



New Insights into the Evolution of *Fusarium* Pathogenesis in Wheat

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www.csiro.au



Where are we?

CSIRO Plant Industry, Brisbane

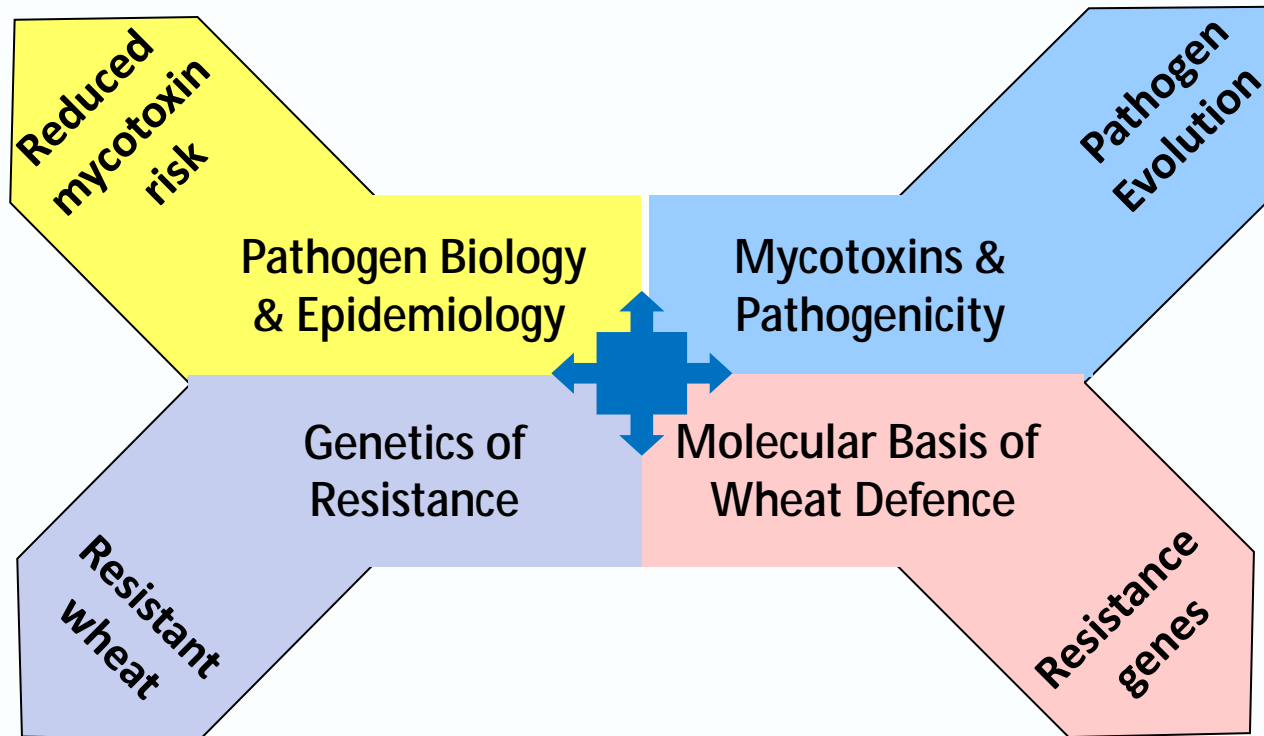


Queensland Bioscience Precinct –
BRISBANE



Research Station – GATTON

Wheat - Fusarium Research in CSIRO



Four inter-connected strands
to deliver industry and science
outputs

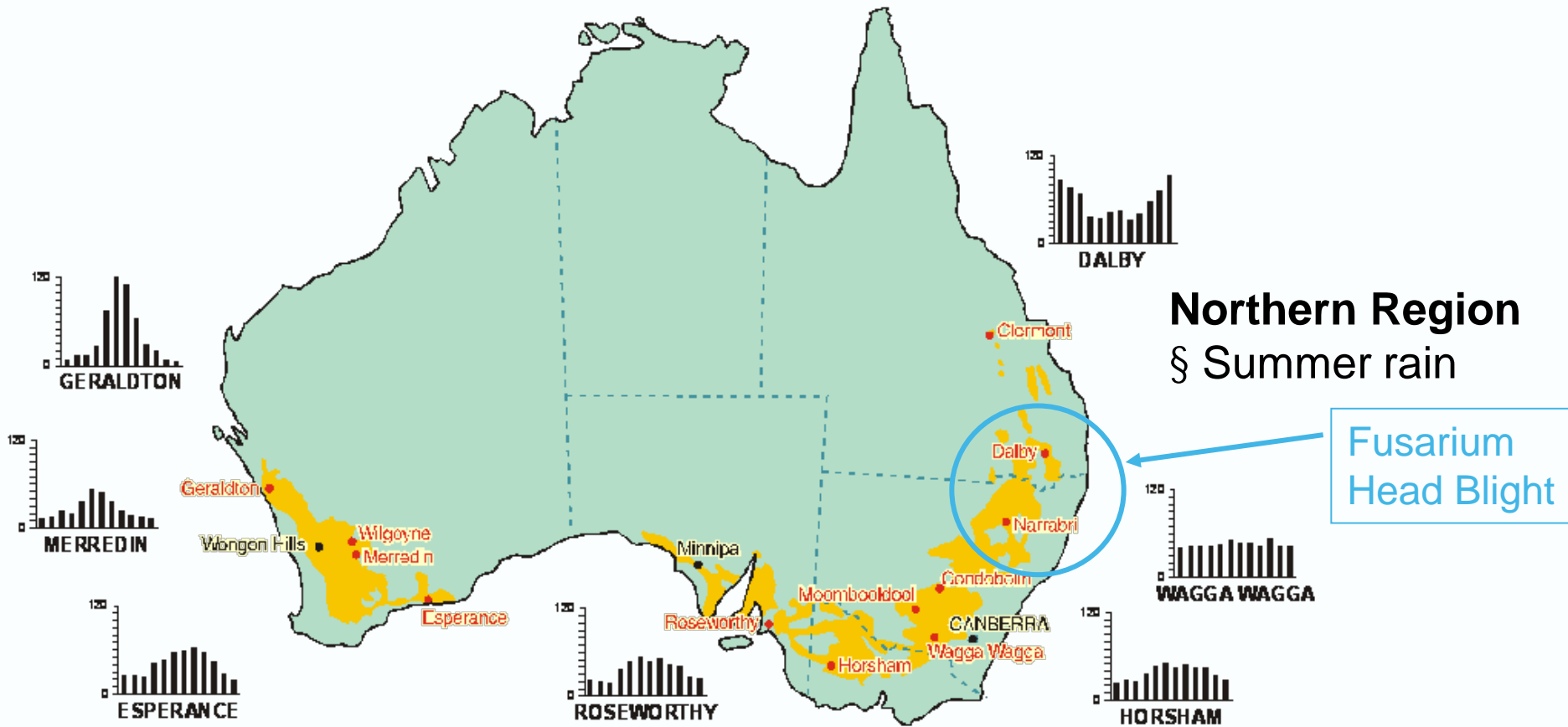
A tale of two diseases

wet finish = head blight - dry finish = crown rot



F. pseudograminearum and *F. graminearum* can cause both crown rot and head blight

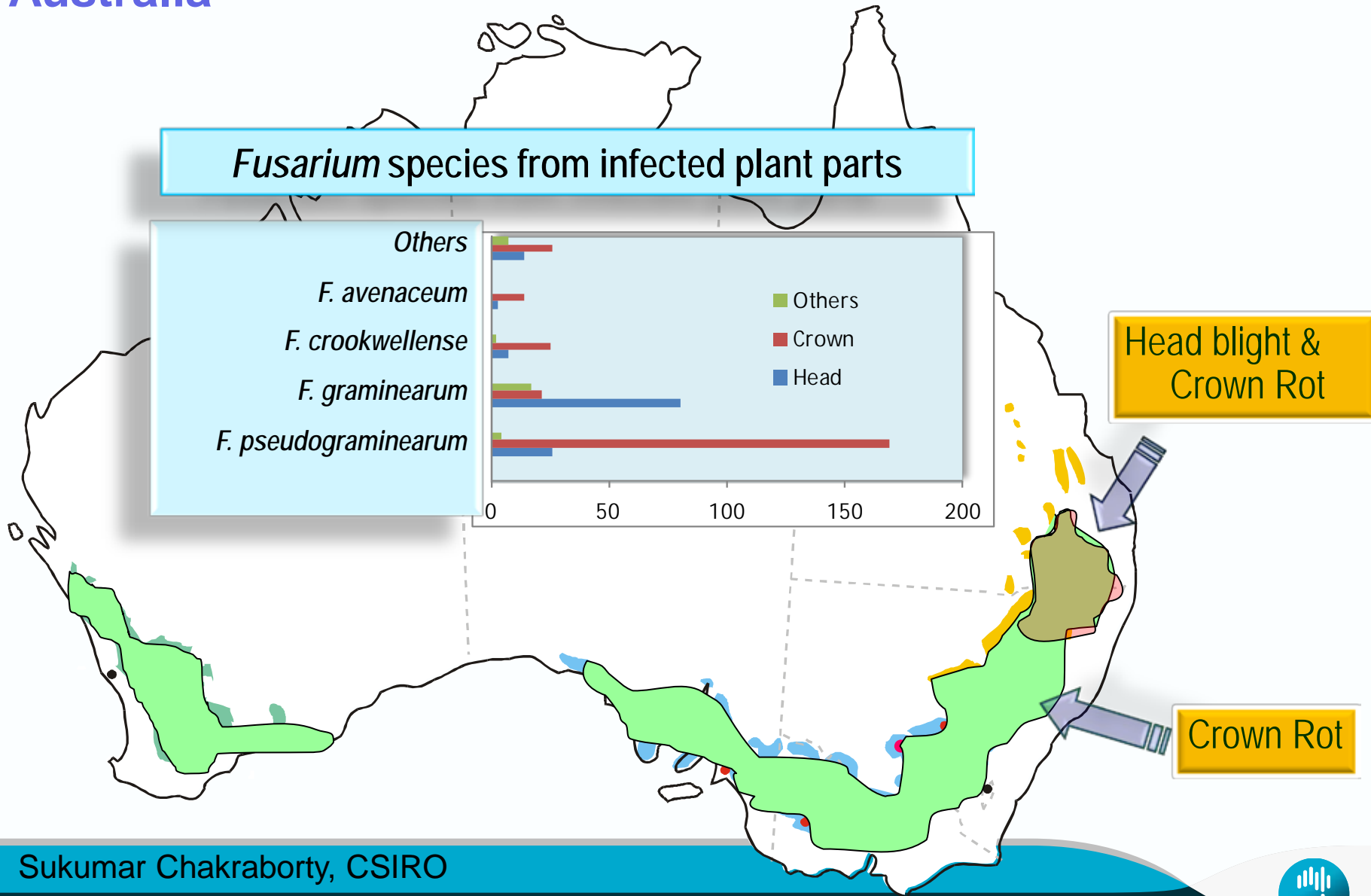
Australian Wheat Belt & Fusarium



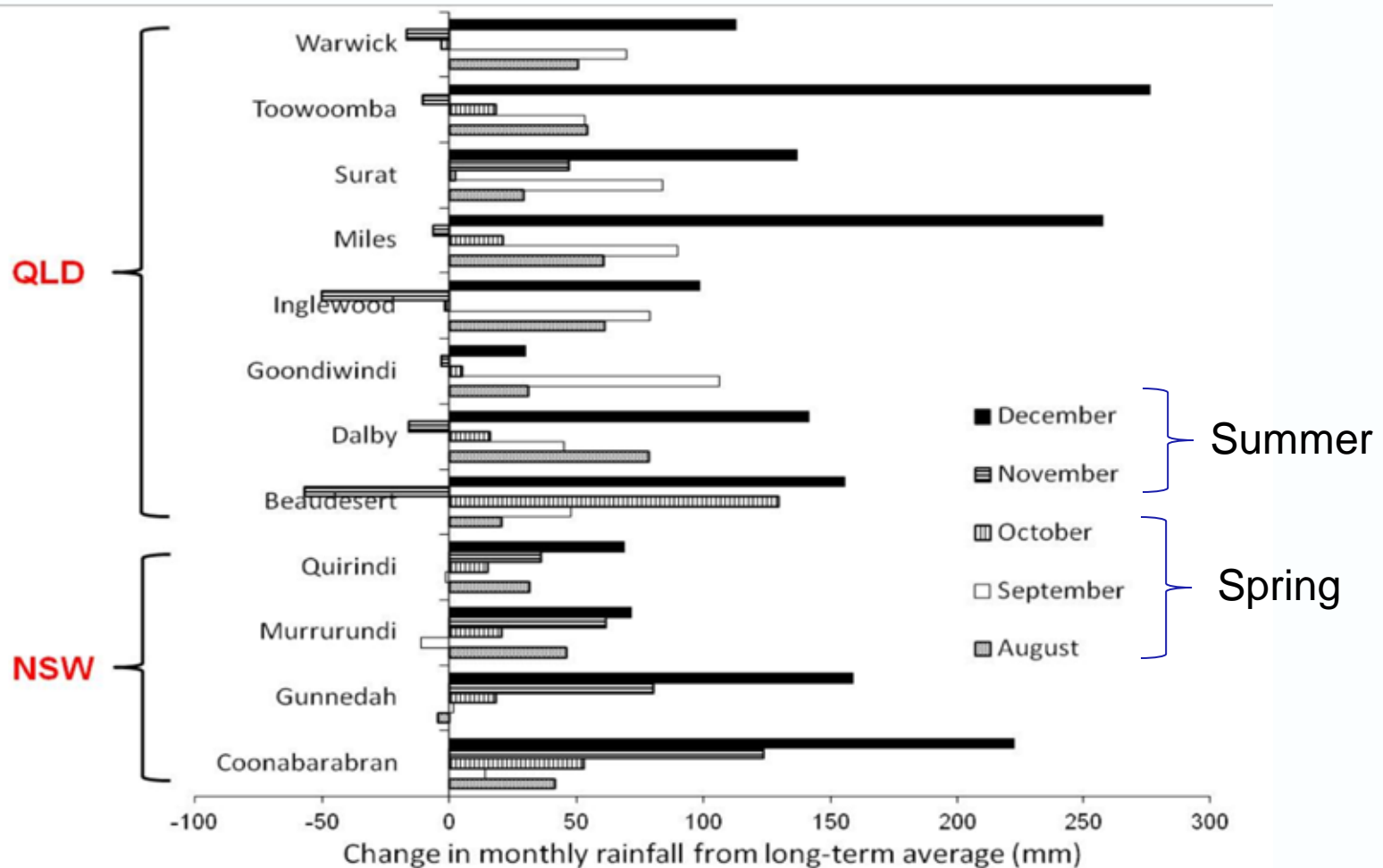
Southern and Western Regions
§ Winter rain

Crown rot found in all regions.
Mainly *F. pseudograminearum*

Fusarium species causing crown rot and head blight in Australia



2010 wheat season had a very wet finish

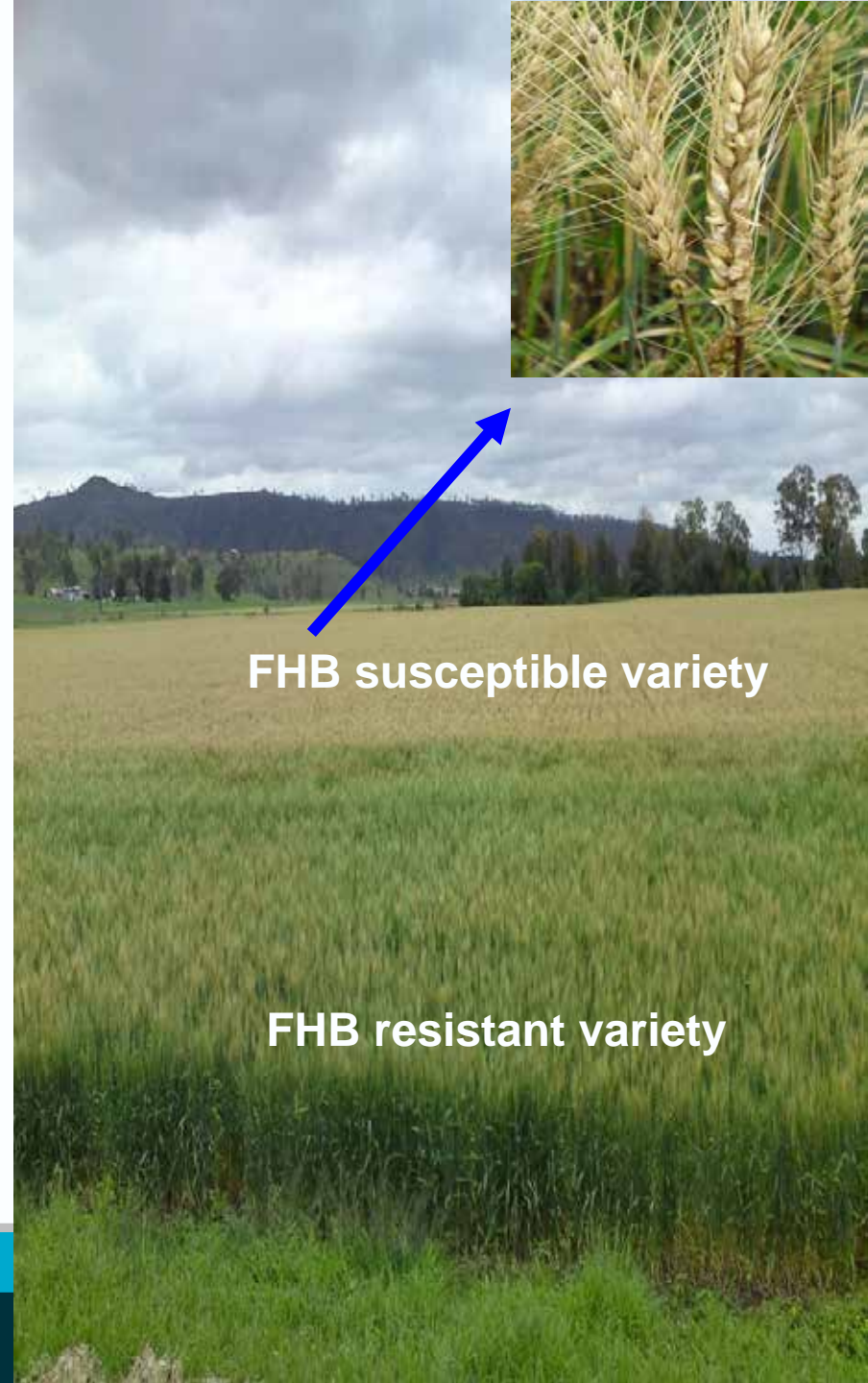


FHB epidemic 2010

Wheat crops were sampled from 25 sites in QLD and 19 in NSW at soft dough or early maturity stage

FHB was widespread on bread wheat and durum

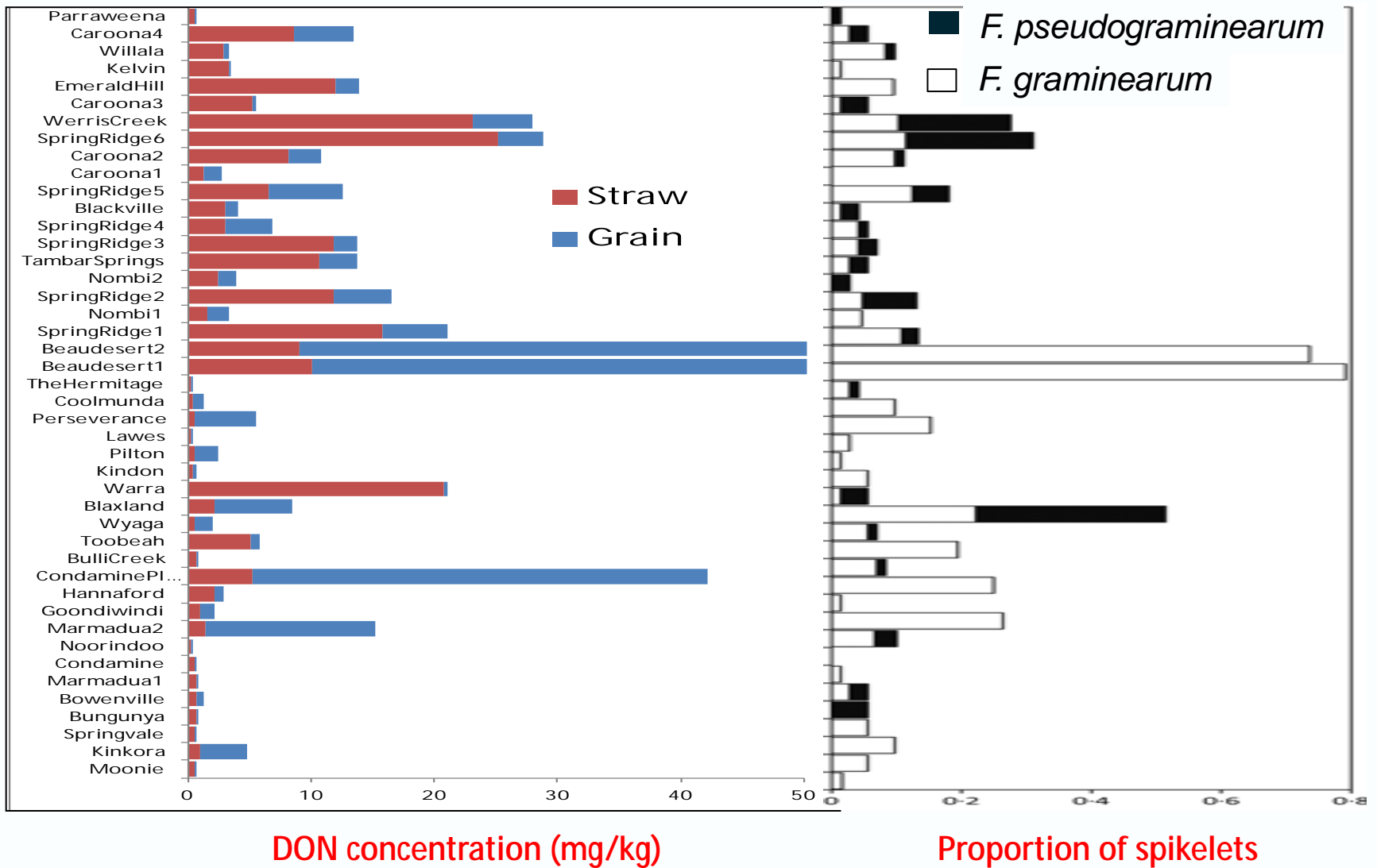
Both *Fusarium graminearum* and *F. pseudograminearum* caused FHB epidemic



FHB susceptible variety

FHB resistant variety

FHB epidemic 2010



What happened to the big wet after December 2010?







DY0960



Major Questions

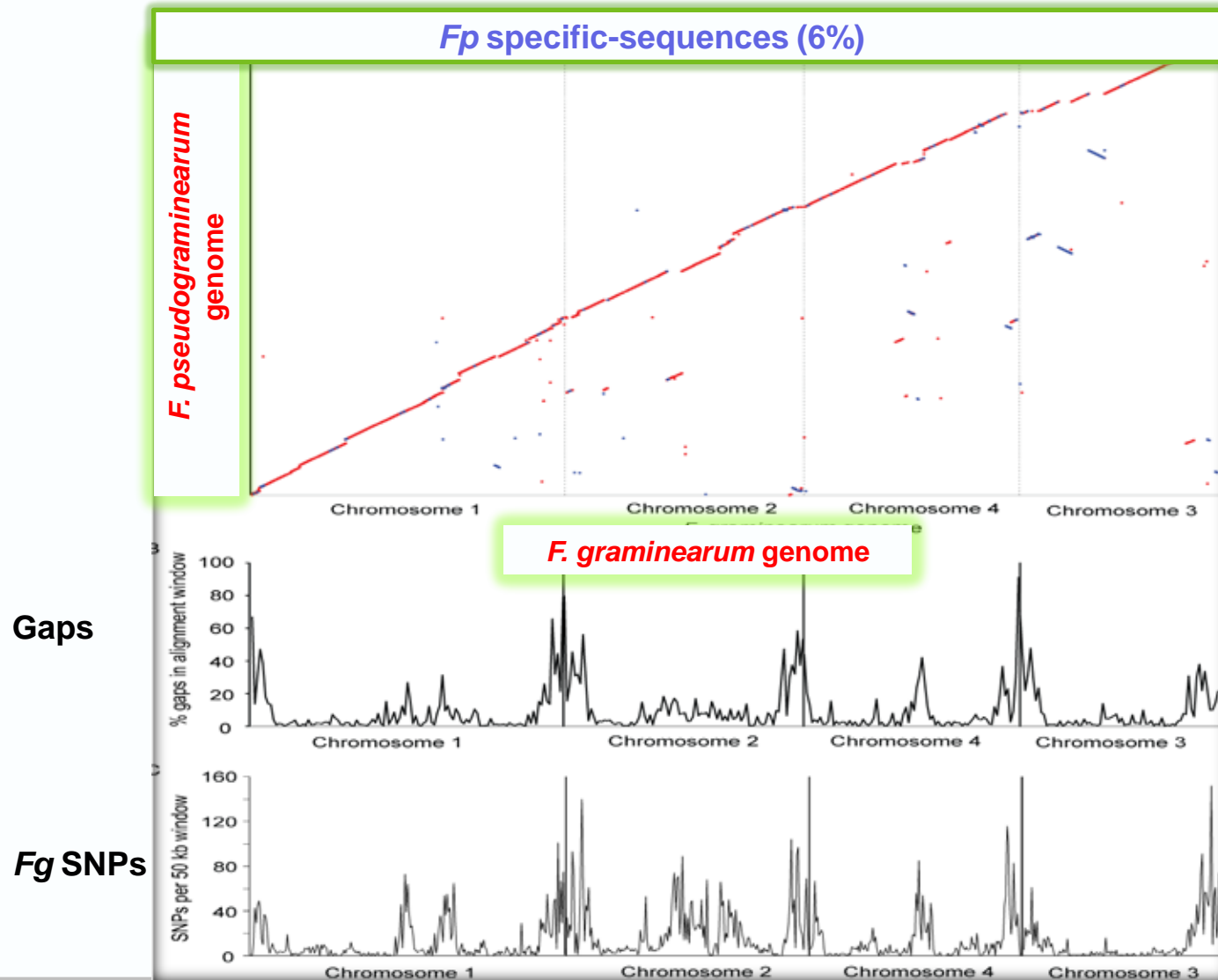
- Why is *F. pseudograminearum* predominant in crown rot?
- Why is *F. pseudograminearum* so broadly adapted?
- What cereal defences are overcome by *F. pseudograminearum* and how?

F. pseudograminearum genome

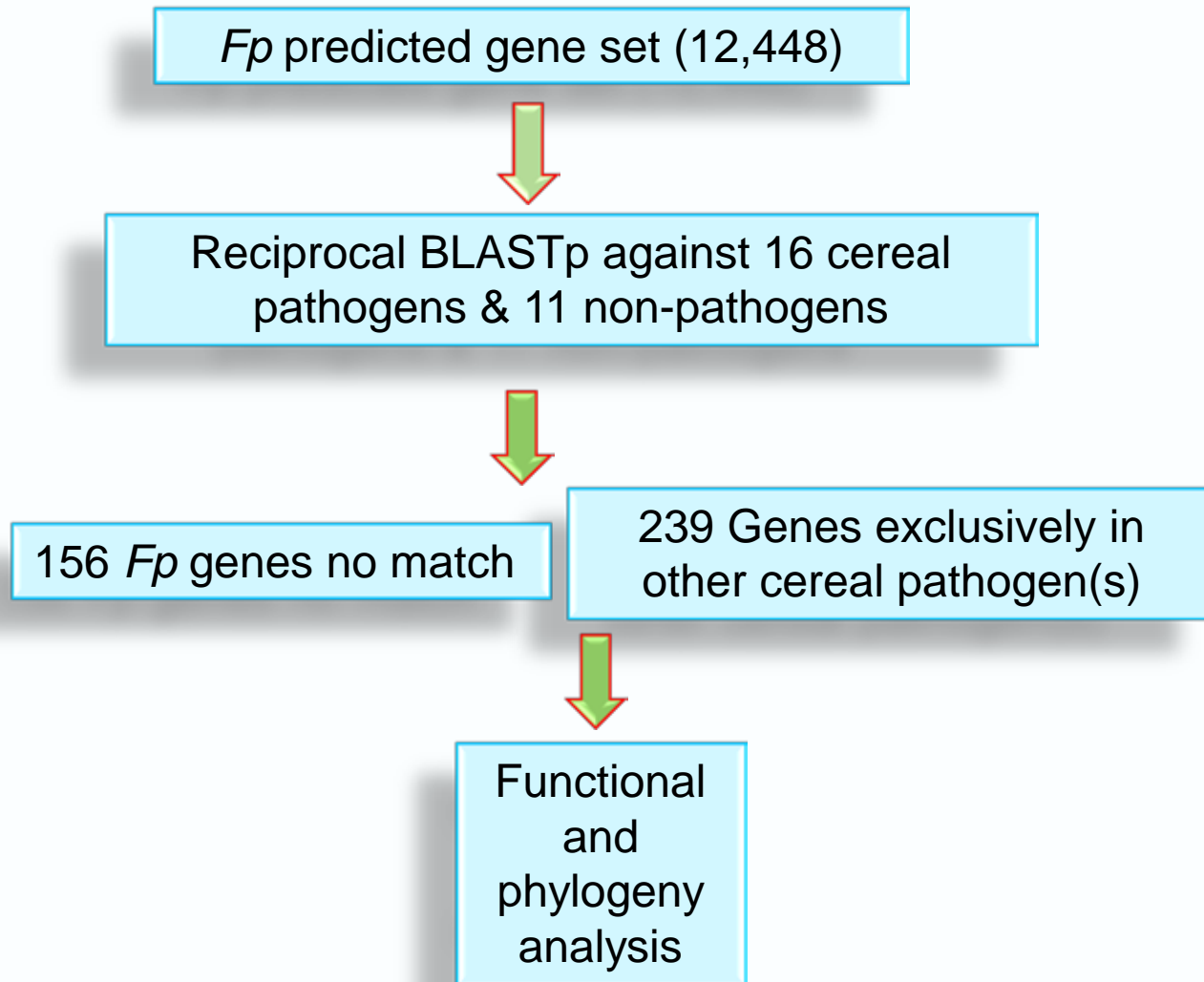
Species	Size	Technology	Coverage
<i>F. pseudograminearum</i>	37Mbp	Illumina	179x
<i>F. graminearum</i> ¹	36Mbp	Sanger	10x
<i>F. oxysporum</i> f. sp. <i>lycopersici</i> ²	60Mbp	Sanger	6x
<i>F. oxysporum</i> 5176 ^{2,3}	55Mbp	454	8x
<i>F. verticillioides</i> ²	41Mbp	Sanger	8x

¹Cuomo et al 2007; ²Ma et al 2010; ³Thatcher et al 2012; Gardiner et al 2012

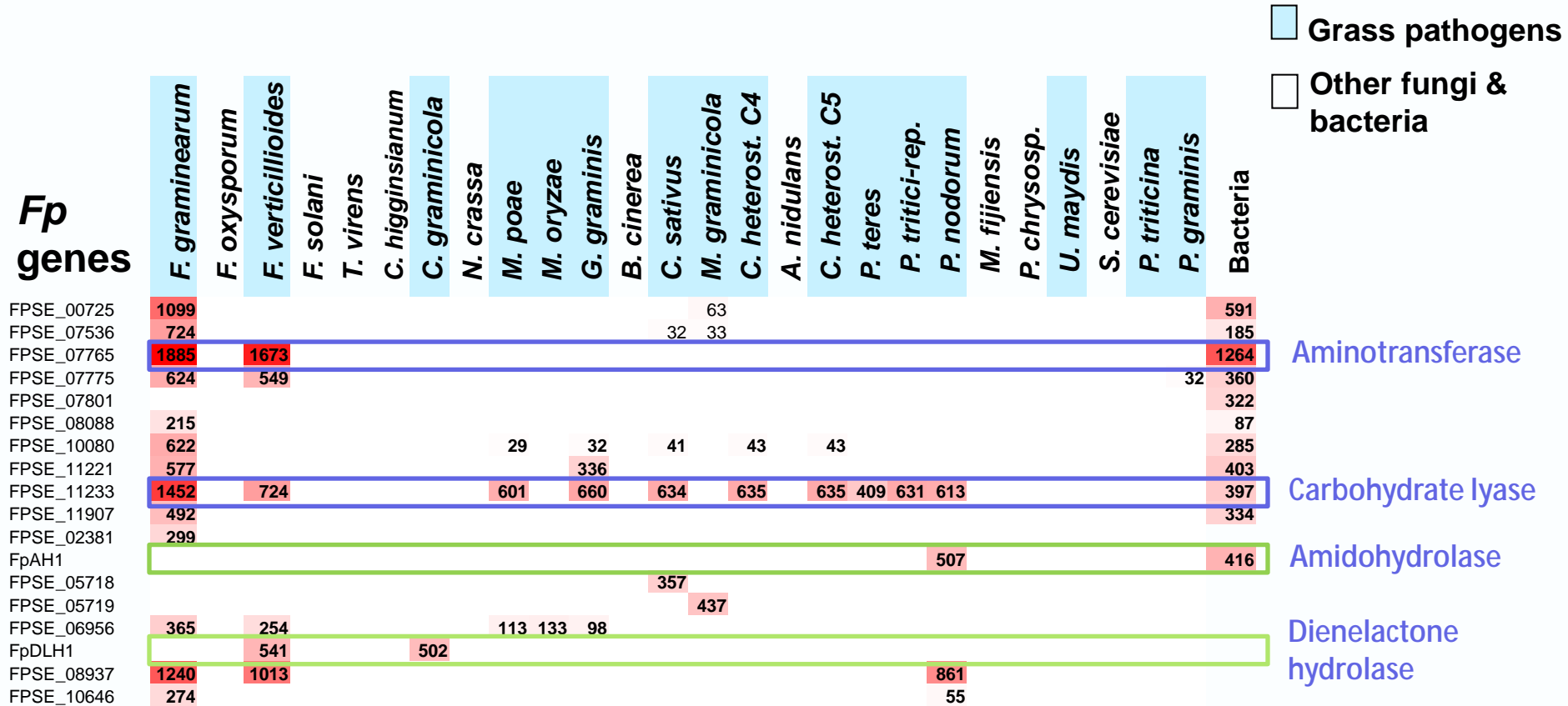
Comparison of *F. pseudograminearum* & *F. graminearum* genomes



Comparative genomics pipeline



Examples of *F. pseudograminearum* genes exclusively shared by cereal pathogens with some acquired from bacteria



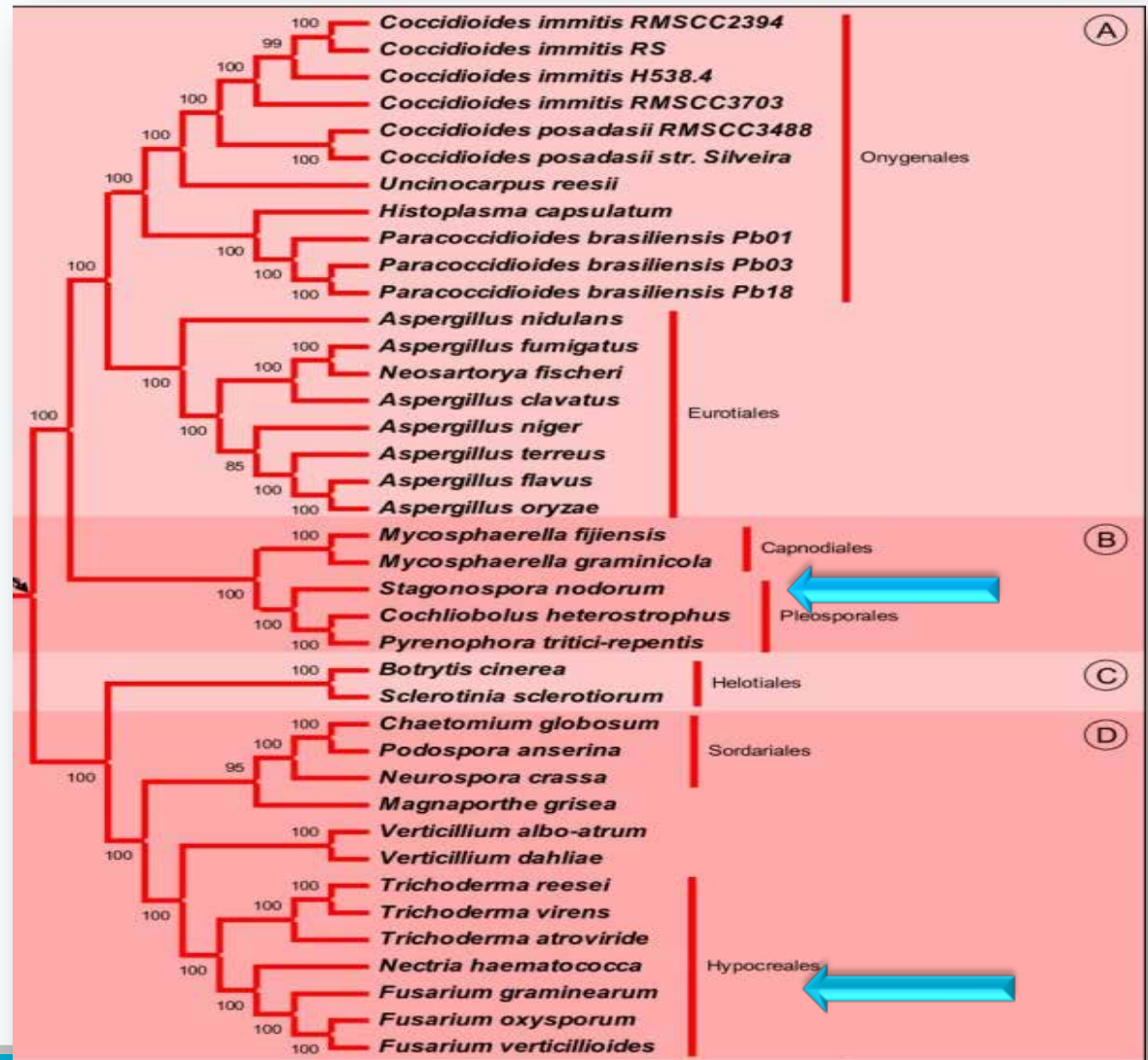
Numbers indicate BLAST bit score

Where did FpAH1 come from?

Genetic exchange
between
Stagonospora
and *Fp*?

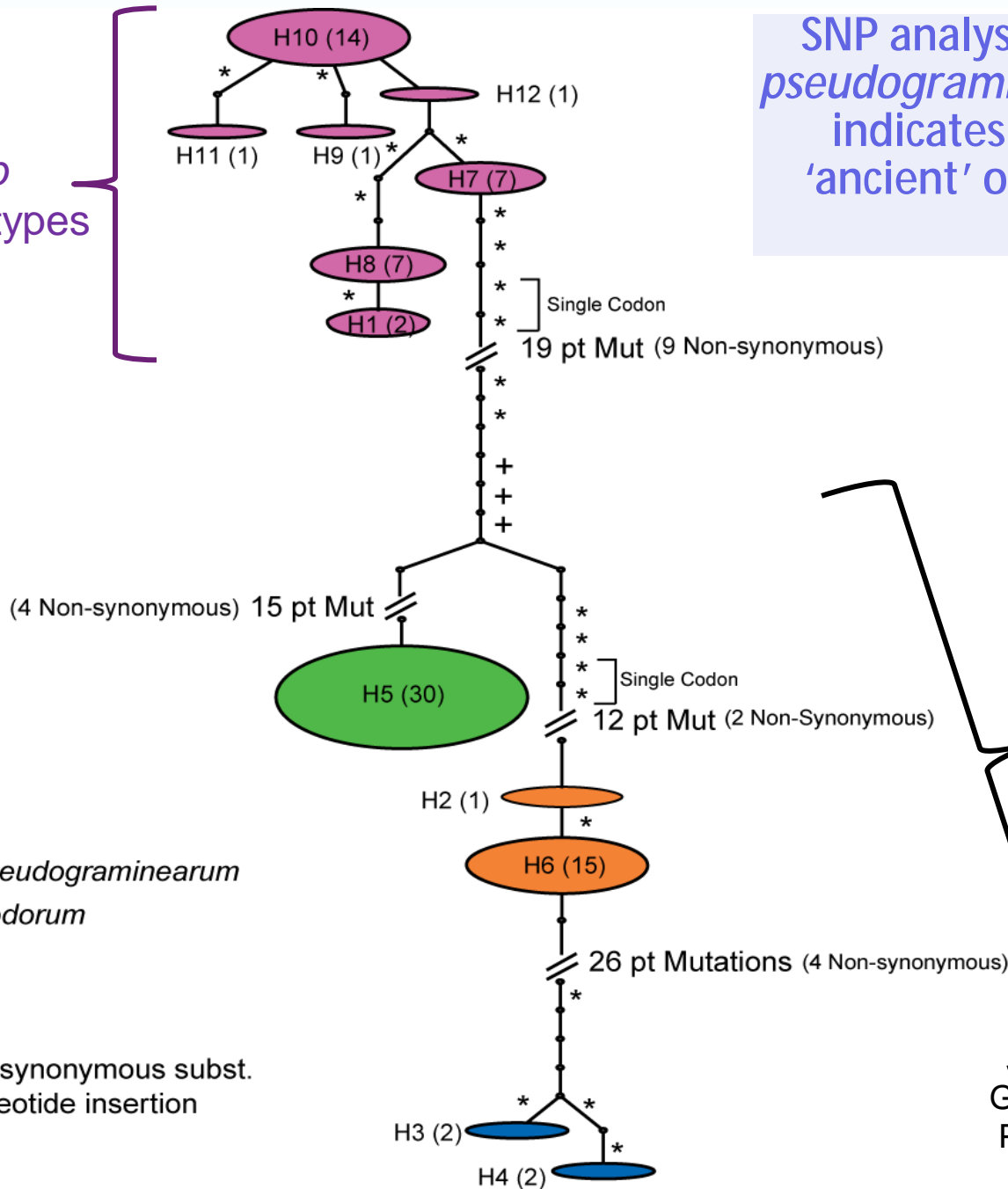
or

Independent
acquisition from
bacteria?



SNP analysis of AH1 genes in *F. pseudograminearum* & *P. nodorum* indicates an independent & 'ancient' origin in each species

Fp
haplotypes



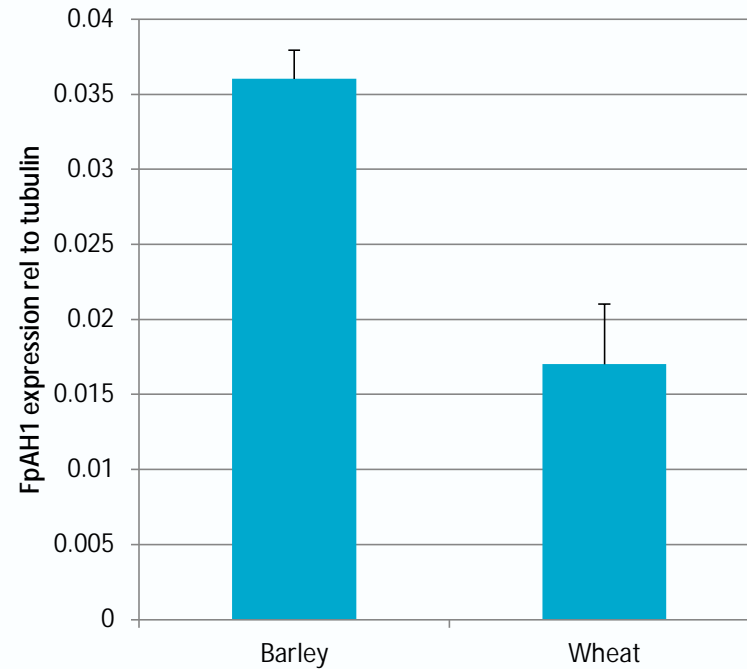
Phaeosphaeria
haplotypes

- F. pseudograminearum*
- P. nodorum*
- Pat1
- Pat3
- * Non-synonymous subst.
- + Nucleotide insertion

Gardiner et al., 2012,
PLOS PATHOGENS

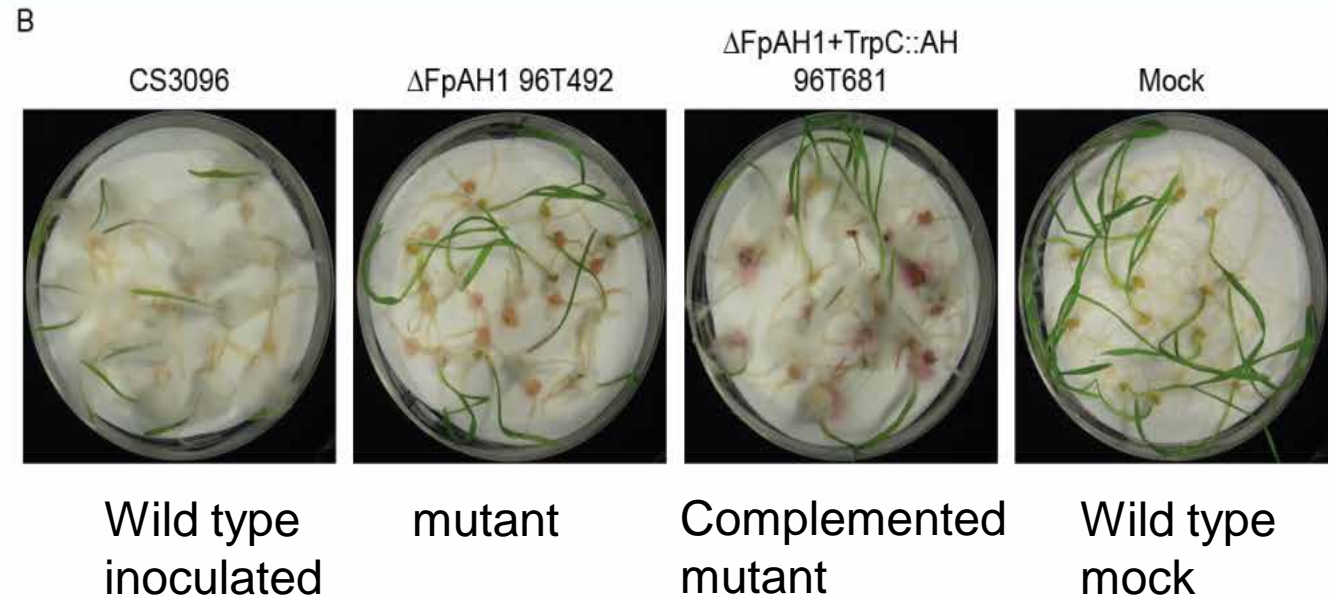
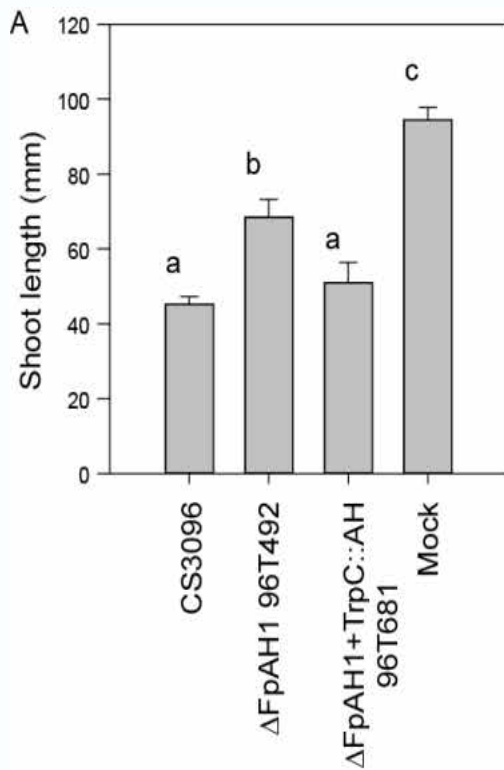


FpAH1 is expressed during crown infection

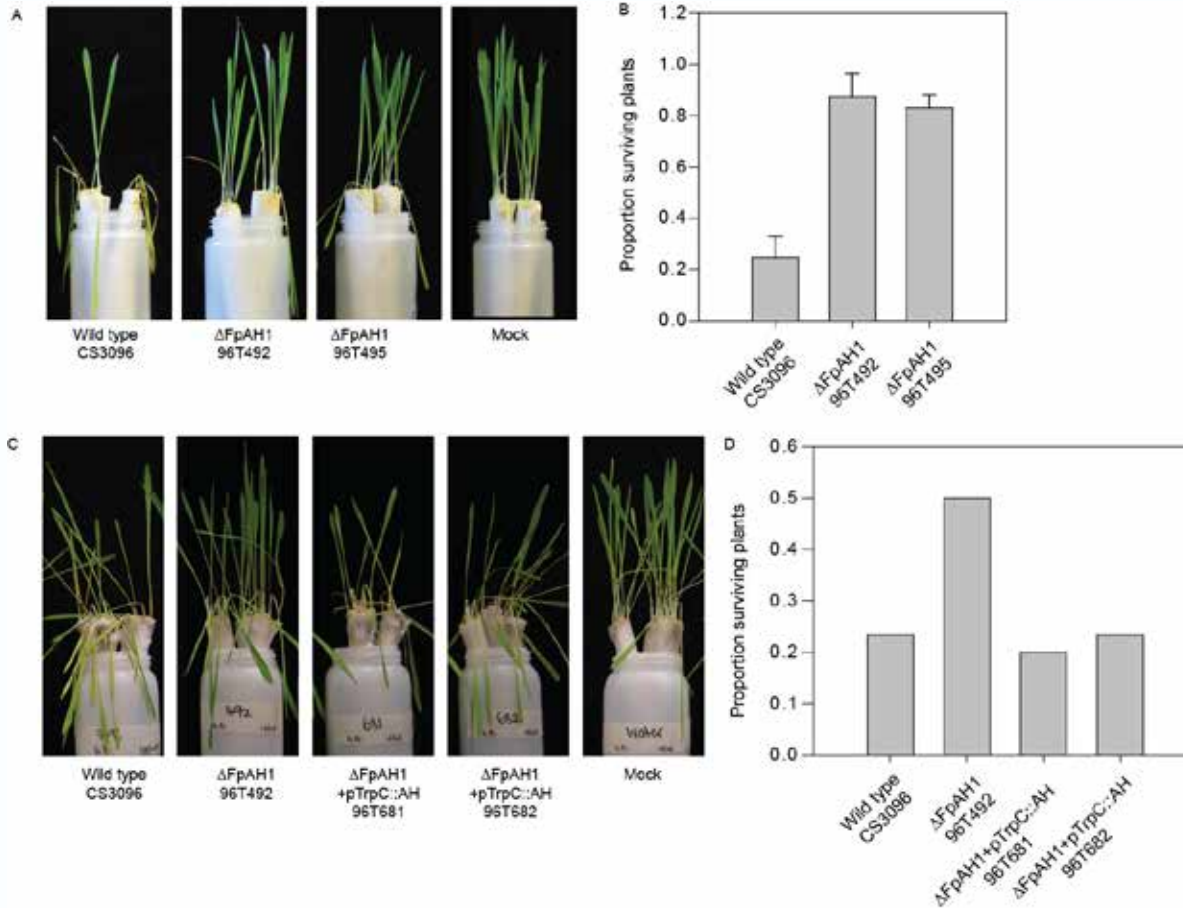


FpAH1 promoter-GFP fusion
and Real-time RT-PCR

FpAH1 is important for full virulence on wheat



FpAH1 is required for full virulence on barley



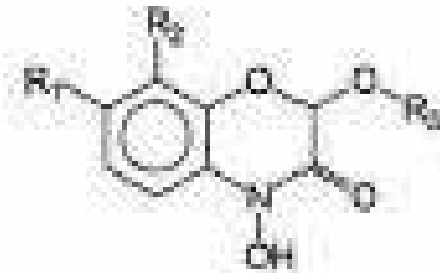
FpAH1 knockouts have reduced virulence (i.e. increased plant survival)

FpAH1 complementation restores virulence in knock outs

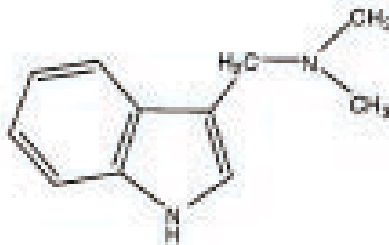
What is the mode of action of FpAH1?

Amidohydrolases are a diverse superfamily of enzymes which catalyse the hydrolysis of amide bonds in a large number of different substrates

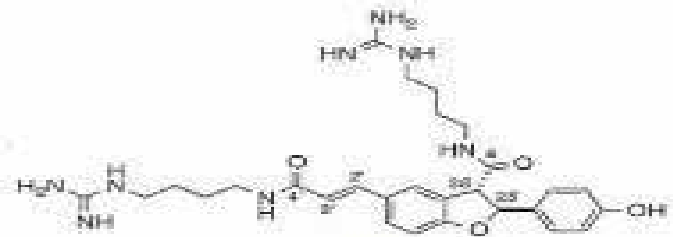
Amide-containing cereal defence molecules



Hydroxamic acids (DIMBOA)

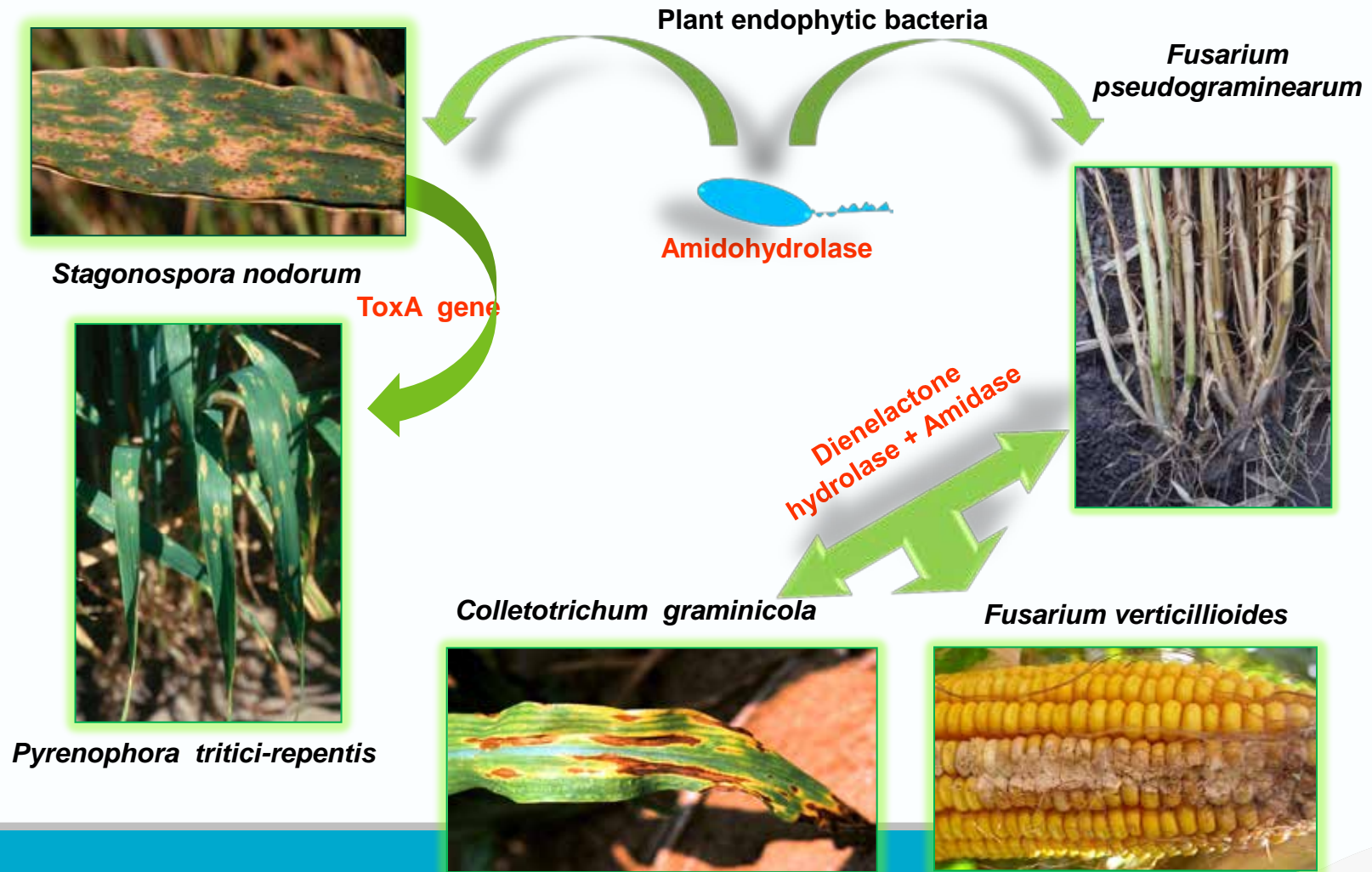


Gramine (indole alkaloid)



Hordatine

Evolution of pathogenicity in cereal pathogens: possible roles for horizontal gene transfer



Genomes now under comparative analysis

Species	Isolate	Interest
F. pseudograminearum	CS3220	Moderate pathogenicity
	CS3427	High pathogenicity
	CS3487	Promiscuous mating isolate
	CS5834	WA isolate
F. acuminatum	CS5907	CR pathogen occasionally isolated in field
F. equiseti	CS3069	CR pathogen occasionally isolated in field
F. culmorum	CS7071	Globally important species for FCR and FHB

Thank you

CSIRO Plant Industry Brisbane

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