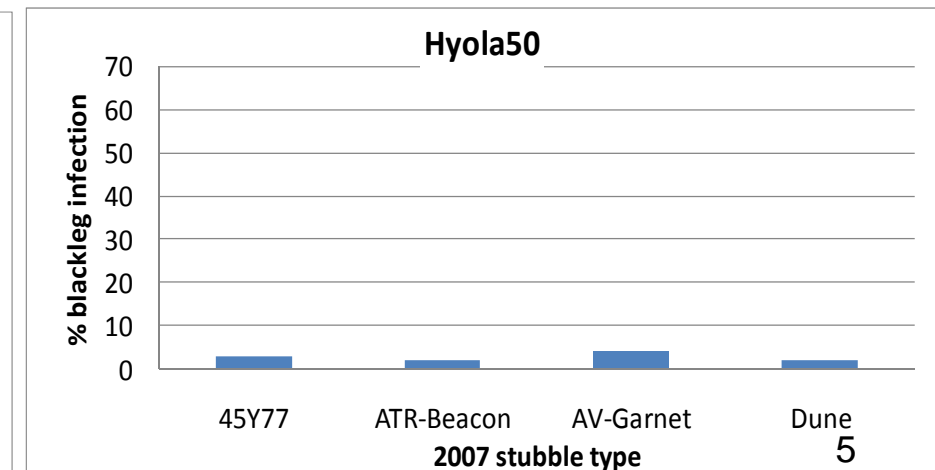
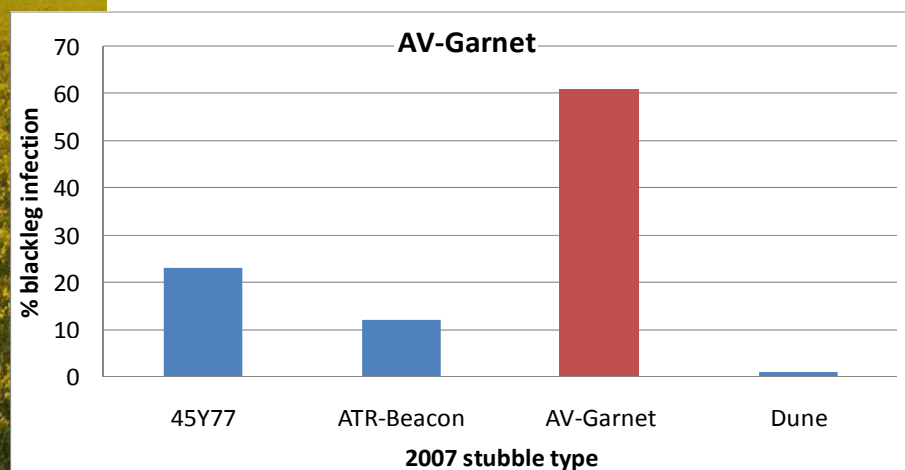
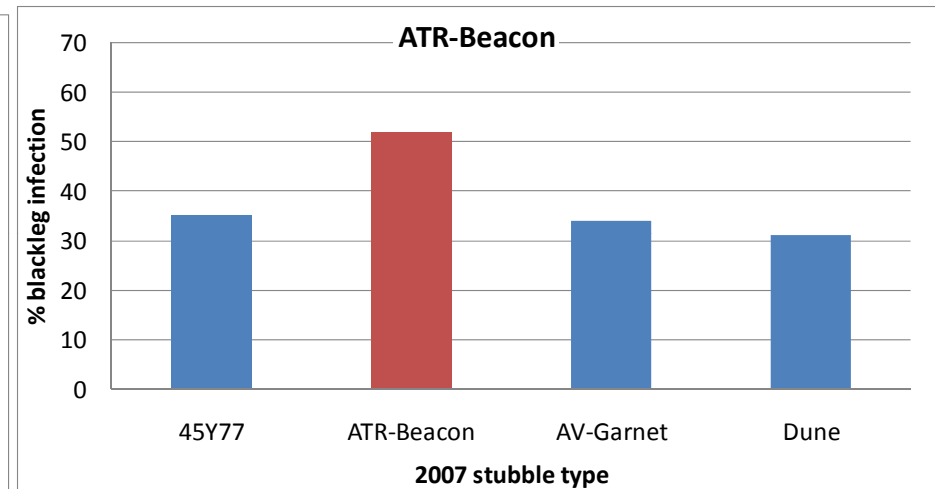
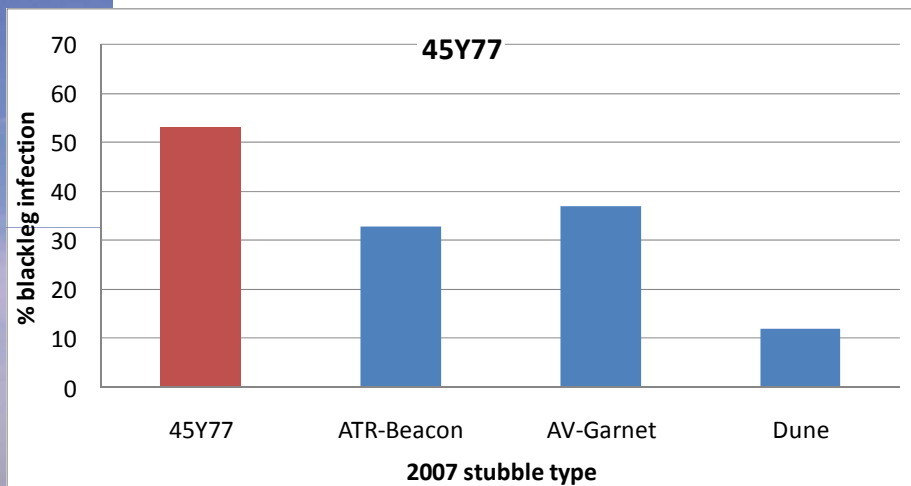
- From 2003-2008 monitored high rainfall sites where sylvestris resistance broke down in 2003
- Cultivars with sylvestris resistance withdrawn for market
- In small plots, disease severity in cultivars with sylvestris resistance decreased over time; similar disease level in cultivars with polygenic resistance
- Fungal populations are dynamic - evolve quickly and resistance becomes effective again



2005

Rotation of different resistance sources:

- minimises selection pressure on fungal populations
- thus enhances durability of resistance genes

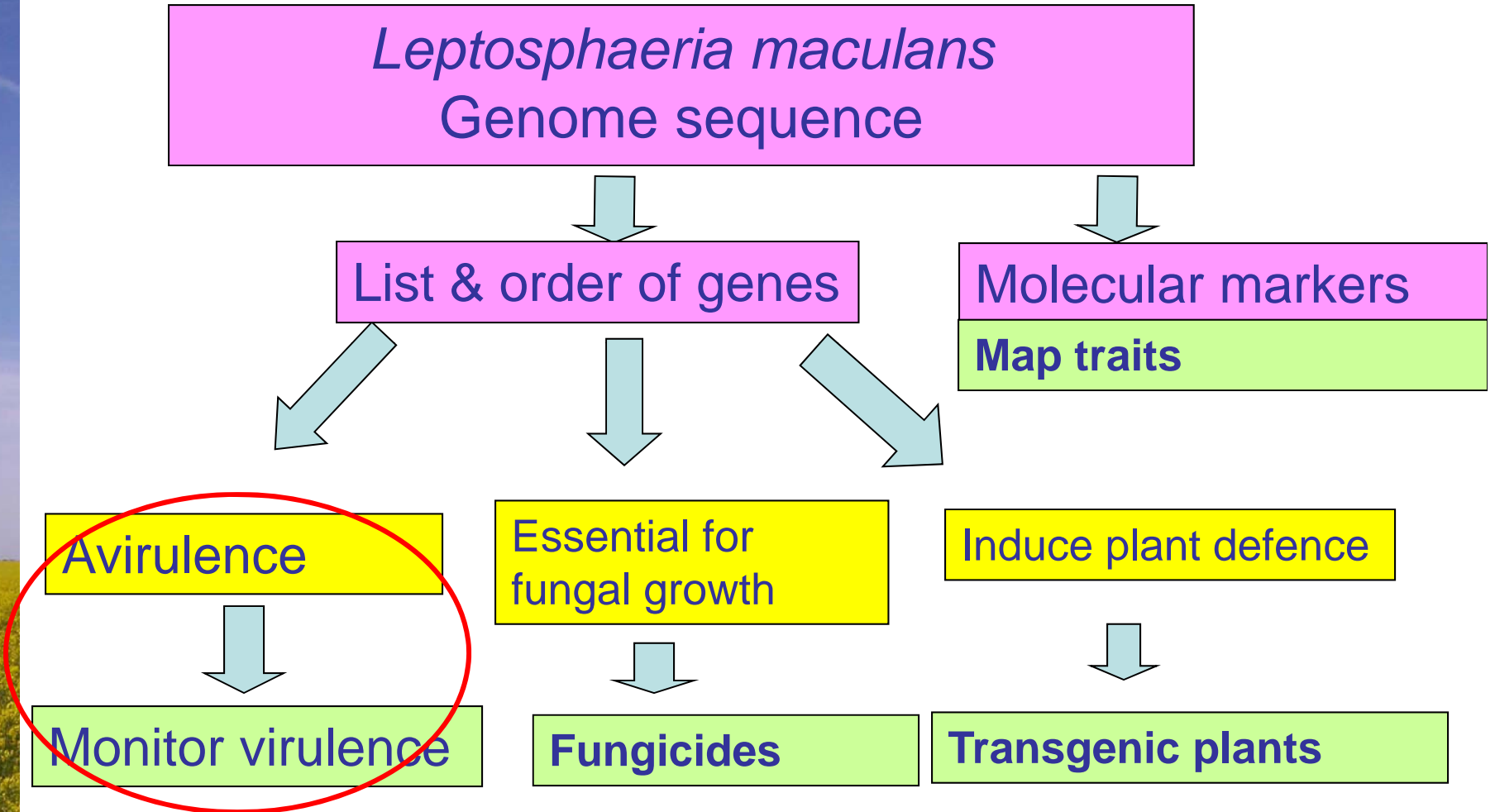




We can't beat blackleg but can try to stay ahead of it

- New GRDC project 'Staying Ahead of Blackleg'
- A/ monitor virulence in Australian fungal populations
 - use knowledge of blackleg genome to develop high throughput assays for risk of breakdown of resistance
 - understand how blackleg fungus overcomes resistance
- B/ develop and implement an **national** blackleg management plan that includes strategies to maximise durability of resistance

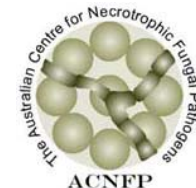
Monitoring blackleg populations



Fundamental knowledge about disease mechanisms & biology of fungus

L. maculans genome

- Rouxel, INRA URGI, France & Howlett, Melb Uni
- Genome has 12,500 genes
- Unusual features
 - Large: 45 Mb; *Stagonospora nodorum* (37 Mb)
 - Repetitive DNA: degenerated transposable elements –
 - 38% genome; 9% of *S. nodorum* genome
 - Alternating regions gene-rich (1 gene/2 kb) & gene-poor (1 gene/30 kb),
 - Disease-related genes (effectors - eg. avirulence) interspersed with repetitive DNA within gene-poor regions

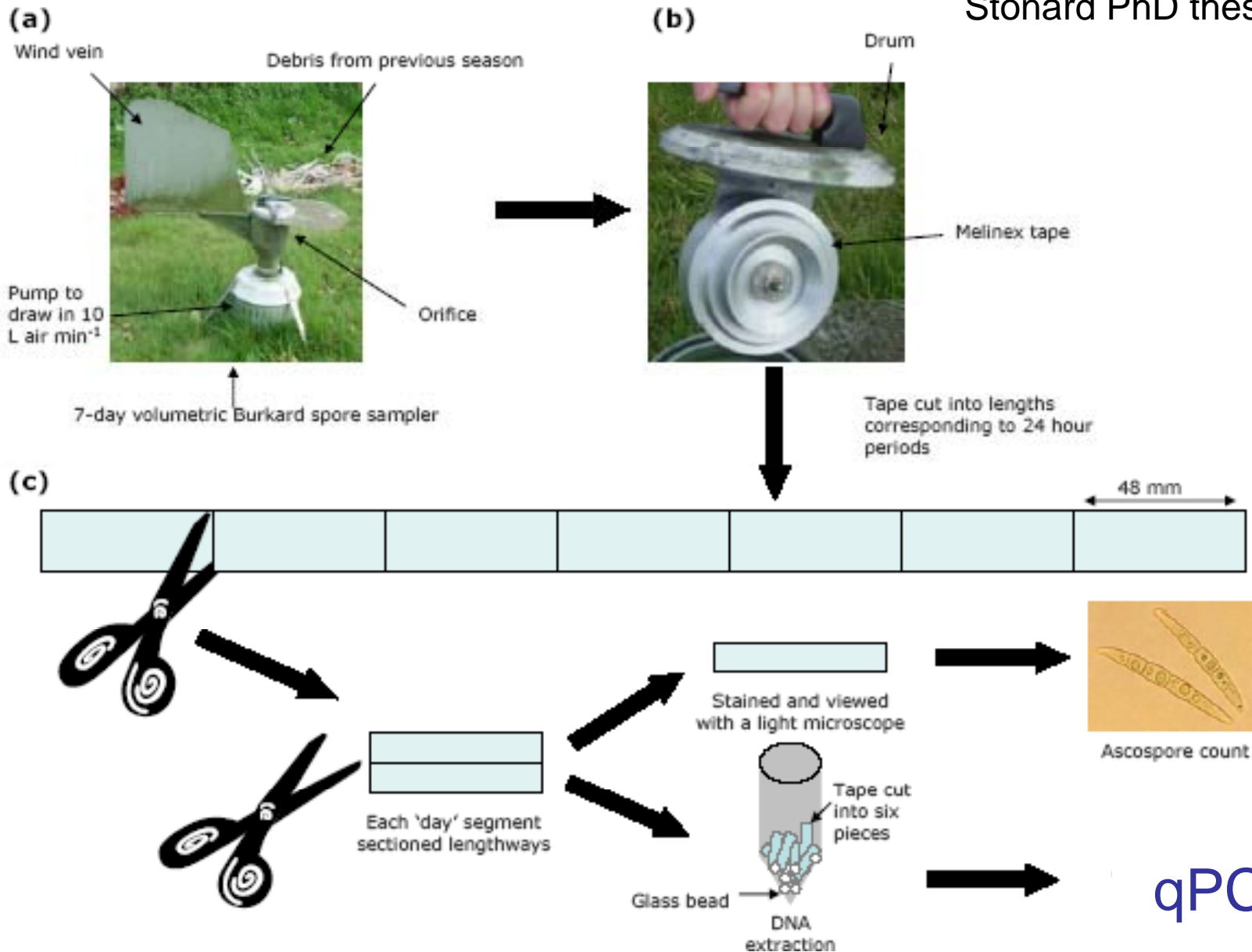


Monitoring blackleg populations

- Molecular markers for
 - *AvrLm1* (*Rlm1* – Columbus, Surpass 400)
 - *AvrLm6* (*Rlm6* – juncea R gene)
 - *AvrLm4-7* (*Rlm4* & *Rlm7*)
- Genes in repetitive rich areas of genome
- PCR assay – eg. *AvrLm1* (*Rlm1*)
Virulence (*avr*) associated with gene deletion
AvrLm1 – band; *avrLm1* – no band
- Determining changes in frequency of virulence in populations towards particular resistance genes
- Advising industry of risk to particular resistance sources

Monitor populations via Burkard spore trap

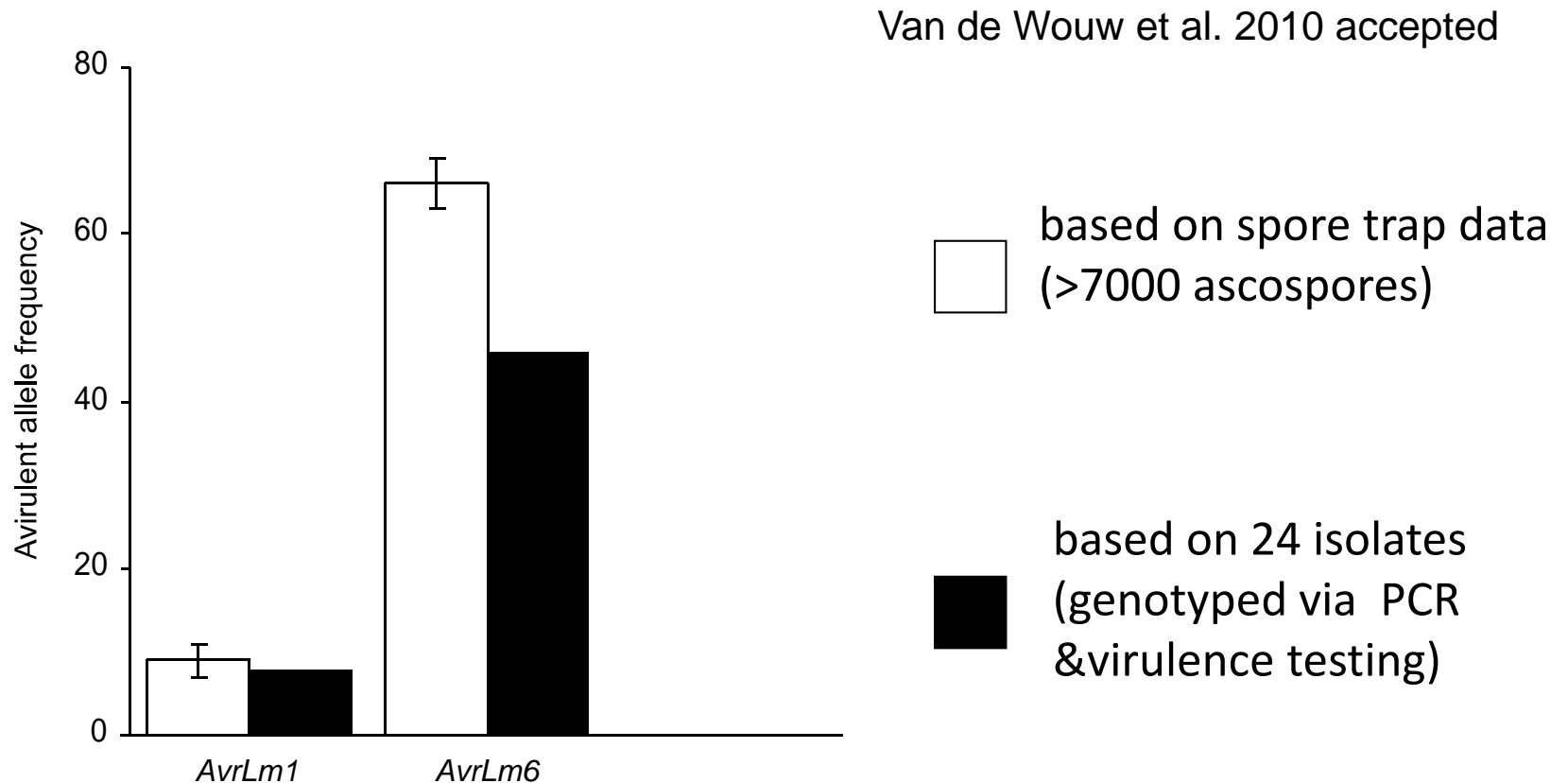
Stonard PhD thesis



qPCR

AvrLm1 and *AvrLm6* allele frequencies estimated from airborne inoculum

- 2006/2007 season in single UK field





Monitor *Avr* allele frequencies nationally

- Collect spore samples or stubble from canola-growing regions
- Liberate spores from stubble using
 - Spore tents
 - Wind liberator
- Determine avirulence gene frequencies
- Assess disease severity nationally – NVT sites
- Feed data into national blackleg management package



National blackleg management package

- **Known resistance genes in each cultivar**
- **Frequency of virulent blackleg isolates against cultivars**
- Blackleg ratings
- Reduced resistance warning on blackleg ratings.
- Regional blackleg severity
- Paddock Risk Assessment test
- Regional performance of cultivars

Blackleg Management Package



Disease assessor: plant pathologist Steve Marcroft says canola growers will soon have a new tool to help them assess blackleg risk.

Time to give blackleg the boot

Weekly Times 17 Feb 2010