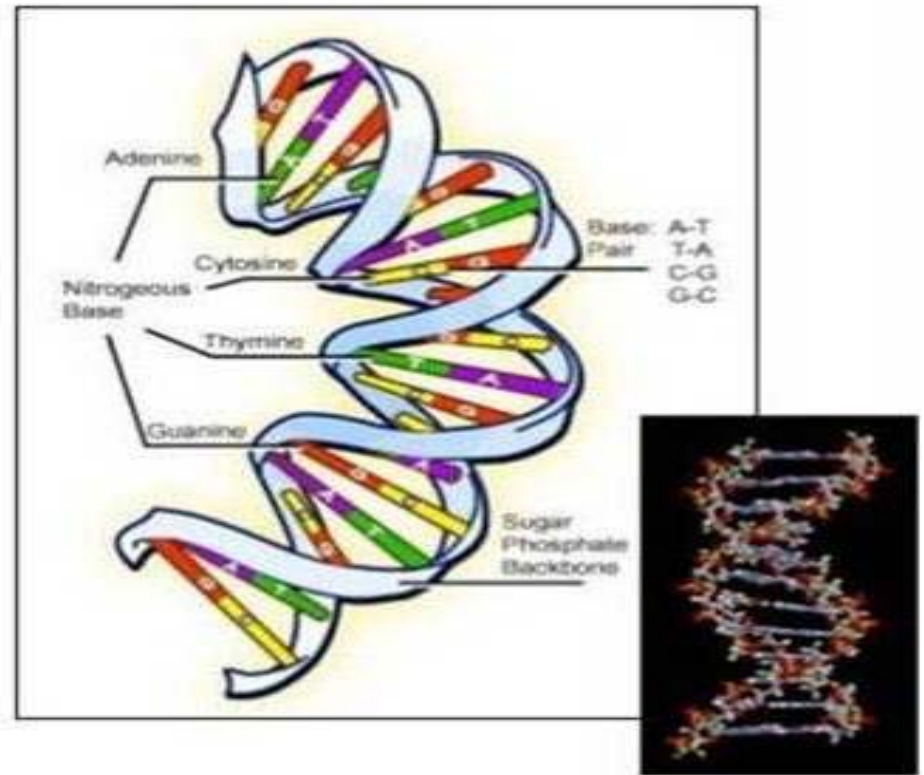


Genomics in plant disease management

What does 'genomics' mean?

- 'Genomics' is the study of the genomes of organisms.



Why to study genomes?

- Pathogen genome sequences help us to understand
 - Pathogenic behaviour and life style of a pathogen
 - Population diversity of a pathogen in a geographical area
 - Evolution of a pathogen over time
 - Relatedness of different fungal species

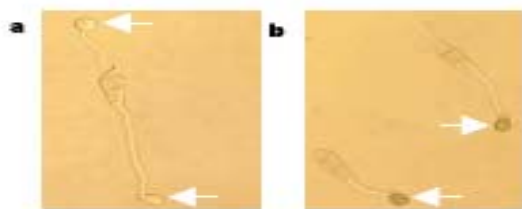
The genome sequence of the rice blast fungus *Magnaporthe grisea*

Ralph A. Dean¹, Nicholas J. Talbot², Daniel J. Ebbole³, Mark L. Farman⁴, Thomas K. Mitchell¹, Marc J. Orbach⁵, Michael Thon³, Resham Kulkarni^{1*}, Jin-Rong Xu⁶, Huaqin Pan¹, Nick D. Read⁷, Yong-Hwan Lee⁸, Ignazio Carbone¹, Doug Brown¹, Yeon Yee Oh¹, Nicole Donofrio¹, Jun Seop Jeong¹, Darren M. Soanes², Slavica Djonovic³, Elena Kolomiets³, Cathryn Rehmeyer⁴, Weixi Li⁴, Michael Harding⁵, Soonok Kim⁸, Marc-Henri Lebrun⁹, Heidi Bohnert⁹, Sean Coughlan¹⁰, Jonathan Butler¹¹, Sarah Calvo¹¹, Li-Jun Ma¹¹, Robert Nicol¹¹, Seth Purcell¹¹, Chad Nusbaum¹¹, James E. Galagan¹¹ & Bruce W. Birren¹¹

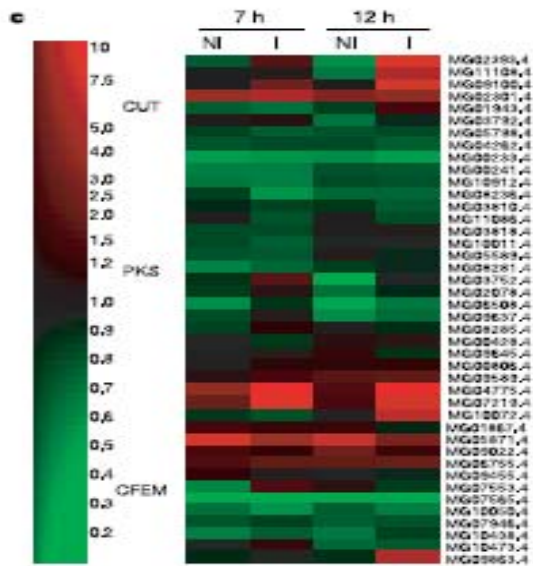
Table 1 *Magnaporthe grisea* assembly features

General genome features	Value
Size (bp)	37,878,070
Chromosomes	7
(G+C) percentage	51.6
Protein-coding genes	11,109
tRNA genes	316
Per cent coding	40.5
Average gene size (bp)	1,683
Average intergenic distance (bp)	1,503
Predicted protein-coding sequences	
Conserved hypothetical proteins	8,868 (79%)
Predicted proteins*	2,233 (20%)

Nature **434**, 980–986 (21 April 2005)



Differential expression of selected *M. grisea* genes during infection-related development. Appressorium formation (arrows) at 7 h (a; cessation of polar growth and tip hooking) and 12 h (b; tip swelling and melanization) after germination.



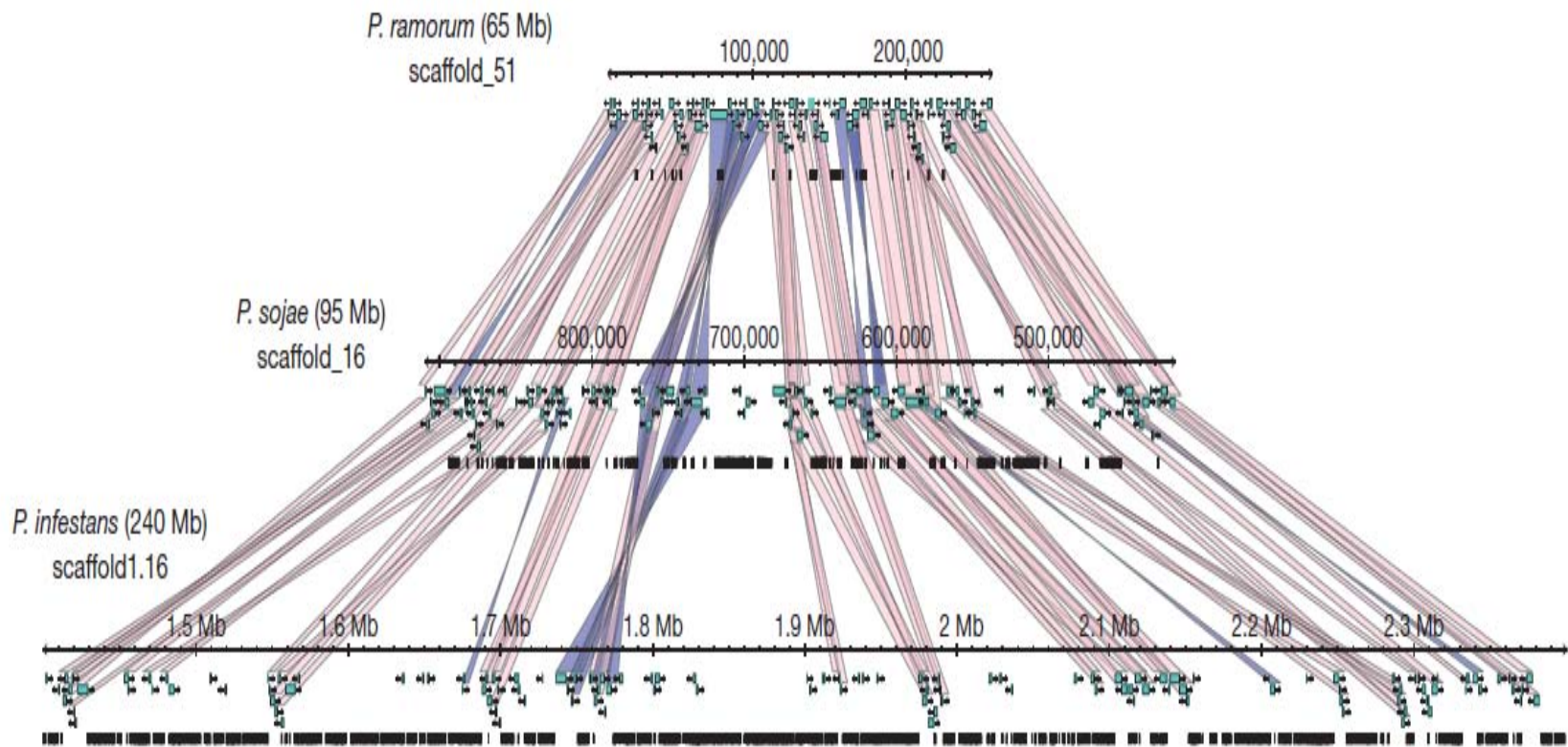
C; Expression profiles of selected genes from conidia germinated on hydrophobic appressorium-inducing (I) and hydrophilic non-appressorium-inducing (NI) surfaces. The colour scale indicates transcript abundance relative to ungerminated conidia: red, increase in transcript abundance; green, decrease in transcript abundance.

Genome sequence and analysis of the Irish potato famine pathogen *Phytophthora infestans*

Brian J. Haas^{1*}, Sophien Kamoun^{2,3*}, Michael C. Zody^{1,4}, Rays H. Y. Jiang^{1,5}, Robert E. Handsaker¹, Liliana M. Cano², Manfred Grabherr¹, Chinnappa D. Kodira^{1†}, Sylvain Raffaele², Trudy Torto-Alalibo^{3†}, Tolga O. Bozkurt²,

Table 1 | Genome assembly and annotation statistics

	<i>P. infestans</i>	<i>P. sojae</i>	<i>P. ramorum</i>
Genome			
Estimated genome size	240 Mb	95 Mb*	65 Mb*
Coverage (fold)	7.6	7.9*	5.6*
Number of scaffolds	4,921	1,810*	2,576*
N50 scaffold length	1,570 kb	463 kb*	308 kb*
Total scaffold length	228.5 Mb	86.0 Mb*	66.7 Mb*
Number of contigs	18,288	5,577*	7,588*
N50 contig length	44.5 kb	105.7 kb*	47.5 kb*
Total contig length	190 Mb	78 Mb*	54.4 Mb*
G+C content	51.0%	54.4%	53.9%
Repeat† (%)	74%	39%	28%
Collinear blocks‡	85 Mb	52 Mb	37 Mb
Repeat† (%) in collinear blocks‡	57%	28%	13%
Repeat† (%) outside collinear blocks‡	86%	60%	56%
Intergenic region spacing in collinear blocks‡ (25–75 percentiles)	224–3,070 bp	307–2,319 bp	270–1,551 bp
Intergenic region spacing outside collinear blocks‡ (25–75 percentiles)	664–19,144 bp	753–5,896 bp	566–4,351 bp
Genes			
Number of genes§	17,797	16,988	14,451
<i>Phytophthora</i> orthologues	11,893	12,427	12,136
<i>Phytophthora</i> core orthologues	9,583	9,550	9,664

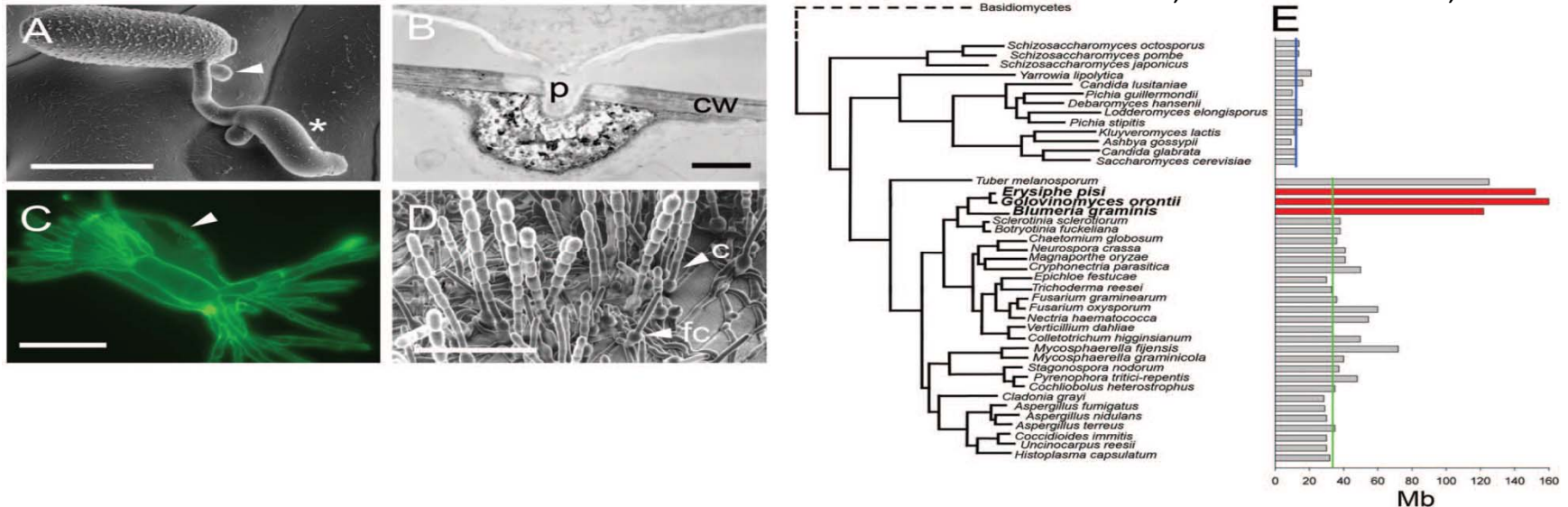


- Expansion of *Phytophthora infestans* resulted from a proliferation of repetitive DNA accounting for 74% of the genome.
- Comparison with two other *Phytophthora* genomes showed rapid turnover and extensive expansion of specific families of secreted disease effector proteins, including many genes that are induced during infection or are predicted to have activities that alter host physiology.
- These fast-evolving effector genes are localized to highly dynamic and expanded regions of the *P. infestans* genome.
- This probably plays a crucial part in the rapid adaptability of the pathogen to host plants and underpins its evolutionary potential.

Genome Expansion and Gene Loss in Powdery Mildew Fungi Reveal Tradeoffs in Extreme Parasitism

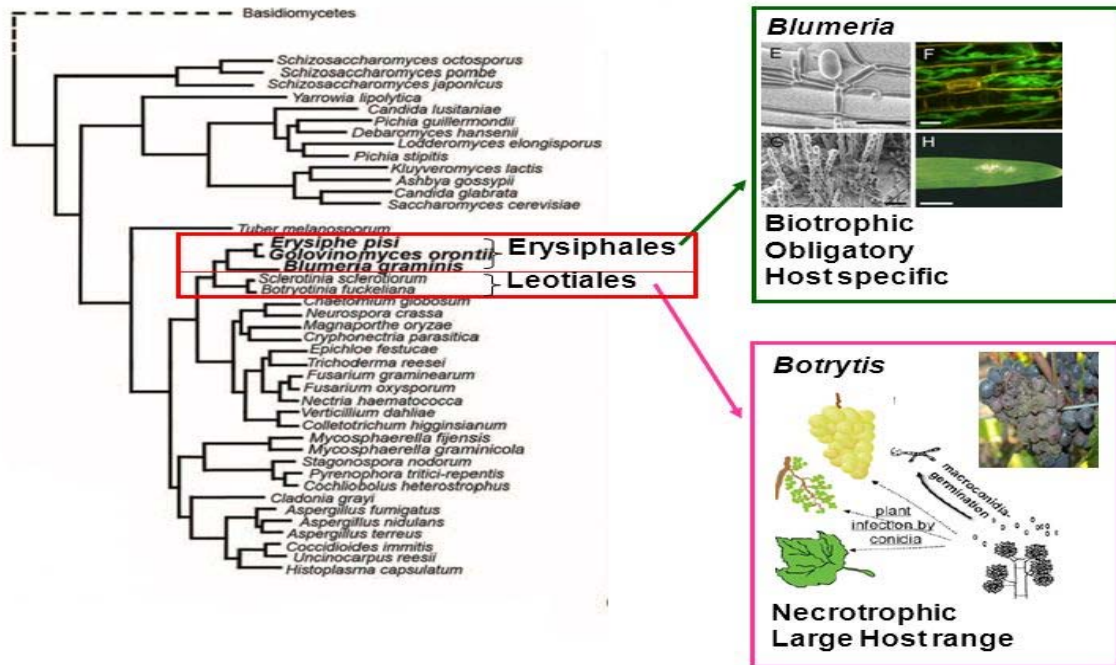
Pietro D. Spanu,^{1*} James C. Abbott,^{1†} Joelle Anselem,^{2,15†} Timothy A. Burgis,^{1†}
Darren M. Soanes,^{3†} Kurt Stüber,^{4†} Emiel Ver Loren van Themaat,^{4†} James K. M. Brown,^{5‡}

Science Vol. 330, 10 December 2010, 1543-1546.



Phylogeny of selected ascomycetes and their genome sizes. *Blumeria*, *Golovinomyces*, and *Erysiphe* are shown in red. The median genome sizes of the hemiascomycetes (blue vertical line, 12.3 Mb) and euascomycetes (green vertical line, 36.7 Mb).

Blumeria and Botrytis are related species with different life styles



Spanu et al. 2010, Science; Amselem et al. 2011 PLOS genetics

Rapid assessment of pathogen diversity from field samples

