Pathogen-secreted effectors: host subversion and what else?

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European Conference on Fungal Genetics, Rome, 2020

Plants perceive pathogens with pattern receptors





Invasion Pattern-Triggered Response (IPTR)







Cook et al., Annu. Rev. Phytopathol. 2015

Effectors are crucial for continued symbiosis







Effectors can become invasion patterns







Pathogens have "two-speed" genomes







- Core genome : household processes
 - Conserve and maintain (purifying selection)

- Flexible genome: effectors and other pathogenicity factors
 - Plasticity and rapid adaptation

Verticillium dahliae





Verticillium plasticity: lineage-specific regions



LS regions: recent duplications & gene loss







Faino et al., Genome Research 2016

LS regions display reduced SNP frequencies





100years

Faino *et al.*, Genome Research 2016 Depotter *et al.*, Molecular Ecology 2019

Why reduced SNP frequencies in LS regions?

Acquisition of LS regions by horizontal transfer?

• Unlikely: phylogeny of LS genes follows phylogeny of *Verticillium* genus





LS regions: intermediate chromatin state



Heterochromatin: DNA methylation and H3K9me3 at specific TEs, closed DNA (low ATAC-seq)

Euchromatin: Devoid of DNA and histone methylation, open DNA (high ATAC-seq)

LS regions

- Devoid of DNA and H3K9 methylation
- Enriched for H3K27me3
- Intermediate ATAC-seq signal

Machine learning prediction of LS regions

- Approached LS identification as a binary classification problem
- Used four machine learning algorithms to assess ability to identify previously unknown LS regions
- Independently re-iterated over the genome to saturate prediction







Proximity ligation: LS regions interact





V. dahliae effector catalogs are highly divergent







Comparative genomics: tomato pathogenicity



Tom1 mediates pathogenicity on tomato







Tom1 can confer pathogenicity to non-pathogens





The Verticillium dahliae Ave1 effector

Tomato immune receptor Ve1 recognizes effector of multiple fungal pathogens uncovered by genome and **RNA** sequencing

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V. dahliae

Ave1 is ubiquitously expressed



in vitro





in soil

VdAve1 displays selective antimicrobial activity





VdAve1 induces microbiome changes



VdAve1 affects antagonistic Sphingomonadales



VdAve1 affects antagonistic Sphingomonadales





Life stage-specific microbiome-manipulation?



Take-home messages



The 2-speed genome of Verticillium involves lineagespecific regions LS regions display an intermediate chromatin state Single lineage-specific effectors can act as host range determinant

Part of the effector catalog is intended for microbiome manipulation

Acknowledgements

Genome evolution: Jasper Depotter (Cologne, GER) David Cook (Kansas, USA) Martin Kramer M Seidl (Utrecht, NL)



Microbiome manipulation: Nick Snelders Hanna Rovenich (Cologne, GER) Gabrielle Petti (Zürich, CH)

Other: Hui Tian David Torres Jasper Vermeulen Katharina Hanika Edgar Chavarro Carrero Nelia Ortega Parra Grardy yayan den Berg



Collaborators: V Lipka (Göttingen, DE) J Mesters (Lübeck, DE) L Hamoen (Amsterdam, NL) M Bolton (Fargo, US) B Zhang (Nanjing, CN) L Zhu (Wuhan, CN) J Rudd (Rothamsted, UK) S Miyashita (Tohoku, JP)

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