

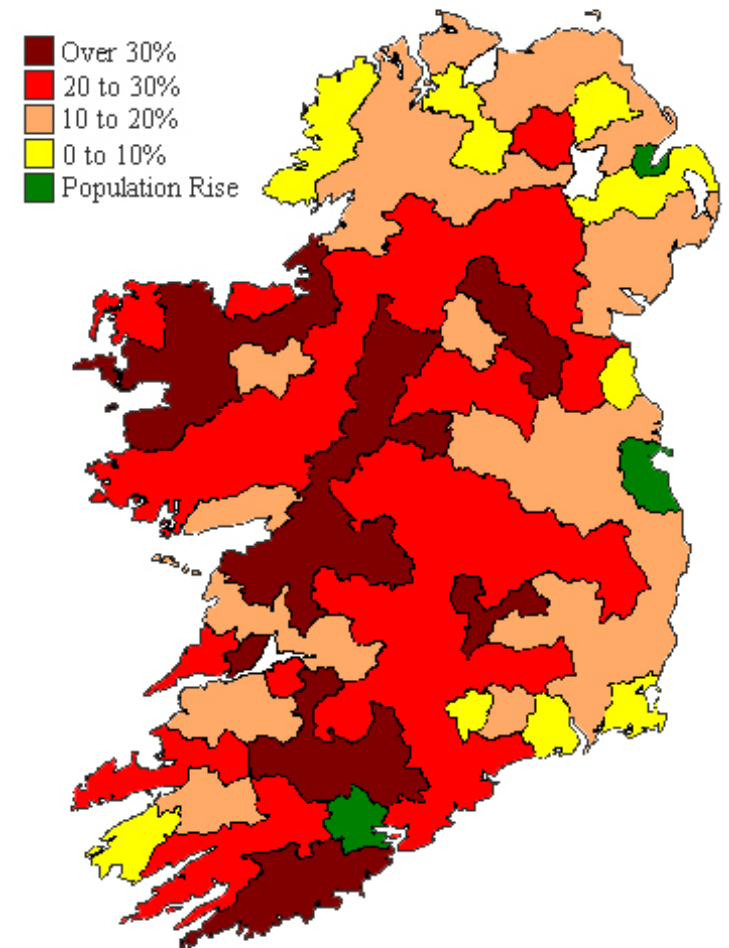
Phytophthora Infestans

Benedict Hempel - Food & Genes

16.12.2019

The Irish Potato Famine

- Major outbreak of the Potato Blight
- 1845 – 1849
- 12% of Irelands population starved
- Forced displacement of 2 million people



Modified from: Edwards & Williams, 1956

Phytophthora infestans

- Causal Agent of the Potato Blight
- Belongs to the Oomycetes
- Main Hosts: Potato and Tomato
- Originated in Mexico
- Favors cool and moist environments



Modified from www.unece.org, 7.12.19

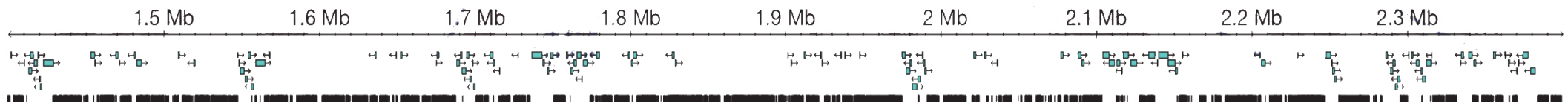


www.knowmoregrowmore.com, 11.12.19

The Genome of *P. infestans*

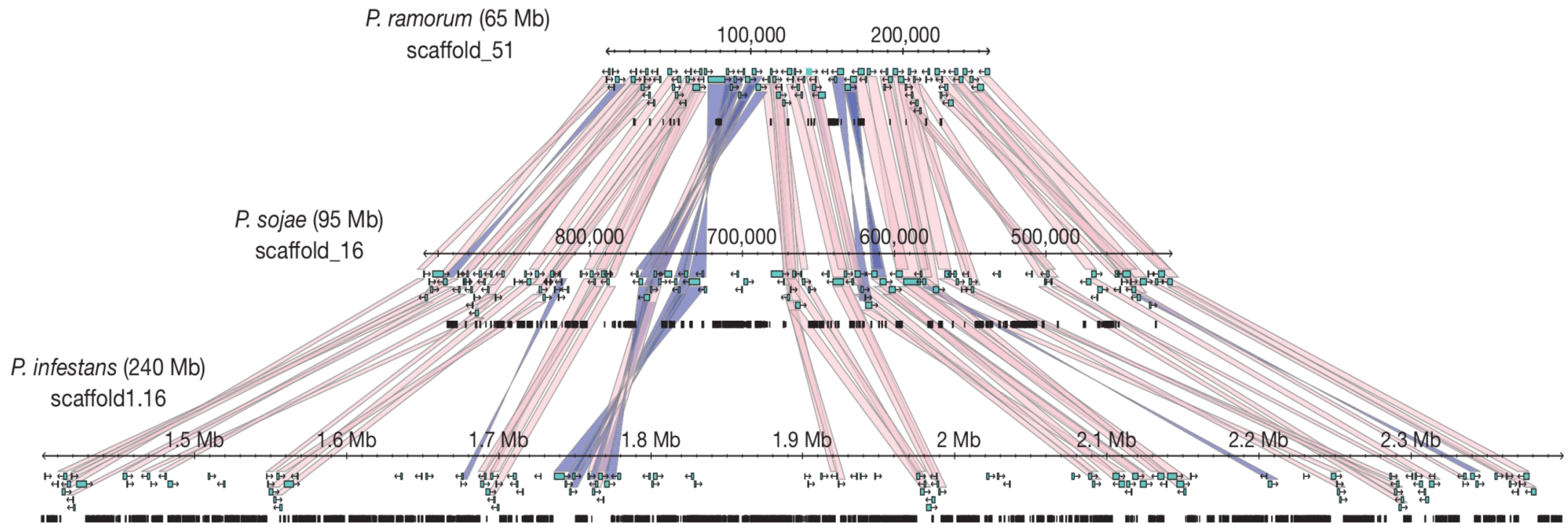
- Genome size: 240 Mb
- Genes: 17,797
- Repeats: 74%
- Big number of Transposons
- Gene-rich, conserved blocks & Gene-sparse, repeat-rich blocks

P. infestans (240 Mb)
scaffold1.16

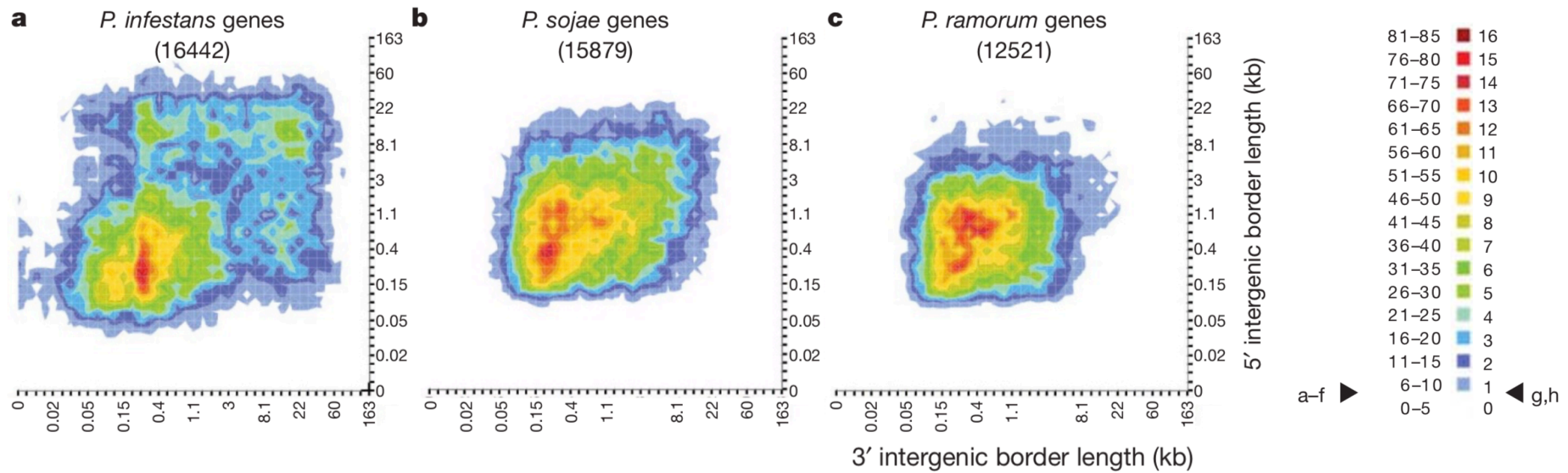


Modified from Haas et al., 2009

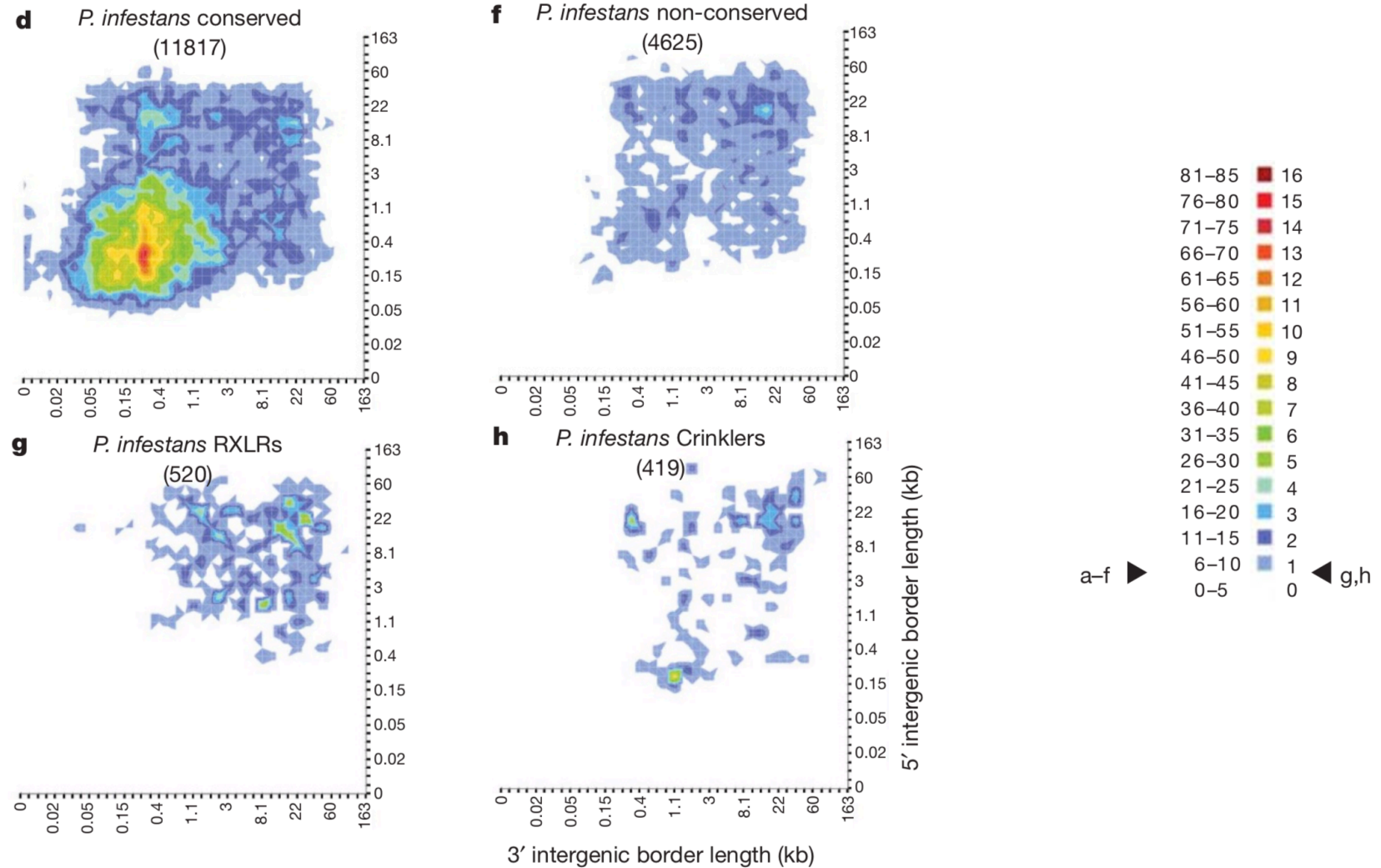
The Genome of *P. infestans*



The Genome of *P. infestans*

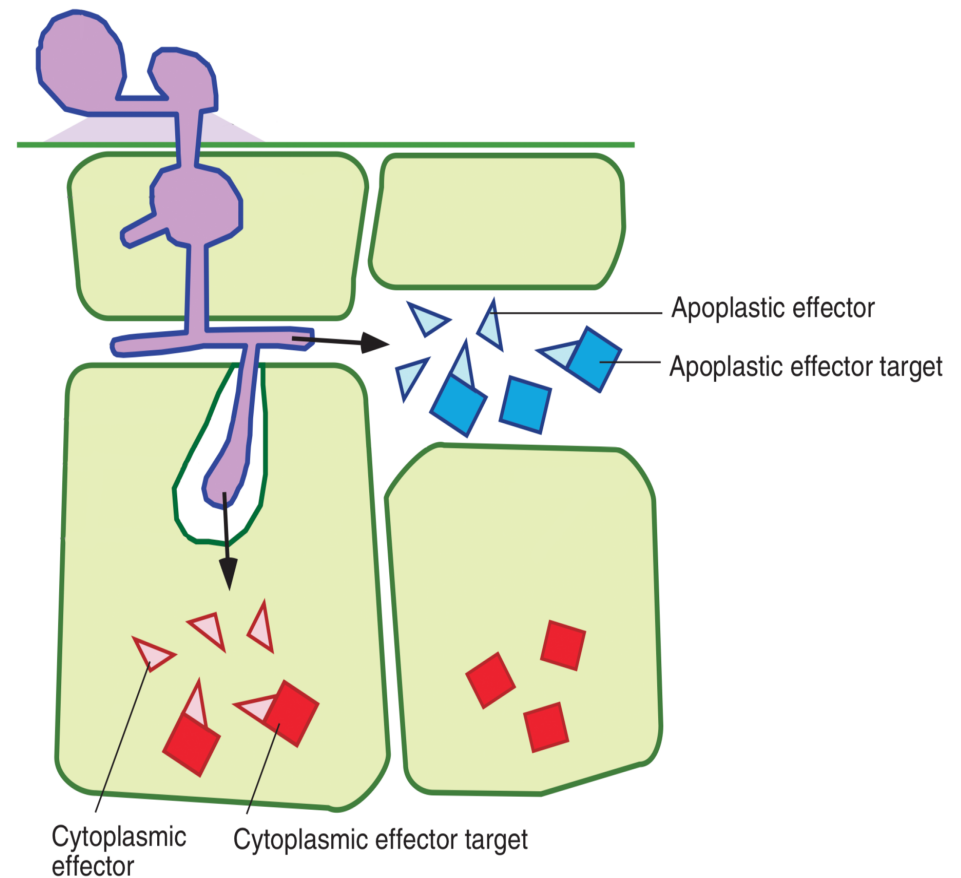


The Genome of *P. infestans*



Pathogene effectors of *P. infestans*

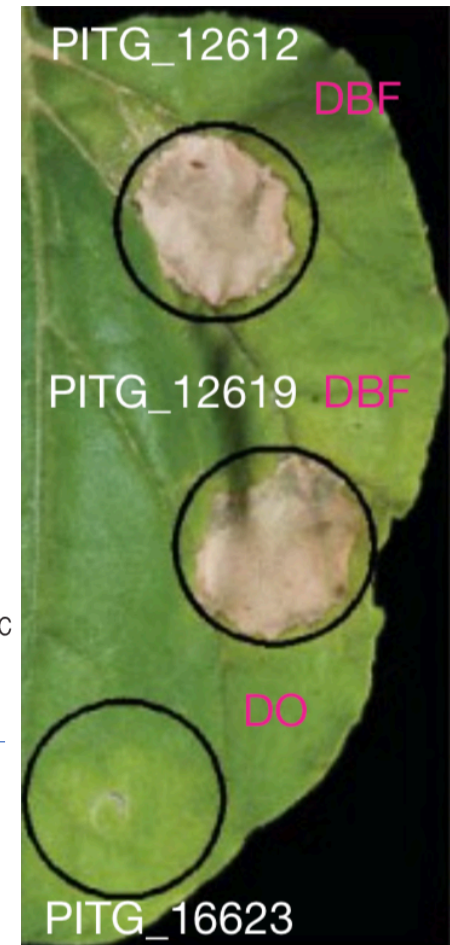
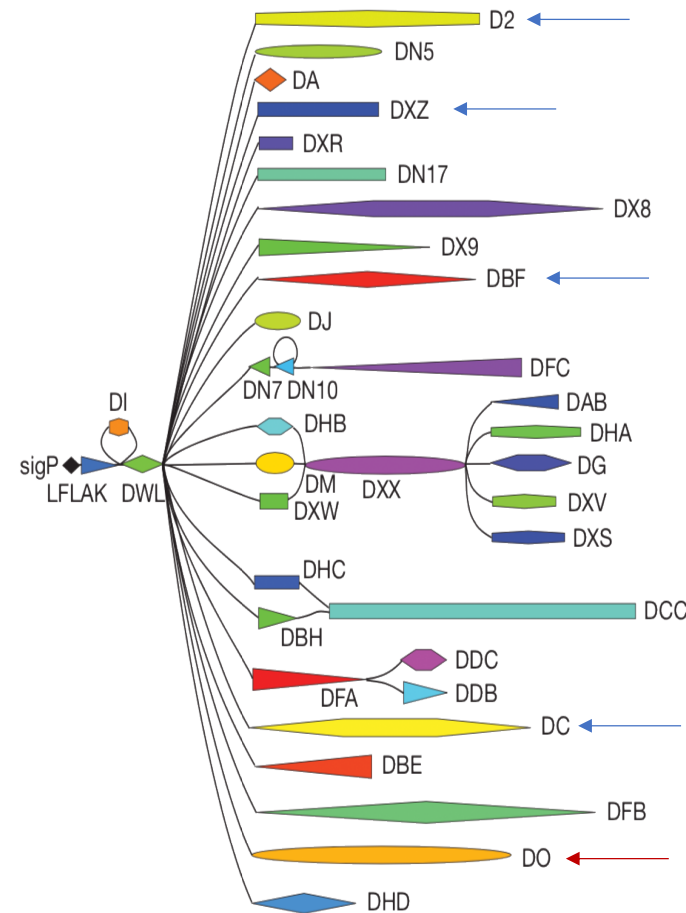
- Located in gene-sparse, repeat-rich regions
- Rapidly evolving
- Apoplastic & cytoplasmic effectors
- Highly diverse and modular
- Proliferation driven by Transposons



Modified from Kamoun, 2006

Pathogene effectors: CRNs

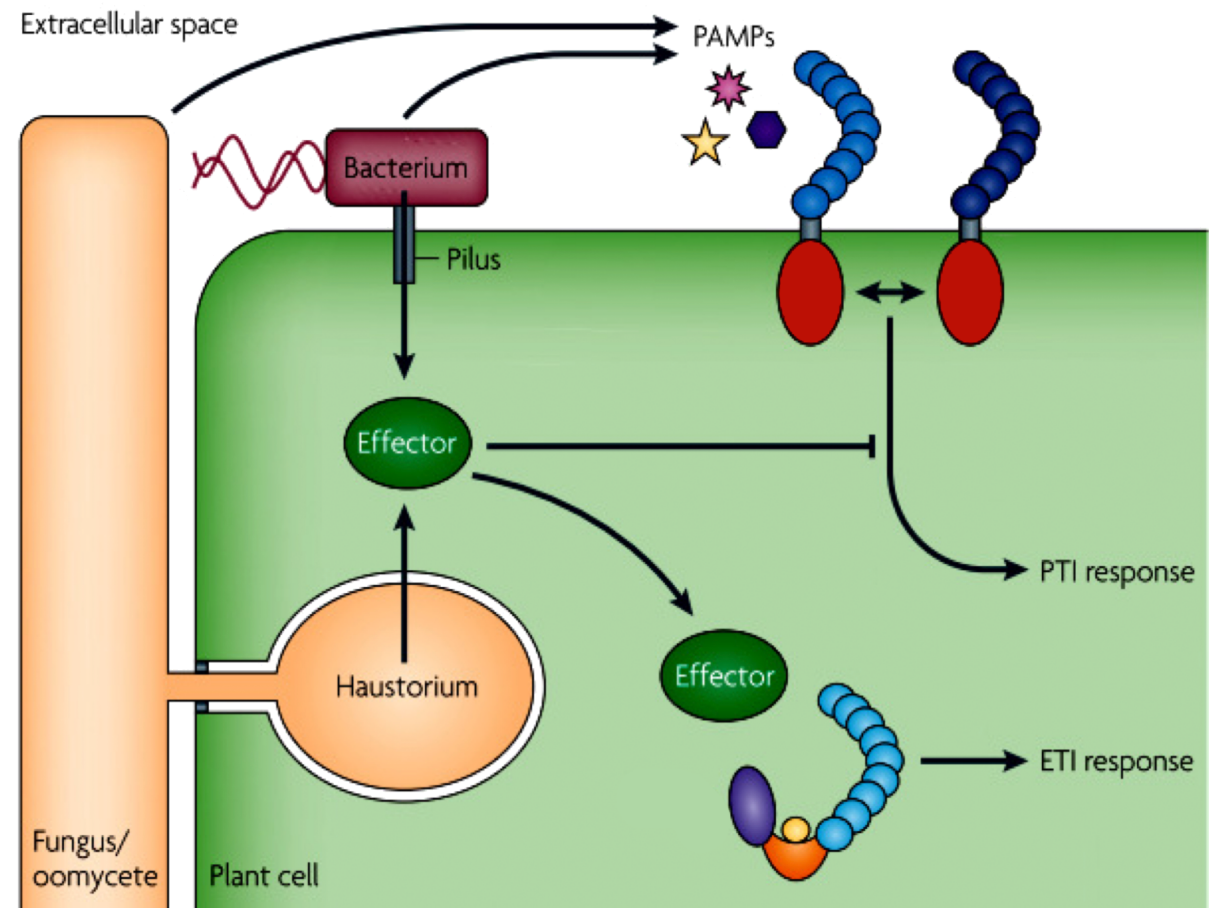
- 196 genes in *P. infestans*
- N-Terminal LFLAK domain
- Various C-Terminal effector domains
- Very common in Oomycetes
- Possible connection to necrotrophy



Haas et al., 2009

Plants vs. Pathogens: An Arms Race

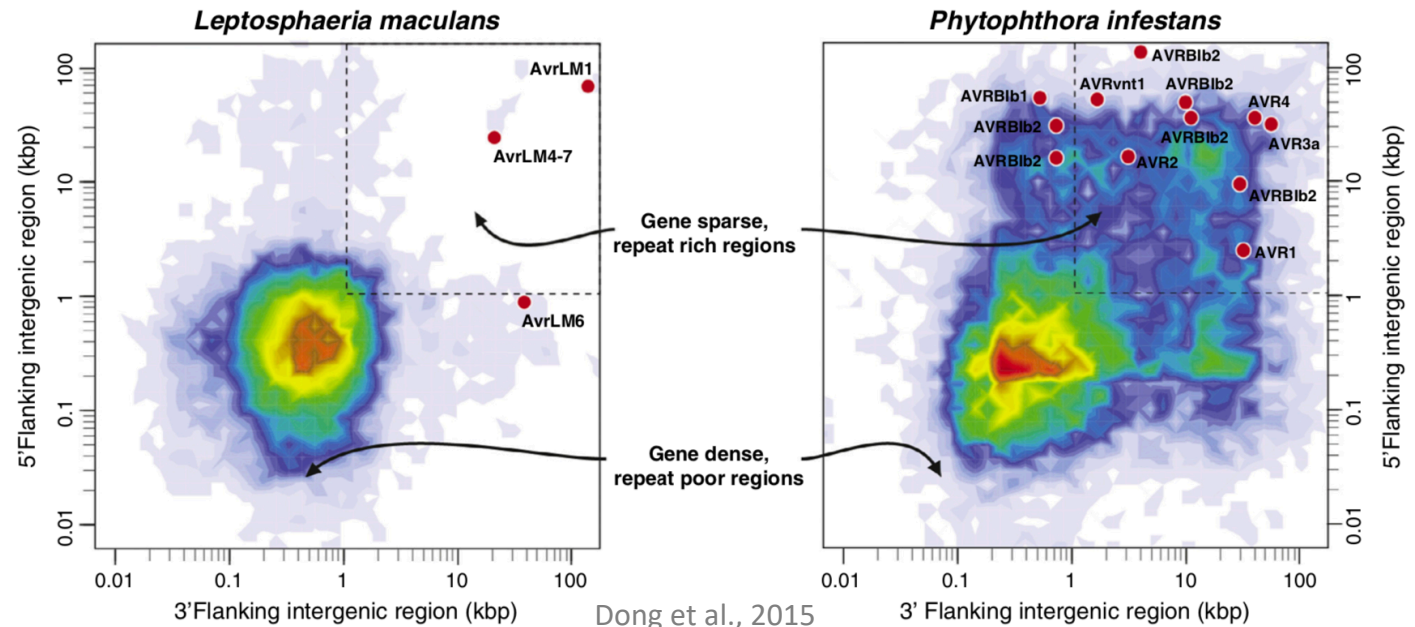
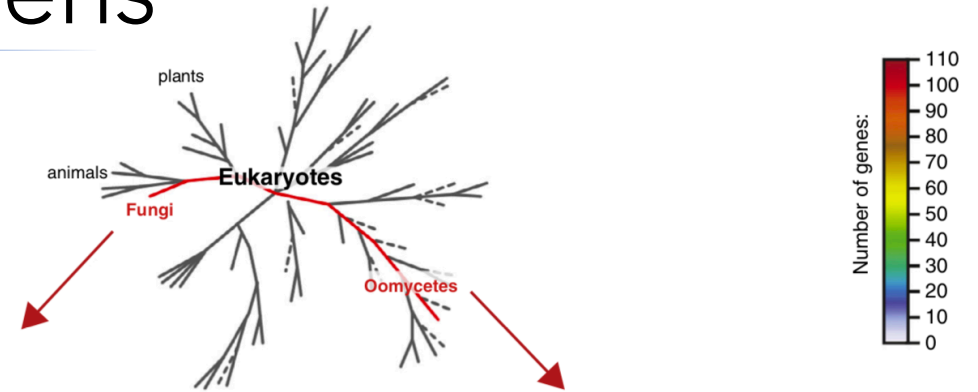
- PAMP Triggered Immunity (PTI)
- Effector Triggered Immunity (ETI)



Taha Abd El Rahman , 2011

The two-speed genomes of filamentous pathogens

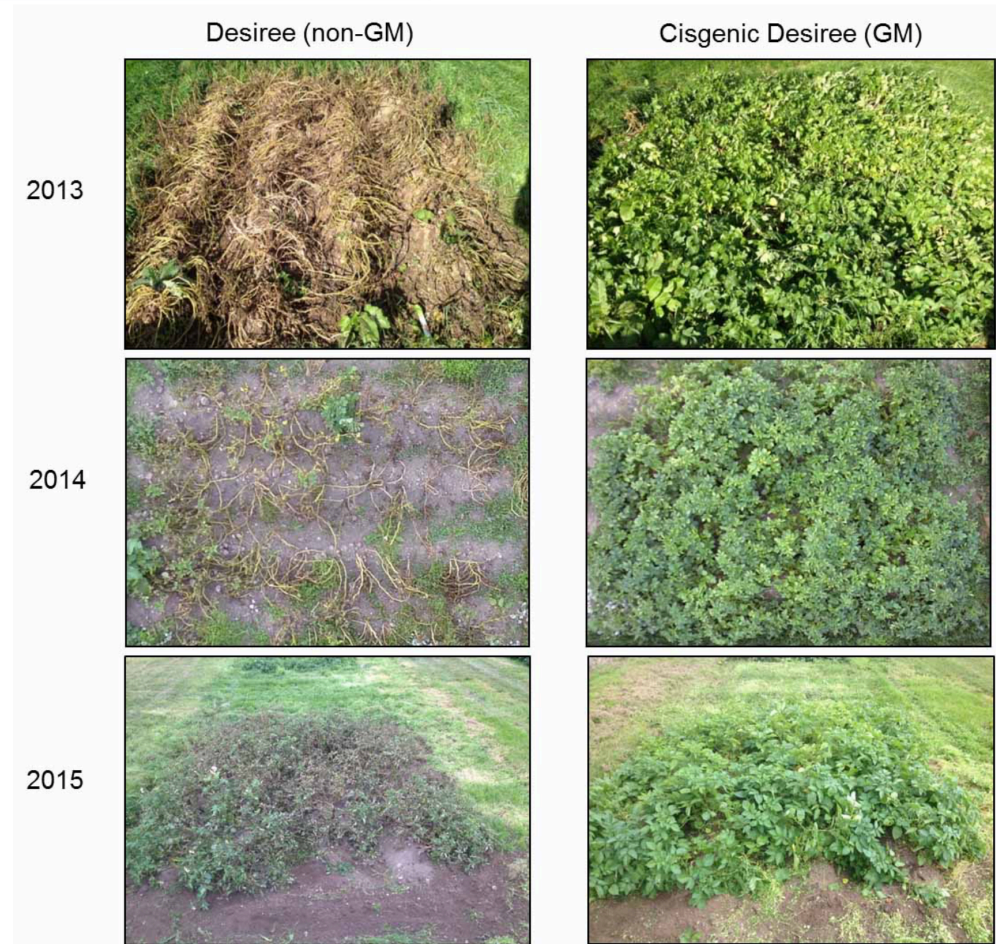
- Bipartite genome structure
 - conservation of house-keeping genes
 - fast modification of virulence genes



Convergence in unrelated plant pathogens!

Impact on crop production & possible countermeasures

- Problem:
 - 6 billion \$ in annual crop loss
 - Solution?
 - Decision Support Systems (DSS)
 - GMOs
 - Novel strategies?
- IPM 2.0



Summary

- Pathogenic Oomycetes are a major threat to global crop production
- Unrelated plant pathogens show a similar genome structure
- House-keeping genes are kept in conserved, gene-rich blocks
- Virulence genes are often located in dynamic, repeat-rich regions
- Modulation and transposon-driven proliferation of effector motifs is essential for host specialisation and virulence

References

- The two-speed genomes of filamentous pathogens: waltz with plants (2015)
 - Dong, Suomeng et al.
- Genome sequence and analysis of the Irish potato famine pathogen *Phytophthora infestans* (2009)
 - Haas, Brian J. et al.
- The Irish potato famine pathogen *Phytophthora infestans* originated in central Mexico rather than the Andes (2014)
 - Goss, Erica M. et al.
- Historic Late Blight Outbreaks Caused by a Widespread Dominant Lineage of *Phytophthora infestans* (2016)
 - Ristaino Jean. et al.
- Identification and Characterisation CRN Effectors in *Phytophthora capsici* Shows Modularity and Functional Diversity (2013)
 - Stam, Remco et al.
- The Great Famine: Studies in Irish History 1845-1852 (1956)
 - Edwards, R. Dudley & Williams, T. Desmond
- Molecular Mechanisms controlling the interaction between *Botrytis cinerea* and its host Tomato (2011)
 - Taha Abd El Rahman
- Development and validation of IPM strategies for the cultivation of cisgenically modified late blight resistant potato (20018)
 - Kessel, Geert J.T. et al.
- A Catalogue of the Effector Secretome of Plant Pathogenic Oomycetes (2006)
 - Sophien Kamoun
- Plant-mediated gene silencing restricts growth of the potato late blight pathogen *Phytophthora infestans* (2015)
 - Jahan, Sultana N et al.

Discussion

- What do you think are farming techniques which could possibly prevent crop loss due to late blight?

Discussion

- Do you think different rules should be applied for cisgenic and transgenic organisms in terms of food production?