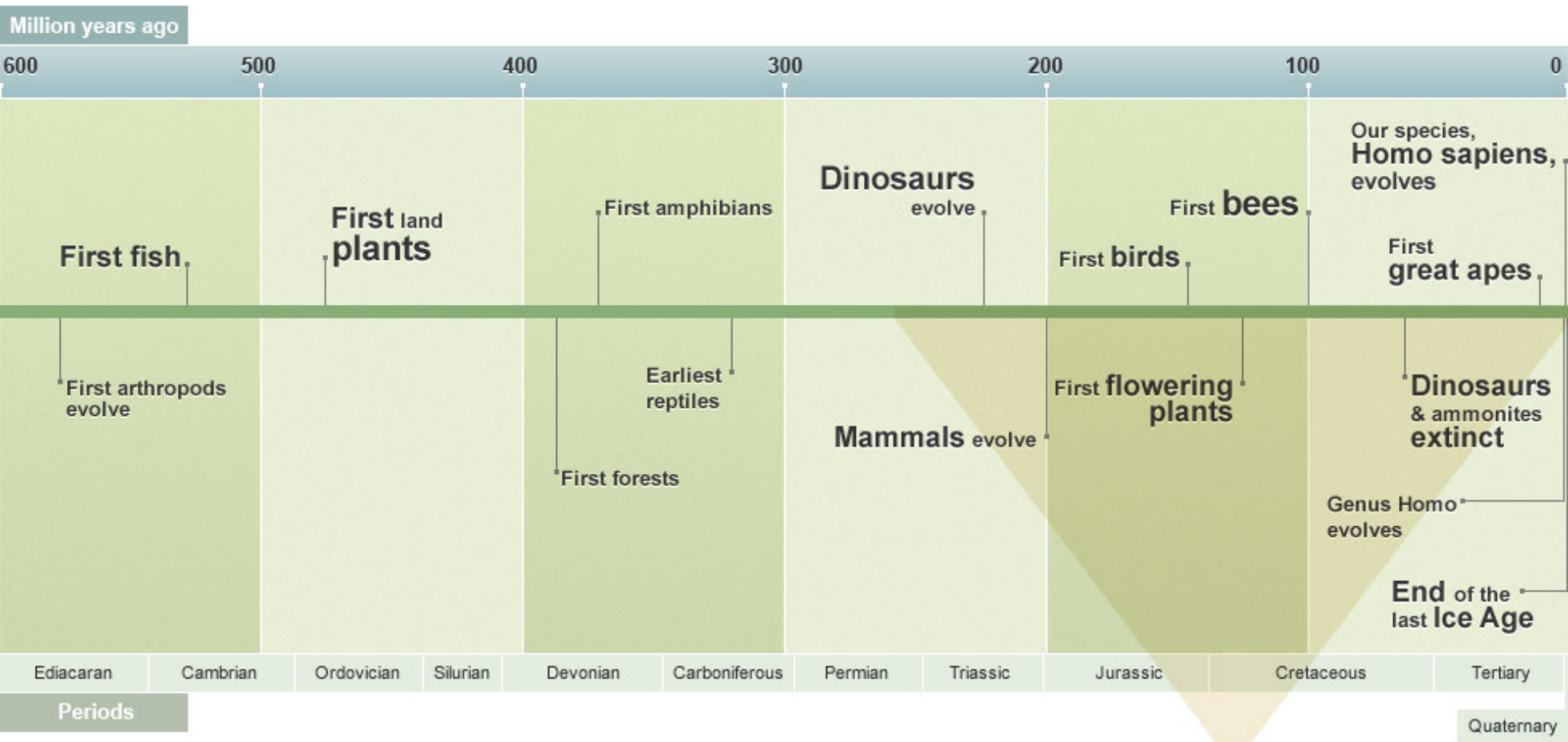


Interação planta-patógeno: comunicação bioquímica e estratégias de defesa e ataque

Dr. Ronaldo J. D. Dalio

ronaldobio@hotmail.com



First fish

First land plants

First amphibians

Dinosaurs evolve

First birds

First bees

Our species, Homo sapiens, evolves

First great apes

First arthropods evolve

Earliest reptiles

Mammals evolve

First flowering plants

Dinosaurs & ammonites extinct

Genus Homo evolves

End of the last Ice Age

First forests

Ediacaran

Cambrian

Ordovician

Silurian

Devonian

Carboniferous

Permian

Triassic

Jurassic

Cretaceous

Tertiary

Periods

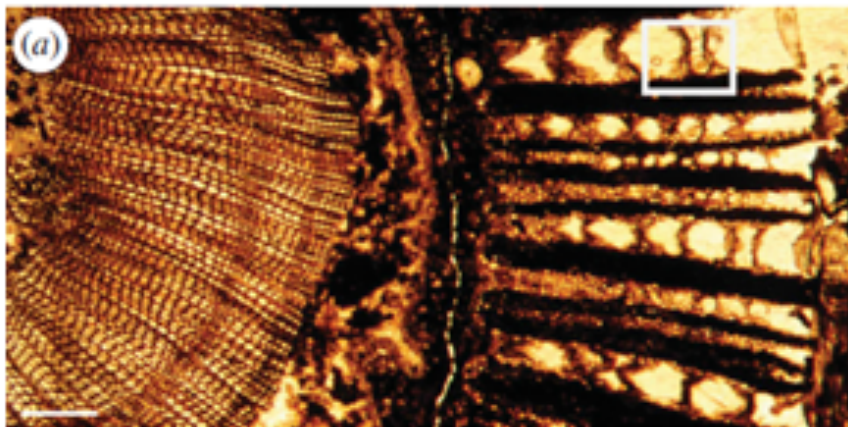
Quaternary



Evidence of parasitic Oomycetes (*Peronosporomycetes*) infecting the stem cortex of the Carboniferous seed fern *Lyginopteris oldhamia*

Strullu-Derrien et al. (2010) Proc. R. Soc. B (2011) 278, 675–680

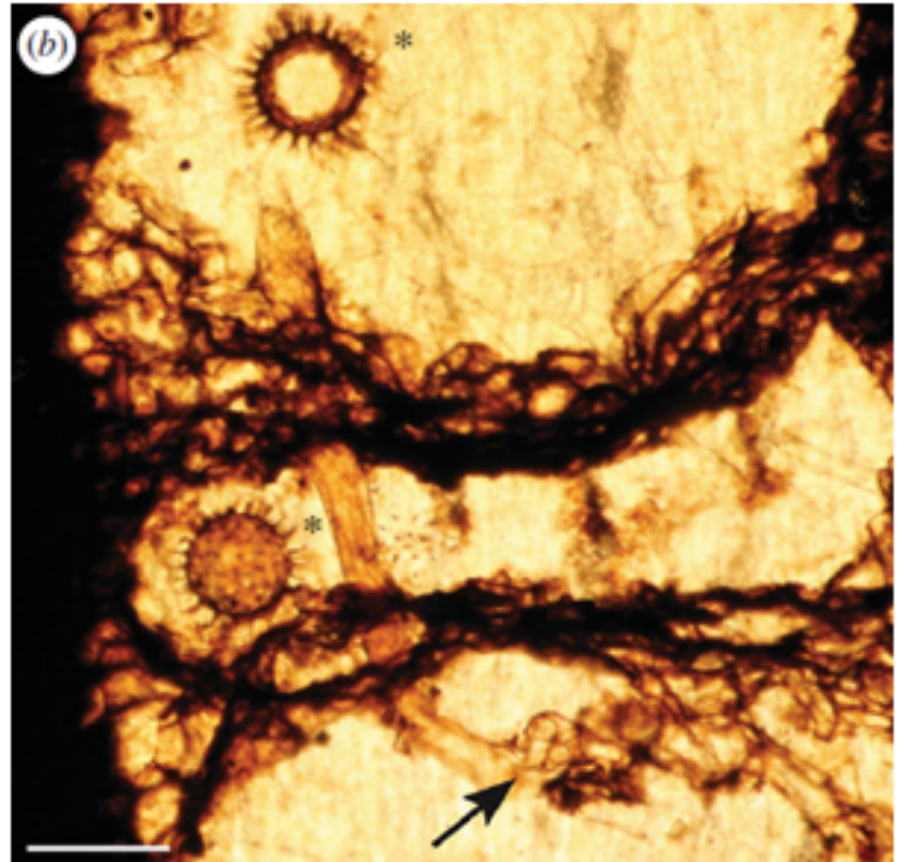
About 320 MY



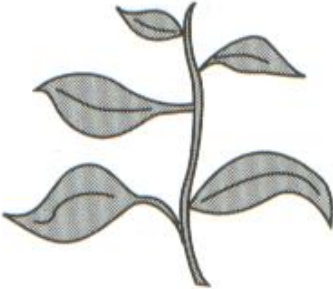

a) Overview of a transverse section of *Lyginopteris oldhamia* stem showing colonization by the Oomycetes in the cortical tissues (frame); the zone in the frame corresponds to

b) Hypha (arrow) and oogonia (asterisk) of *Combresomyces williamsonii* within the parenchyma that separates the fibres of the dictyoxylon outer cortex of the stem.

Note the occurrence of a knot of hyphae (arrow), scale bar, 400 μ m.



Sistema imune de plantas e animais

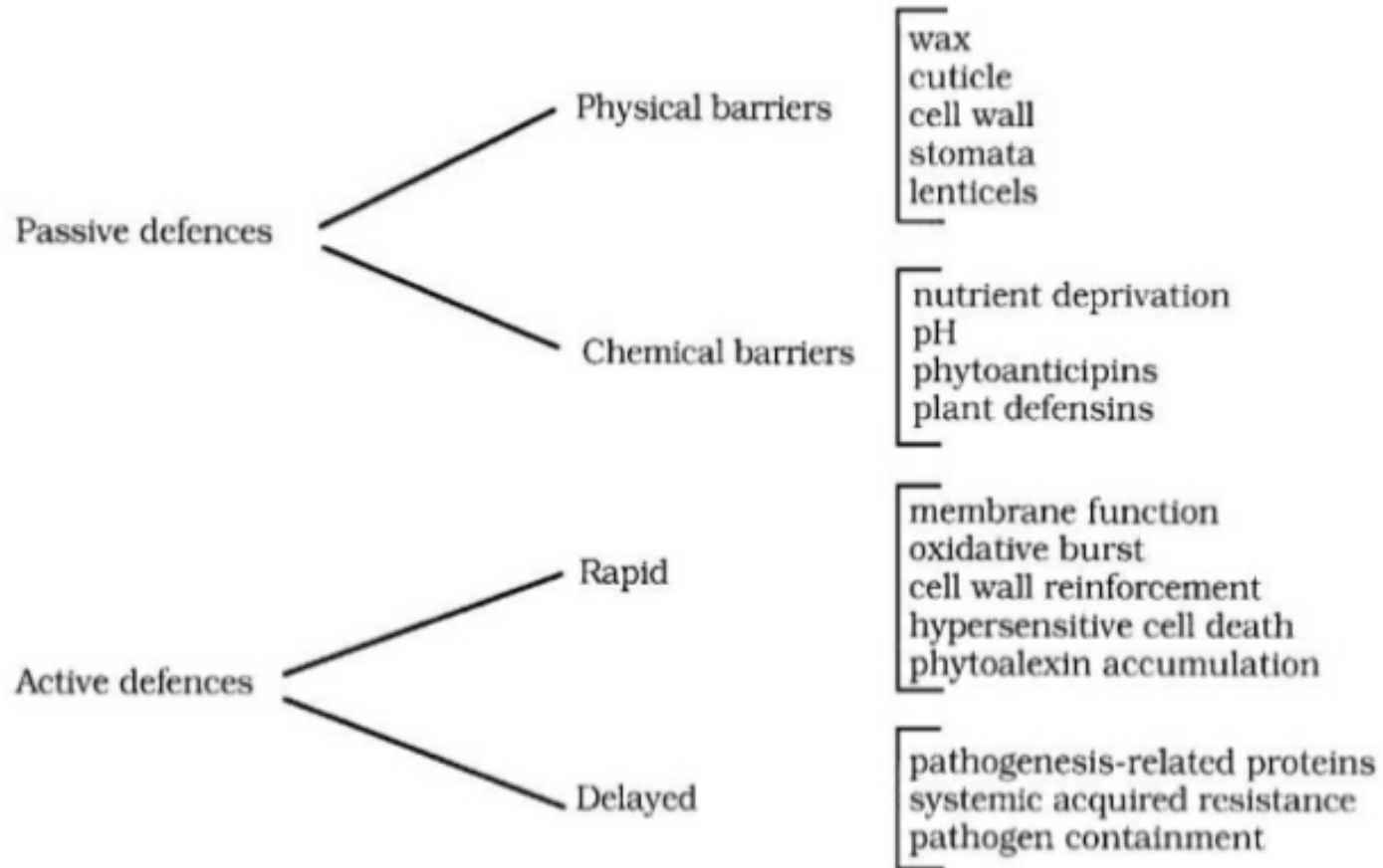
		
Recognize	✓	✓
Respond	✓	✓
Remember	?	✓

Quem são os patógenos de plantas?

- Virus
- Bactéria
- Fungos
- Oomicetos
- Nematóides

Como as plantas se defendem?

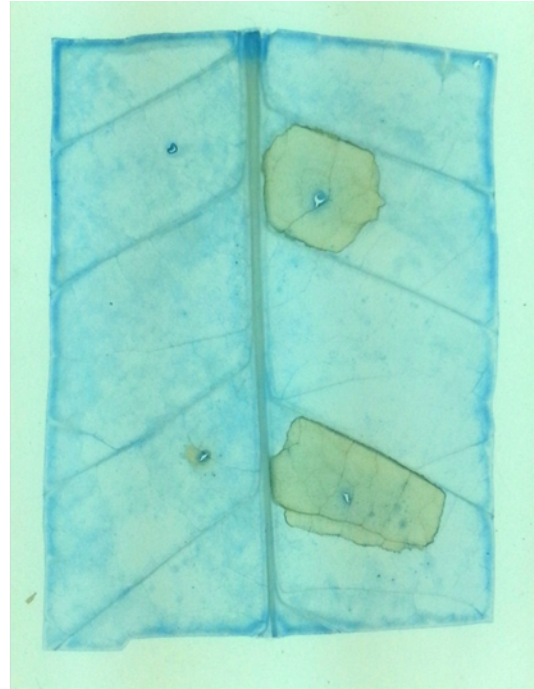
Defense mechanism in plants



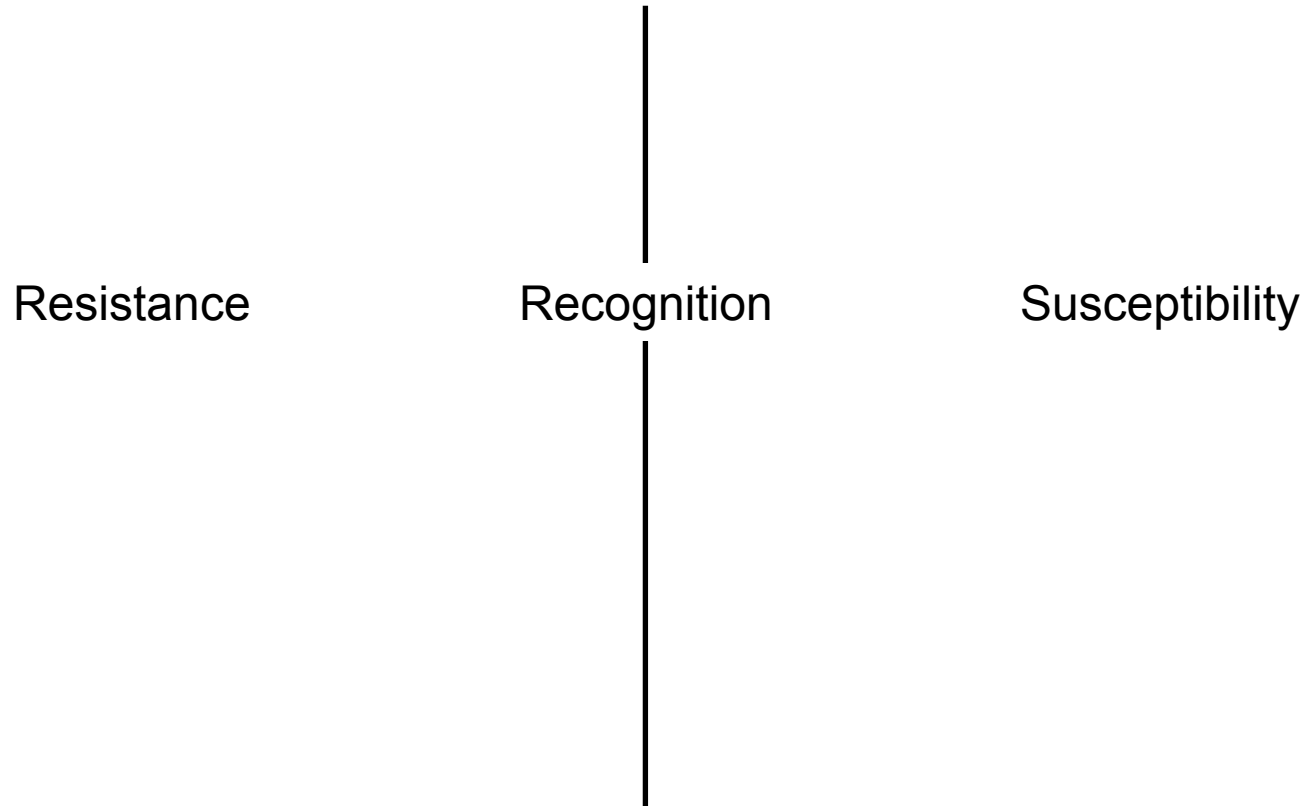
5. Hypersensitive response

- Rapid [death](#) of cells in the local region surrounding an infection.
- Restrict the growth and spread of pathogens to other parts of the plant.
- Favor growth of pathogens with a necrotrophic lifestyle

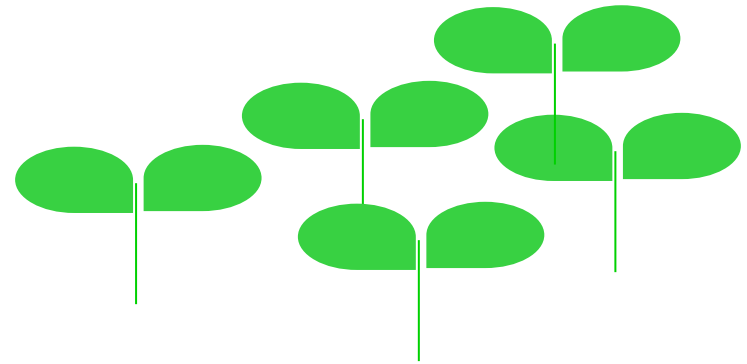
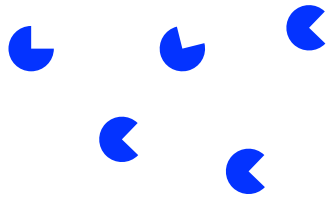




Plant-pathogen interactions

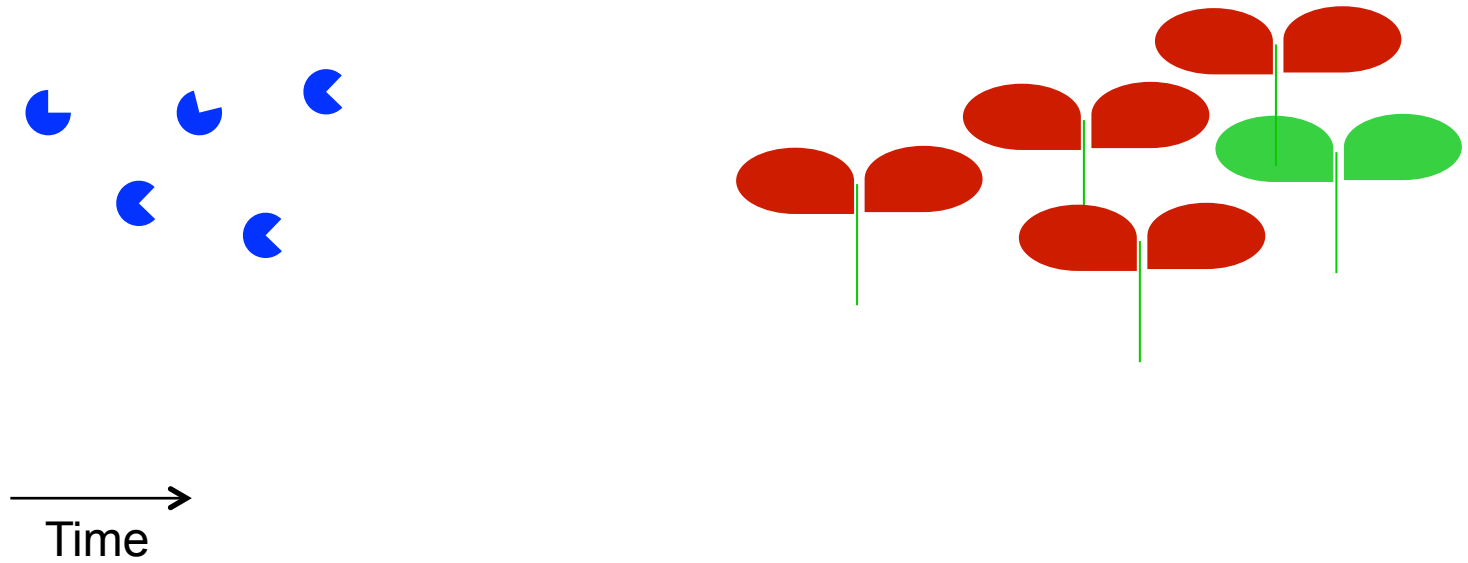


Co-evolution (Arms- race)



Time →

Co-evolution (Arms- race)

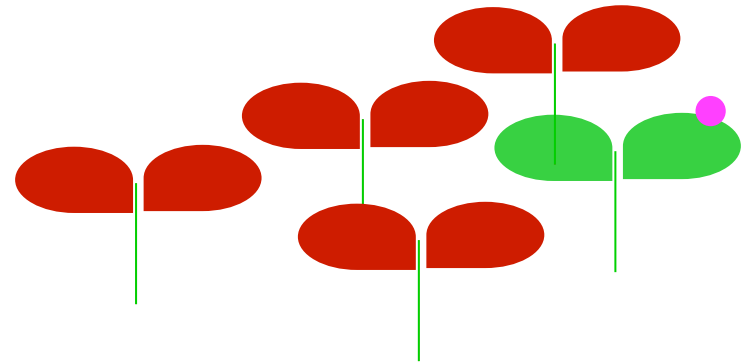
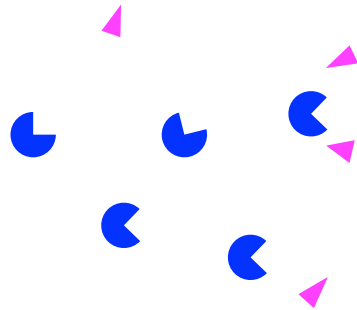
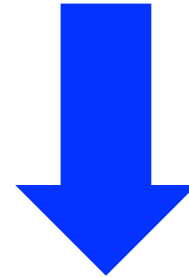


Co-evolution (Arms- race)

◀ PAMPs= Pathogen Associated molecular patterns

PTI= PAMP triggered immunity

**Selection
Pressure**

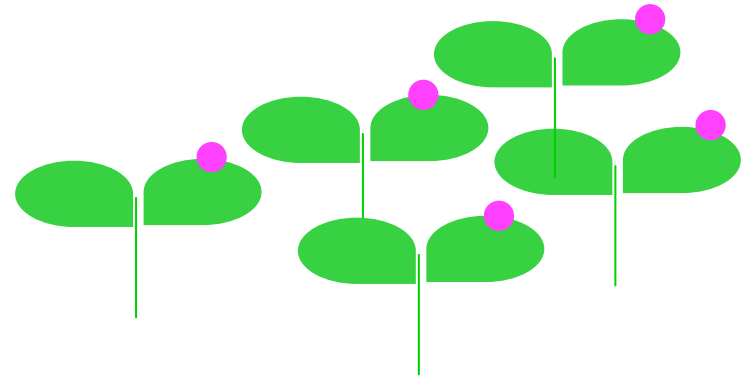
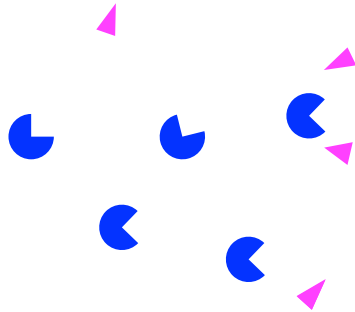
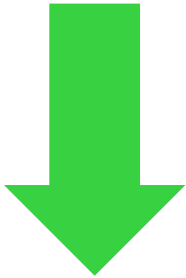


● PRRs= Pattern-recognition receptor

→
Time

Co-evolution (Arms- race)

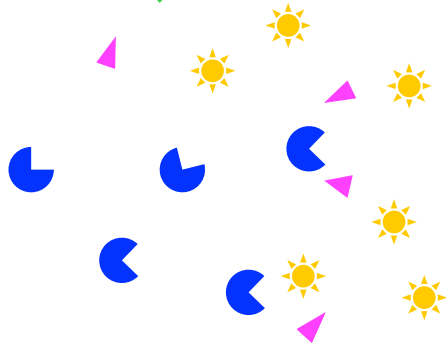
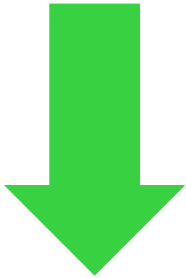
**Selection
Pressure**




Time →

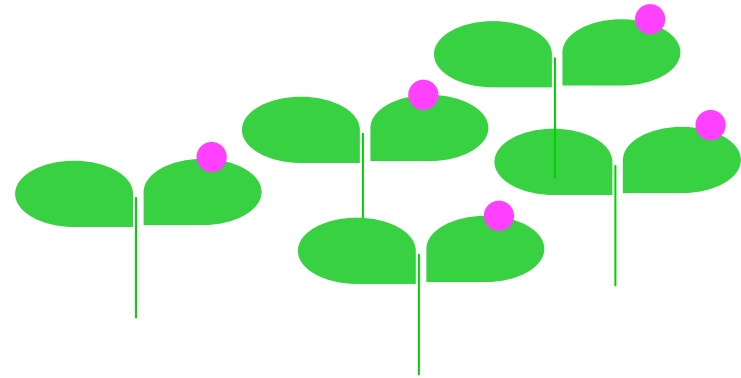
Co-evolution (Arms- race)

**Selection
Pressure**



 Effector= a molecule released by an organism to modify physiology of another organism

Manipulation of host defenses

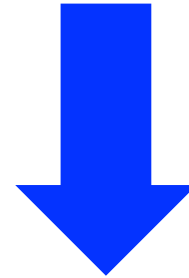


Time

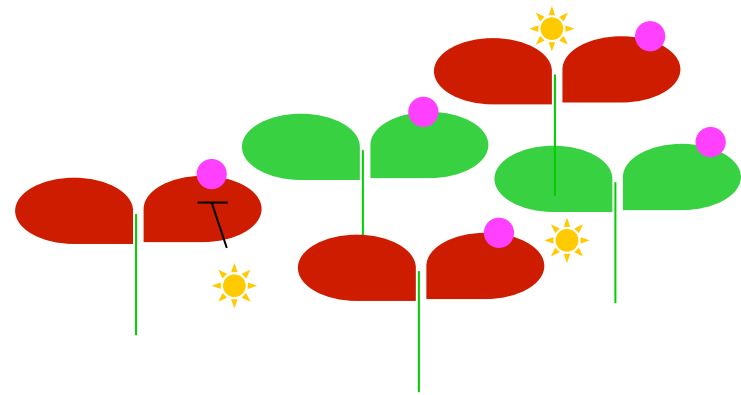
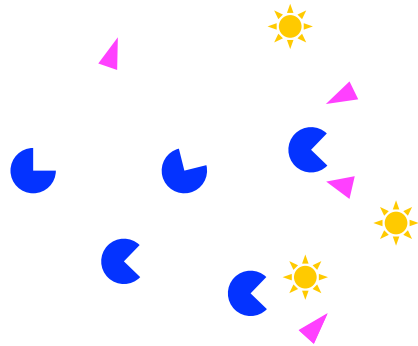


Co-evolution (Arms- race)

**Selection
Pressure**



ETS= Effector triggered susceptibility



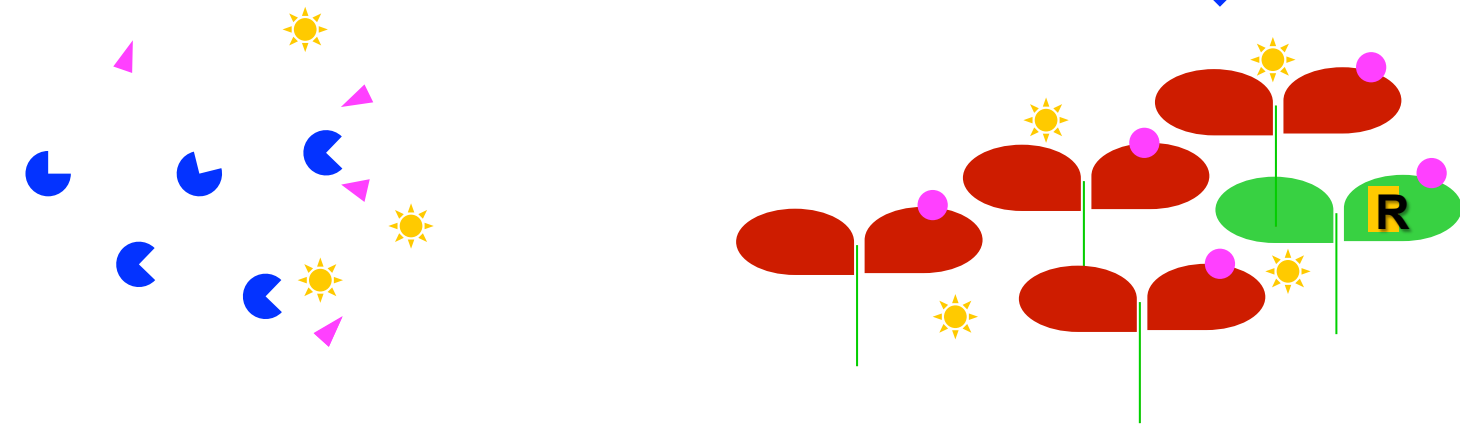
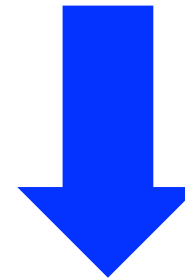
Time →

Co-evolution (Arms- race)

R R-genes= Resistance genes encoding proteins that detect pathogens effectors

ETI= Effector triggered immunity

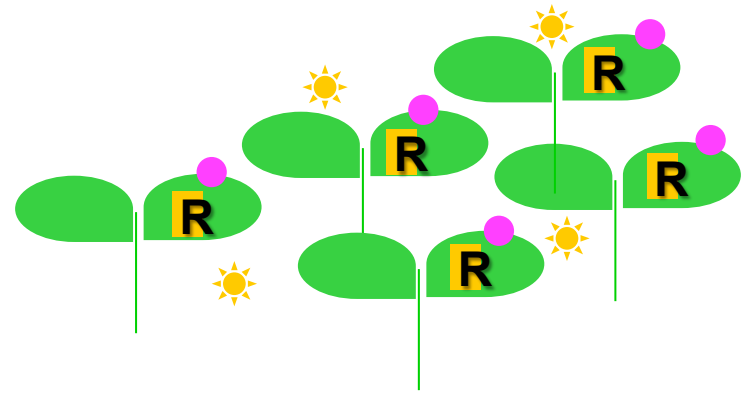
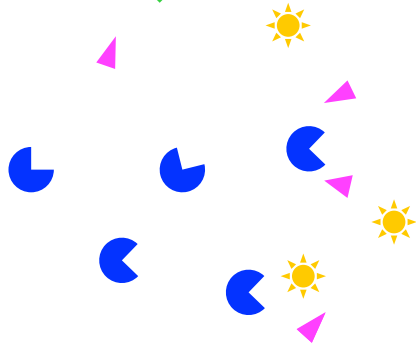
**Selection
Pressure**



Time →

Co-evolution (Arms- race)

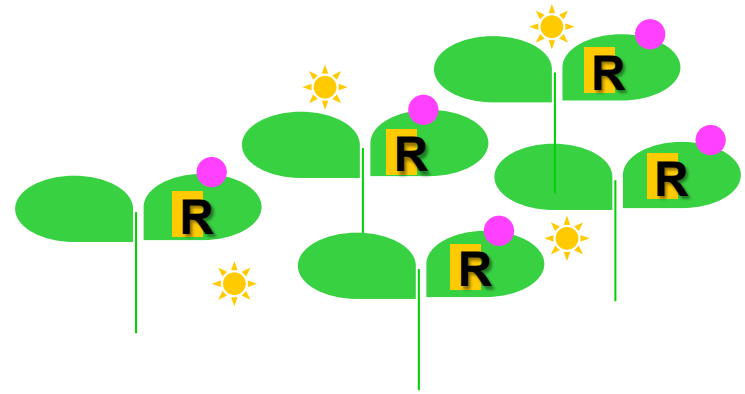
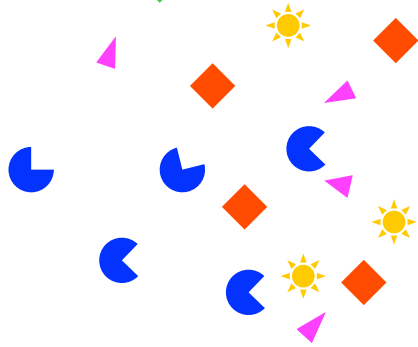
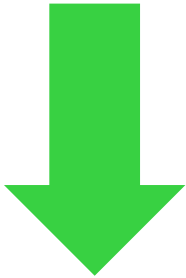
Selection
Pressure



Time →

Co-evolution (Arms- race)

Selection
Pressure

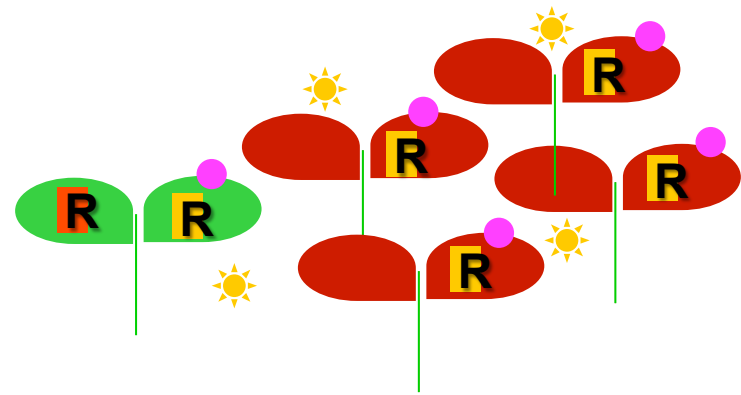
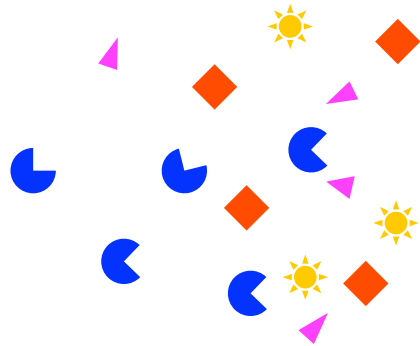
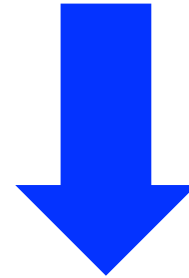


Time



Co-evolution (Arms- race)

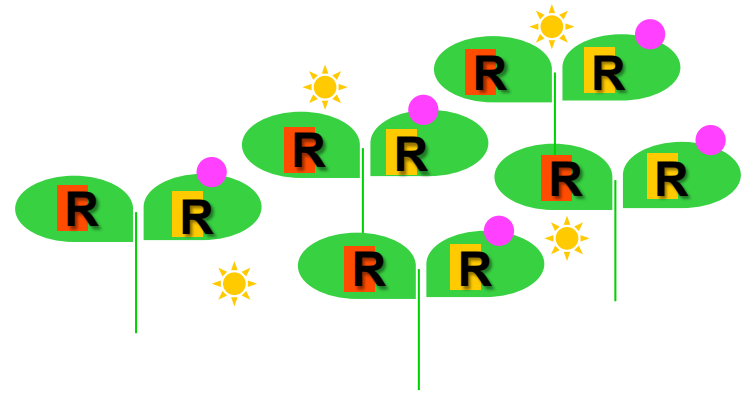
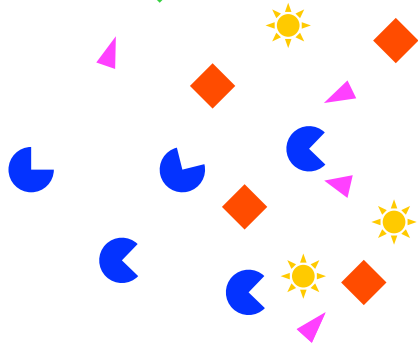
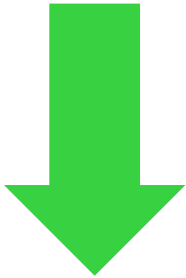
**Selection
Pressure**



Time →

Co-evolution (Arms- race)

Selection
Pressure



Time



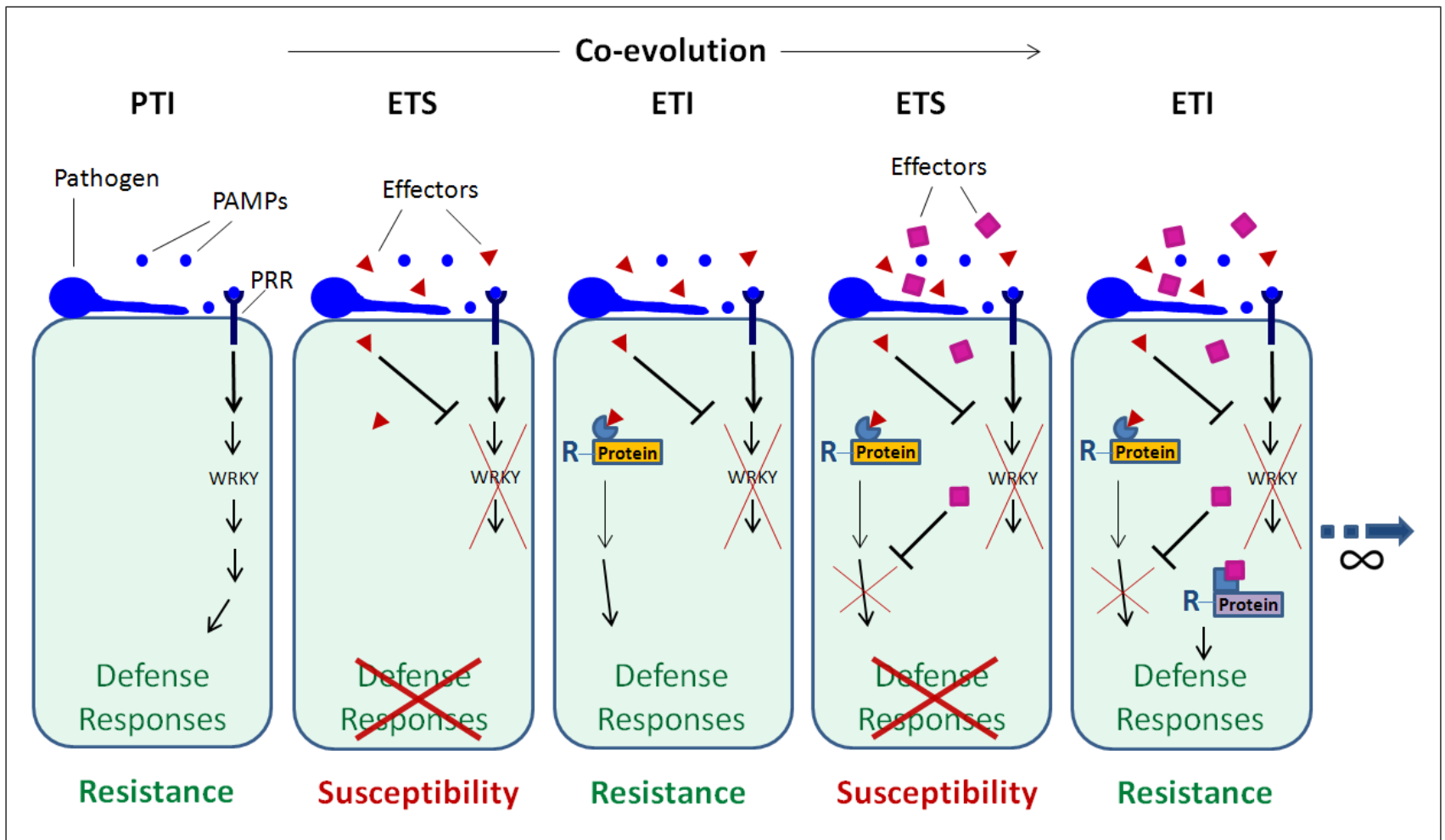
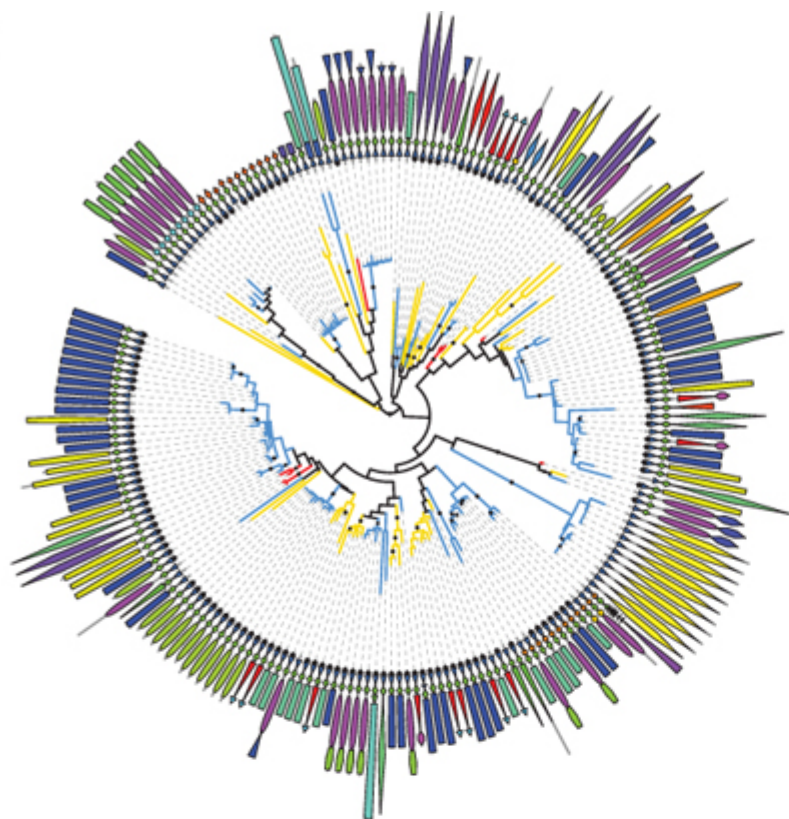


Table 2. Number of candidate RXLR effectors identified in oomycete genomes

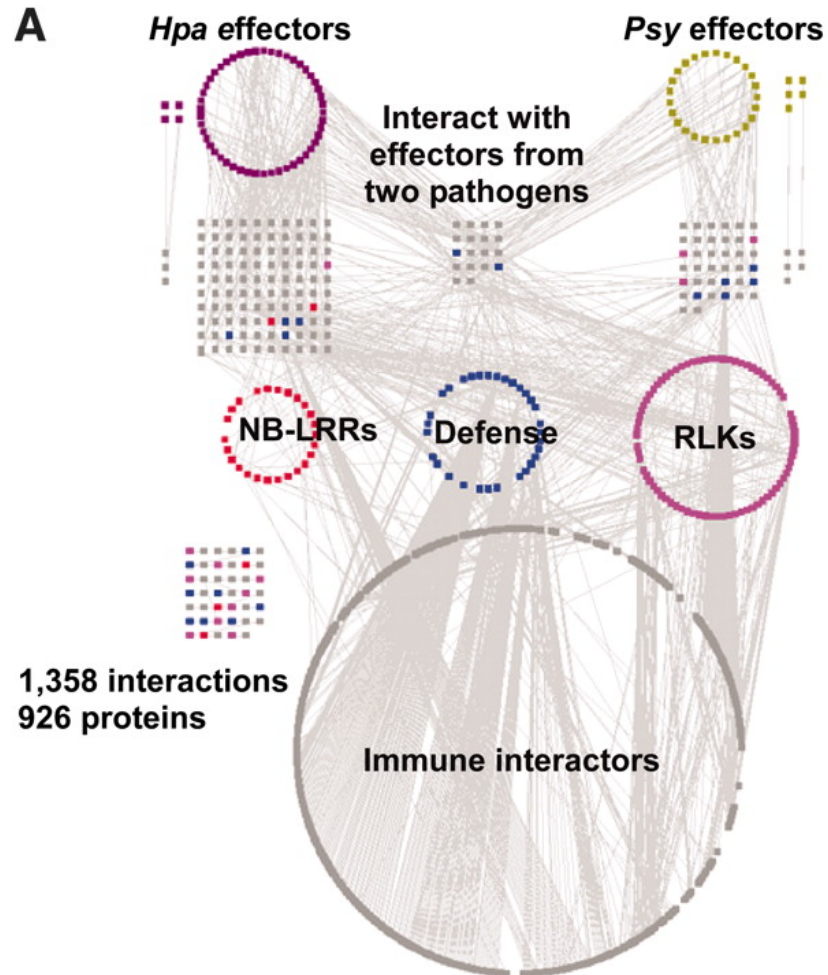
Species	Reference	Genome size (Mbp)	Total RXLR*
<i>Hyaloperonospora parasitica</i>	Washington University	75	149
<i>Phytophthora capsici</i>	JGI	65	420
<i>Phytophthora infestans</i>	Broad Institute	240	716
<i>Phytophthora ramorum</i>	Tyler et al. (2006)	65	531
<i>Phytophthora sojae</i>	Tyler et al. (2006)	95	672

a



CRN family phylogeny on the basis of the conserved N-terminal sequence.

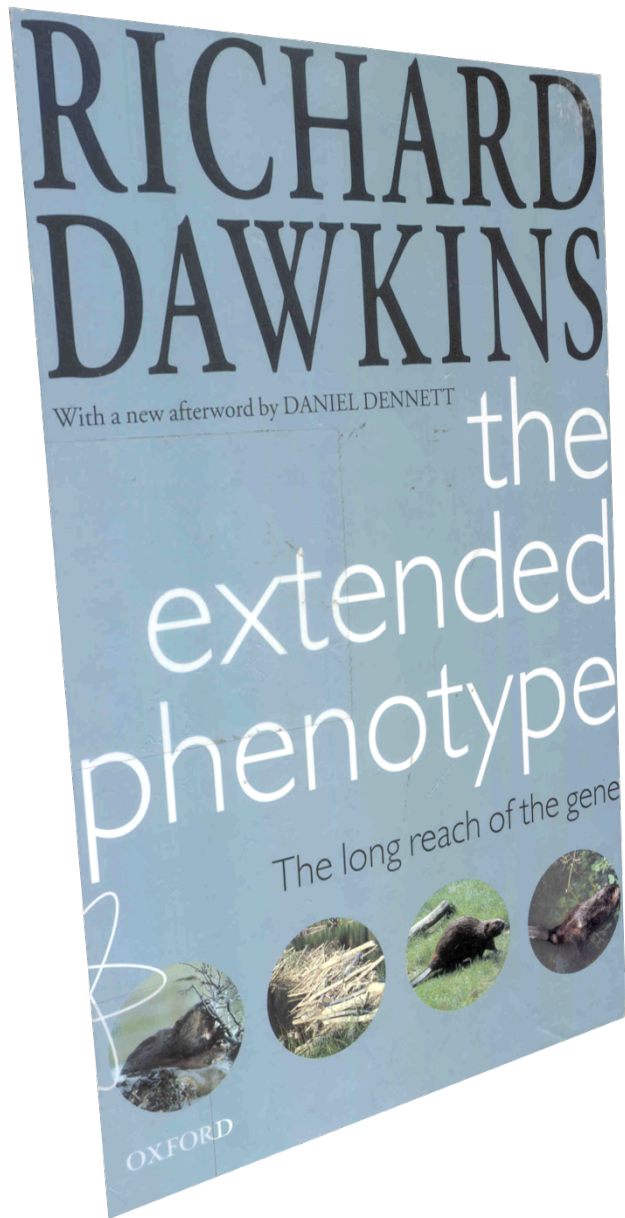
A



Experimentally determined plant-pathogen immune network.



$$1 \times 10^{260}$$



“parasite genes having phenotypic expression in host bodies and behavior”

Dawkins, R; Oxford, 1982.



Xanthomonas-H D.mp4

Função

Table 1

A selection of filamentous plant pathogen effectors

Pathogen species	Effector	Localization in plant tissue ^a	Signal peptide length ^b	Positive selection	Virulence activities	Reference(s)
<i>Blumeria graminis</i> f. sp. <i>hordei</i>	AVRa10	Cytoplasmic	NA		Enhances infection in susceptible barley plants ^c	[29**]
	AVRk1	Cytoplasmic	NA		Enhances infection in susceptible barley plants ^c	[29**]
<i>Cladosporium fulvum</i>	Avr2	Apoplasmic	20		Cysteine protease inhibitor; inhibits tomato Rcr3 ^c	[43]
	Avr4	Apoplasmic	18		Contains CBM14 chitin binding domain; protects fungal cell walls from hydrolysis by plant chitinases ^c	[44]
	Avr9	Apoplasmic	23		Structural similarity to cystine knot carboxypeptidase inhibitor ^d	[57]
<i>Fusarium oxysporum</i> f. sp. <i>lycopersici</i>	SIX1	Apoplasmic (xylem)	21			[49]
<i>Hyaloperonospora parasitica</i>	ATR1	Cytoplasmic	15	Yes		[30]
	ATR13	Cytoplasmic	18	Yes		[52]
<i>Leptosphaeria maculans</i>	AvrLm1	Probably cytoplasmic	22			[24]
<i>Magnaporthe oryzae</i>	Avr-Pita	Cytoplasmic	16		Metalloprotease ^d	[25]
<i>Melampsora lini</i>	AvrL567	Cytoplasmic	23	Yes		[16,18**]
	AvrM	Cytoplasmic	28	Yes		[17*]
	AvrP123	Cytoplasmic	23		Kazal-like protease inhibitor ^d	[17*]
	AvrP4	Cytoplasmic	28	Yes		[17*]
<i>Phytophthora infestans</i>	Avr3a	Cytoplasmic	21	Yes	Cell death suppressor ^c	[33**,50]
	CRN1	Cytoplasmic	17		Elicits cell death in host plants ^c	[31]
	CRN2	Cytoplasmic	22		Elicits cell death in host plants ^c	[31]
	CRN8	Cytoplasmic	17		Similarity to RD kinase ^d ; elicits cell death in host plants ^c	[40], C Cakir et al., unpublished
	EPI1	Apoplasmic	16		Kazal-like serine protease inhibitor; inhibits tomato P69B ^c	[45]
	EPI10	Apoplasmic	21		Kazal-like serine protease inhibitor; inhibits tomato P69B ^c	[46]
	EPIC1	Apoplasmic	21	Yes	Cystatin-like cysteine protease inhibitor ^d	[47]
	EPIC2B	Apoplasmic	21	Yes	Cystatin-like cysteine protease inhibitor; inhibits tomato PIP1 ^c	[47]
<i>Phytophthora sojae</i>	Avr1b-1	Cytoplasmic	21	Yes		[58]
<i>Rhynchosporium secalis</i>	NIP1	Apoplasmic	20	Yes	Toxin; elicits necrosis in host plants ^c	[54]
<i>Uromyces fabae</i>	Uf-RTP1	Cytoplasmic	19		Localizes to host nucleus ^c	[19**]

^a Cytoplasmic vs. apoplasmic effectors based on the classification described in the text and in Reference [w3].




^b Length in amino acids, based on SignalP v2.0-NN (<http://www.cbs.dtu.dk/services/SignalP-2.0>); NA, not applicable.

^c Evidence is based on wet lab experimental data.

^d Evidence is based on computational analyses.



Major Transcriptome Reprogramming Underlies Floral Mimicry Induced by the Rust Fungus *Puccinia monoica* in *Boechera stricta*

Liliana M. Cano , Sylvain Raffaele , Riston H. Haugen, Diane G. O. Saunders, Lauriebeth Leonelli, Dan MacLean, Saskia A. Hogenhout, Sophien Kamoun 

Published: September 17, 2013 • DOI: 10.1371/journal.pone.0075293

Article

About the Authors

Metrics

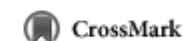
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Abstract

Puccinia monoica is a spectacular plant parasitic rust fungus that triggers the formation of flower-like structures (pseudoflowers) in its Brassicaceae host plant *Boechera stricta*. Pseudoflowers mimic in shape, color, nectar and scent co-occurring and unrelated flowers such as buttercups. They act to attract insects thereby aiding spore dispersal and sexual reproduction of the rust fungus. Although much ecological research has been performed on *P. monoica*-induced pseudoflowers, this system has yet to be investigated at the molecular or genomic level. To date, the molecular alterations underlying the development of pseudoflowers and the genes involved have not been described. To address this, we performed gene

Abstract

Introduction

Results and Discussion

Conclusions

Materials and Methods

Supporting Information

Acknowledgments

Author Contributions

-



Figure 1. Illustration of floral mimicry produced by the pseudoflower-forming rust fungus *Puccinia monoica*.

Abstract

Puccinia monoica is a spectacular plant parasitic rust fungus that triggers the formation of flower-like structures (pseudoflowers) in its Brassicaceae host plant *Boechea stricta*. Pseudoflowers mimic in shape, color, nectar and scent co-occurring and unrelated flowers such as buttercups. They act to attract insects thereby aiding spore dispersal and sexual reproduction of the rust fungus. Although much ecological research has been performed on *P. monoica*-induced pseudoflowers, this system has yet to be investigated at the molecular or genomic level. To date, the molecular alterations underlying the development of pseudoflowers and the genes involved have not been described. To address this, we performed gene expression profiling to reveal 256 plant biological processes that are significantly altered in pseudoflowers. Among these biological processes, plant genes involved in cell fate specification, regulation of transcription, reproduction, floral organ development, anthocyanin (major floral pigments) and terpenoid biosynthesis (major floral volatile compounds) were down-regulated in pseudoflowers. In contrast, plant genes involved in shoot, cotyledon and leaf development, carbohydrate transport, wax biosynthesis, cutin transport and L-phenylalanine metabolism (pathway that results in phenylethanol and phenylacetaldehyde volatile production) were up-regulated. These findings point to an extensive reprogramming of host genes by the rust pathogen to induce floral mimicry. We also highlight 31 differentially regulated plant genes that are enriched in the biological processes mentioned above, and are potentially involved in the formation of pseudoflowers. This work illustrates the complex perturbations induced by rust pathogens in their host plants, and provides a starting point for understanding the molecular mechanisms of pathogen-induced floral mimicry.

Zombies



Horrifying Fungus Creates Zombie Ants

Added by James Fenner on September 14, 2013.

Saved under James Fenner, Science, Zombie ants



Ophiocordyceps unilateralis

From Wikipedia, the free encyclopedia

Ophiocordyceps unilateralis is an [entomopathogenic fungus](#) predominantly found in tropical forest ecosystems. In order to increase its own fitness *O. unilateralis* utilizes the evolutionary trait of an extended phenotype to manipulate the behavioral patterns of an infected [formicidae](#), specifically *Camponotus leonardi* of the tribe of campotini. The infected ants leave their canopy nest and foraging trails, heading for the forest floor in search of an area with a temperature and humidity level that is suitable for fungal growth. The infected ant will then use its mandible to affix themselves to a major vein on the underside of a leaf and eventually die.^[2]



Duas principais estratégias dos patógenos:

1- Impedir / Driblar o reconhecimento da infecção

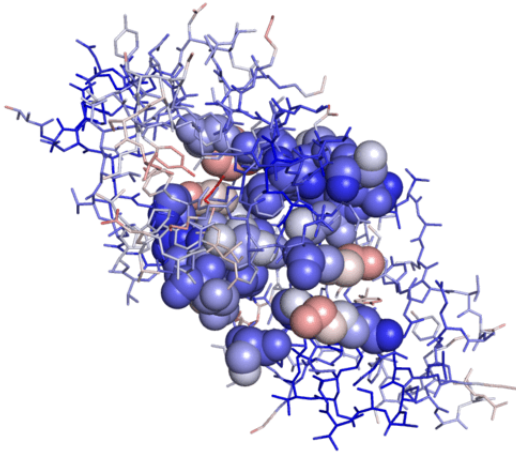
2- penetrar e crescer rápida e exponencialmente nos tecidos da planta

Quais seriam então as nossas estratégias para impedir o desenvolvimento de doenças?

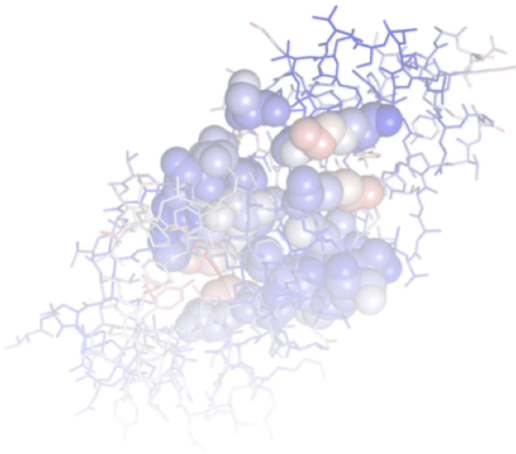
1- Facilitar o reconhecimento da infecção

2- Aumentar a capacidade e rapidez da resposta das plantas ao ataque

- Indução de resistência,
- controle biológico,
- priming,
- manipulação de efetores e PAMPs,
- plantas transgênicas



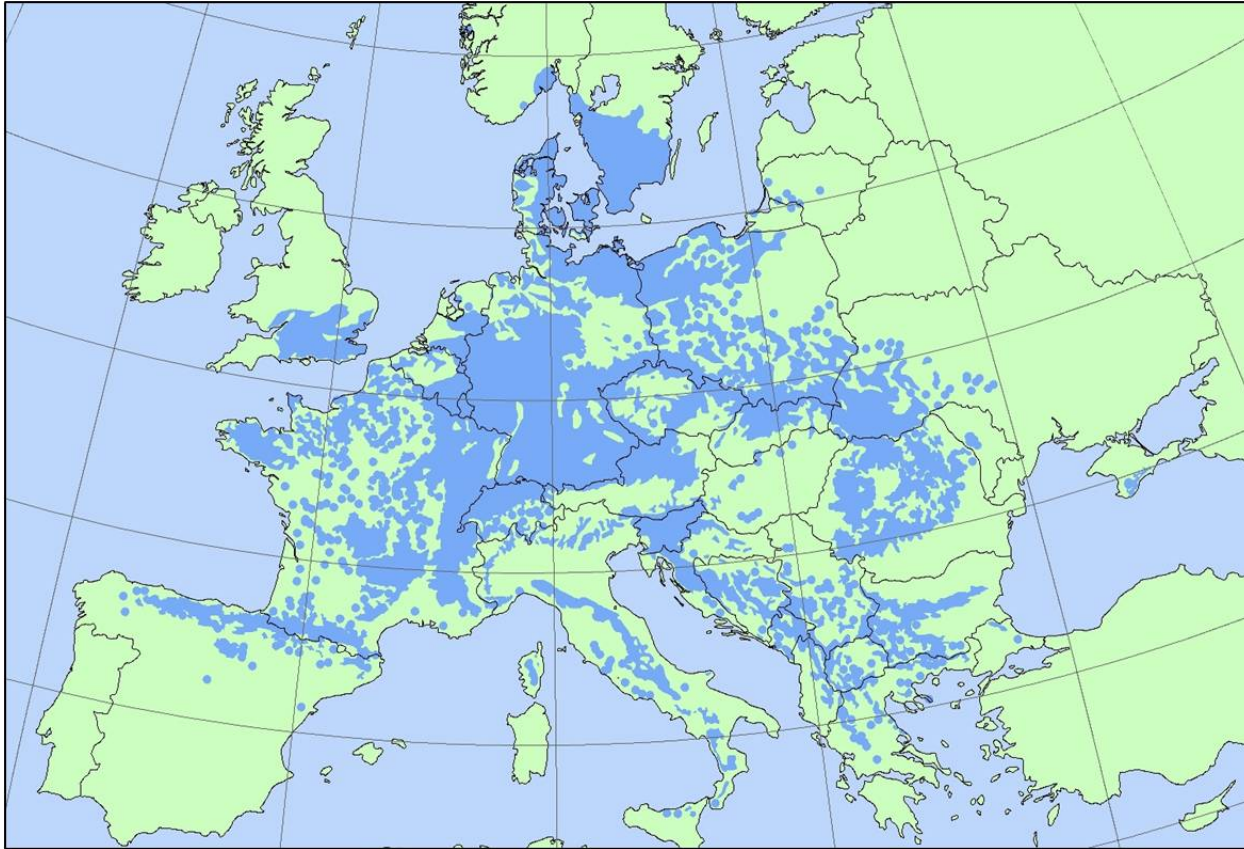
α -plurivorin (elicitin) on
Phytophthora plurivora Vs *Fagus sylvatica*



Fagus sylvatica – Beech - Faia
européia „Mother of forests“



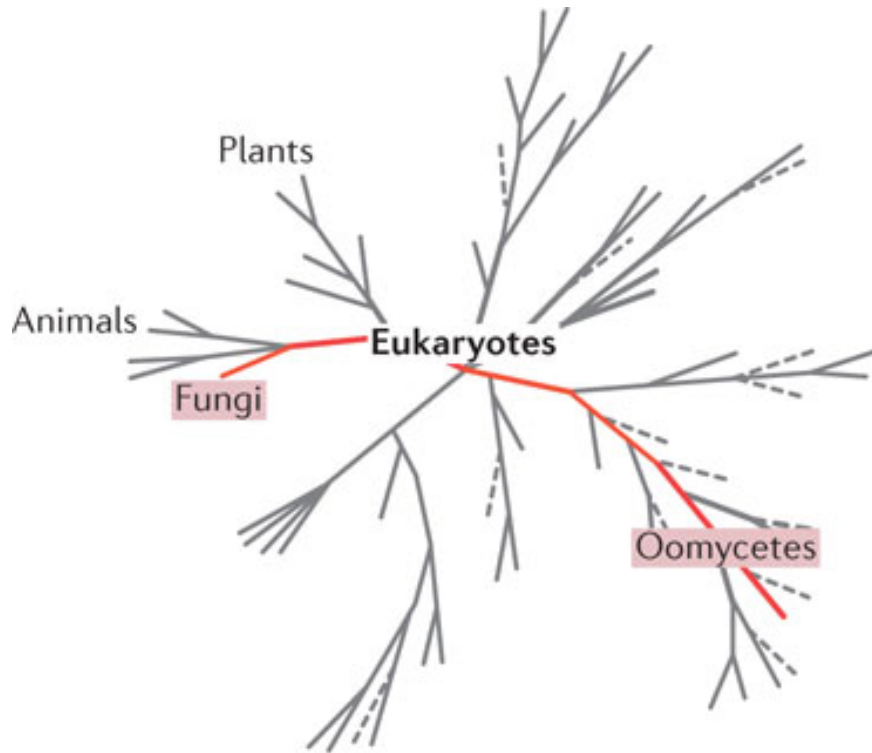
Fagus sylvatica – Distribution map



Spike in the mortality of trees in the last decade.

- Climate change
- Phytophthora infection

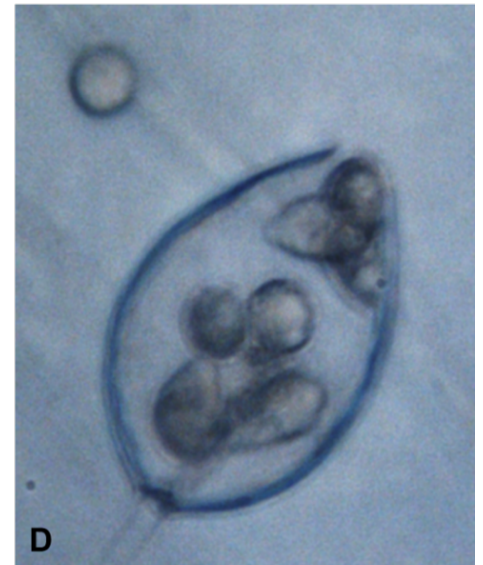
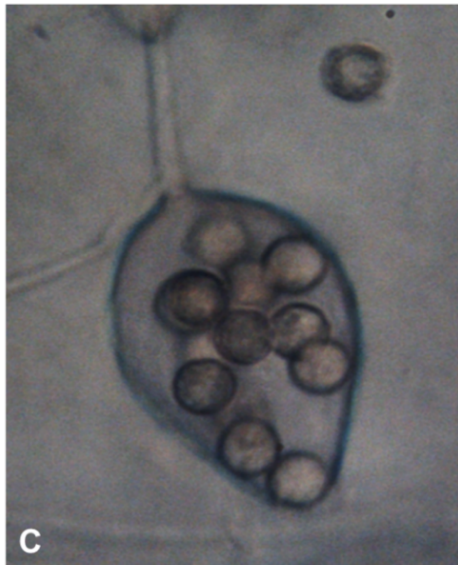
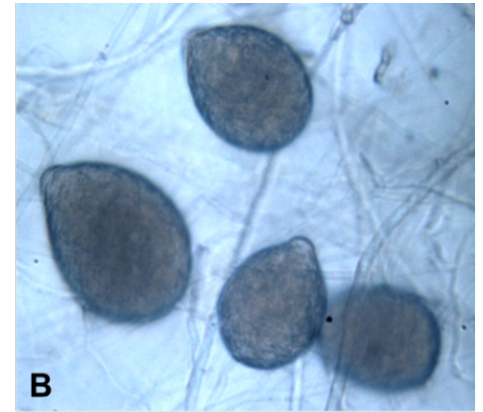
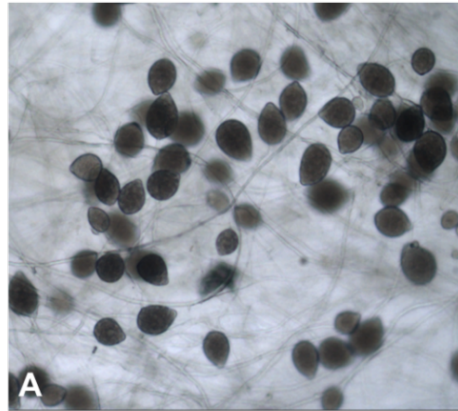
Oomycetes - Phytophthora



Bats are not birds
Dolphins are not fish
Oomycetes are not fungi!

Phytophthora plurivora

- Broad host range
- World-wide distribution
- Very aggressive soil born pathogen attacking roots
- motile zoospores



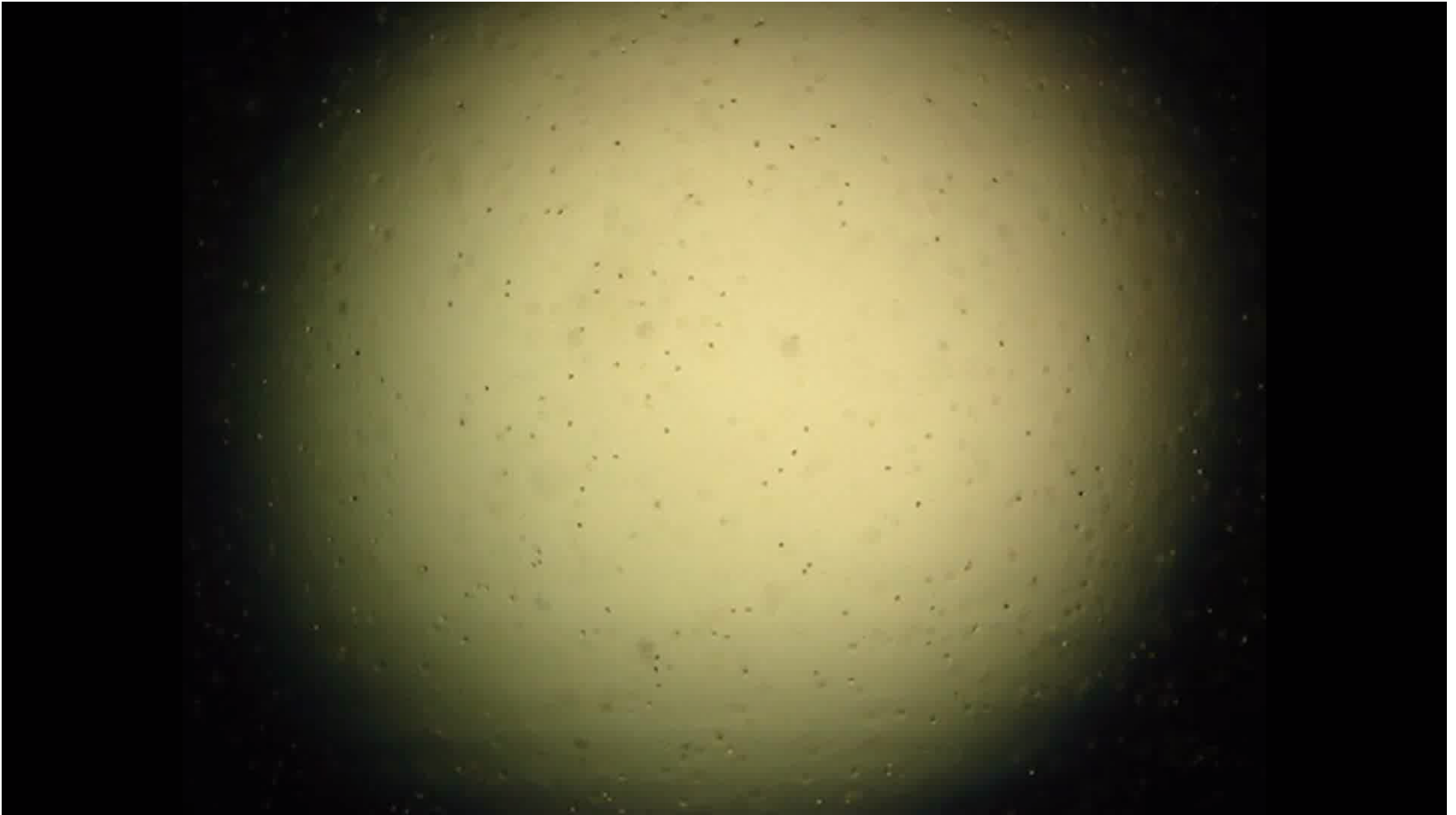


Sporangia releasing zoospores

Attraction to Beech root exudates: <http://www.youtube.com/watch?v=F4sITLkhwuY>



Zoospore attraction to root exudates.wmv



Attacking Beech root piece: http://www.youtube.com/watch?v=_vhlVak2z-U

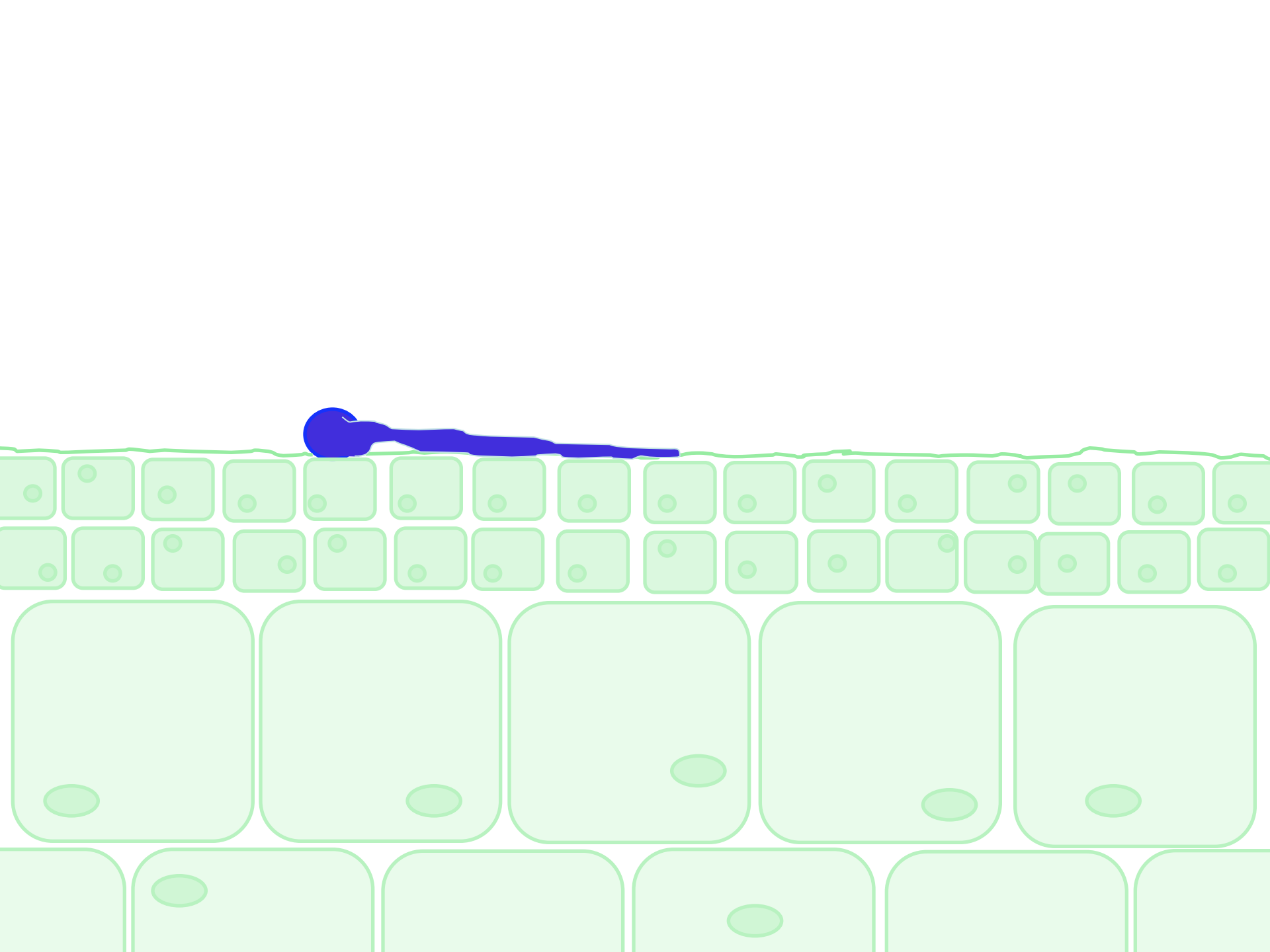
Micélio em raízes

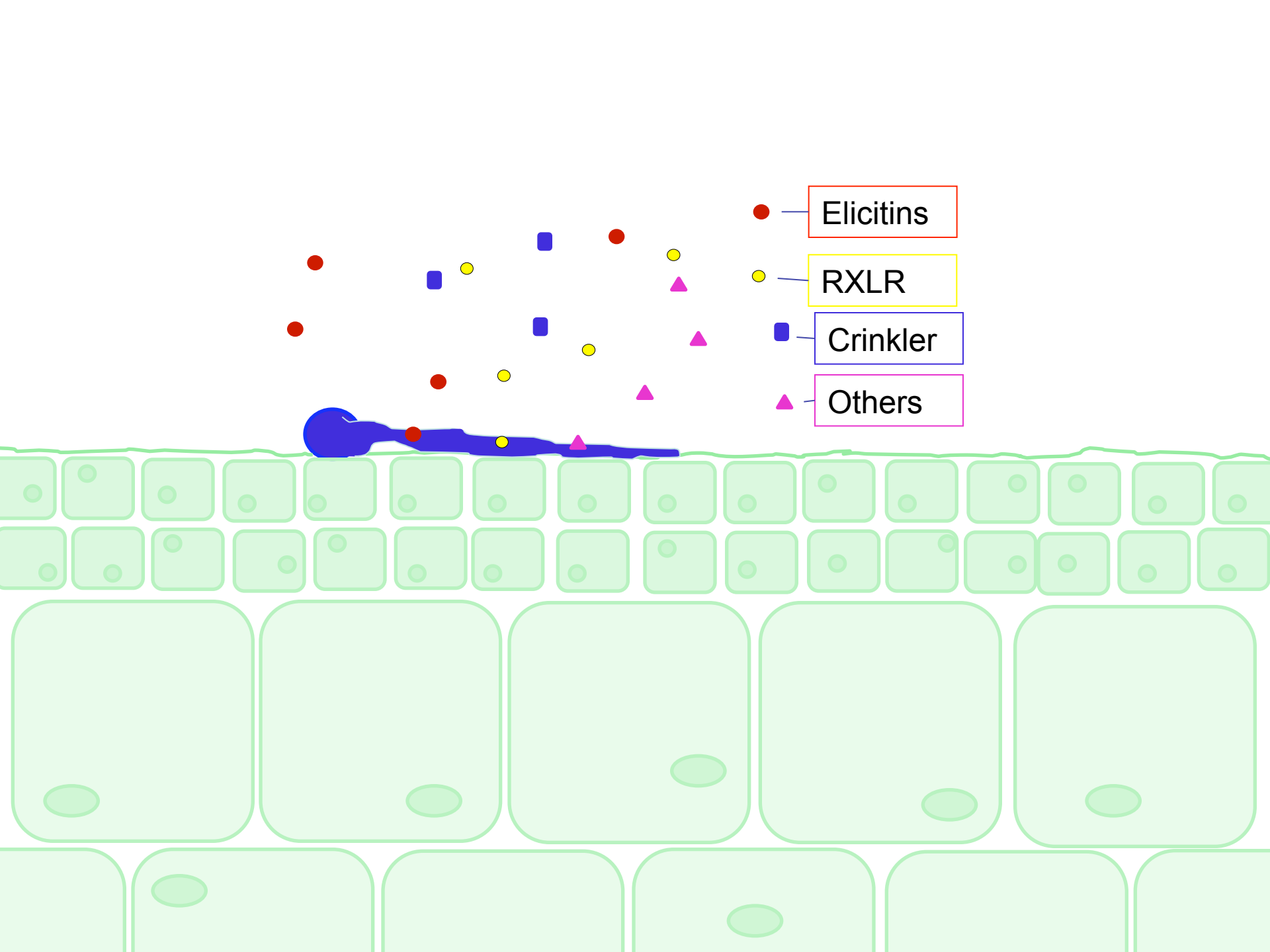


Controle

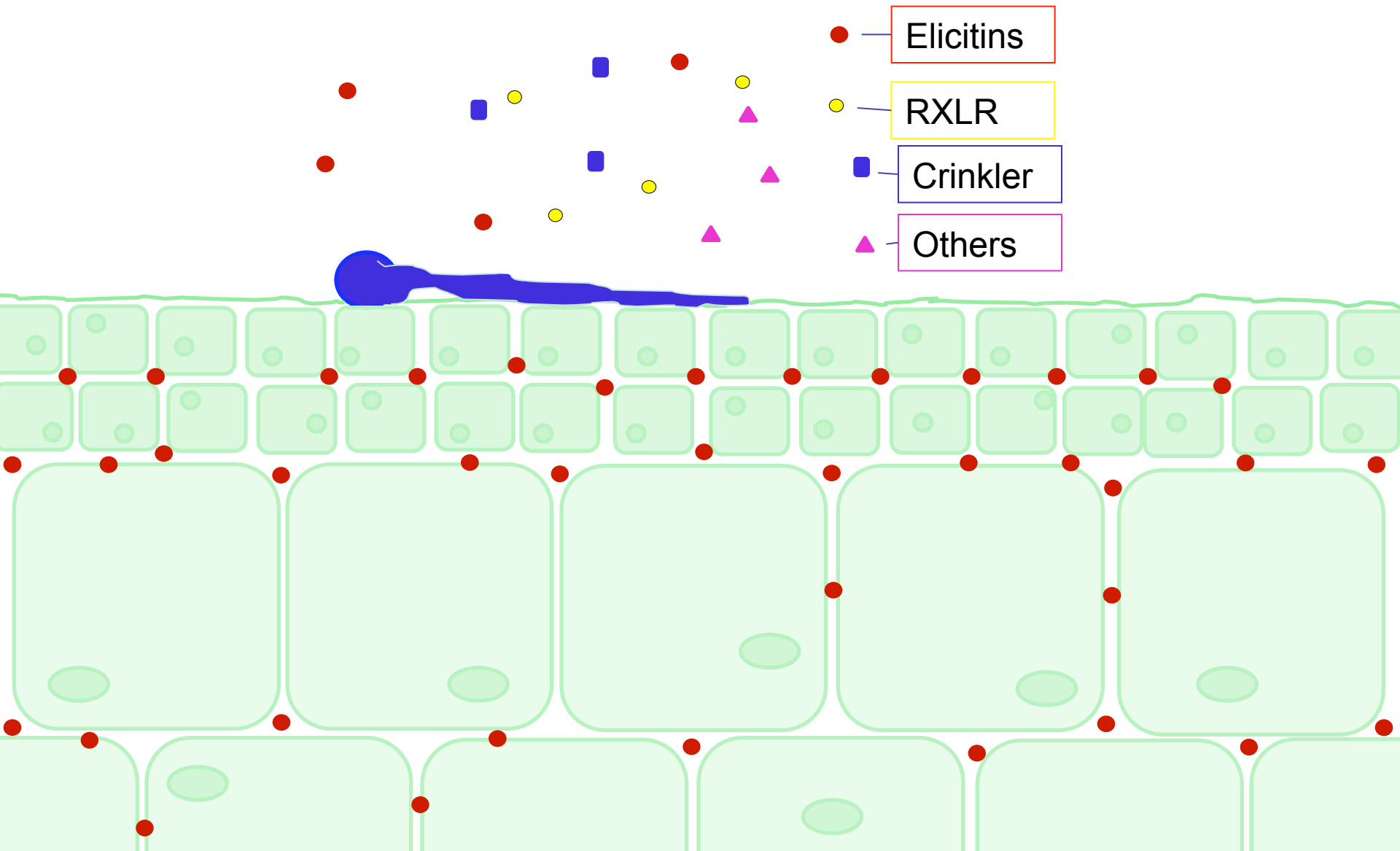


Inoculado

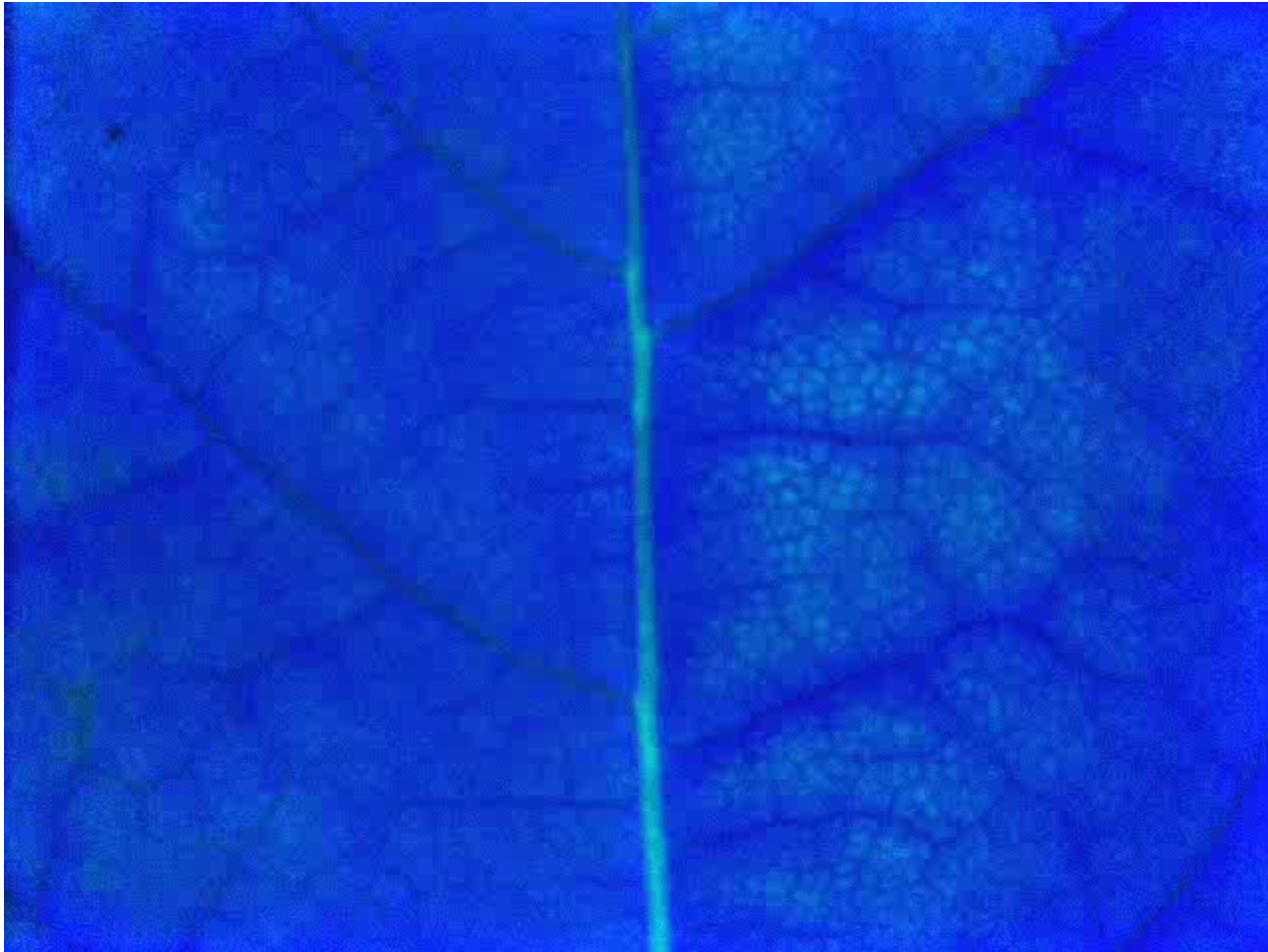




- Elicitins
- RXLR
- Crinkler
- ▲ Others

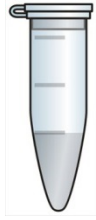


Video: Chlorophyll fluorescence of a *P. plurivora*-infected *F. sylvatica* seedling.



Imaging Pam Yield analyzer

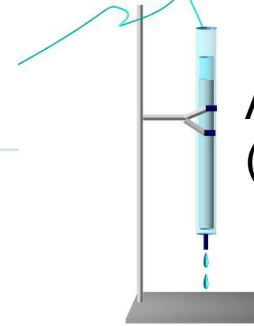
α -plurivorin



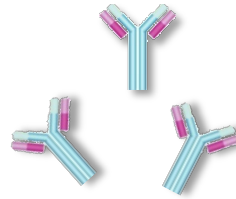
Chicken



Antiserum

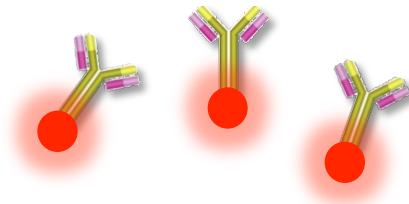


Affinity purification
(elicitin column)

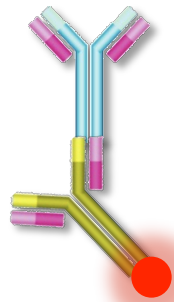


Highly purified primary antibodies against plurivorin

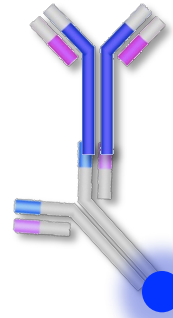
goat



Secondary antibodies against chicken in
goat conjugated with a fluorescence die.

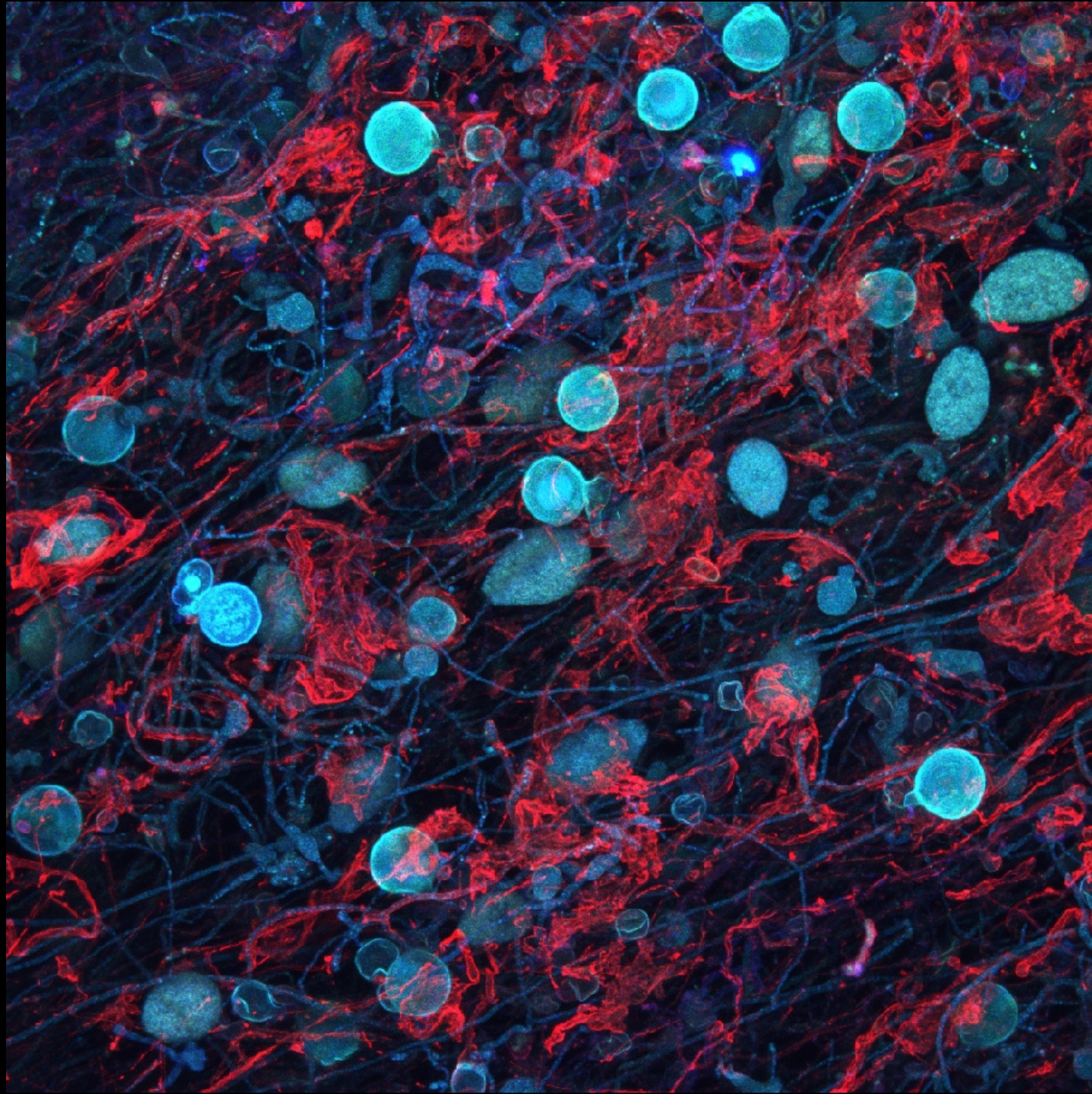


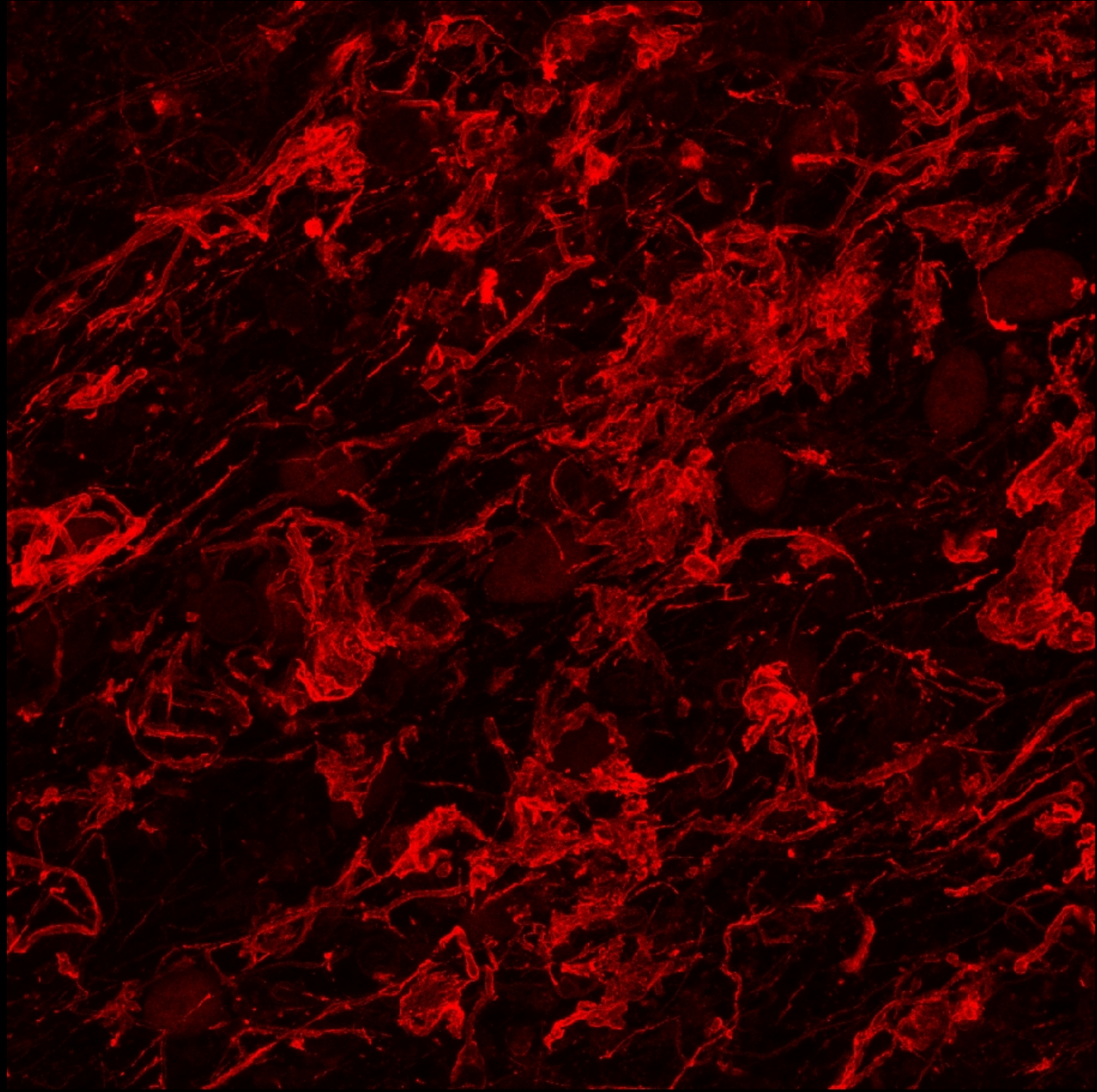
Plurivorin

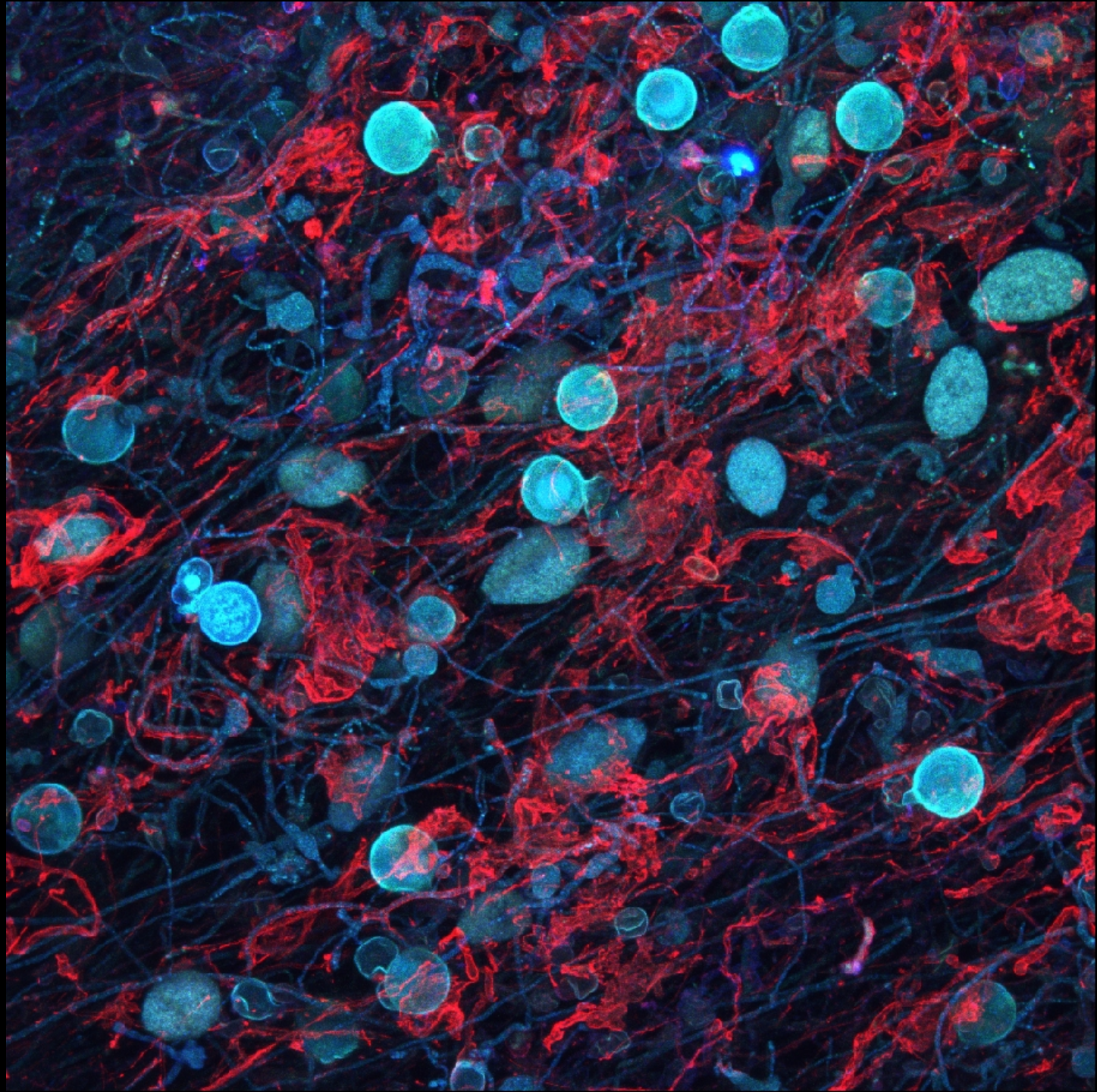


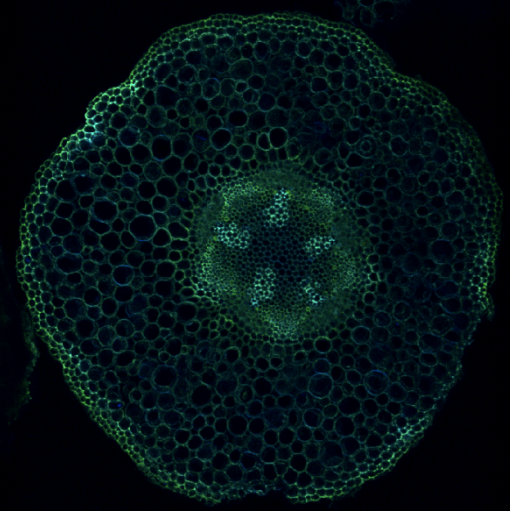
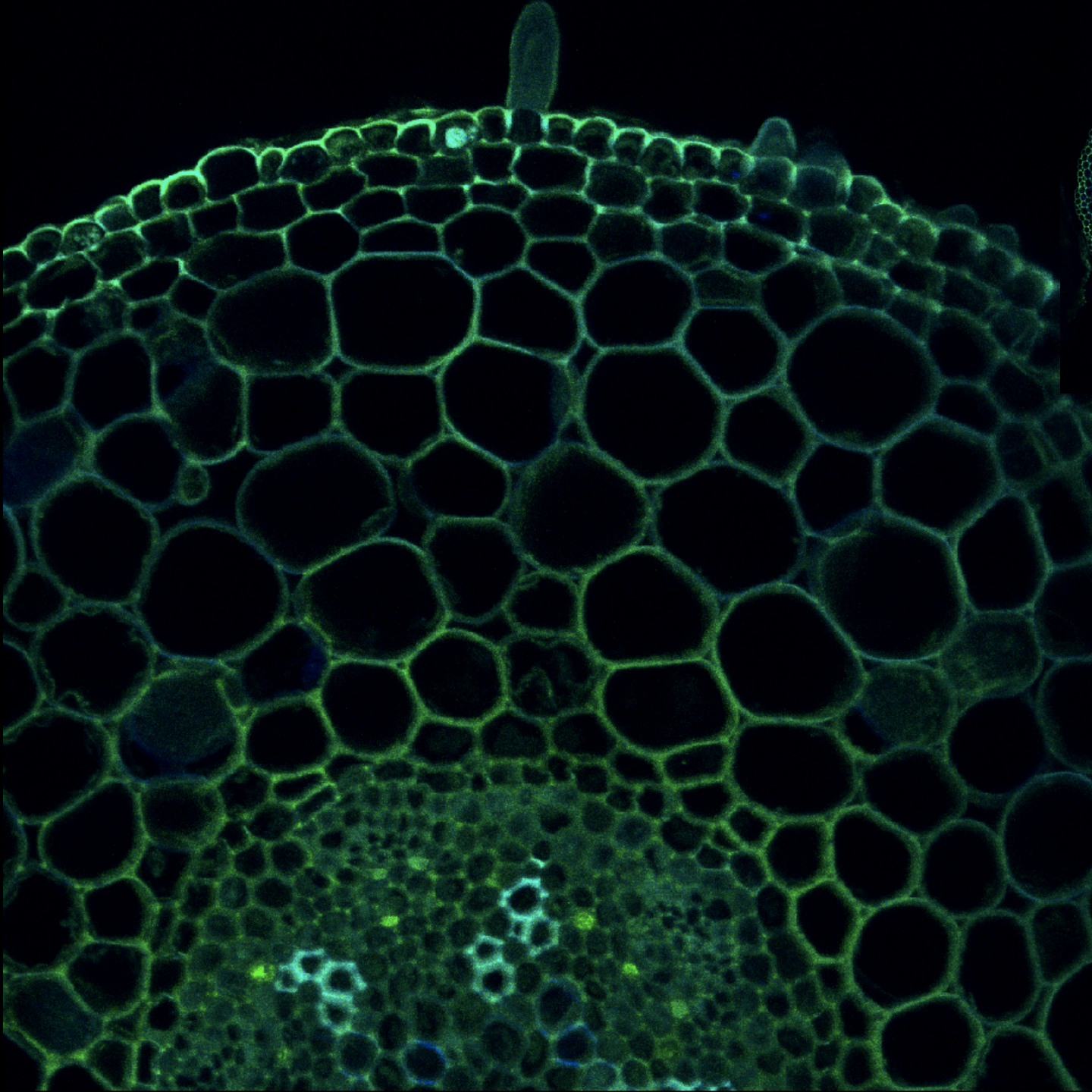
P. plurivora

In vitro

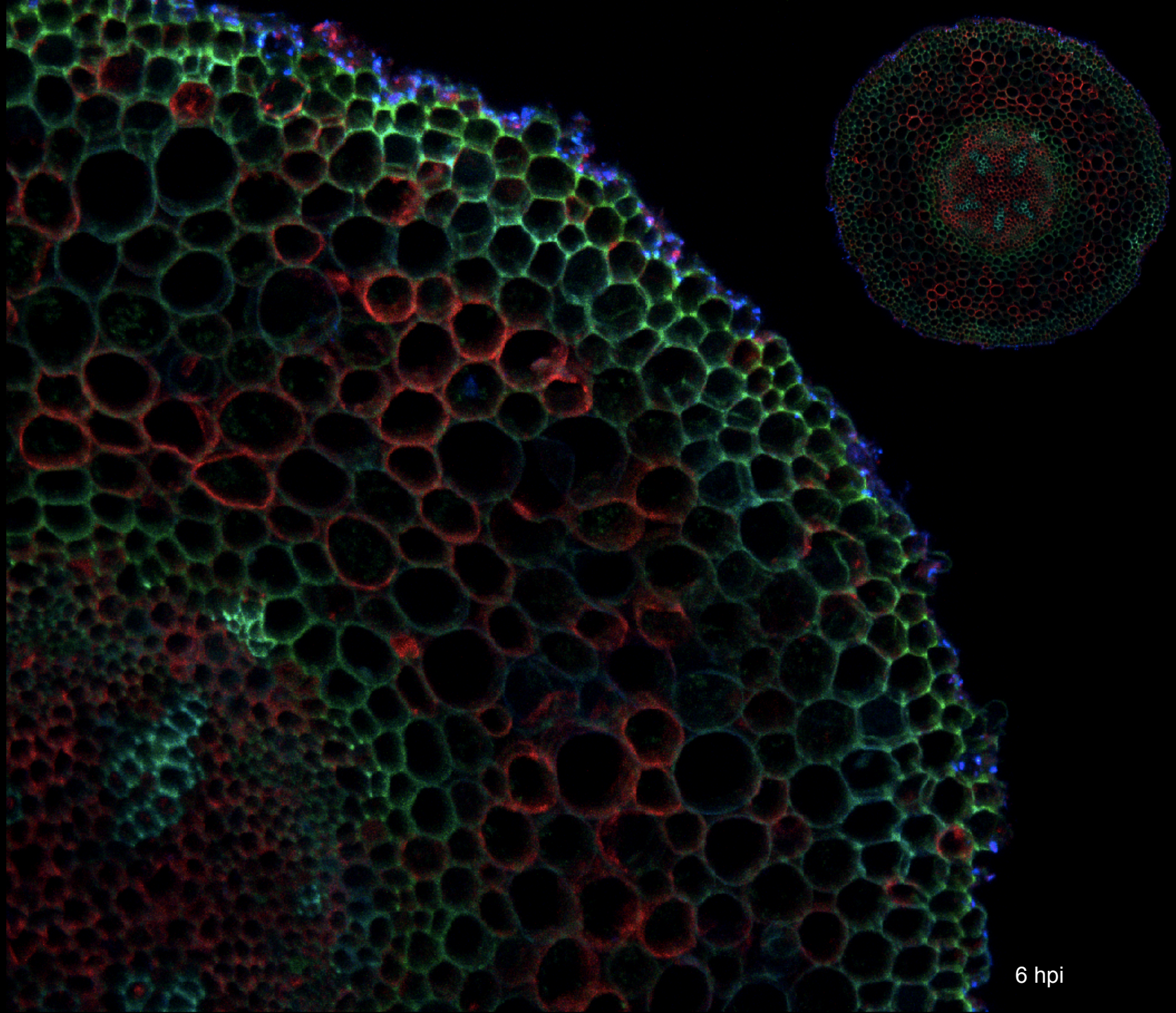




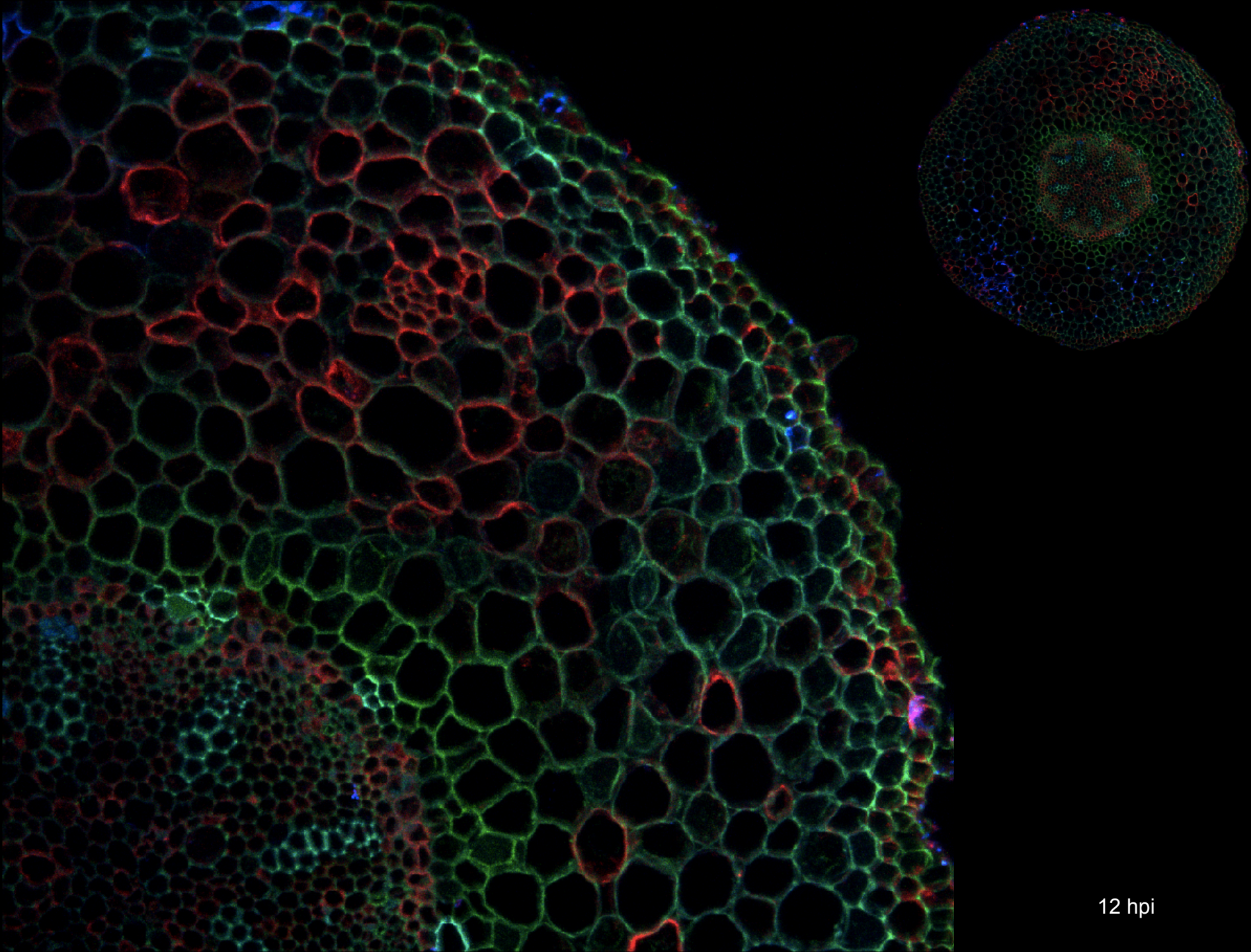




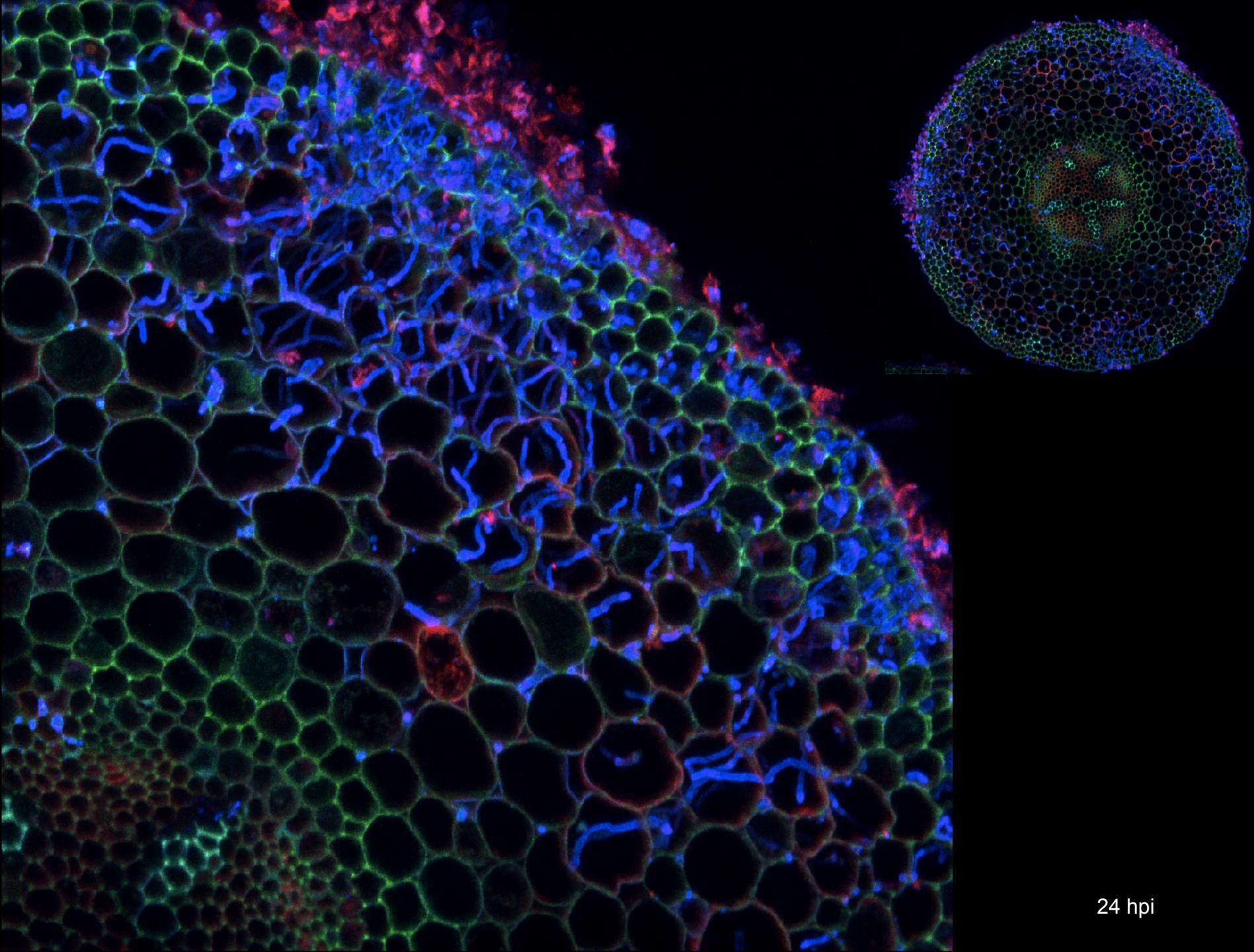
Control
0 hpi



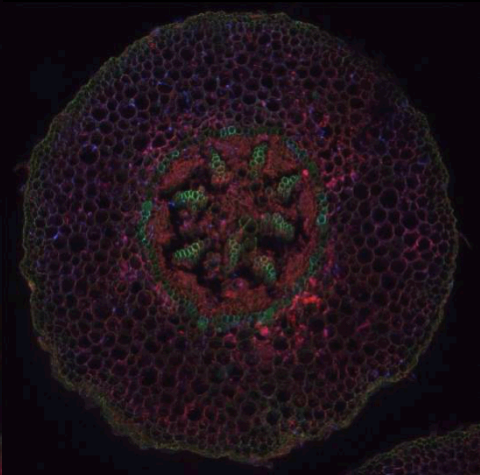
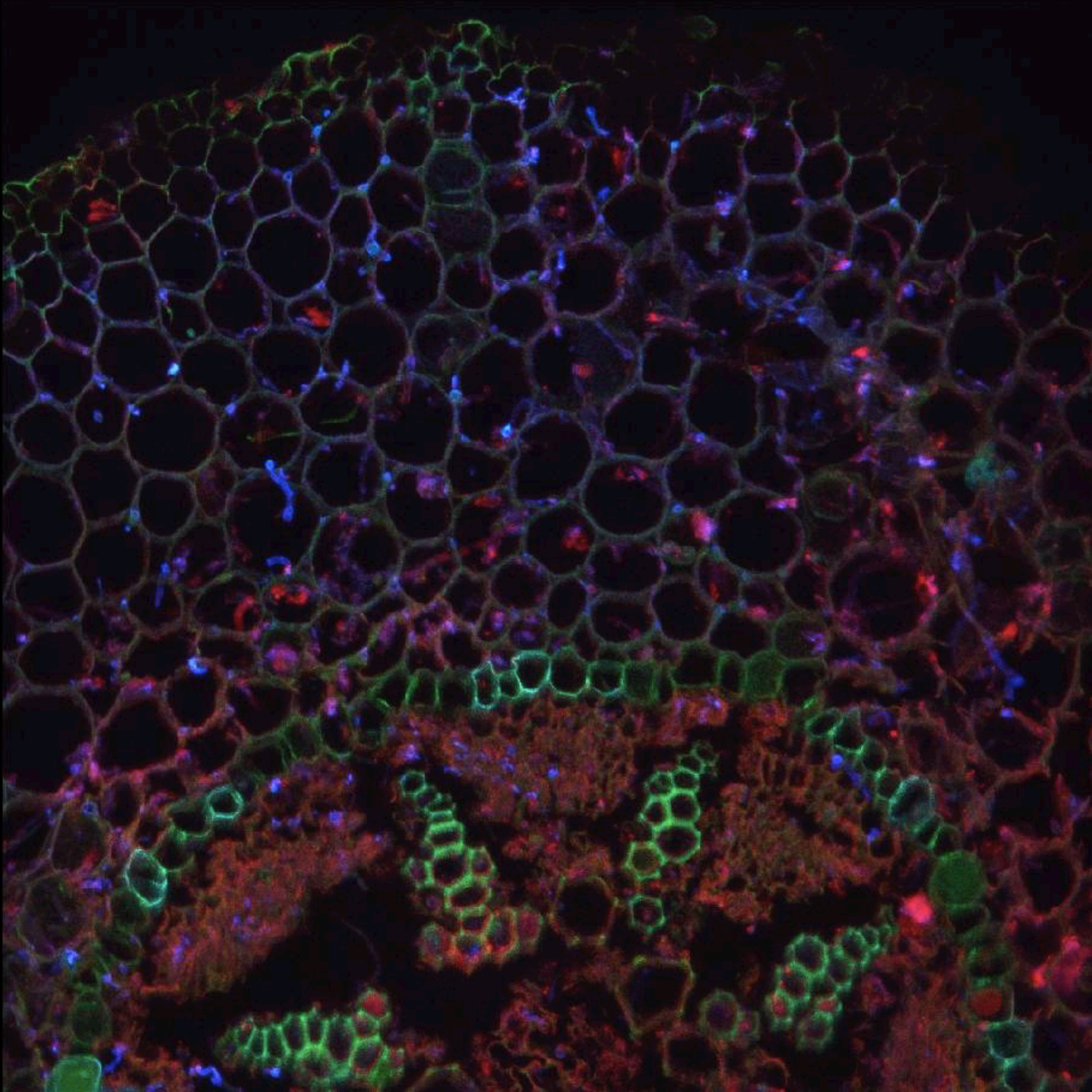
6 hpi



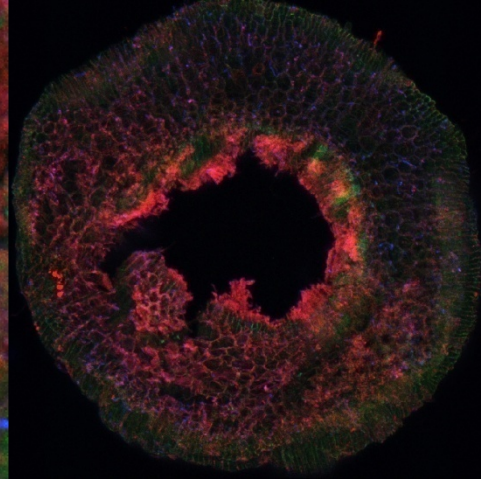
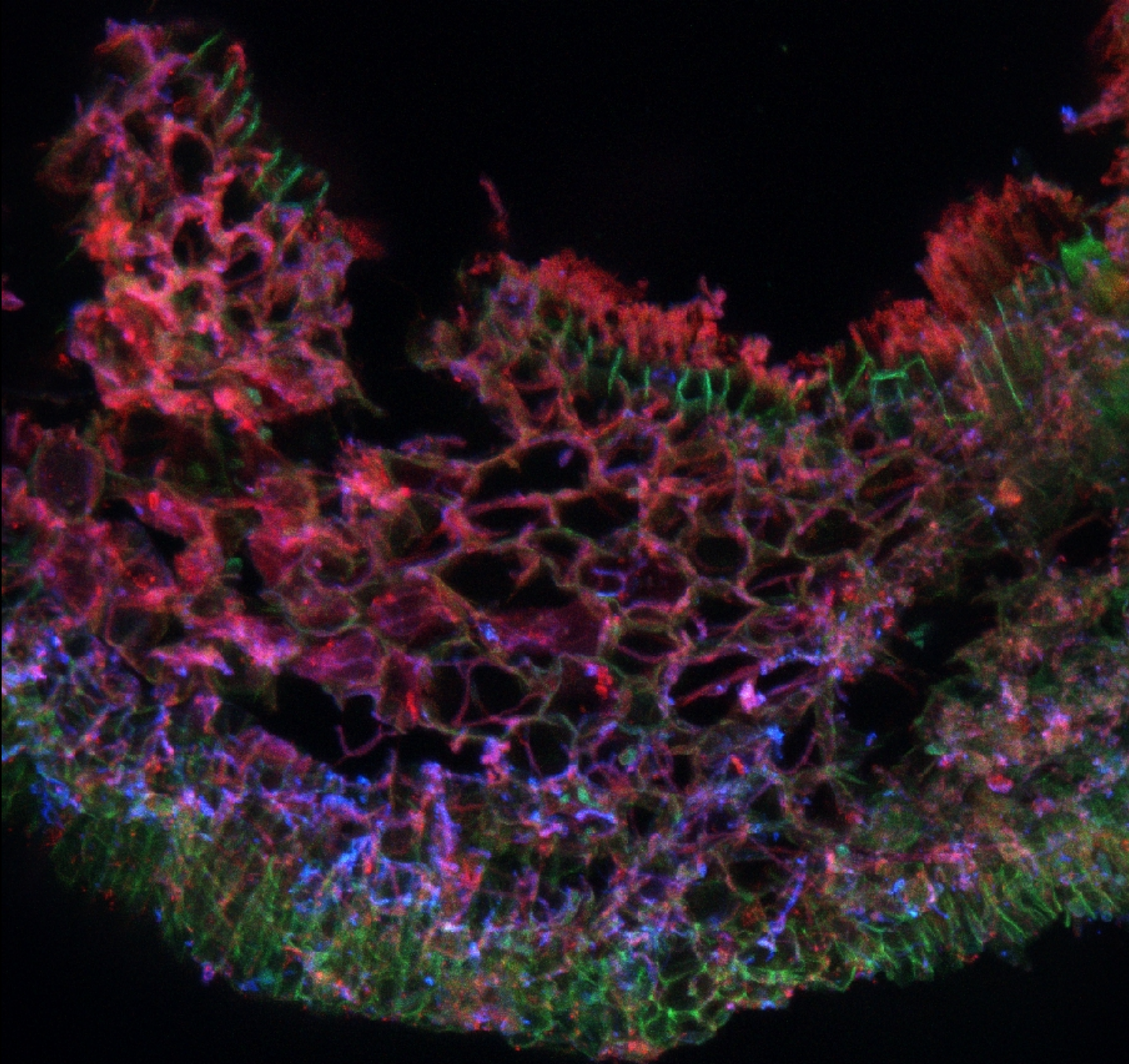
12 hpi



24 hpi

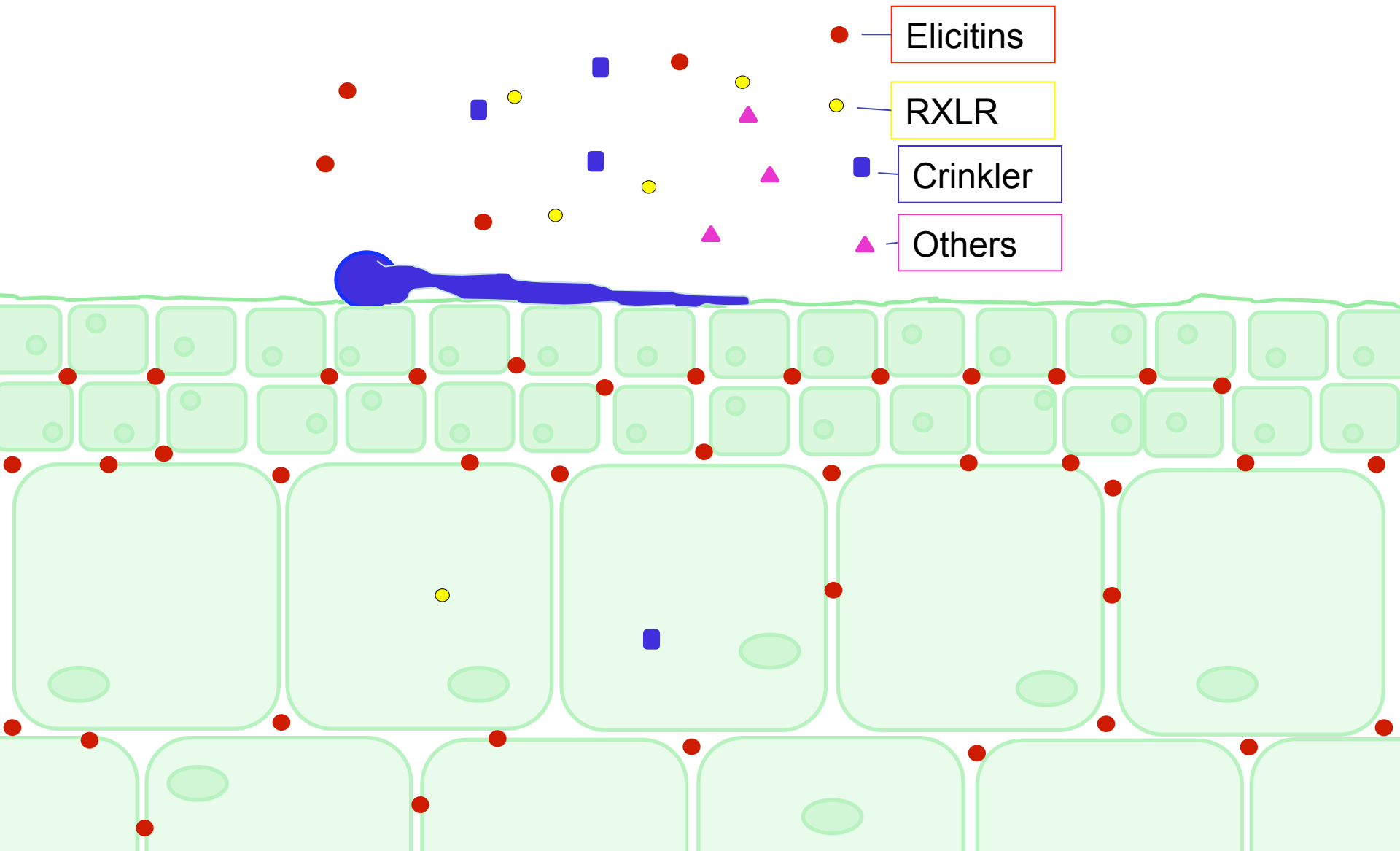


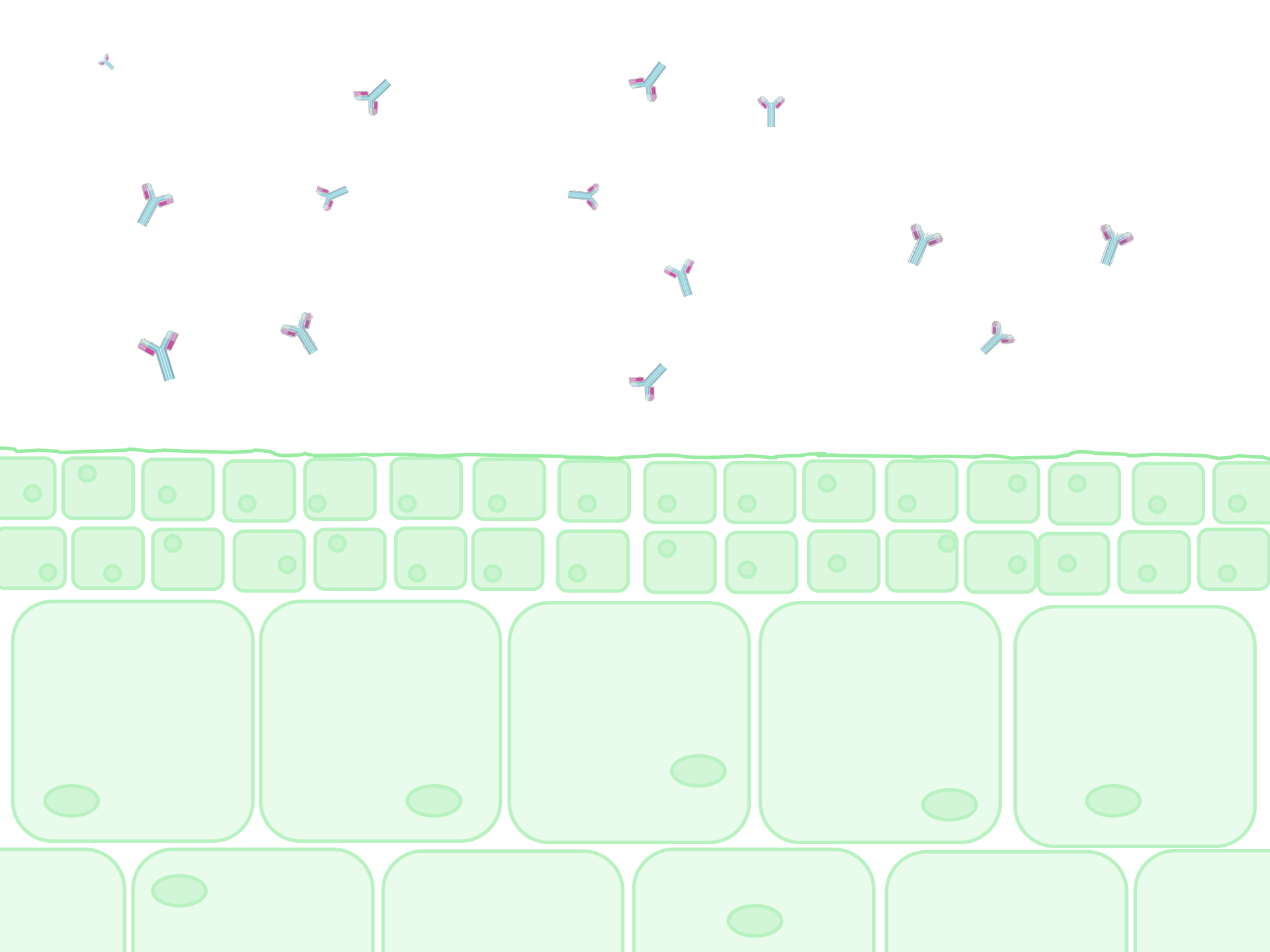
96 hpi

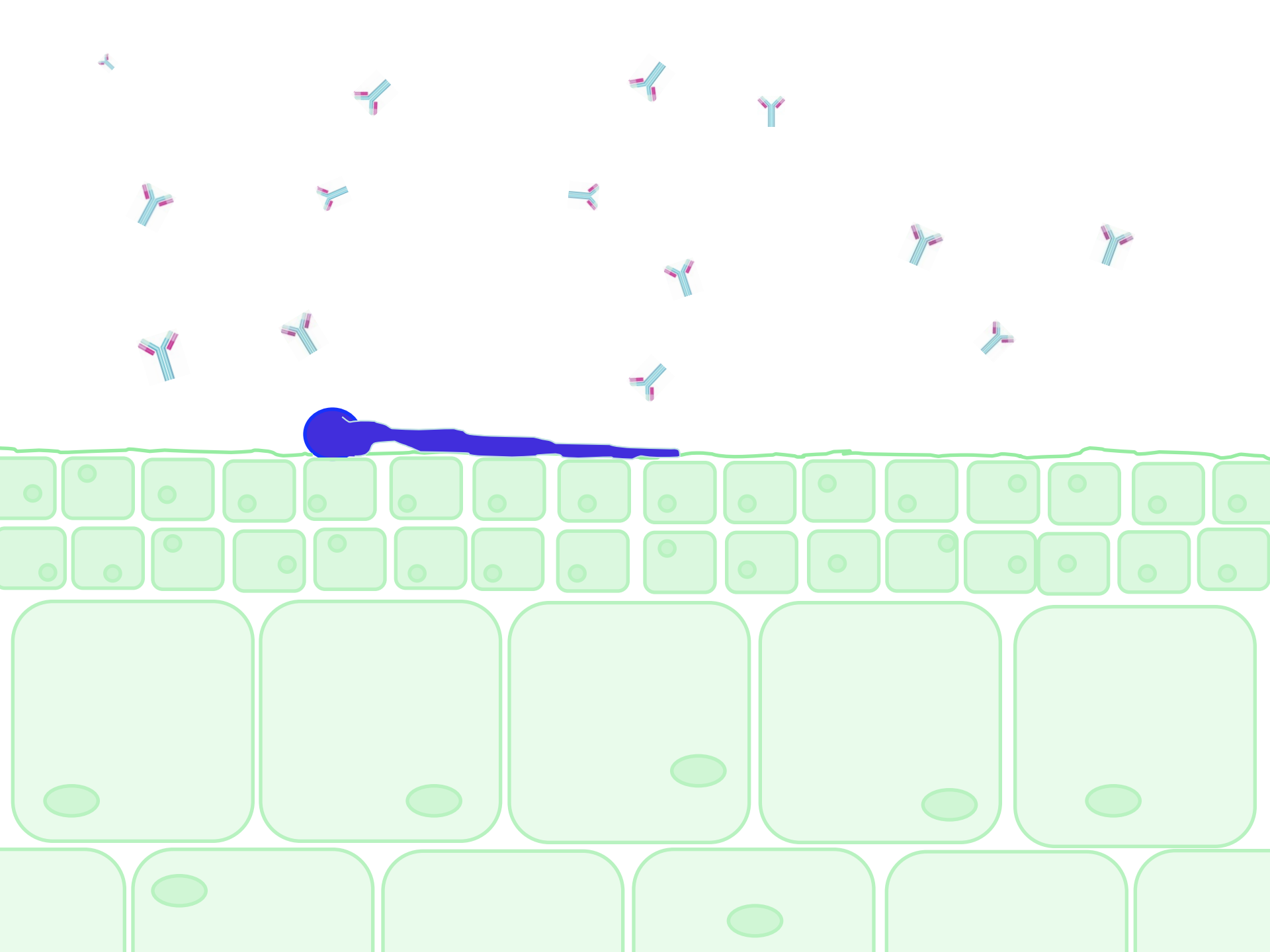


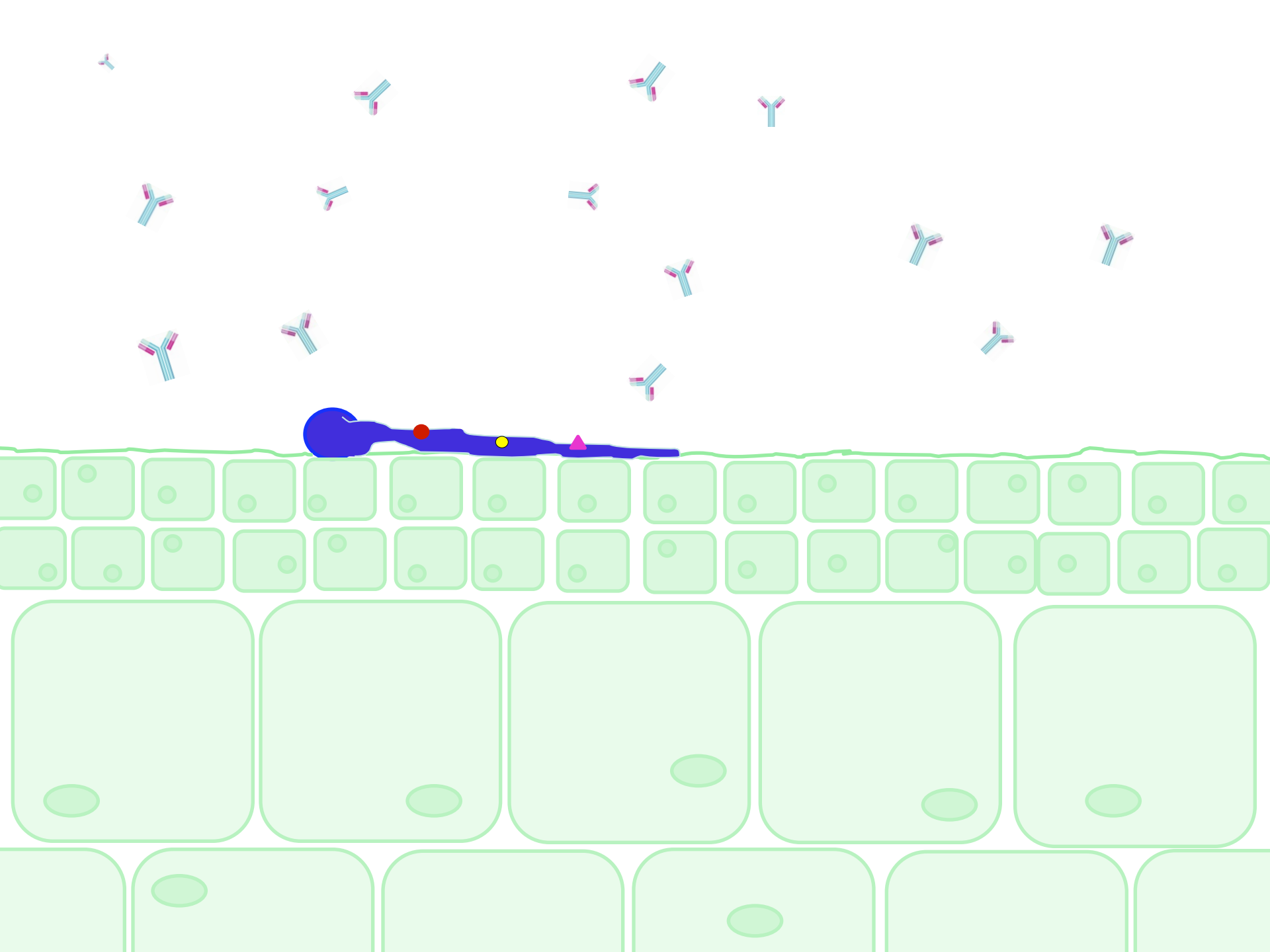
100 % Mortality

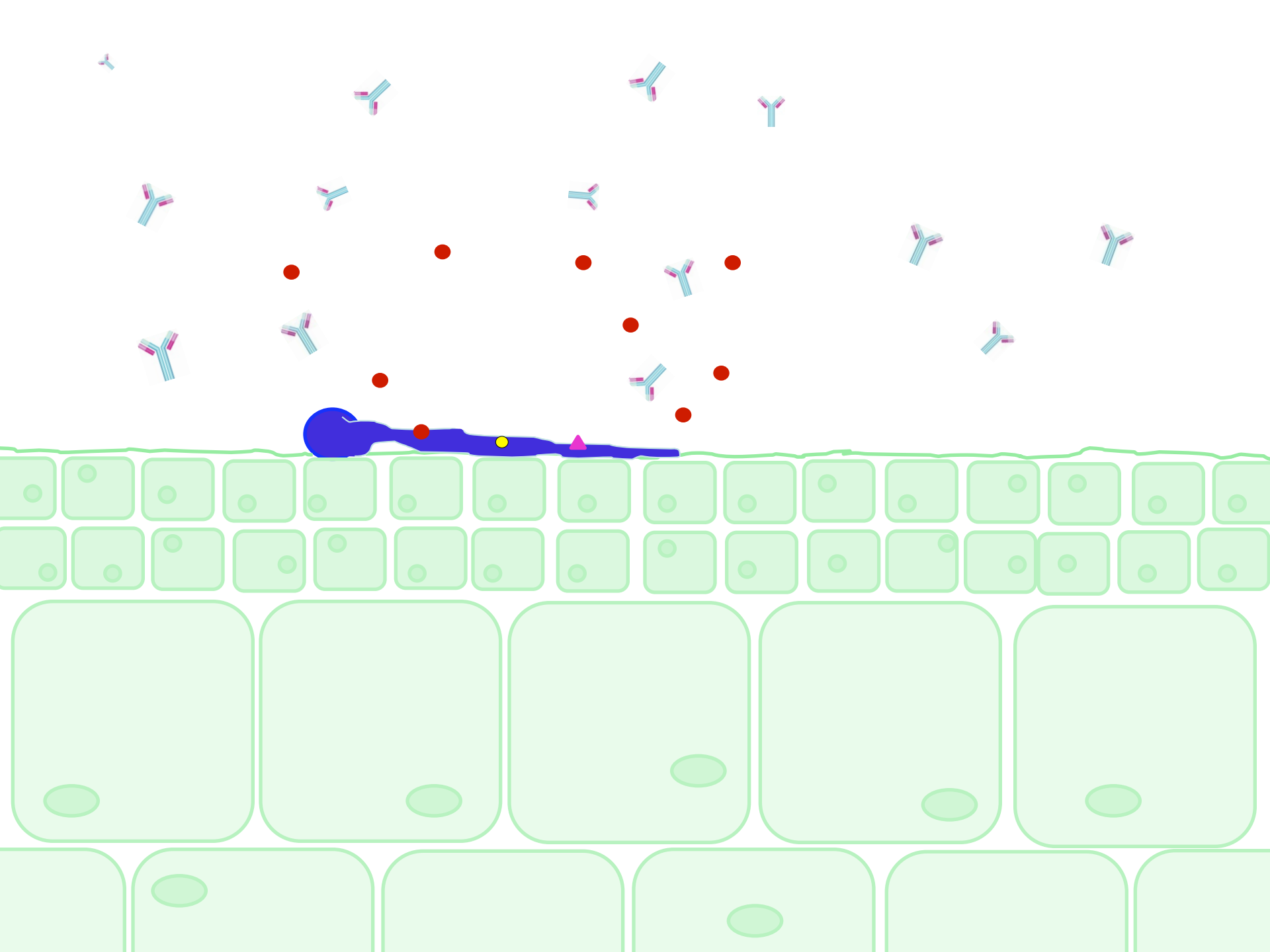
192 hpi

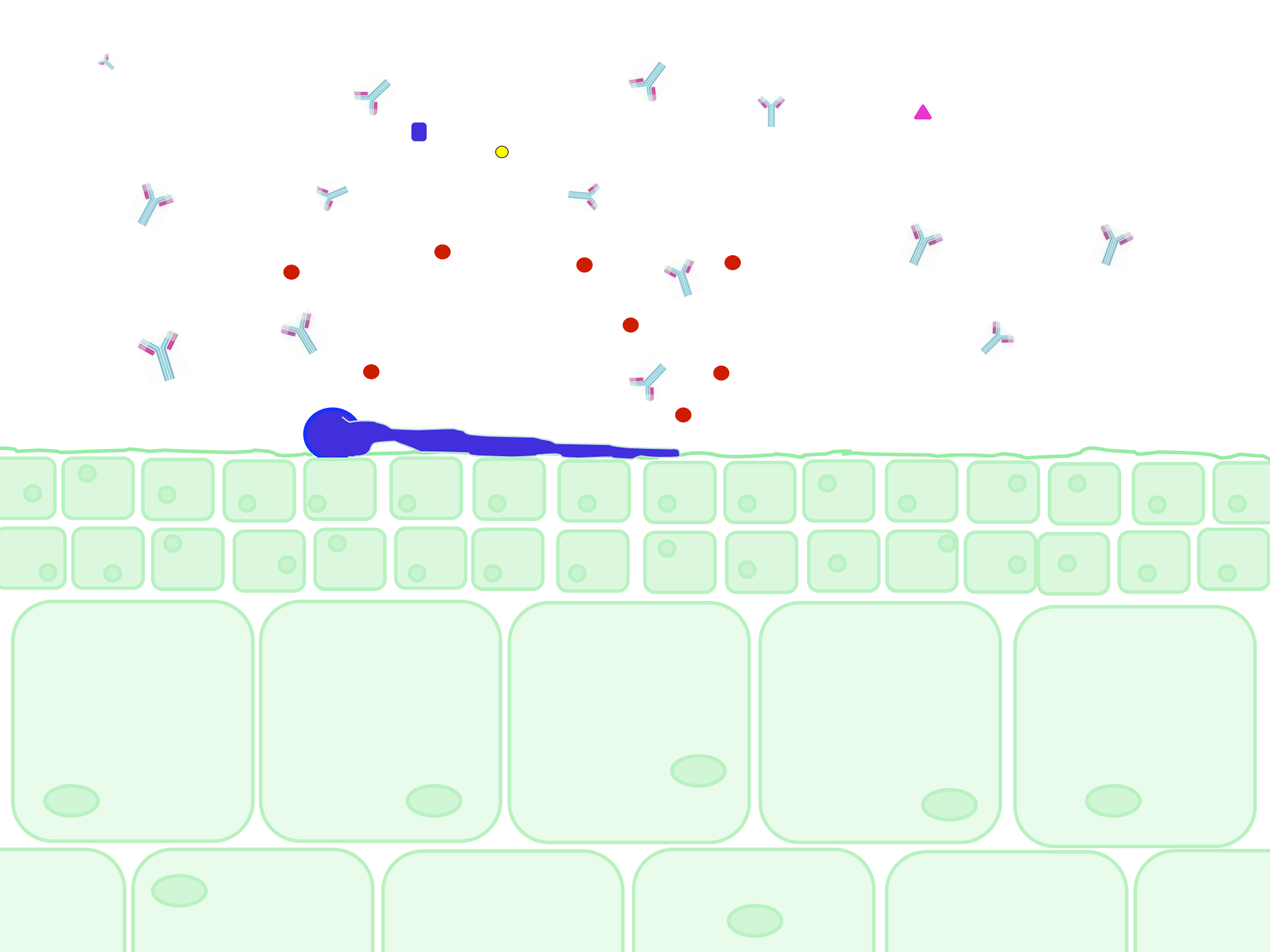


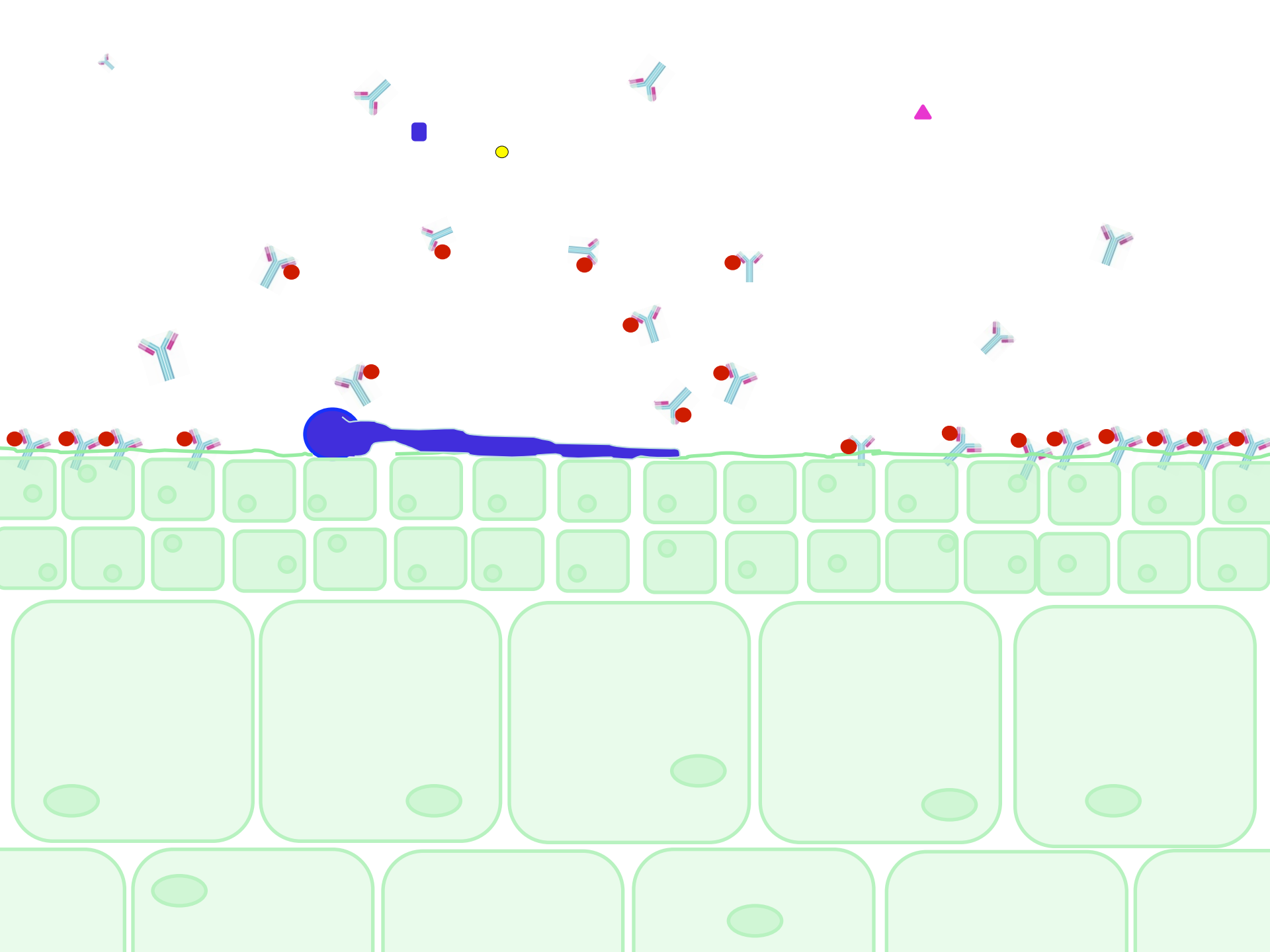




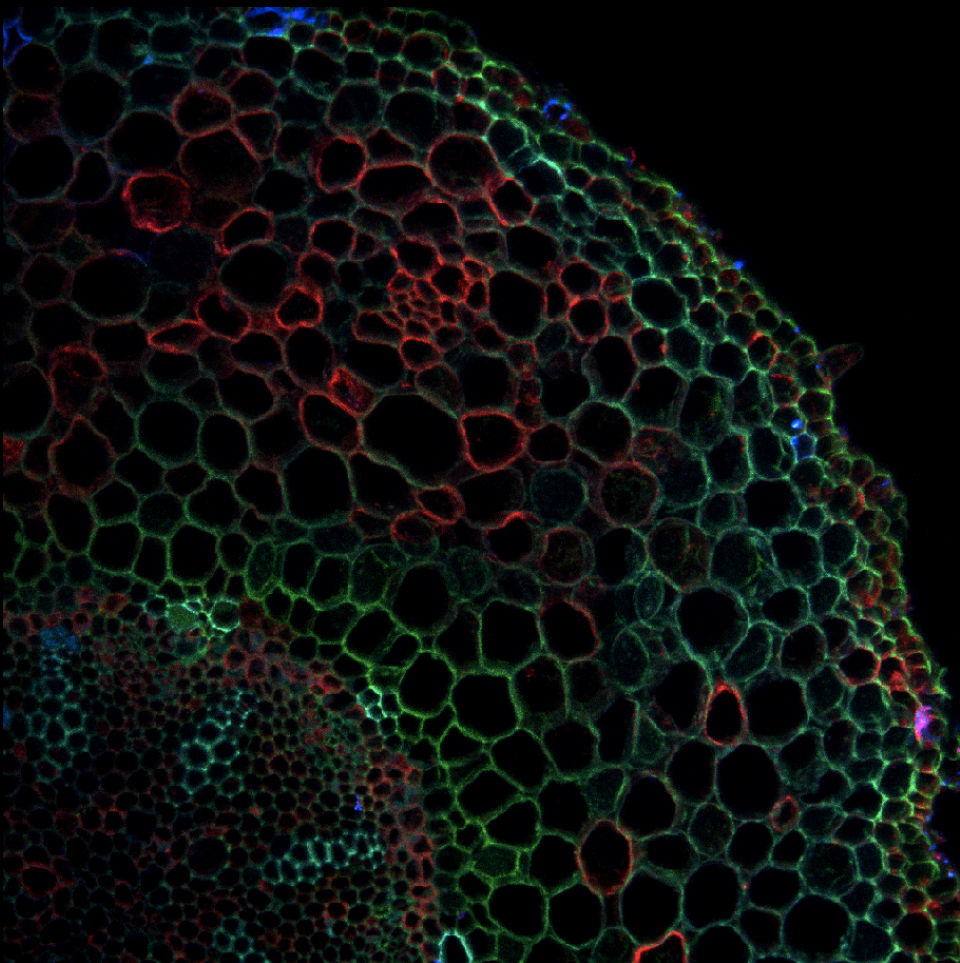




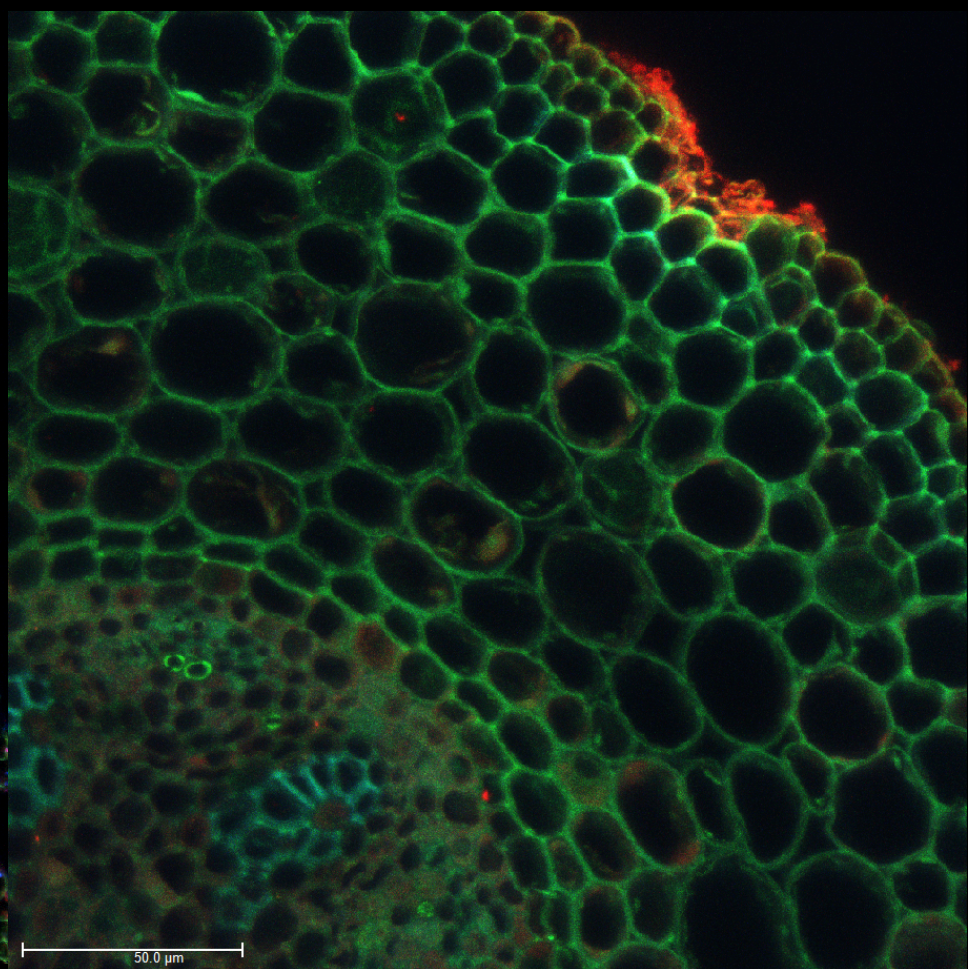




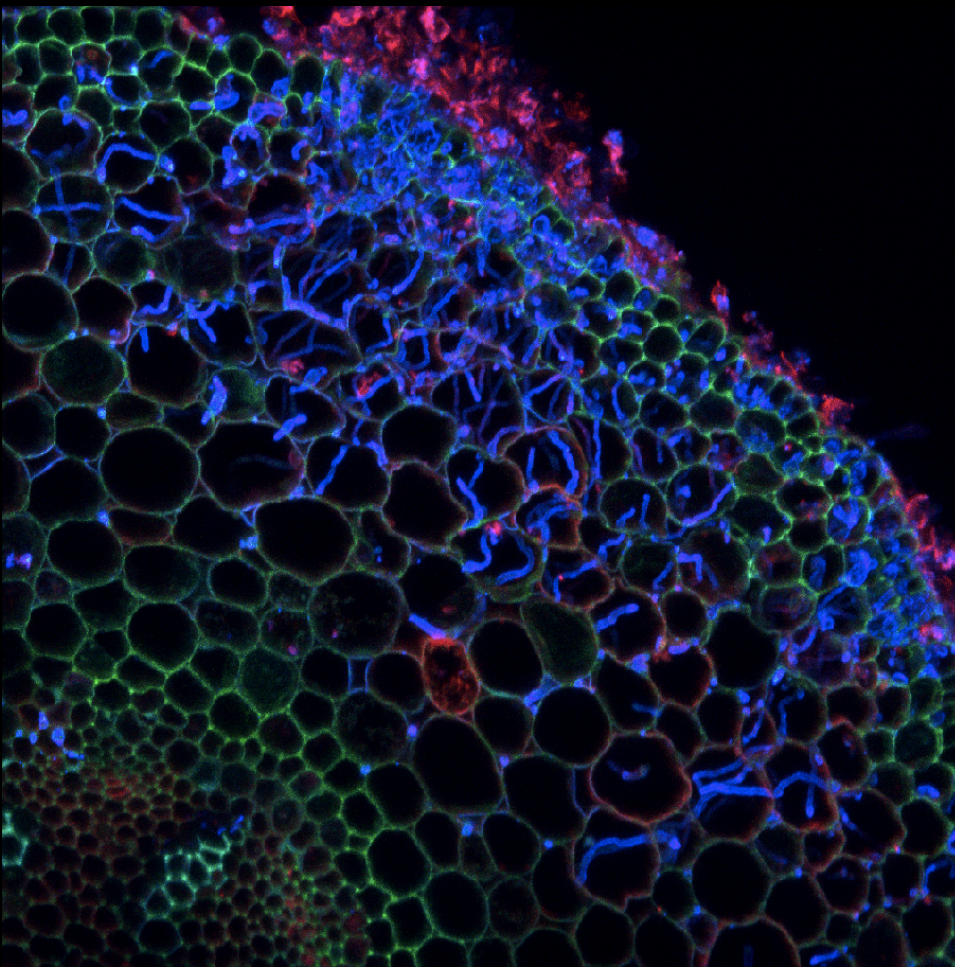
12h



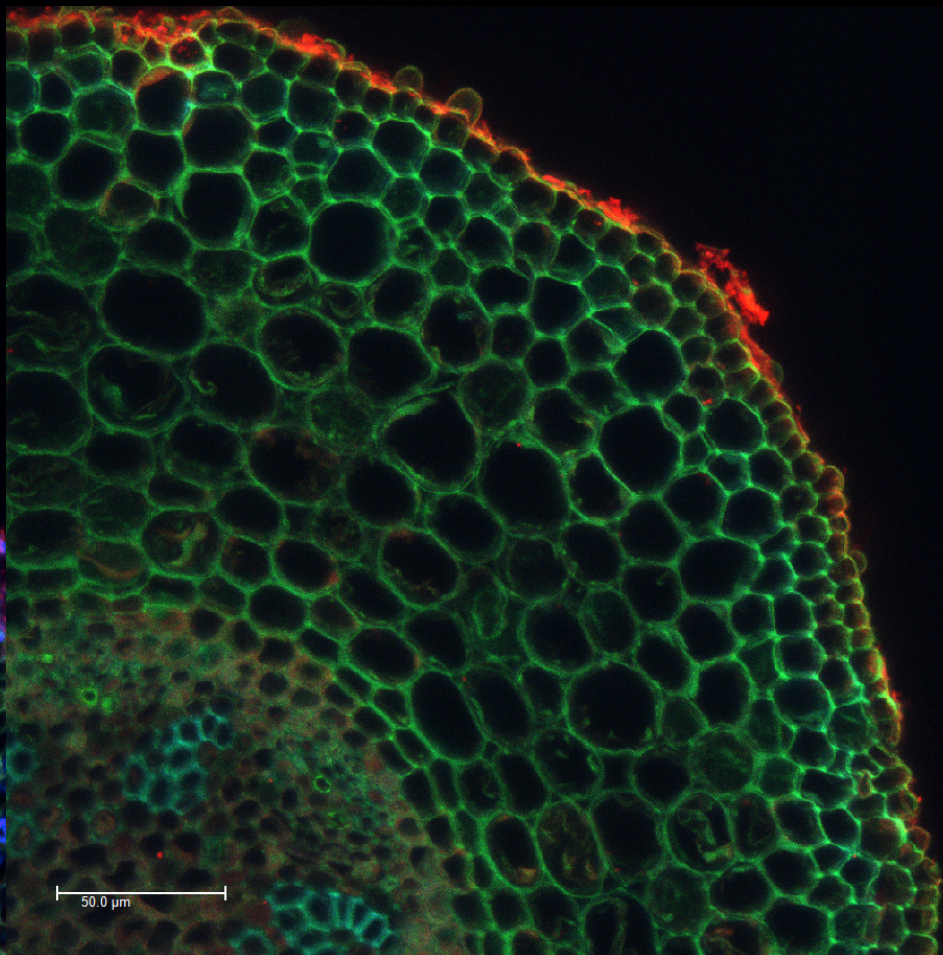
12h + Antibody



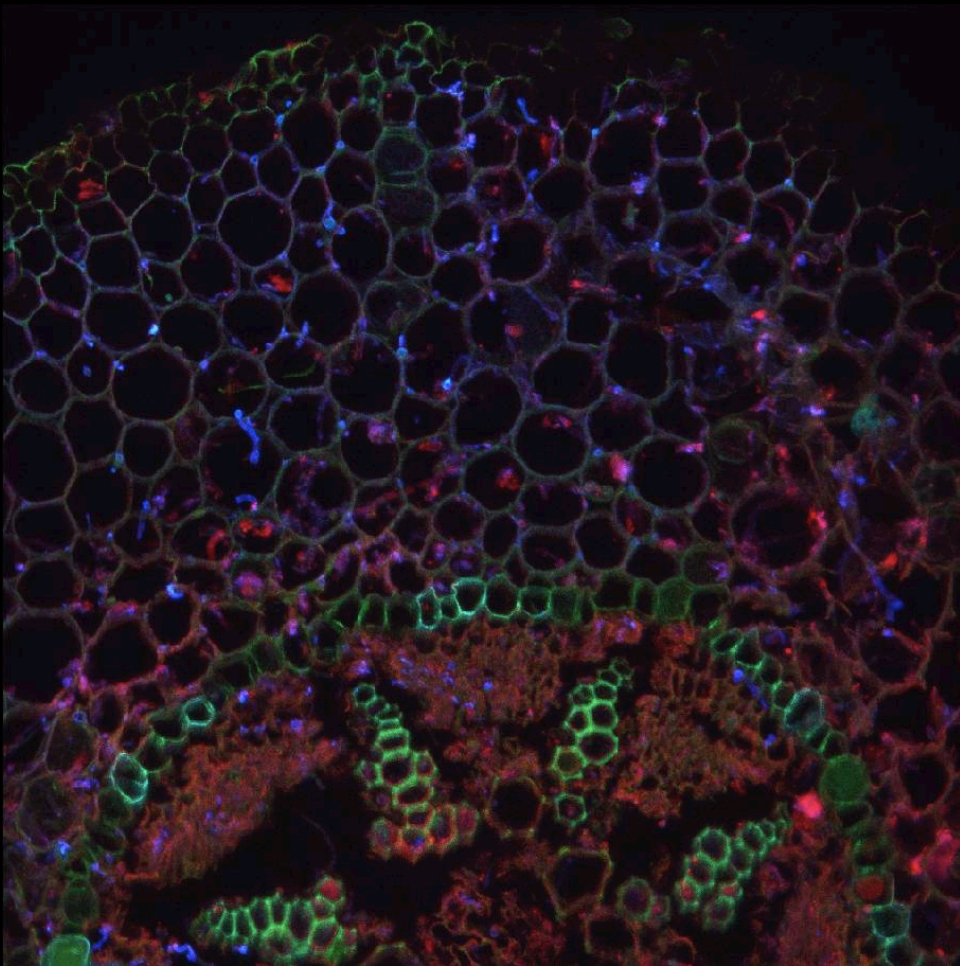
24h



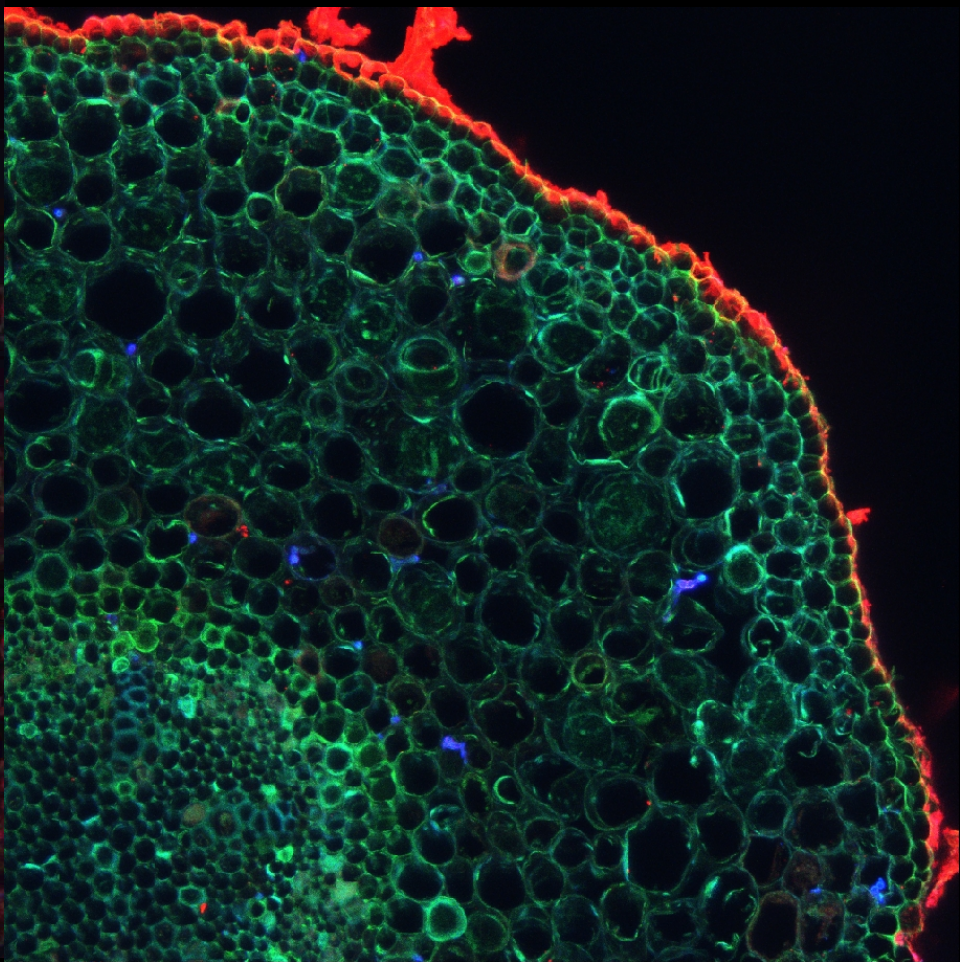
24h + Antibody



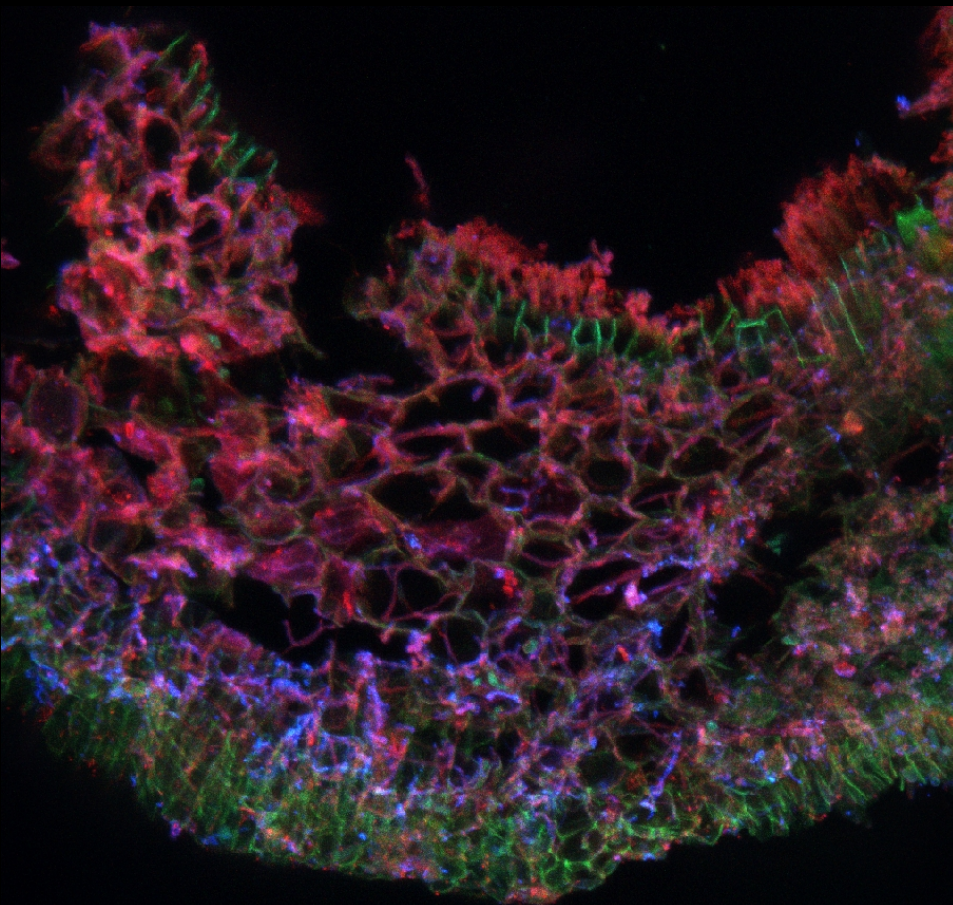
96h



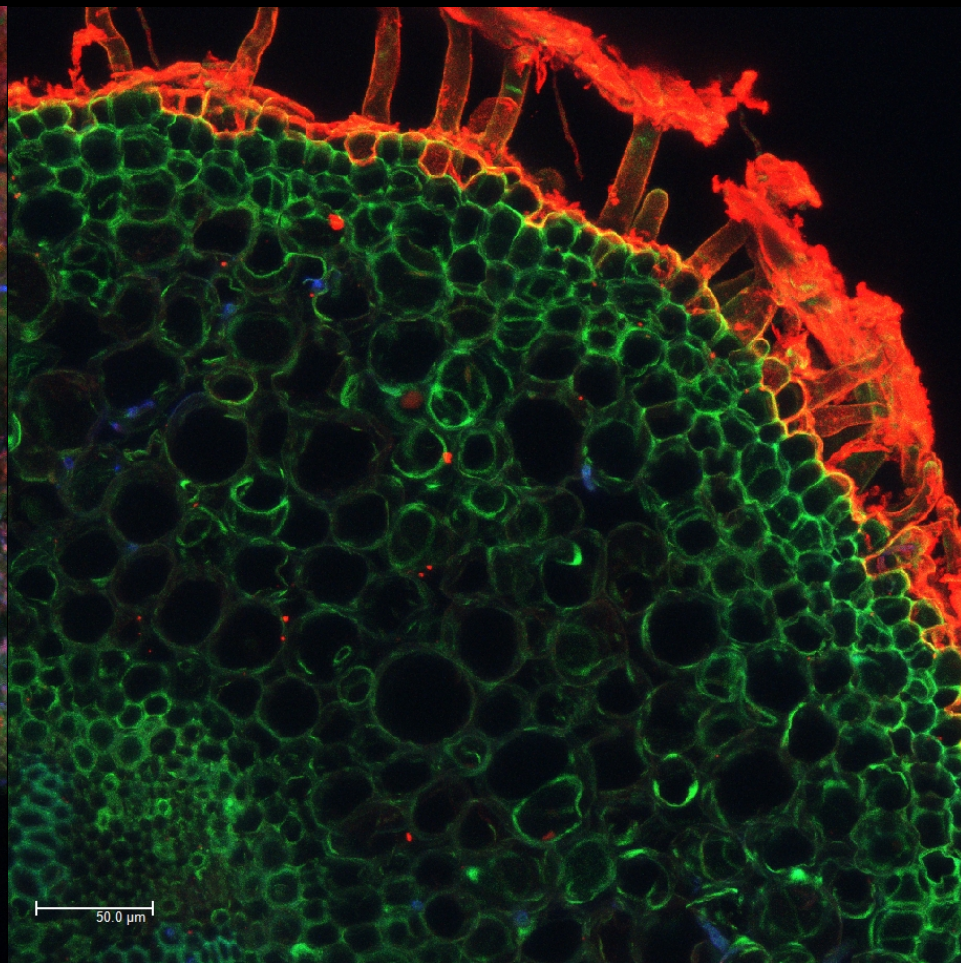
96h + Antibody



192h



192h + Antibody



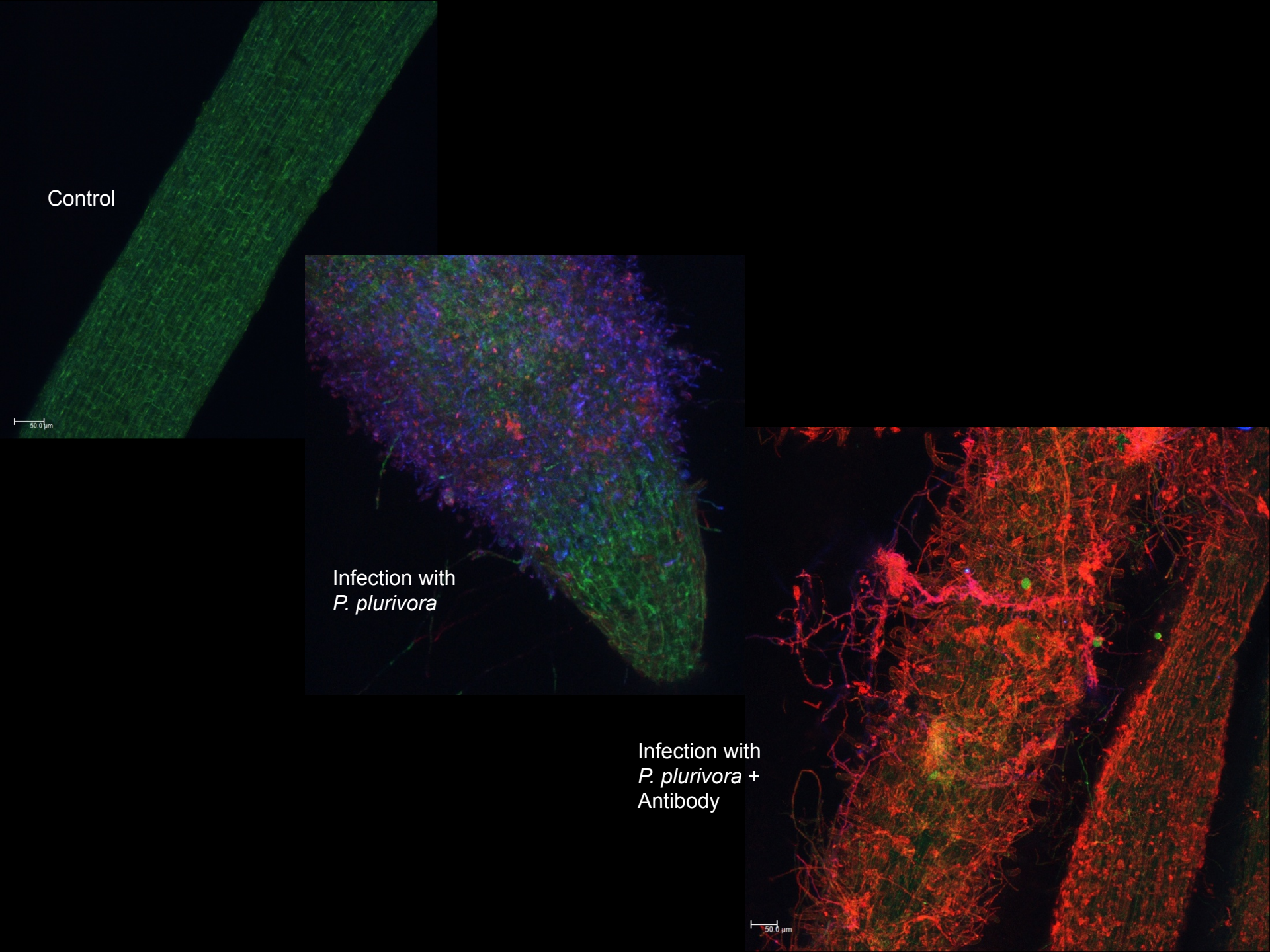
Control

50.0 μ m

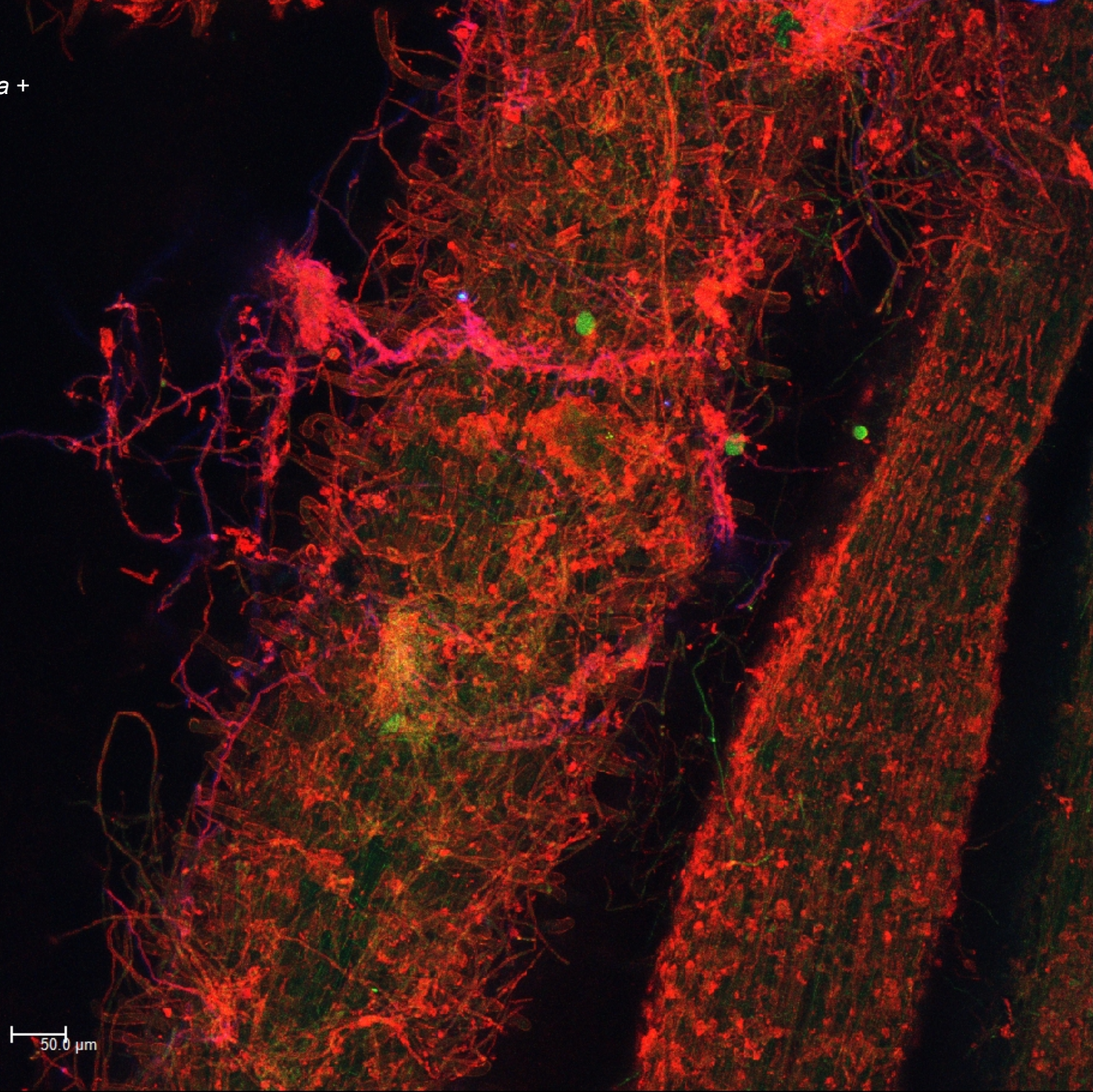
Infection with
P. plurivora

Infection with
P. plurivora +
Antibody

50.0 μ m



96 h *P. plurivora* +
antibody



50.0 μm

Absence of α -plurivirin – resistant interaction



Presence of α -plurivirin – susceptible interaction

Co-evolution (Arms- race)

