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Managing on-farm biosecurity risk in wheat through pre-emptive breeding

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Background

- This project has three main objectives:
  - To incorporate resistance genes identified for the key exotic pests and pathogens into elite Australian varieties, and make the germplasm available to breeding entities
  - Generate new knowledge of the relative resistance status of current Australian wheat varieties
  - Develop and identify molecular markers linked to the key exotic pests and disease that can be employed in routine breeding

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Target pests & pathogens

Sunn pest

- **Wheat yield loss:** as high as 90%.
- **Grain quality loss:** 100%

Hessian fly

- **Wheat yield loss:** as high as 40%.
- **Potential economic loss** = $28 million/year

Karnal bunt

- **Wheat yield loss:** Light, about 0.5%
- **Potential economic loss** = $491 million/year

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Pipeline for outputs delivery - Who's doing what?

ICARDA	CIMMYT	NSW DPI
• Hessian fly • Sunn pest • Backcross breeding • Doubled haploid production	• Karnal bunt phenotyping • Genetic mapping through SeeD affiliation	• Genetic mapping • Haplotyping • Development of diagnostic markers

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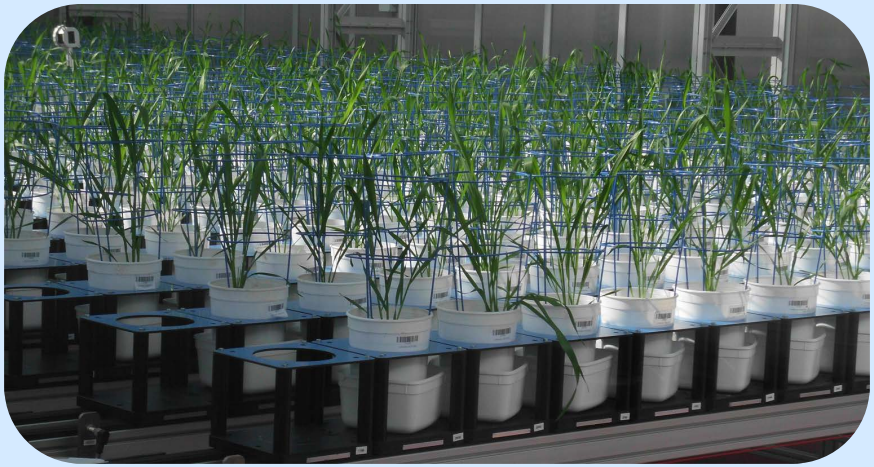
Phenotyping @ ICARDA & CIMMYT



- 209 Australian varieties have been sent to ICARDA for evaluating resistance to Sunn pest and Hessian fly

- Crosses between resistant and elite bread wheat have been initiated at ICARDA by Dr Tadesse Wuletaw

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Characterization of Australian wheat varieties for pest resistance using linked markers

- So far, 192 varieties genotyped with markers linked to H9, H13, H16, H17, H22, H25, H26, H32.
- None of the varieties carried alleles associated with resistance, and most notably not for H26/H32
- H26/H32 confer resistance to the world's most virulent Hessian fly populations.

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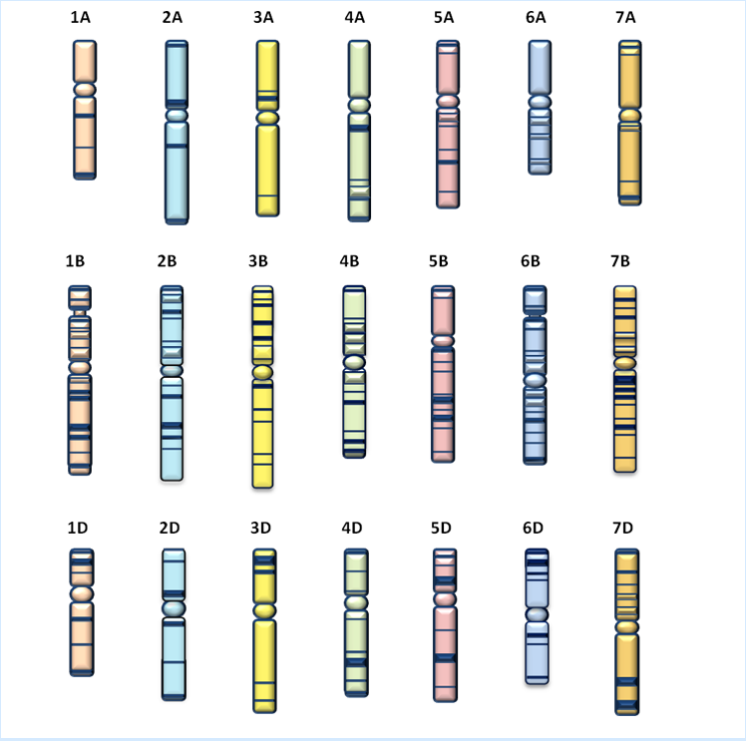
Approaches to developing functional molecular markers

- Association genetics
- Genetic linkage
- Next G sequencing

Convert significant SNPs to PCR-based markers or for KASP assays



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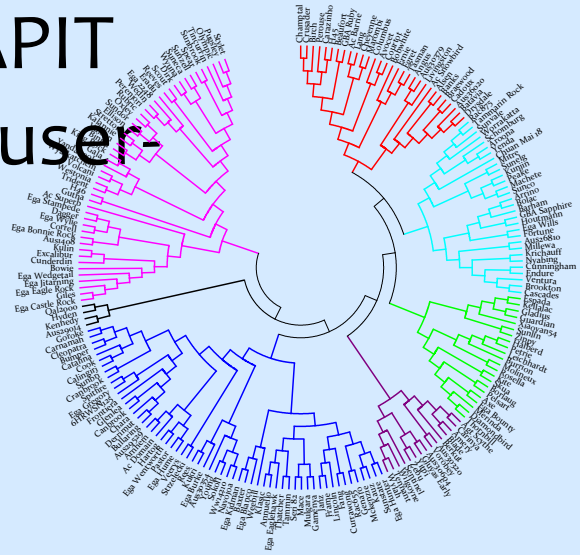
High-density genome-wide association mapping using SNP markers

- 209 varieties
- Genotyped with 9k SNP
- 85% of SNPs with MAF > 0.05
- Association mapping with GAPIT
- Convert informative SNPs to user-friendly markers



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Genetic linkage mapping with bi-parental crosses

- Sunn pest resistance - Three crosses
  - Cham6 x 139883 (n = 169)
  - Cham6 x 139431 (n = 147)
  - Cham6 x 140411 (n = 96)

  } 90K SNP

- Karnal bunt resistance - Two crosses
  - WH542 x HD29 (n = 110)
  - WH542 x W485 (n = 121)

  } 90K SNP + G-by-S

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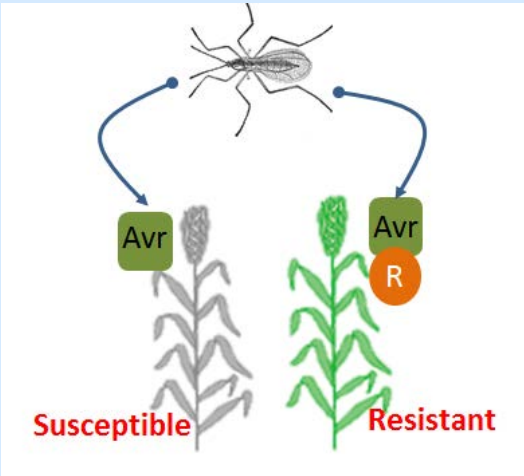
Sequencing of *R* genes

Resistance (R) genes encode proteins that indirectly or directly detect specific pathogen avirulence genes products thus triggering a resistance response



- Wheat *R* genes (RAR1, SGT1, NLR, XA21, TGA, NRR, NPR1-like)
- These will be sequenced for SNP polymorphism in Aust. varieties

- Correlate polymorphisms with resistance
- Determine chromosome locations
- Develop functional markers for routine use

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Acknowledgments

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- Dr. Wuletaw Tadesse - Senior Wheat Breeder, ICARDA
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- Dr. Sukhwinder Singh - Wheat Lead for SeeD, CIMMYT