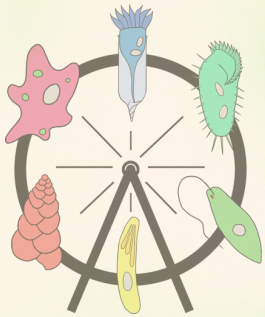


Genomic and transcriptomic advances in understanding the tripartite interactions between host plants, viruses and the protist vectors *Polymyxa*

GENARD Margaux, DECROËS Alain, BRAGARD Claude, LEGRÈVE Anne

Plant health (SAVE)
Earth and Life Institute



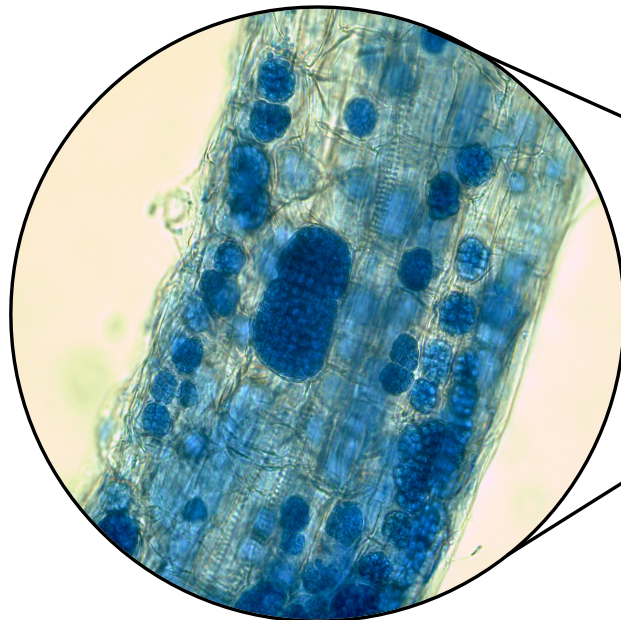
ECOP-ISOP joint meeting



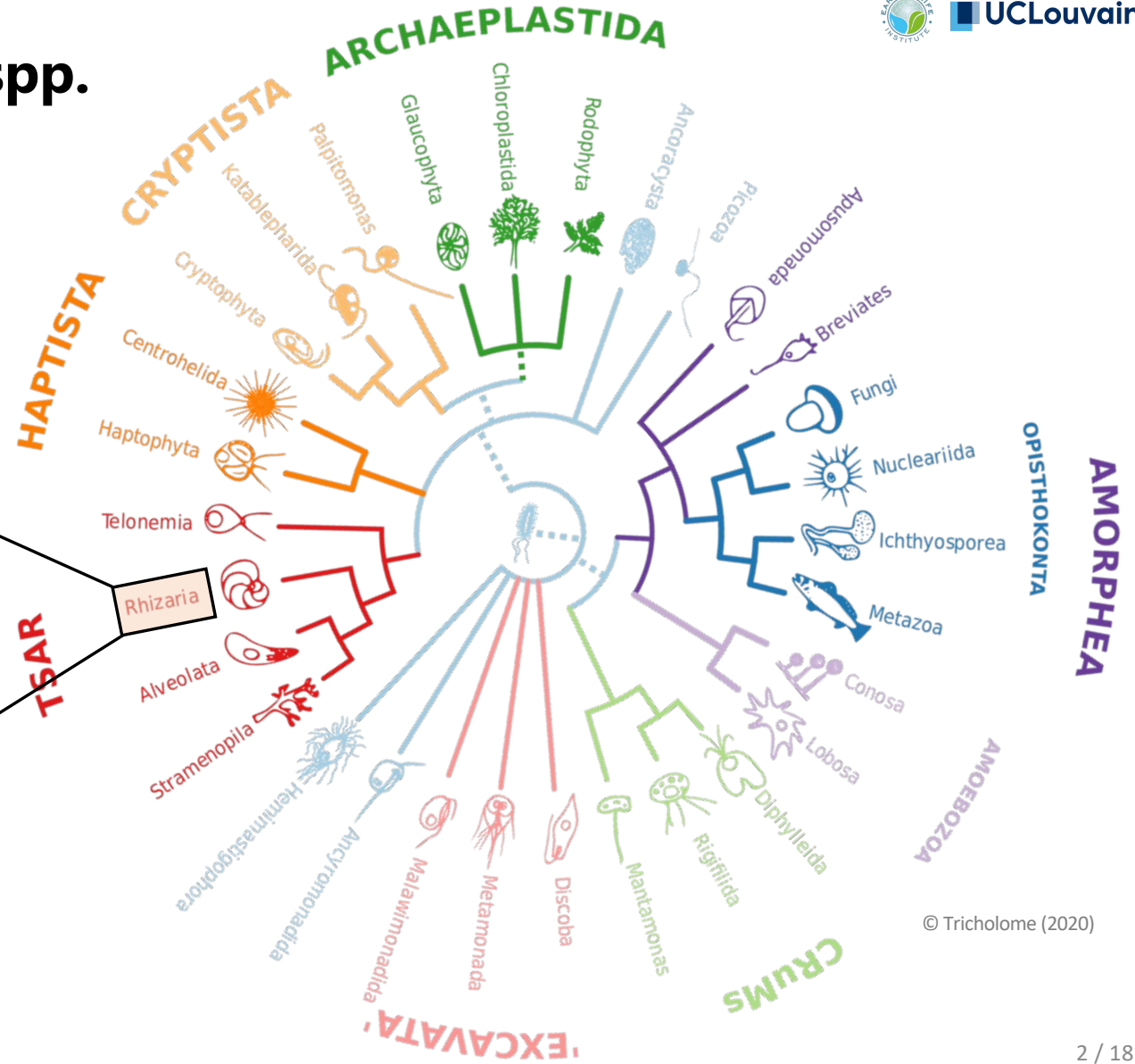
 **UCLouvain**

Classification of *Polymyxa* spp.

Rhizaria
Phytomyxea
Plasmodiophorida



Polymyxa spp.



© Tricholome (2020)

Plasmodiophorids involved in plant diseases



Polymyxa graminis

No symptoms

Virus vector

BaMMV, BaYMV, CWMV, IPCV, JSBWMV, OGSV, OMV, PCV, RNMV, RSNV, SBCMV, SBWMV, SrCSV, WhSMV, WSSMV, WYMV



Polymyxa betae

No symptoms

Virus vector

BNYVV, BSBV, BVQ, BSBMV



Plasmodiophora brassicae

Gall maker

Not a virus vector



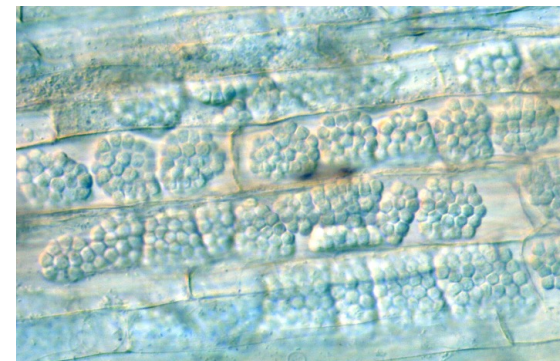
Spongospora subterranea

Gall maker

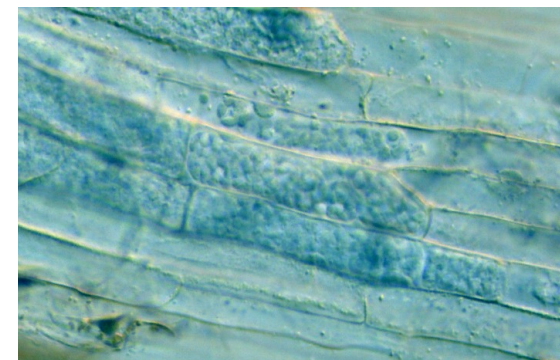
Virus vector

PMTV

Polymyxa spp. life cycle



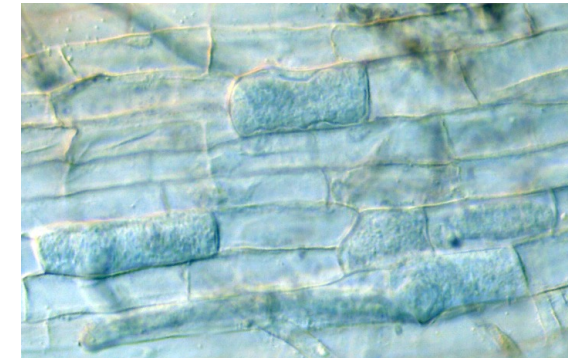
(6) Sporosori



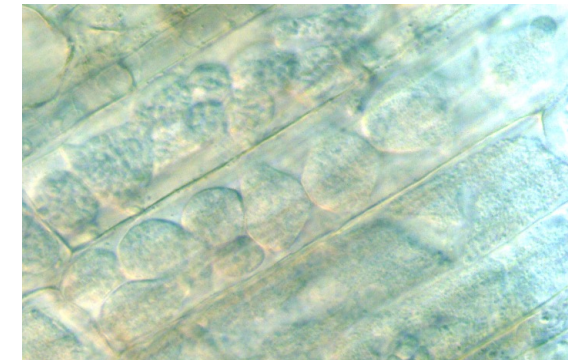
(5) Sporogenic plasmodium



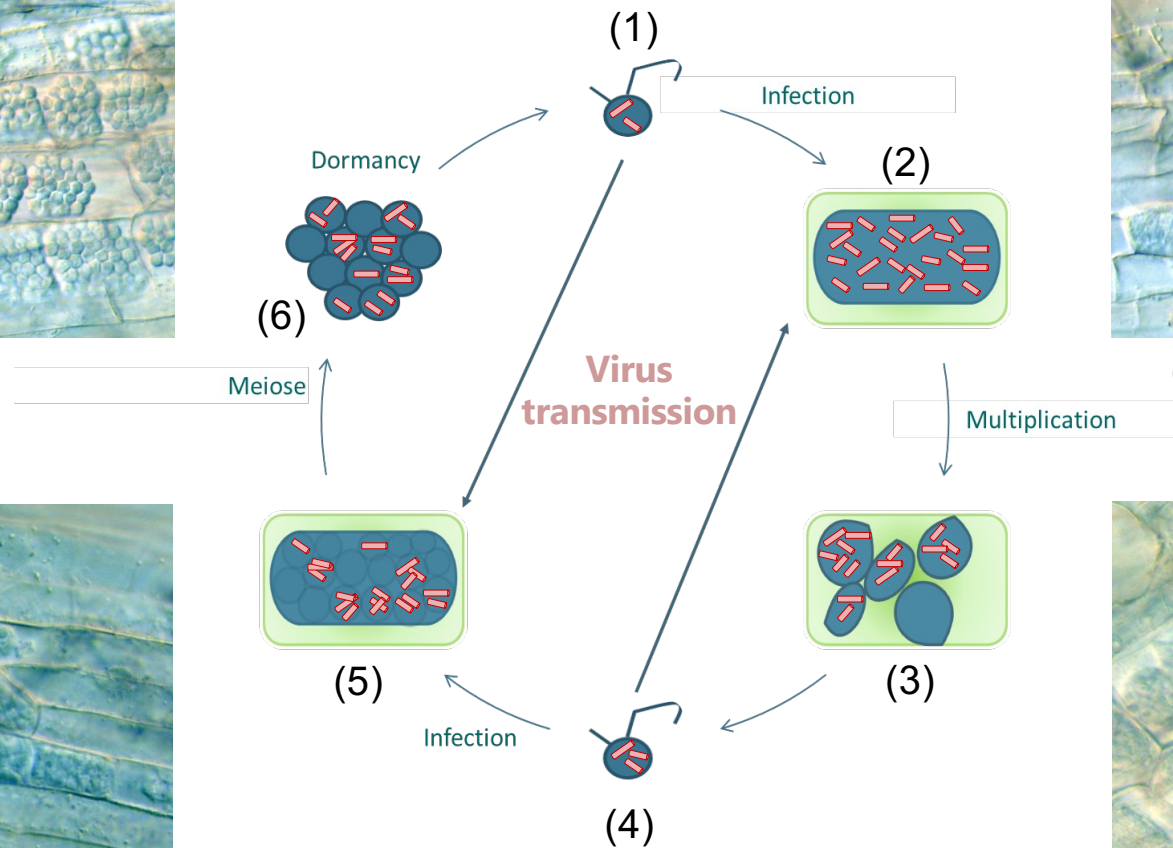
(1) Zoospore
(4) Zoospore



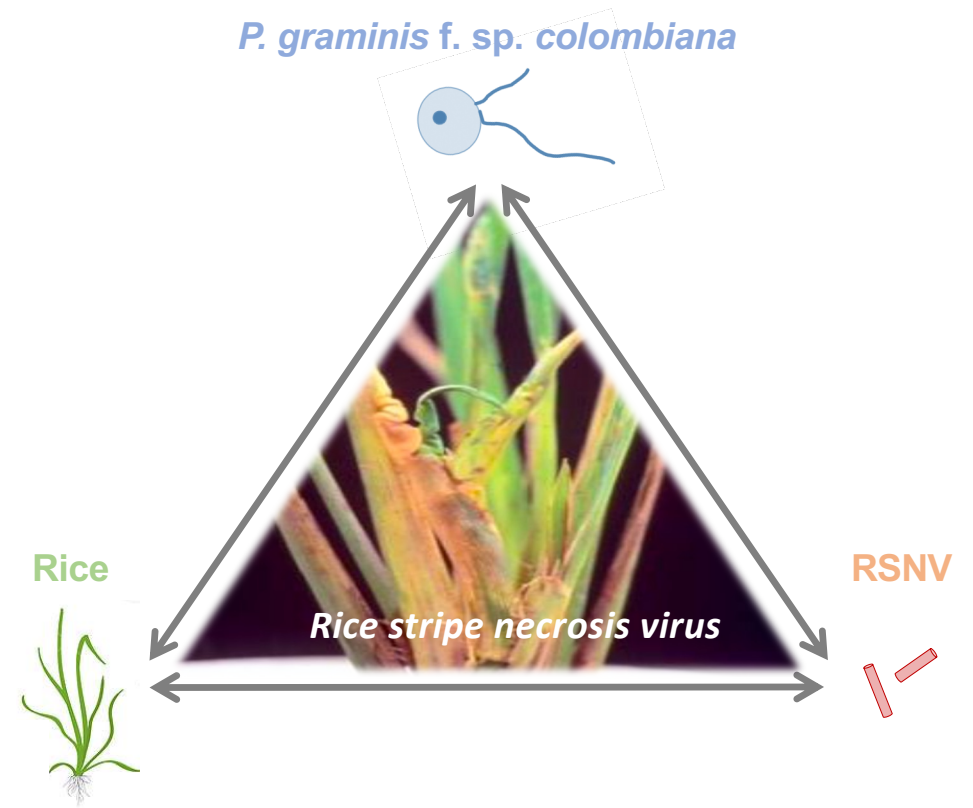
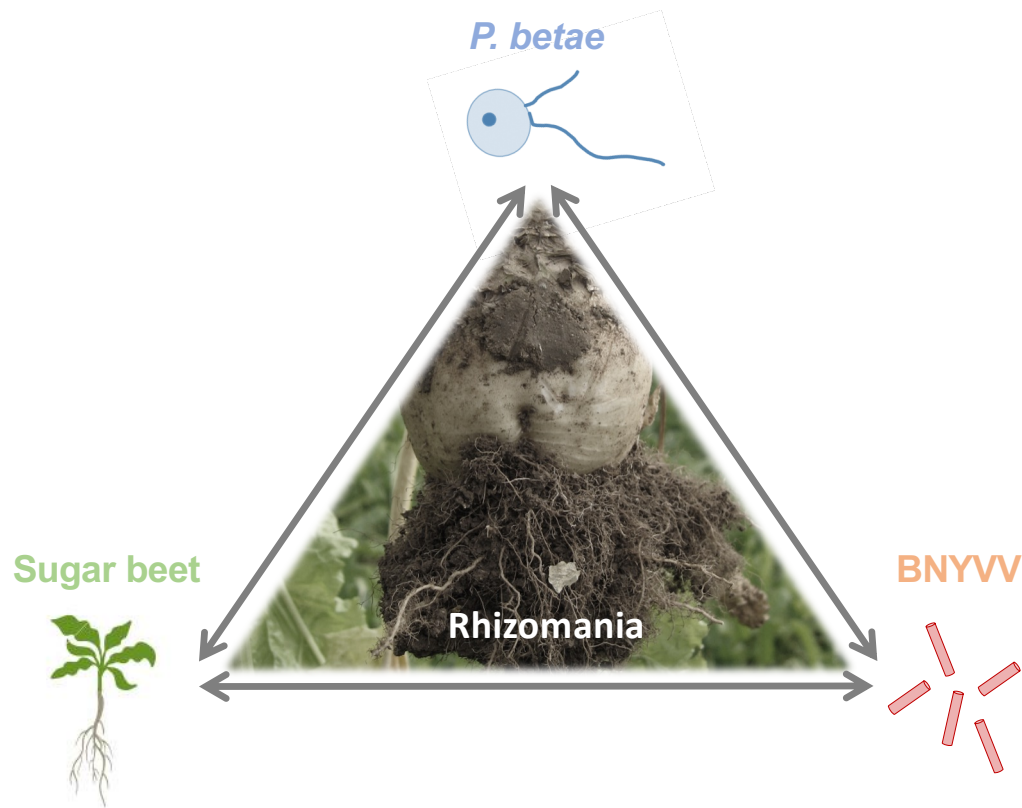
(2) Sporangial plasmodium



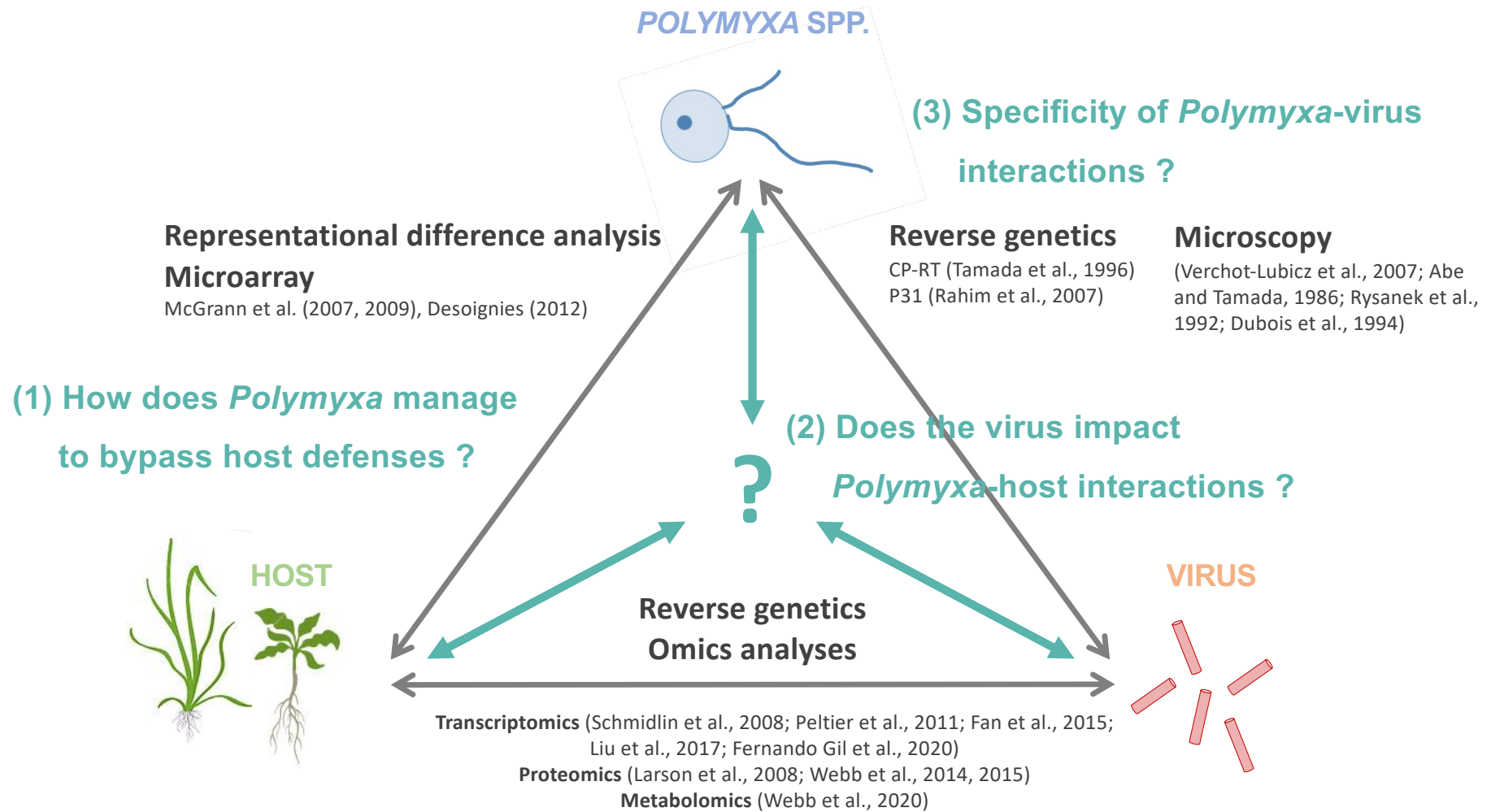
(3) Zoosporangia



Two pathosystems with *Benyvirus*



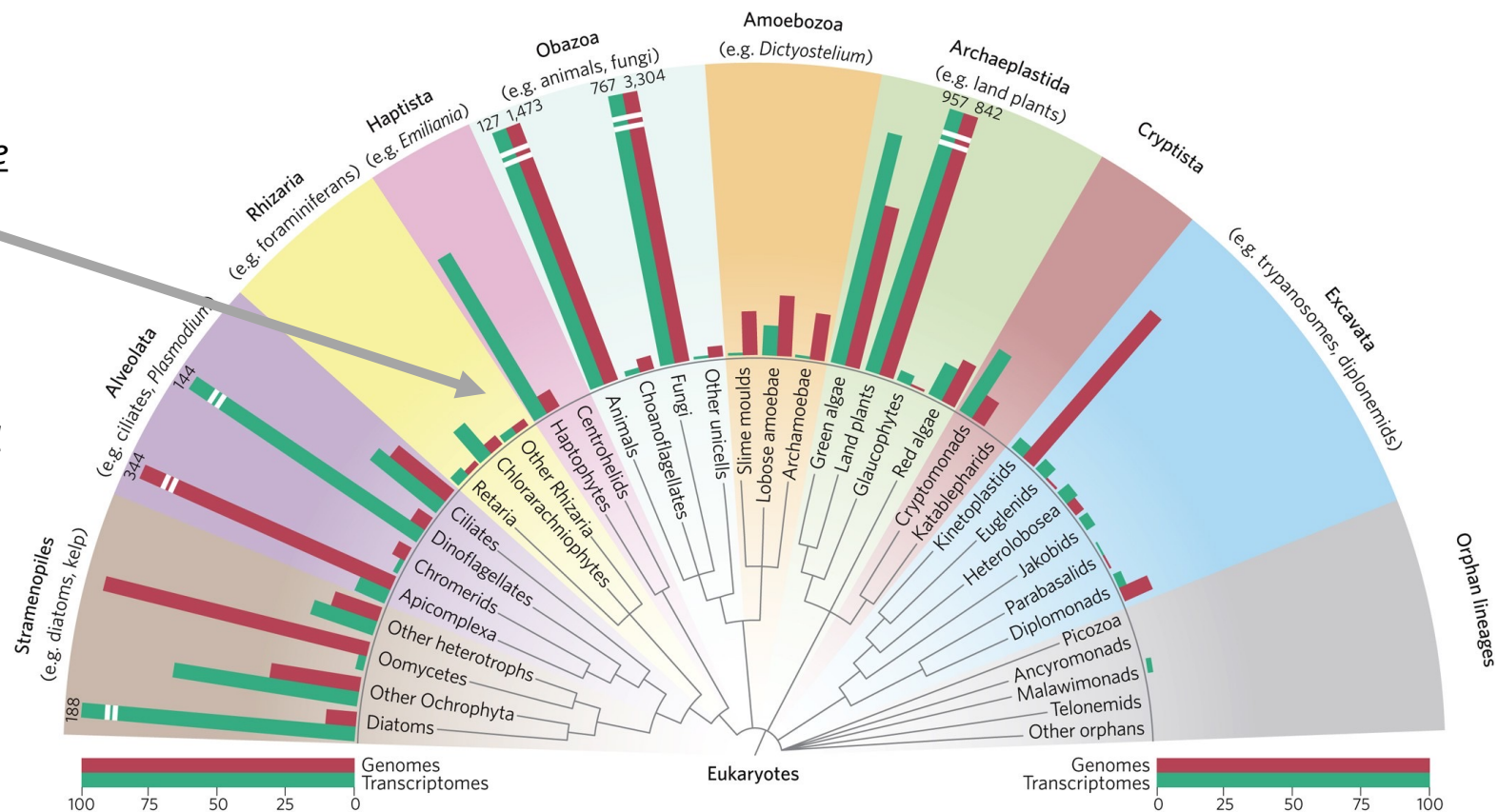
Host-*Polymyxa*-virus interactions



Plasmodiophorids genomes

Plasmodiophorids

- *Hillenburgia nasturtii*
- *Ligniera junci*
- *Plasmodiophora brassicae*
- *Polymyxa betae*
- *Polymyxa graminis*
- *Pseudoligniera verrucosa*
- *Sorosphaerula viticola*
- *Sorosphaerula veronicae*
- *Spongospora subterranea*
- *Tetramyxa parasitica*
- *Woronina pythii*



© Sibbald and Archibald (2017)

Lack of genomic data for Plasmodiophorids

First *Polymyxa betae* genomes

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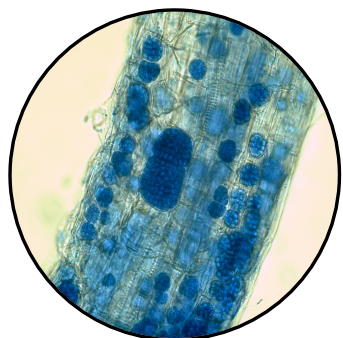
journal homepage: www.elsevier.com/locate/ygeno



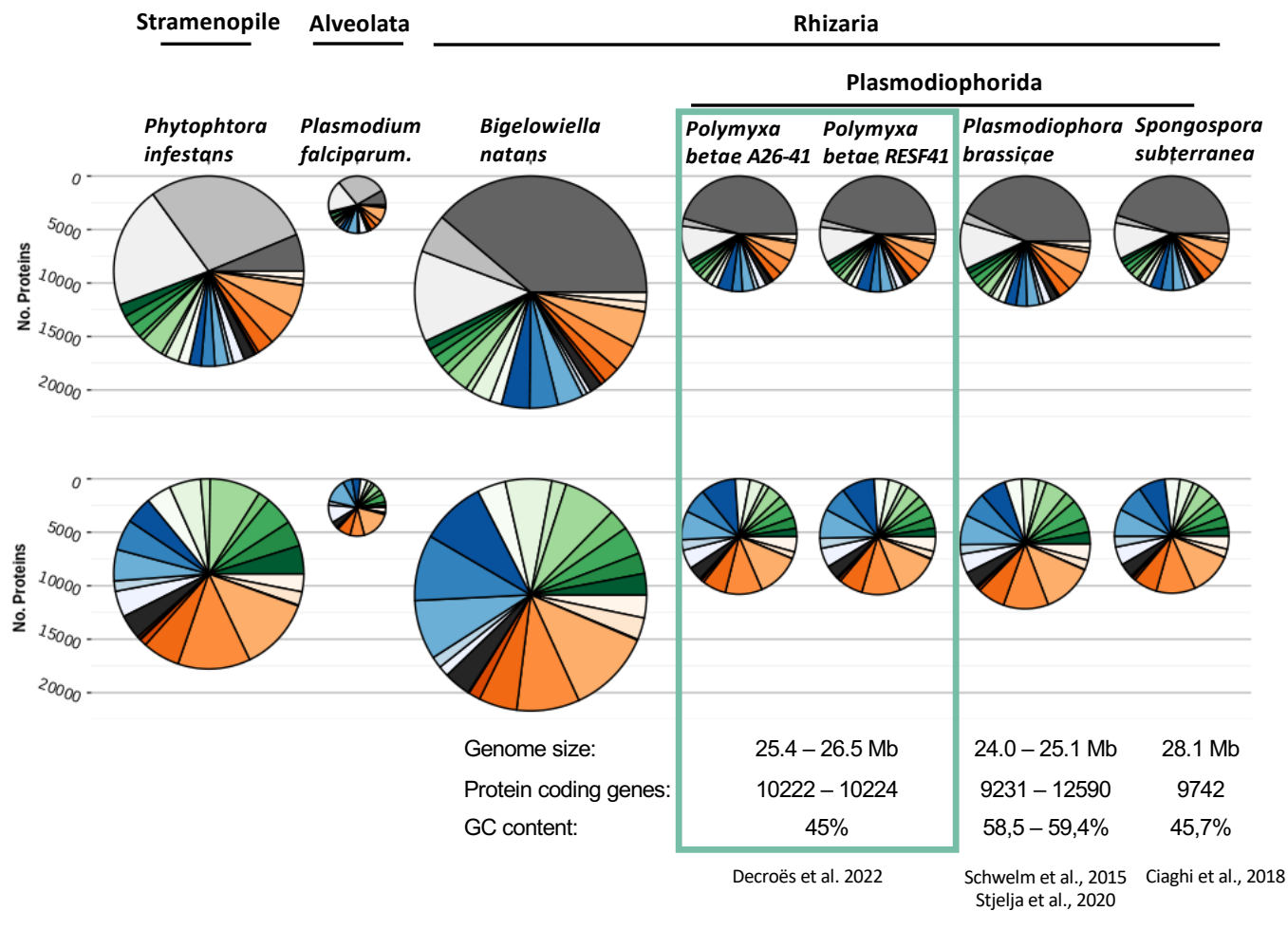
Metagenomics approach for *Polymyxa betae* genome assembly enables comparative analysis towards deciphering the intracellular parasitic lifestyle of the plasmodiophorids

Alain Decroës^{a,*}, Jun-Min Li^b, Lorna Richardson^c, Euphemia Mutasa-Gottgens^{c,d}, Gipsi Lima-Mendez^e, Mathieu Mahillon^{a,1}, Claude Bragard^a, Robert D. Finn^c, Anne Legrève^{a,*}

Alain Decroës


table
Genome size:	25.4 – 26.5 Mb
Protein coding genes:	10222 – 10224
GC content:	45%

Genomes comparison



CELLULAR PROCESSES AND SIGNALING

- [D] Cell cycle control, cell division, chromosome partitioning
- [M] Cell wall/membrane/envelope biogenesis
- [N] Cell motility
- [O] Post-translational modification, protein turnover, and chaperones
- [T] Signal transduction mechanisms
- [U] Intracellular trafficking, secretion, and vesicular transport
- [V] Defense mechanisms
- [W] Extracellular structures
- [Y] Nuclear structure
- [Z] Cytoskeleton

INFORMATION STORAGE AND PROCESSING

- [A] RNA processing and modification
- [B] Chromatin structure and dynamics
- [J] Translation, ribosomal structure and biogenesis
- [K] Transcription
- [L] Replication, recombination and repair

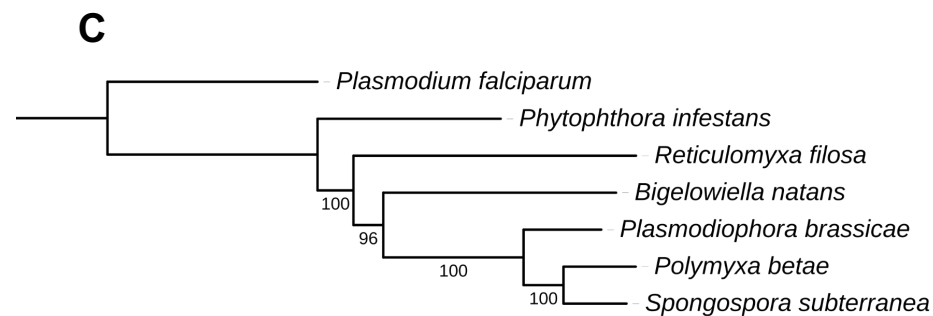
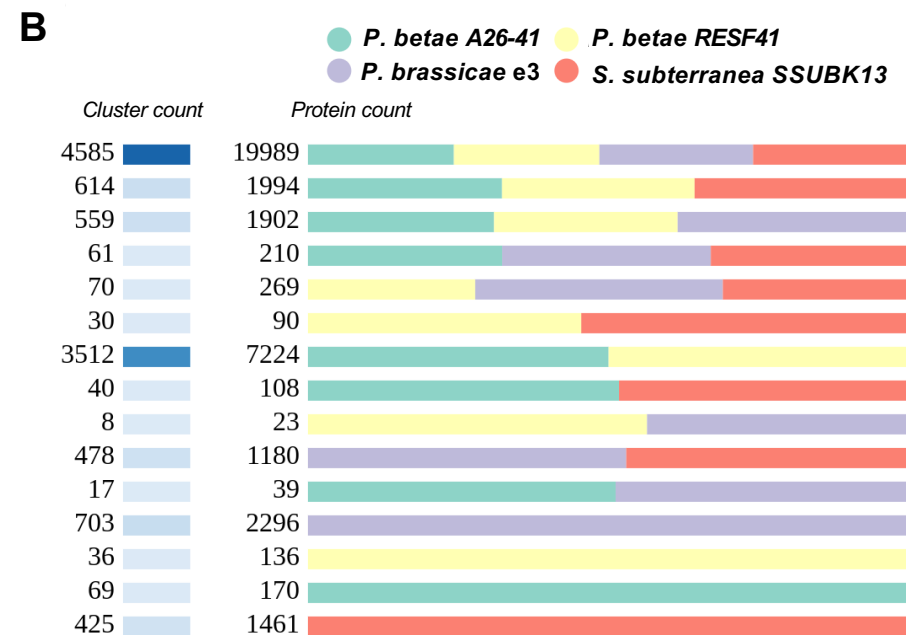
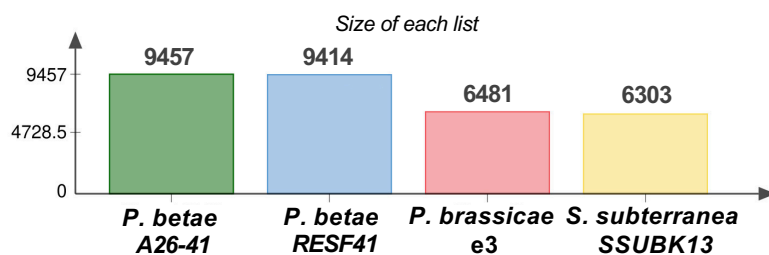
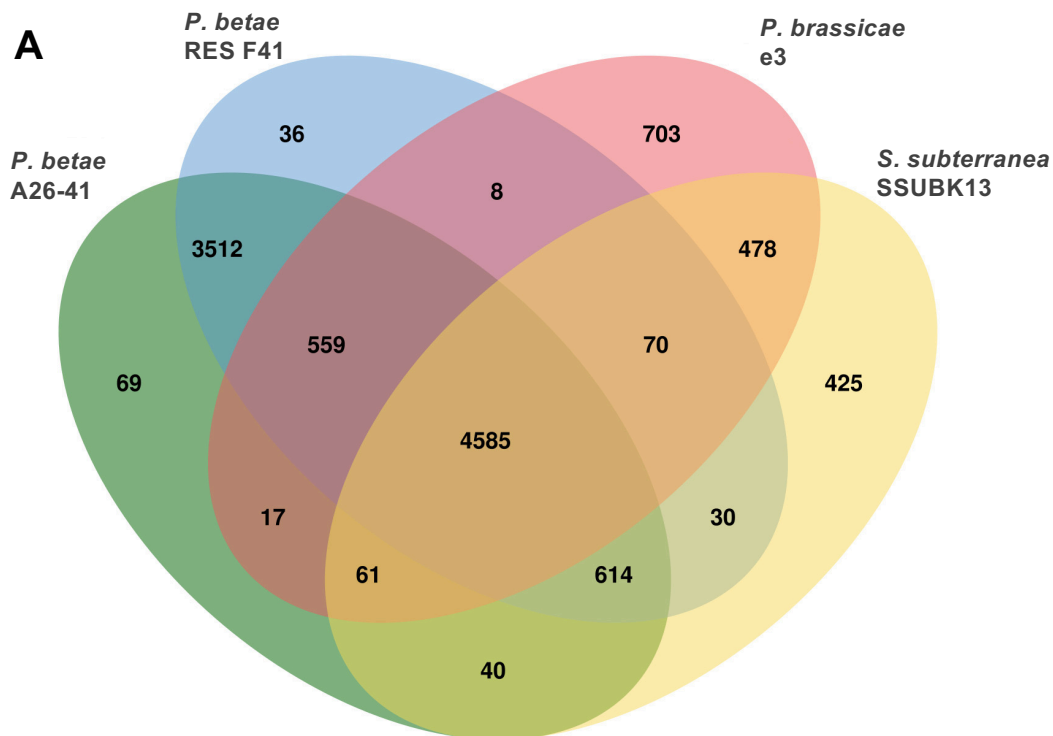
METABOLISM

- [C] Energy production and conversion
- [E] Amino acid transport and metabolism
- [F] Nucleotide transport and metabolism
- [G] Carbohydrate transport and metabolism
- [H] Coenzyme transport and metabolism
- [I] Lipid transport and metabolism
- [P] Inorganic ion transport and metabolism
- [Q] Secondary metabolites biosynthesis, transport, and catabolism

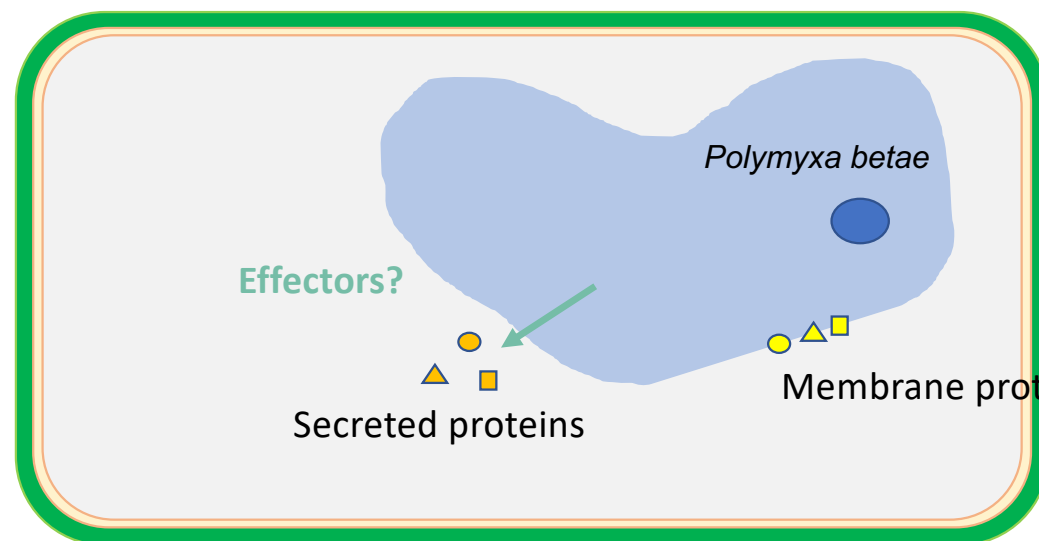
POORLY CHARACTERIZED

- [S] Function unknown
- [UA] Unassigned = No function assigned
- [UM] Unmapped = No ortholog found

Genomes comparison



Secreted and membrane proteins



Specific interactions with viruses?

	<i>P. betae</i> A26-41		<i>P. betae</i> RES F41		<i>P. brassicae</i> e3		<i>S. subterranea</i> SSUBK13	
Proteome	10799		10808		12163		10700	
Step 1	3423		3420		4332		3098	
Step 2	3413		3409		4319		3092	
	Secreted	Membr.	Secreted	Membr.	Secreted	Membr.	Secreted	Membr.
Step 3	991	2422	1010	2399	1283	3036	796	2296
Step 4	655	1525	670	1514	834	1942	526	1489
					↑	↑	↑	↑

Tripartite sugar beet – *P. betae* – BNYVV interactions

MPMI Vol. 35, No. 11, 2022, pp. 989–1005, <https://doi.org/10.1094/MPMI-03-22-0063-R>

Rhizomania: Hide and Seek of *Polymyxa betae* and the Beet Necrotic Yellow Vein Virus with *Beta vulgaris*

Alain Decroës,¹  Mathieu Mahillon,² Margaux Genard,¹ Charlotte Lienard,¹ Gipsi Lima-Mendez,³ David Gilmer,⁴ Claude Bragard,¹ and Anne Legrève^{1,†}

¹ Phytopathology-Applied Microbiology, Earth and Life Institute, UCLouvain, Louvain-la-Neuve, 1348, Belgium

² Plant Protection Department, Agroscope, Nyon, 1260, Switzerland

³ Louvain Institute of Biomolecular Science and Technology, UCLouvain, Louvain-la-Neuve, 1348, Belgium

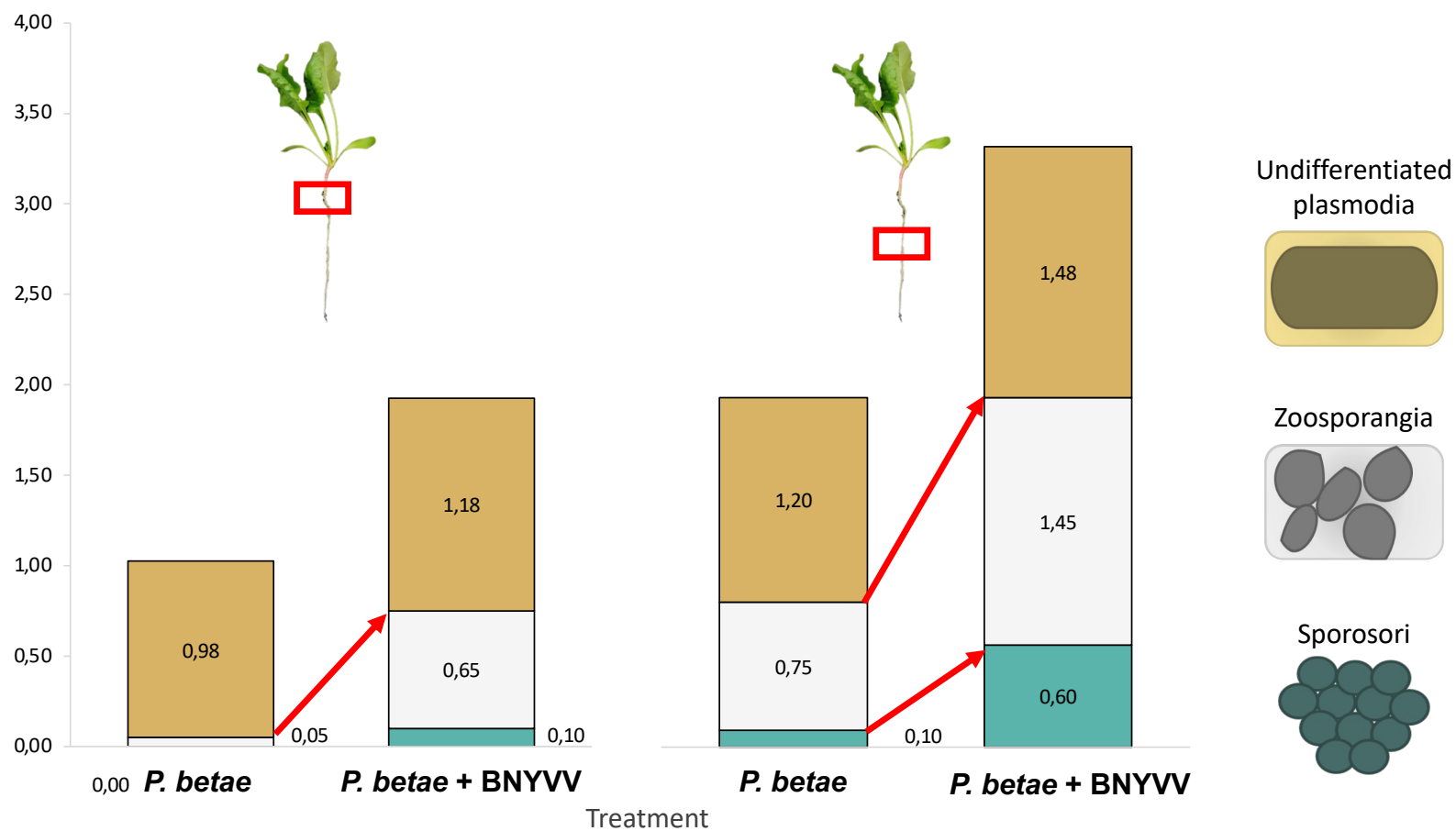
⁴ Institut de biologie moléculaire des plantes, CNRS UPR2357, Université de Strasbourg, Strasbourg, 67084, France

Accepted for publication 8 July 2022.



BNYVV accelerate *P. betae* life cycle

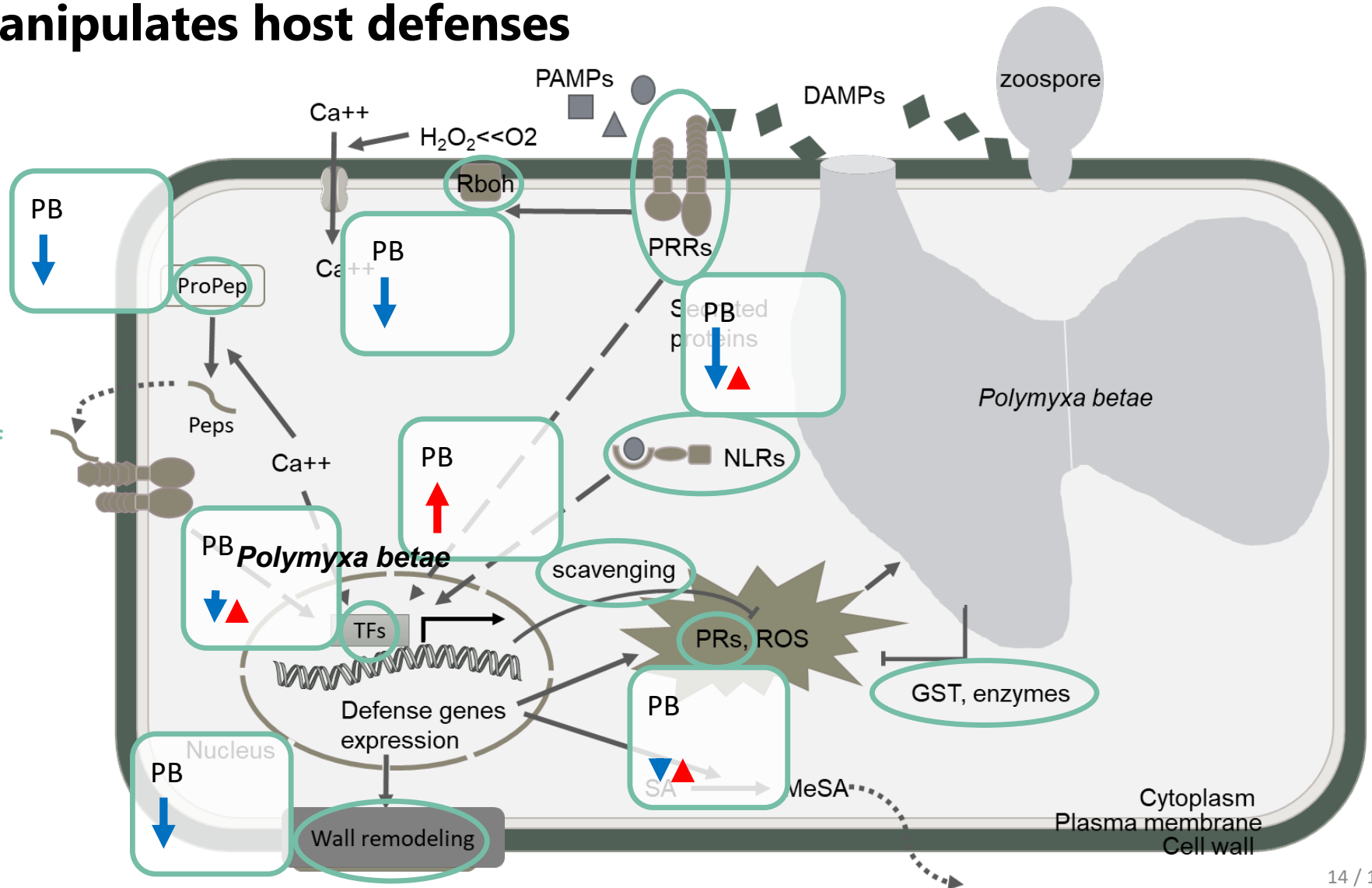
Microscopical observations



P. betae manipulates host defenses



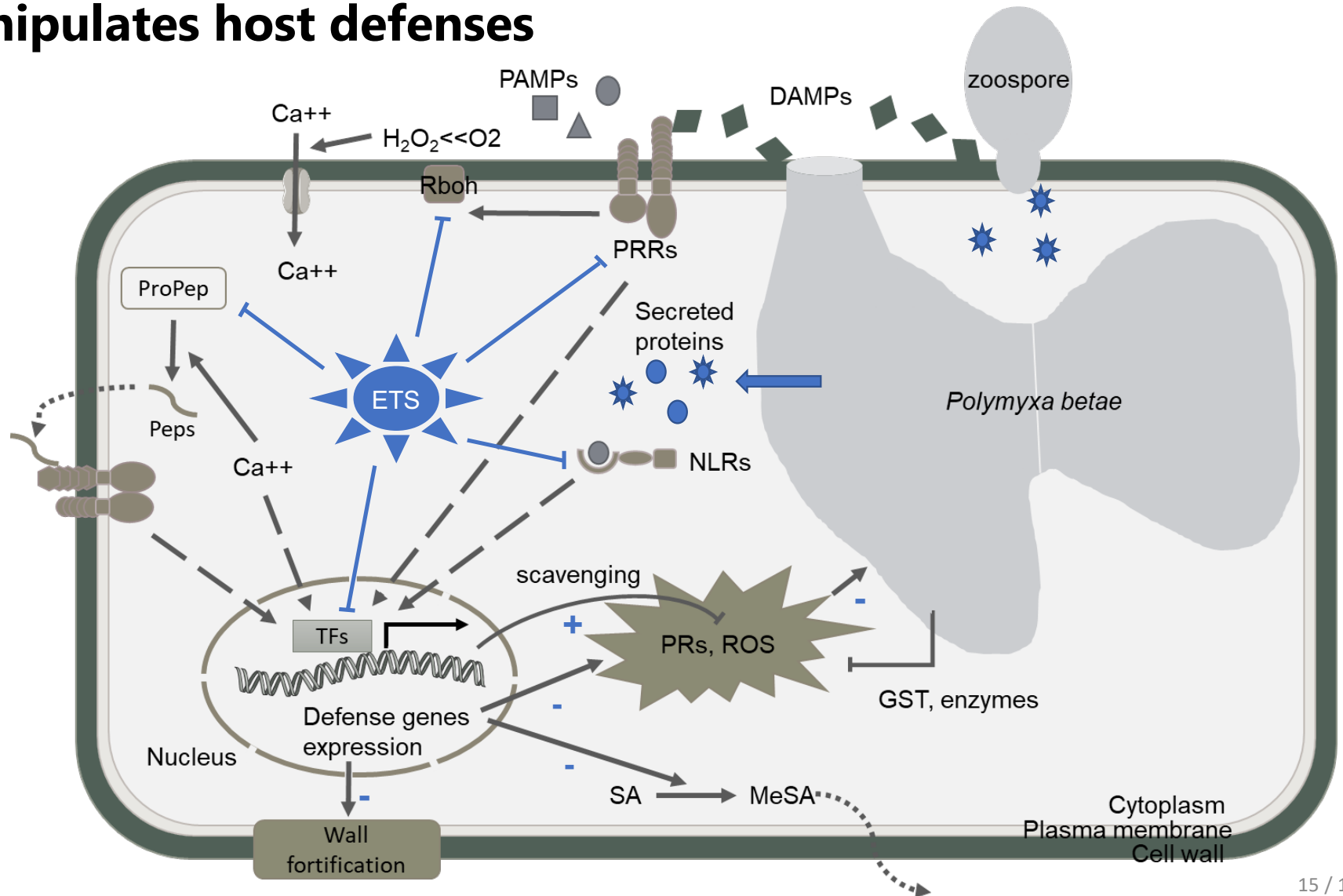
Down-regulation of plant defenses



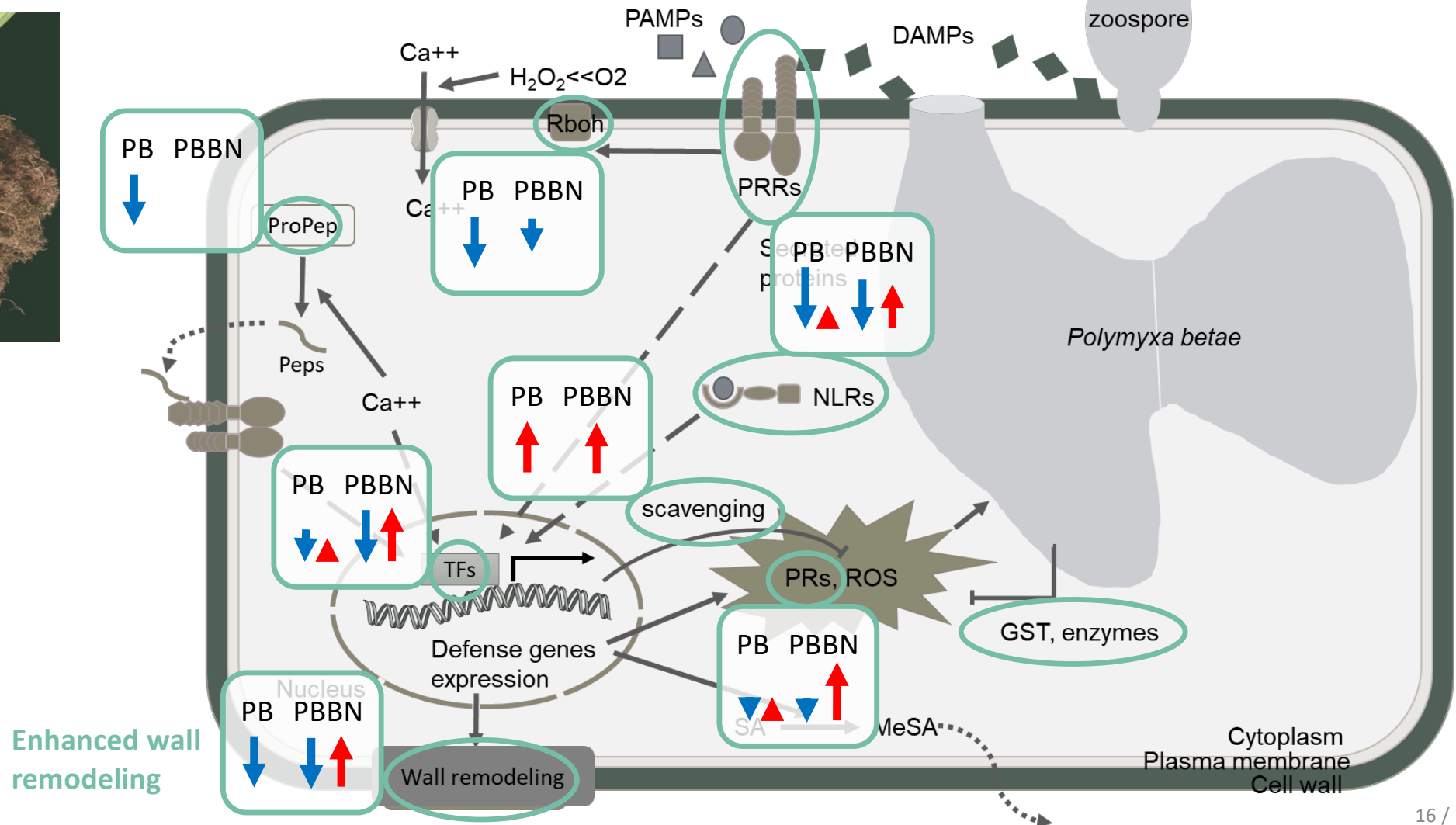
P. betae manipulates host defenses



Effector triggered susceptibility ?



BNYVV induces stronger plant defense response



Conclusion

Genomic

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- ✓ First *P. betae* genomes
- ✓ *P. betae* closer to *S. subterranea* than *P. brassicae*
- ✓ Identification of effectors and membrane proteins

Transcriptomic

MPMI Vol. 35, No. 11, 2022, pp. 989–1005, <https://doi.org/10.1094/MPMI-03-22-0063-R>

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⁴ Institut de biologie moléculaire des plantes, CNRS UPR2357, Université de Strasbourg, Strasbourg, 67084, France

Accepted for publication 8 July 2022.



- ✓ *P. betae* circumvent plant defenses
- ✓ BNYYV accelerates *P. betae* life cycle
- ✓ *P. betae* and BNYYV have a win-win relationship

Perspective

- ✓ *Polymyxa graminis* genome ?
- ✓ Role of *Polymyxa* effectors in compatible interactions ?
- ✓ Specificity of virus transmission ?

Acknowledgments



Anne Legrève

Claude Bragard



Alain Decroës

