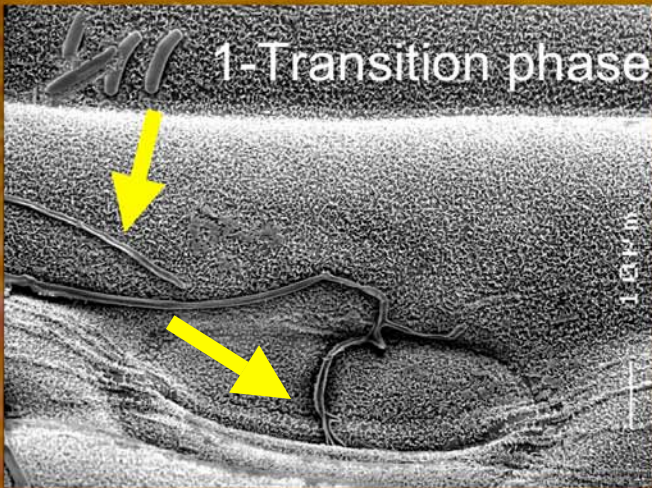


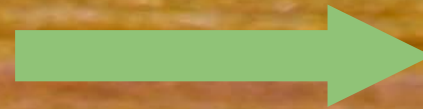


Genes controlling the infection process
the septoria tritici blotch pathogen
Mycosphaerella graminicola

Rahim Mehrabi



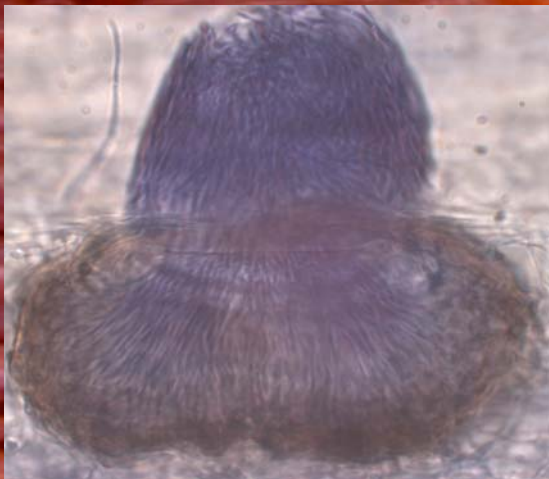
2-Penetration



3-Colonization

Biotrophic

Necrotrophic

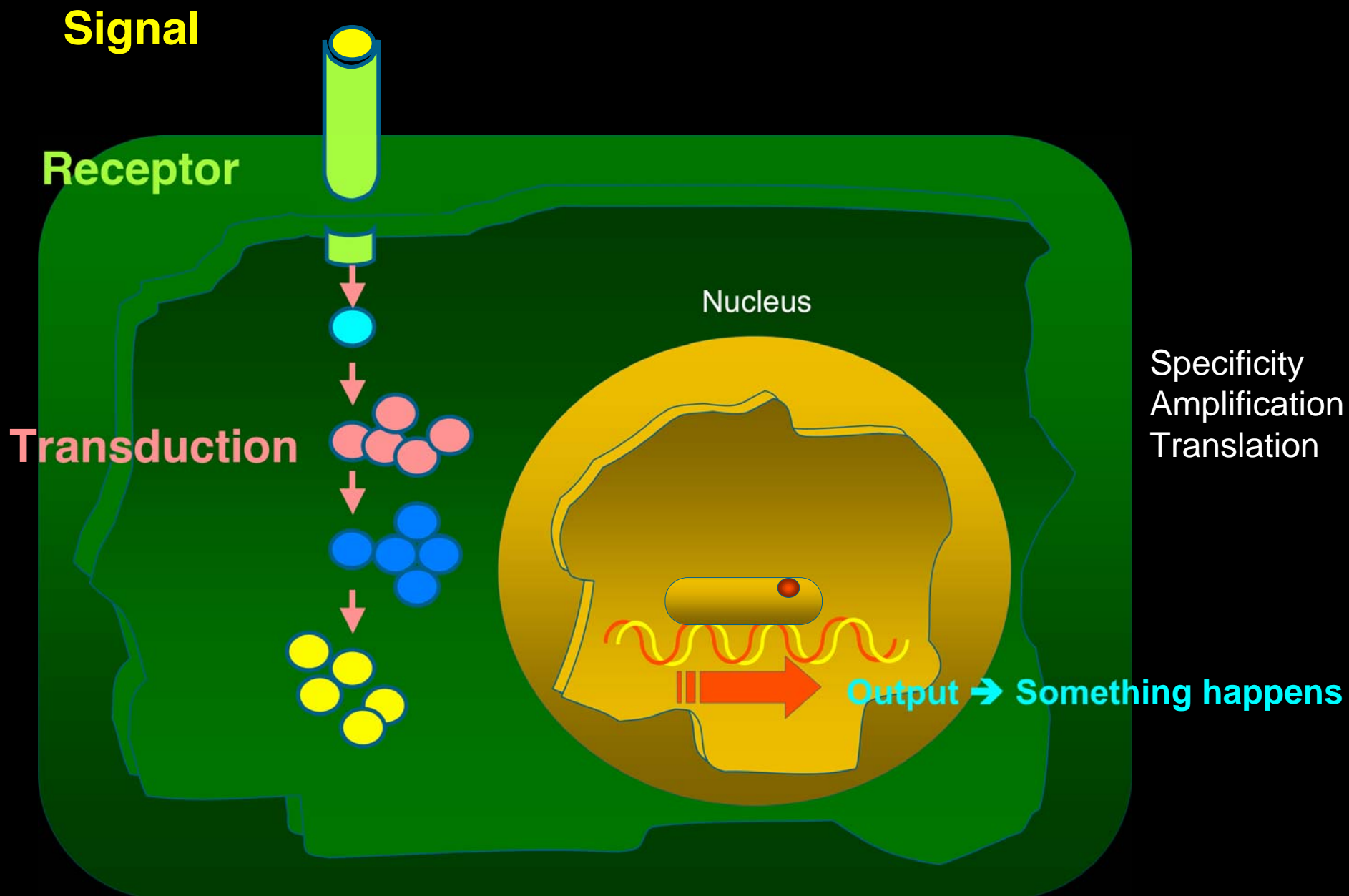


5-Pycnidia maturation



4-Pycnidia formation

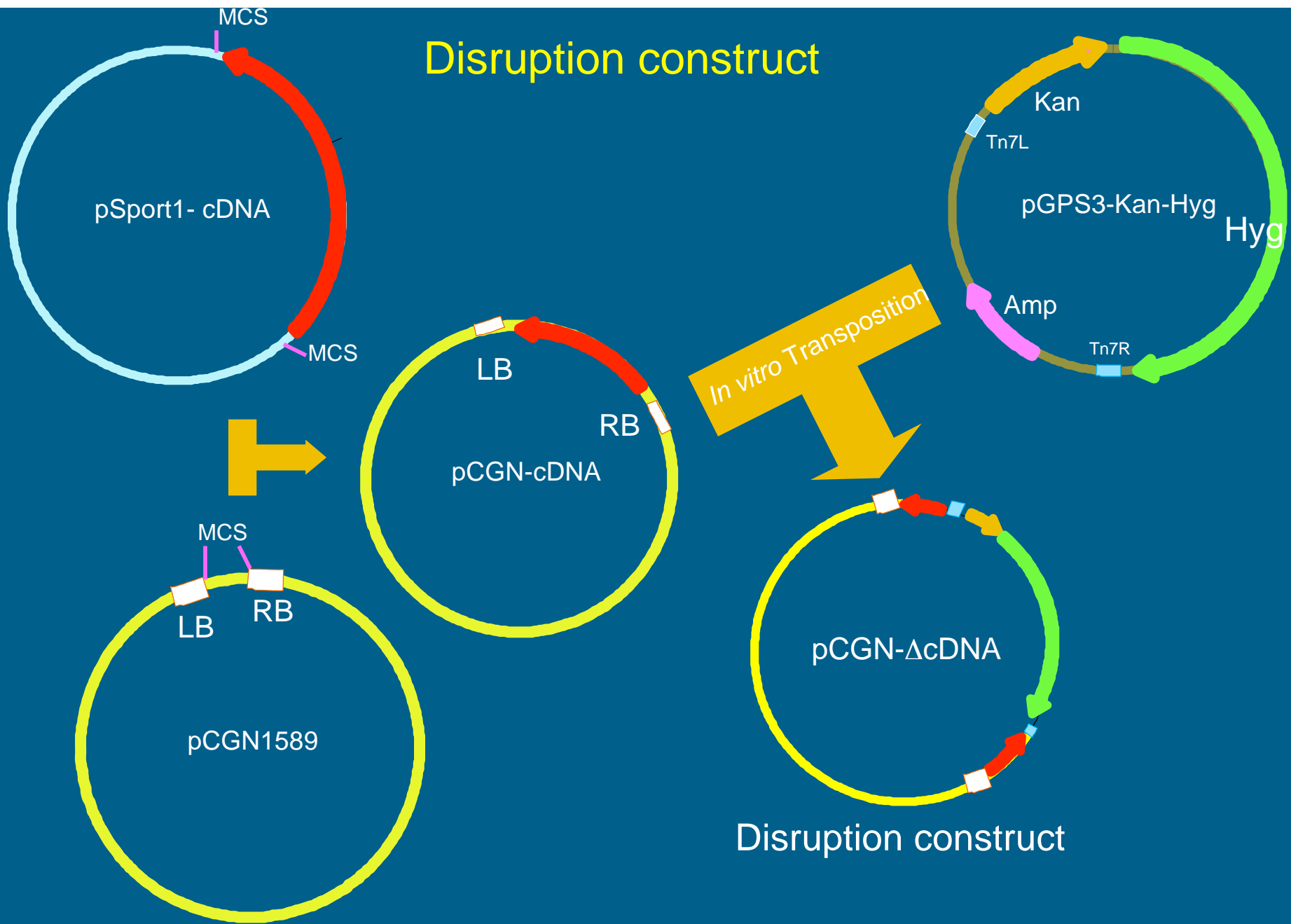
Signaling pathways



Methodology

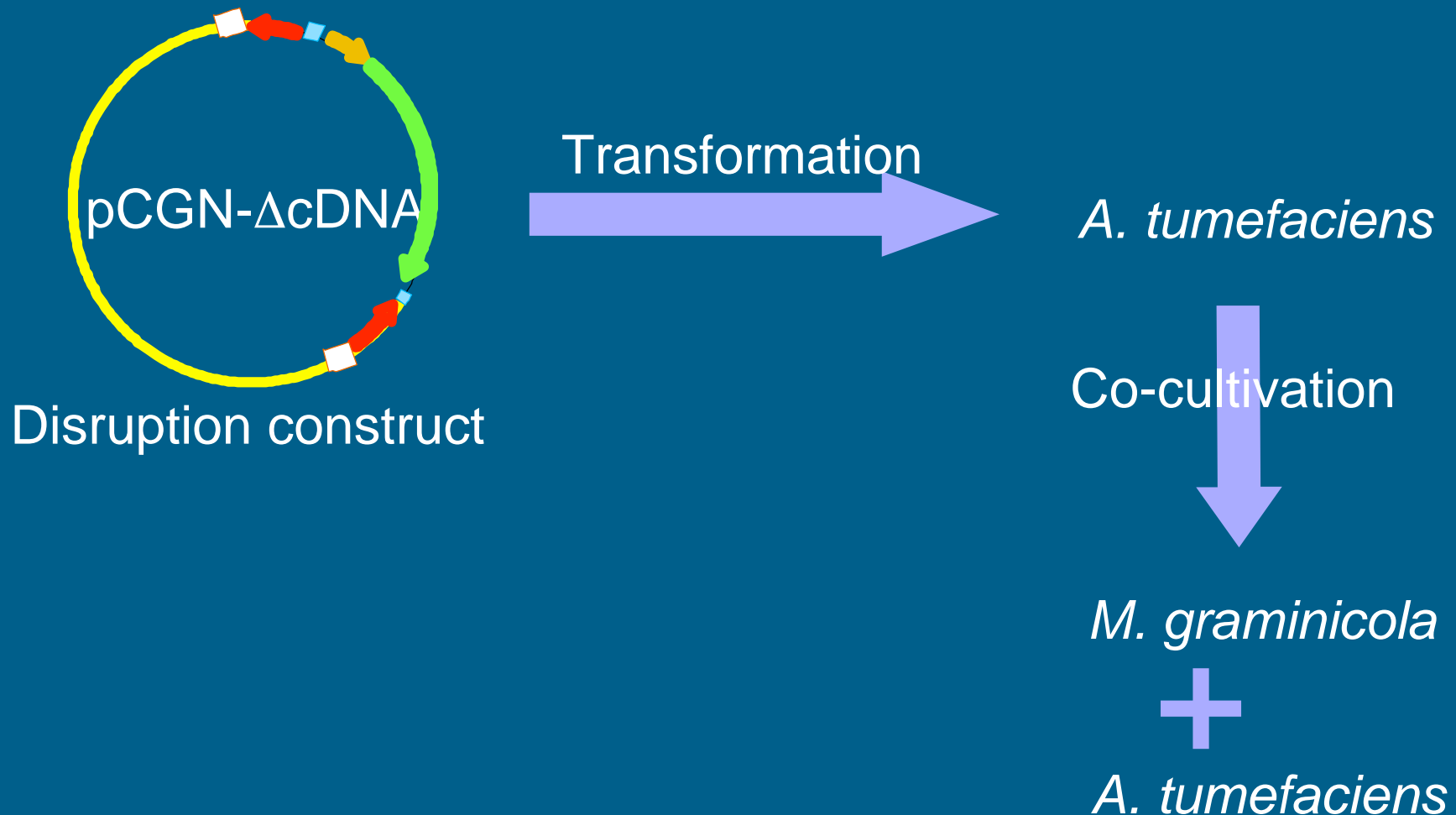
- Identify targets
 - EST libraries
 - 30,000 ESTs (11000 unigenes)
 - >40 genes implicated in signal transduction pathways
- Targeted gene disruption
 - Disruption construct
 - *Agrobacterium tumefaciens*-mediated transformation
- Functional analyses

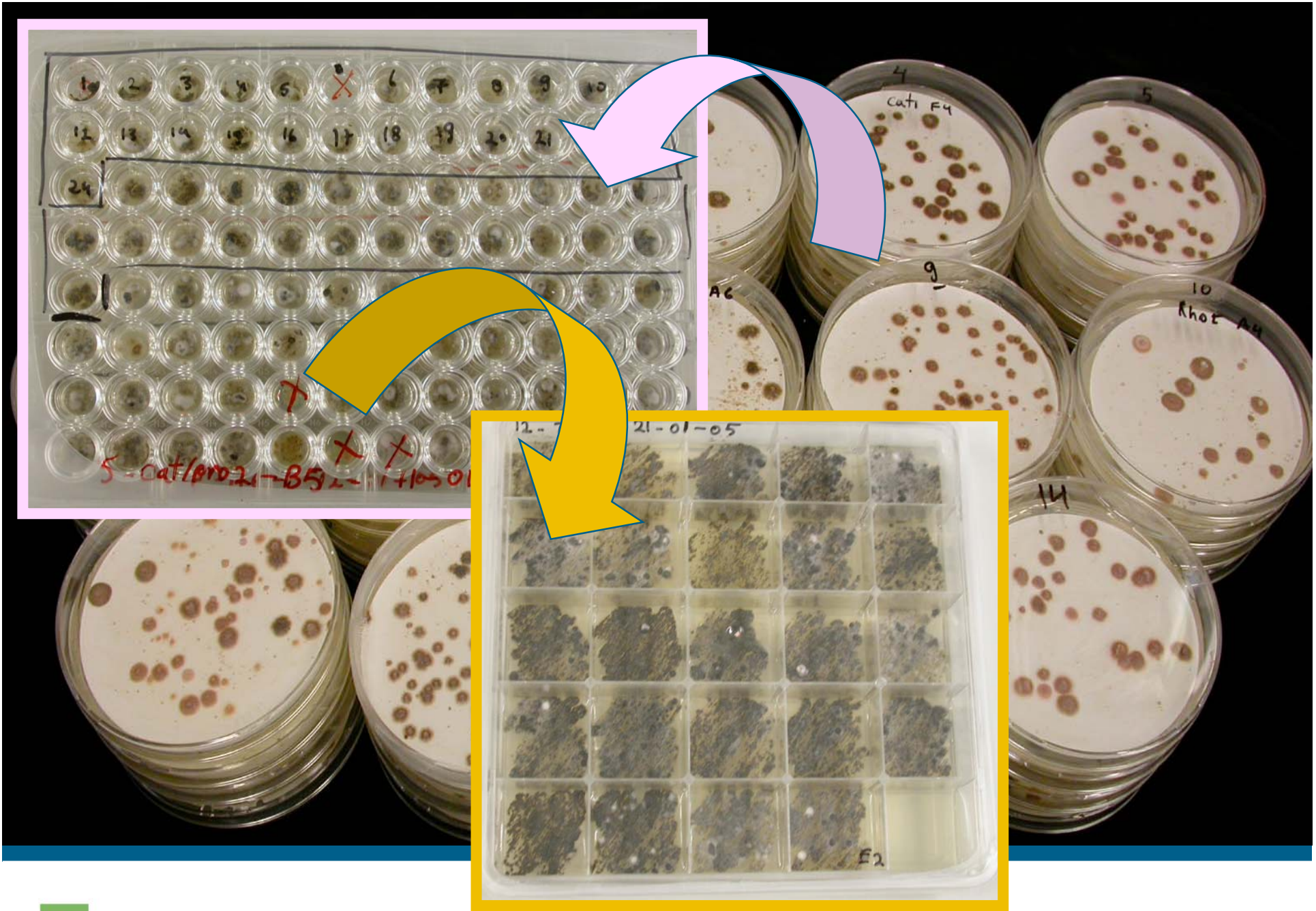
Disruption construct



Disruption construct

Agrobacterium tumefaciens-mediated transformation





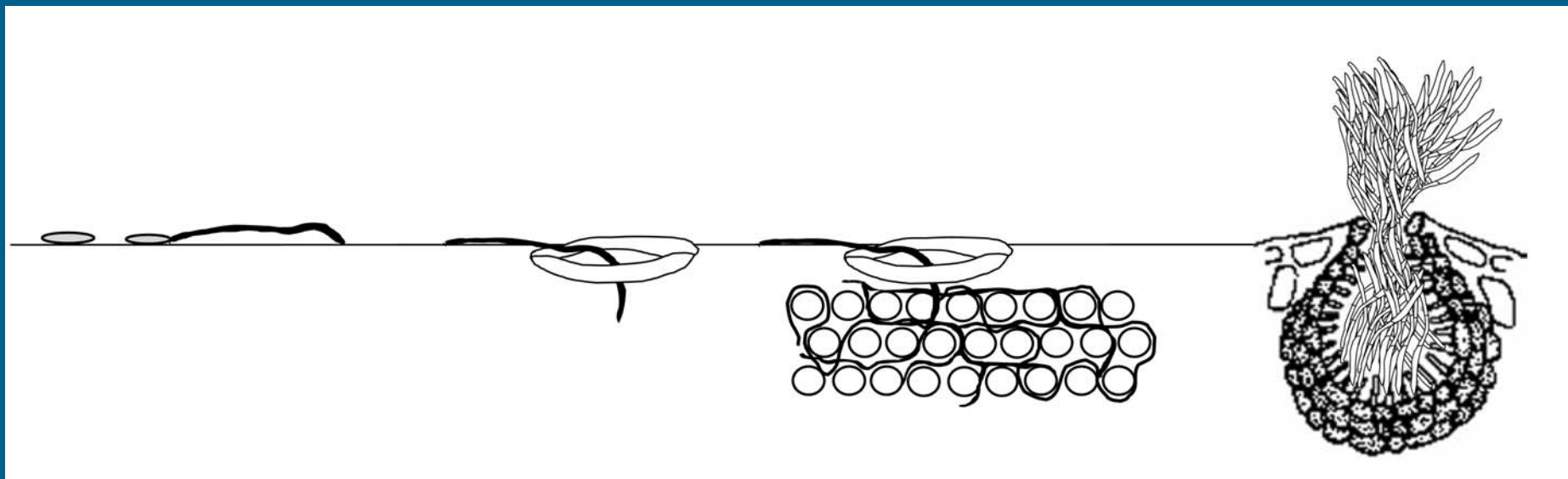
Infection Process

1- Transition

2- Penetration

3- Colonization

4- Fructification



Receptor

Sln1

Sho1

small
GTPase

Ypd1

Ste20

protein
kinase

Ssk1

Ste50

MAP3K

Ssk2,22

Ste11

MAP2K

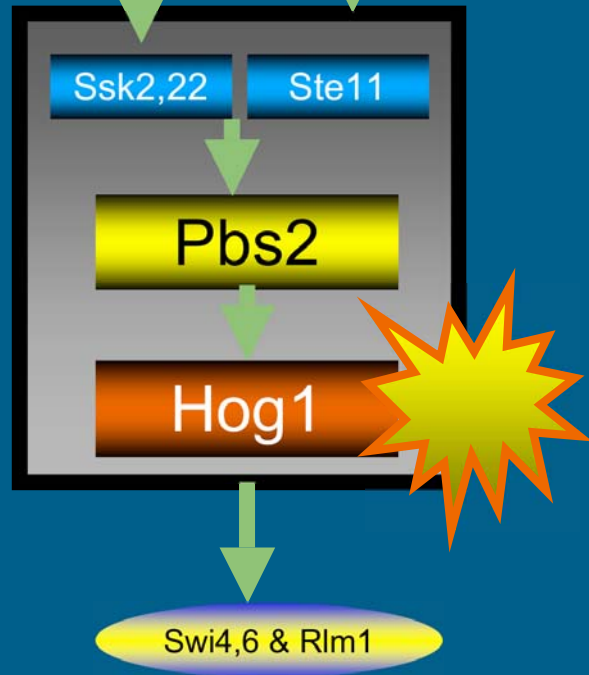
Pbs2

MAPK

Hog1

TF

Swi4,6 & Rlm1



Phenotype

IPO323 (WT) Δ MgHog1-E1 Δ MgHog1-2 Δ MgHog1-5

Osmosensitive



Resistant to fungicide

Fludioxonil (>30x)

Fenpiclonil (> 30x)

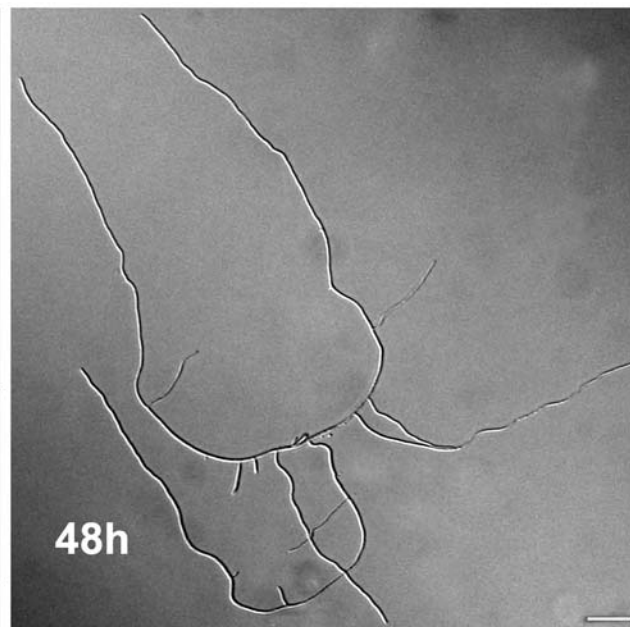
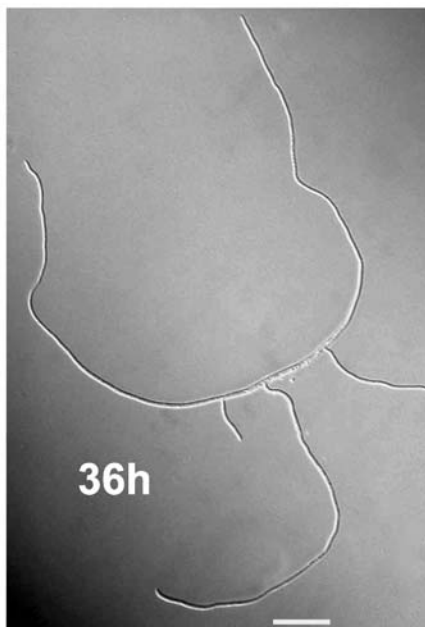
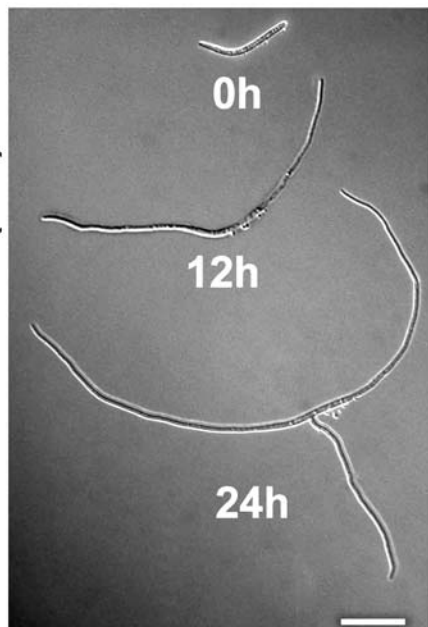
Iprodione (>5x)



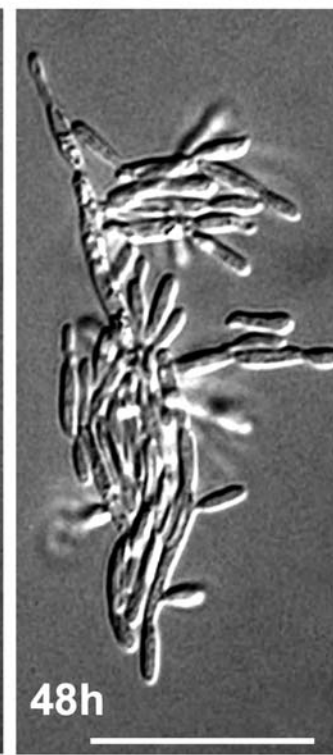
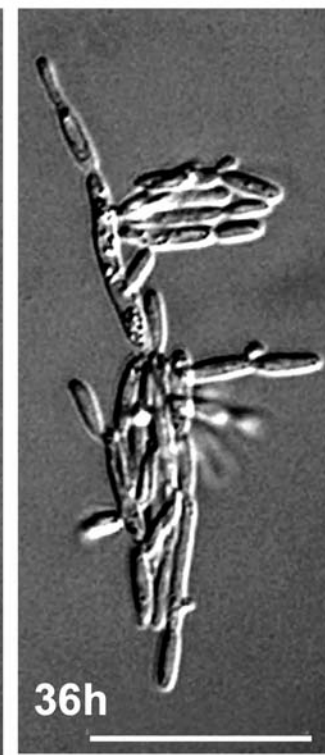
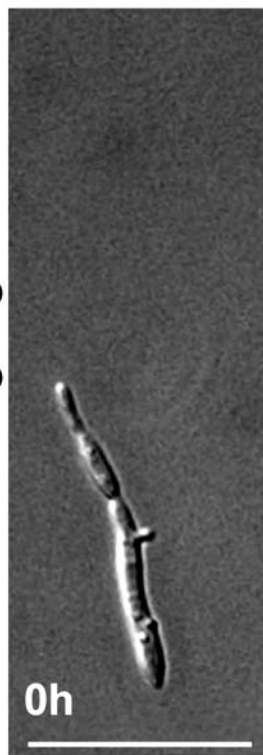
Non-melanized
yeast like growth

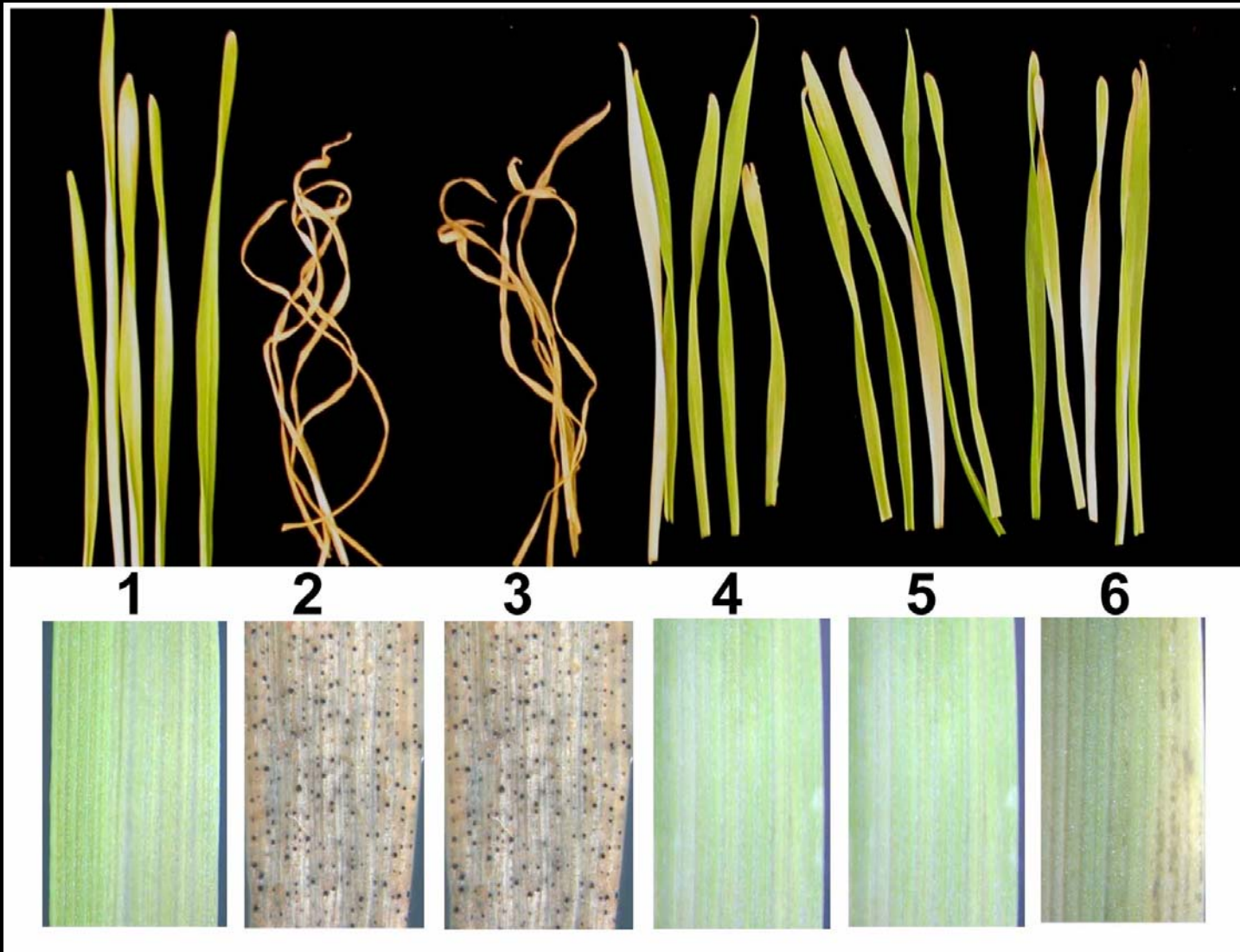


IPO323 (WT)



Δ MgHog1-5

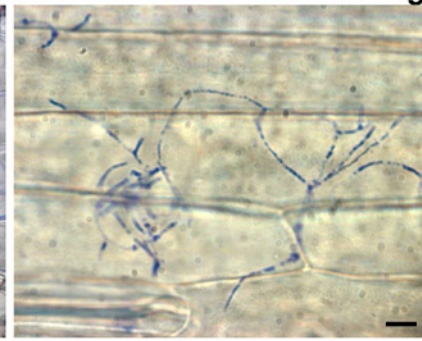
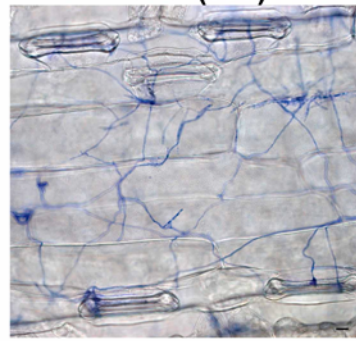




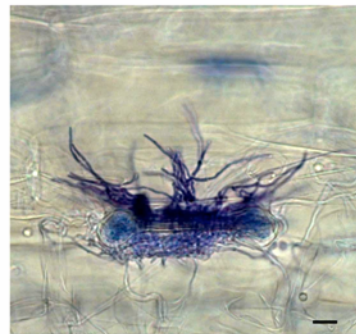
WT

Mghog1

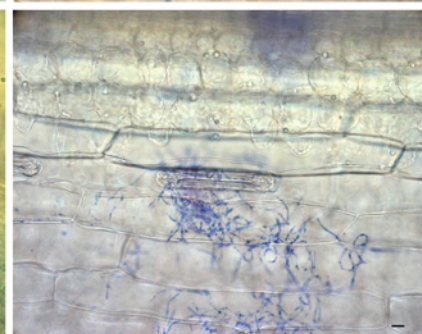
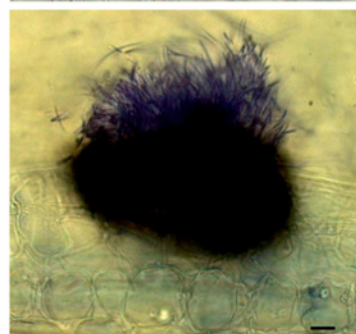
8dpi



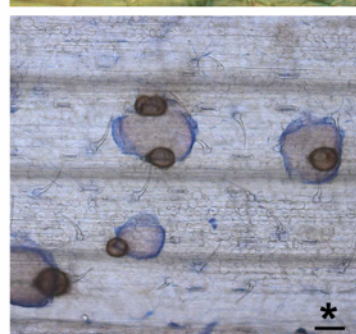
12dpi



16dpi



20dpi



Conclusion (biological function of *MgHog1*)

- Involvement in osmo-stress growth
- Fungicide resistance through interference with the MgHOG1
- Regulation of dimorphic switch
- Virulence factor



Dimorphic switch → Penetration → Colonization → Fructification

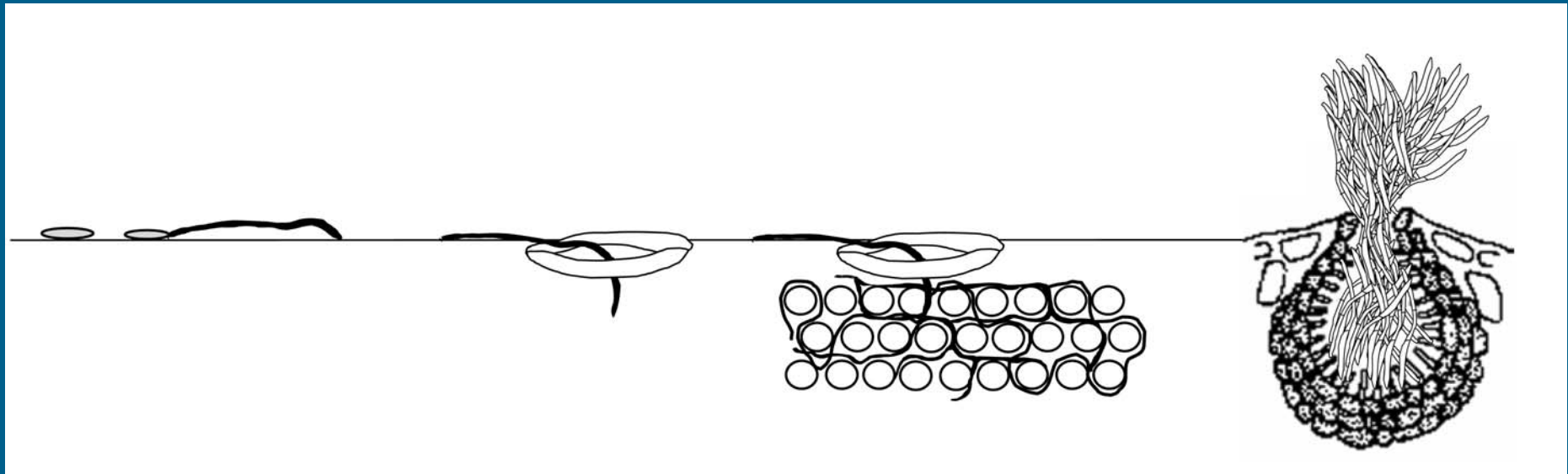
Infection Process

1- Transition

2- Penetration

3- Colonization

4- Fructification



Receptor

Ste2/Ste3

Gp ($\alpha\beta\gamma$)

G α 1

Ste18

Ste4

MAP4K

Ste20/50

MAP3K

Ste11

MAP2K

Ste7

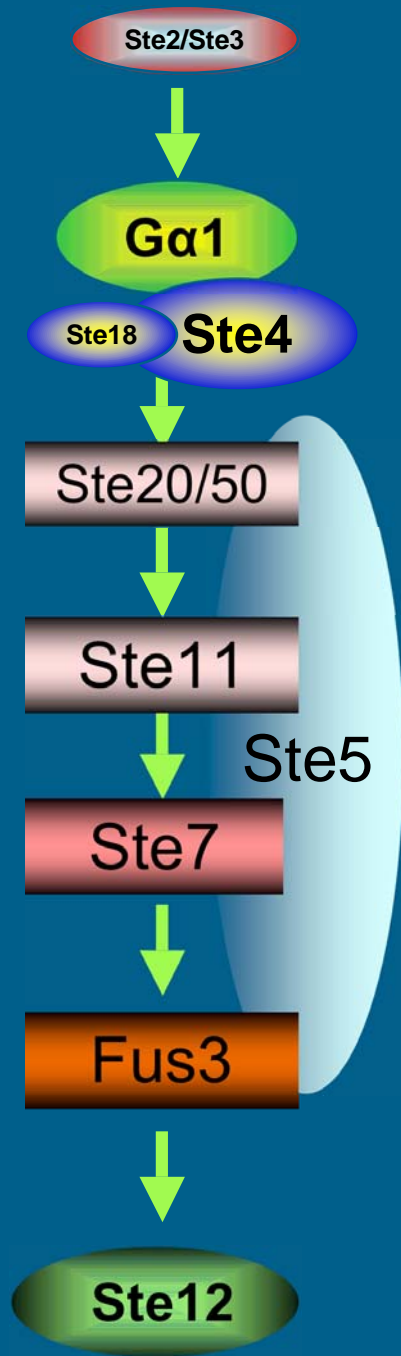
Ste5

MAPK

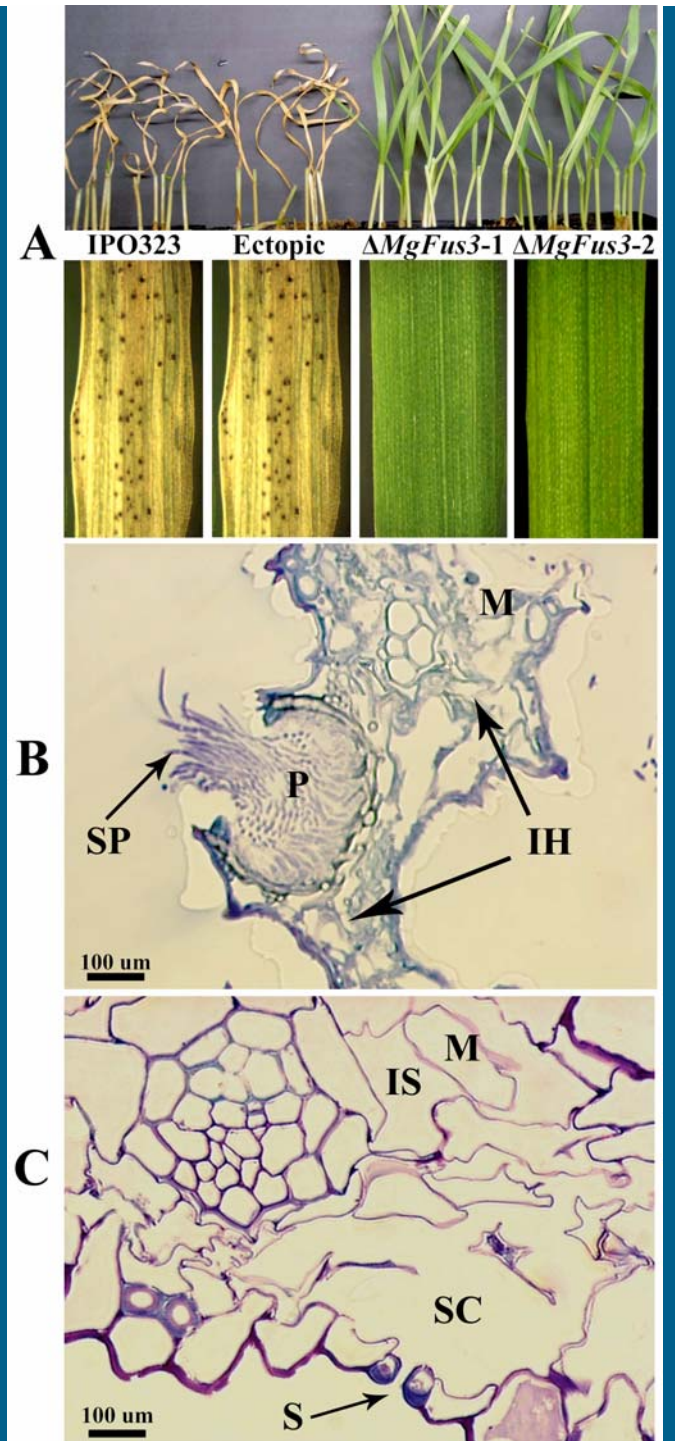
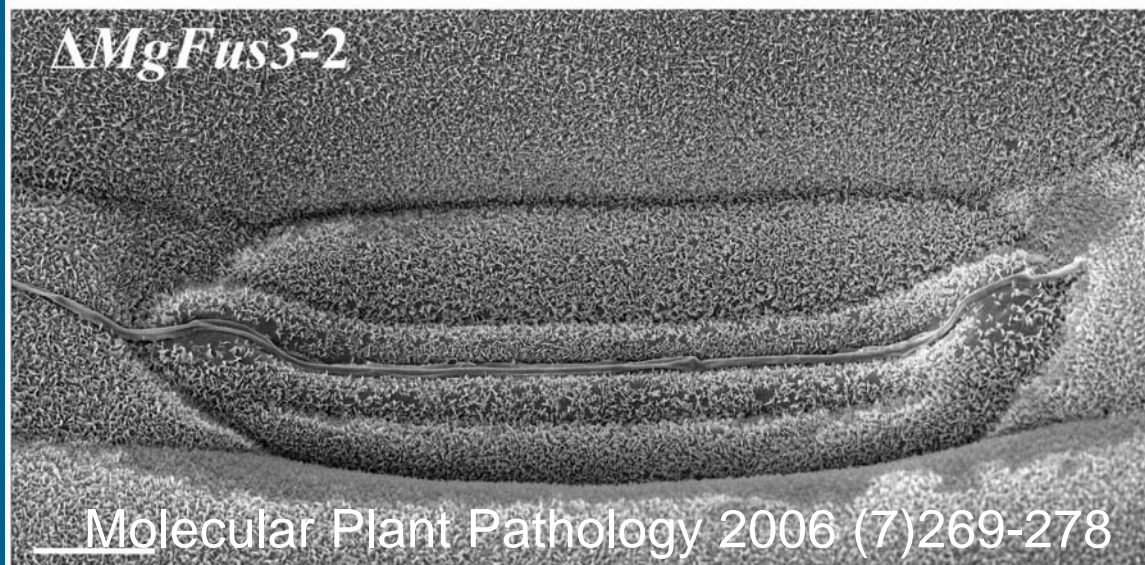
Fus3

TF

Ste12



MgFus3 disruptants are unable to penetrate stomata



Conclusion (biological function of *MgFus3*)

- No role in dimorphic switch
- Regulation of early stage of infection, perception of the host tissue, stomatal penetration
- Probably MgFUS3 have other downstream effector(s) rather than MgSTE12



Dimorphic switch → Penetration → Colonization → Fructification

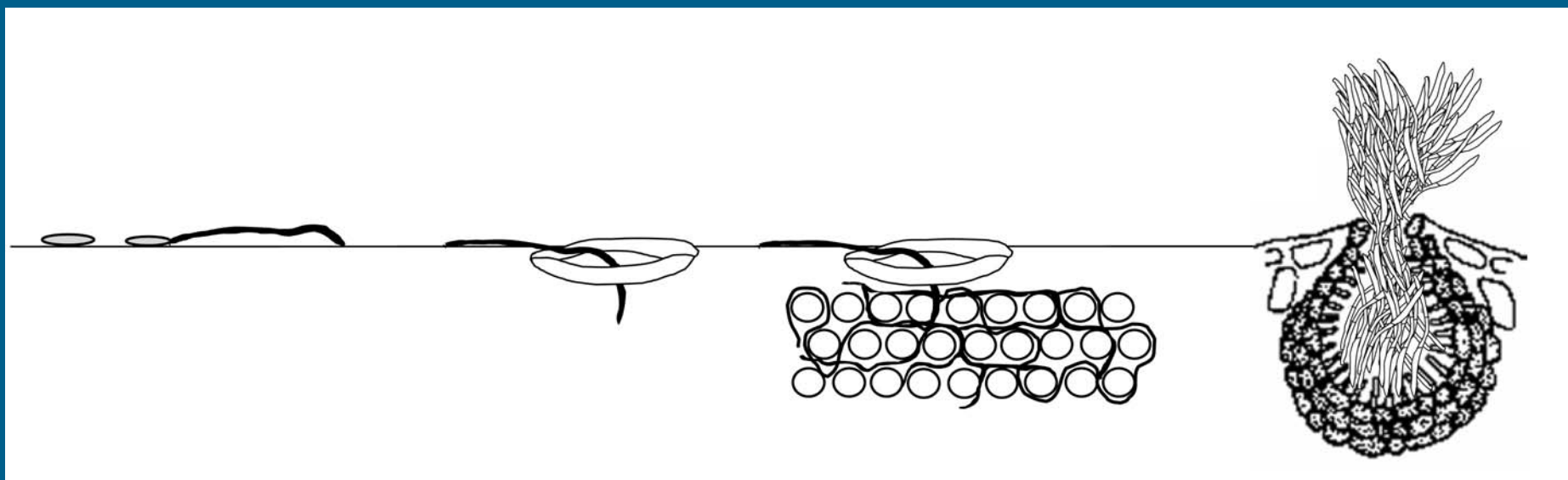
Infection Process

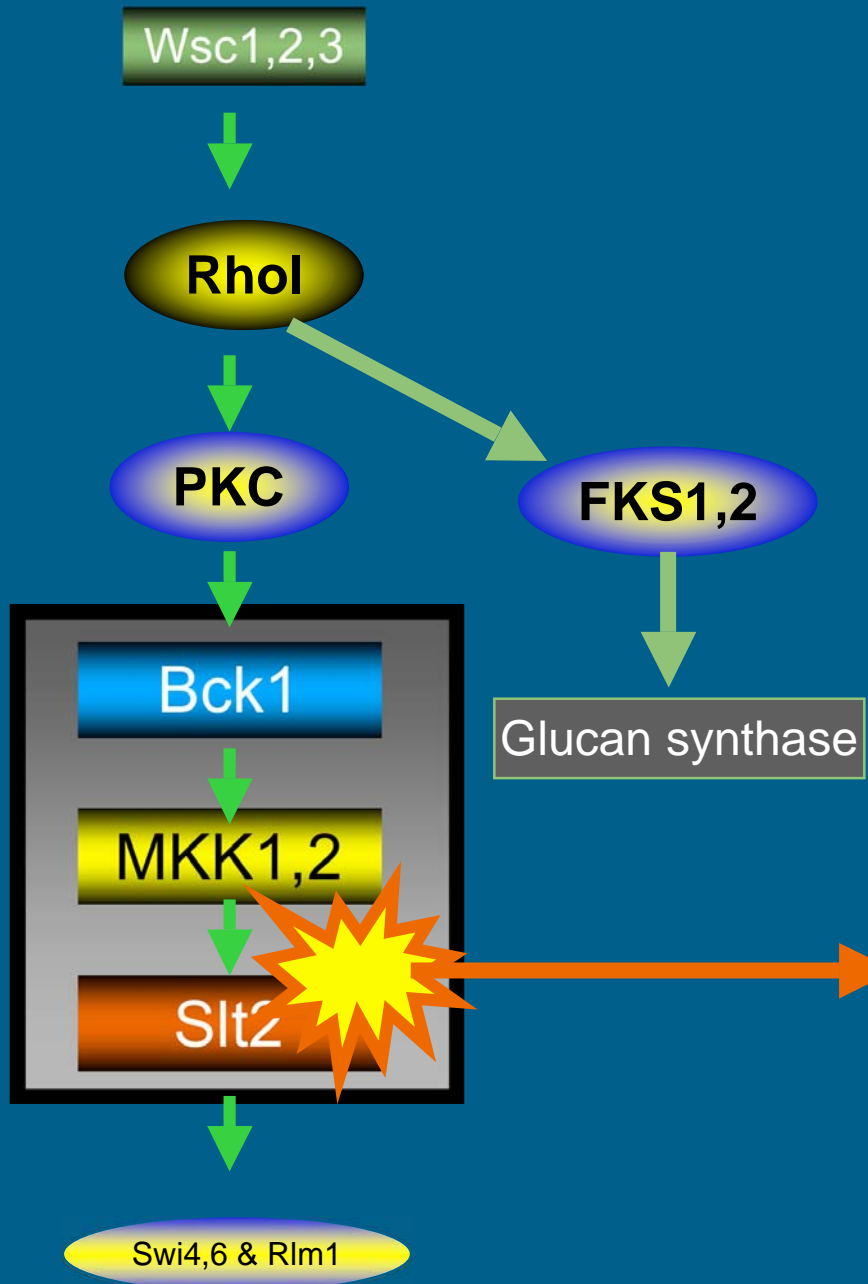
1- Transition

2- Penetration

3- Colonization

4- Fructification



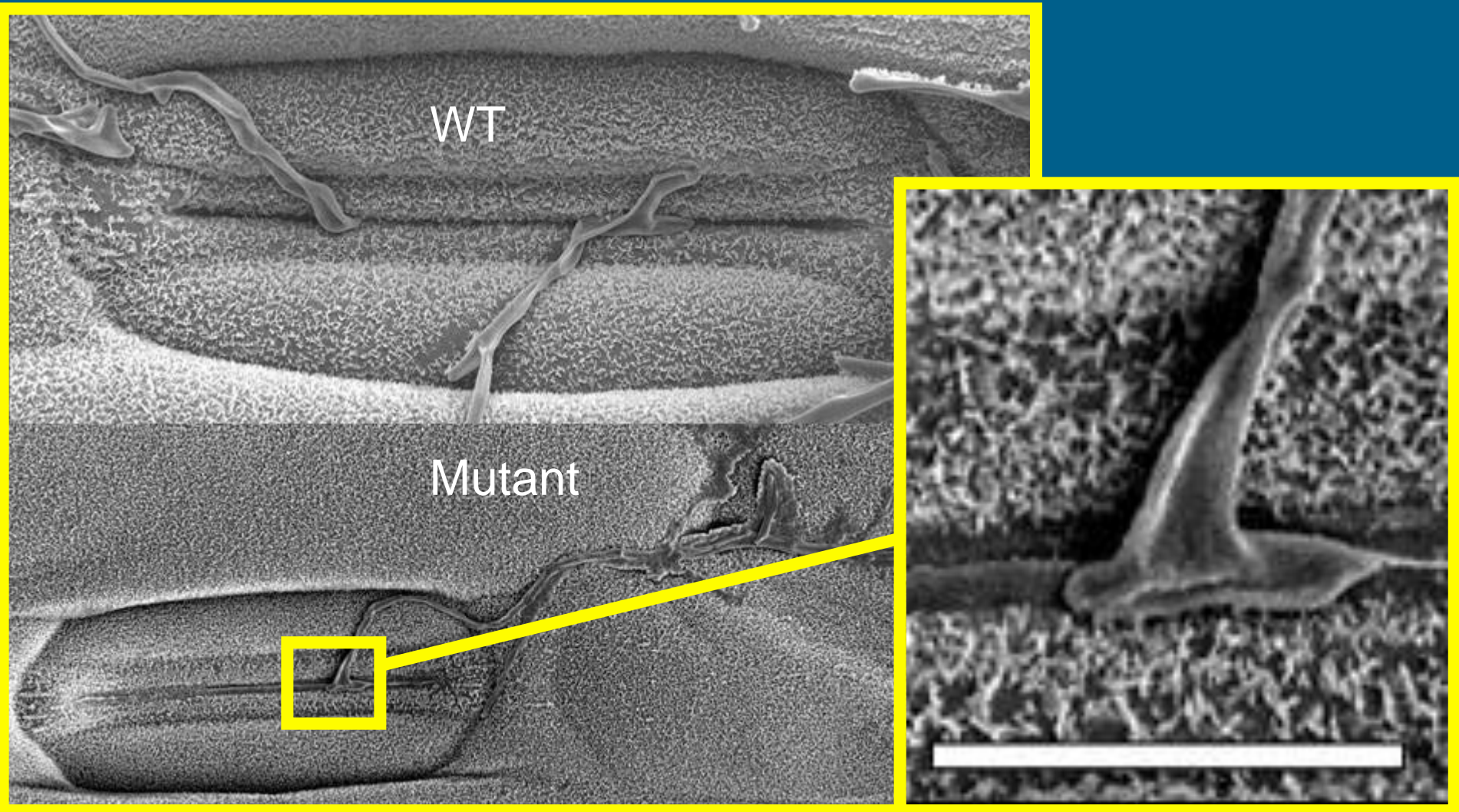


WT

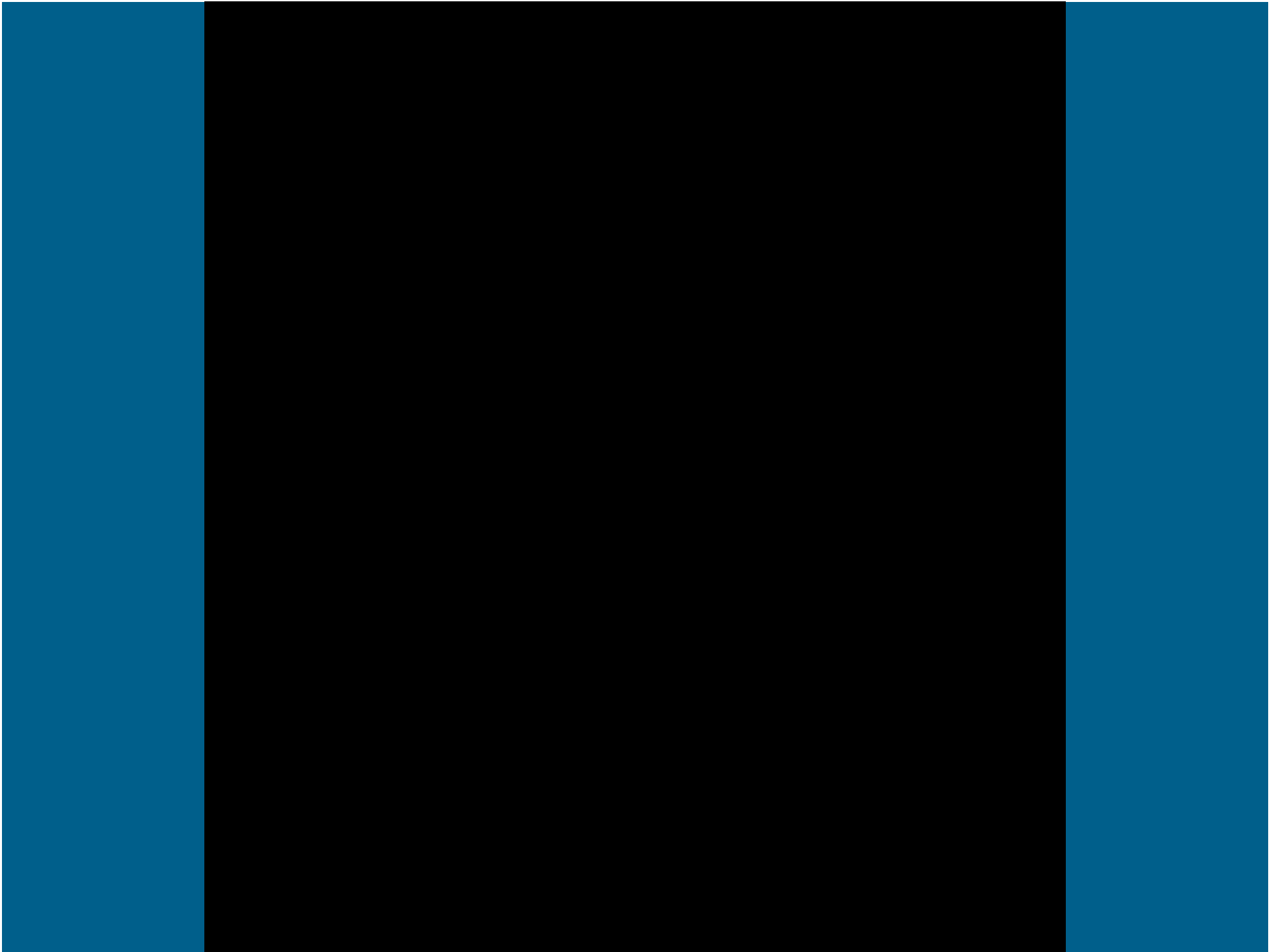
Ectopic

Mutants

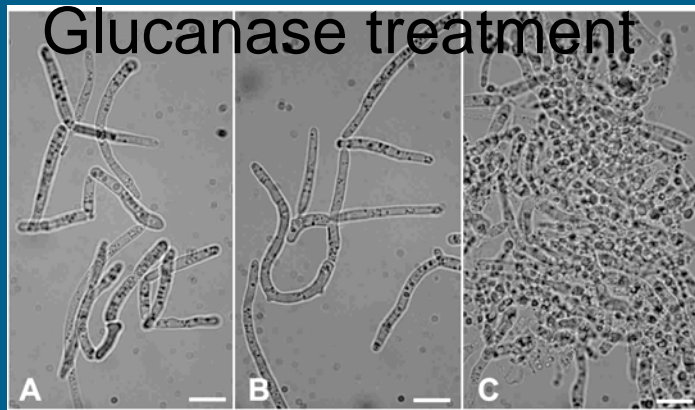
MgSlt2 mutants show attempts of penetration similar to the WT



Scanning electronic microscopy images of infected wheat leaves 72 h postinoculation



MgSlt2 is involved in cell wall strengthening and protects the cells from toxic compounds



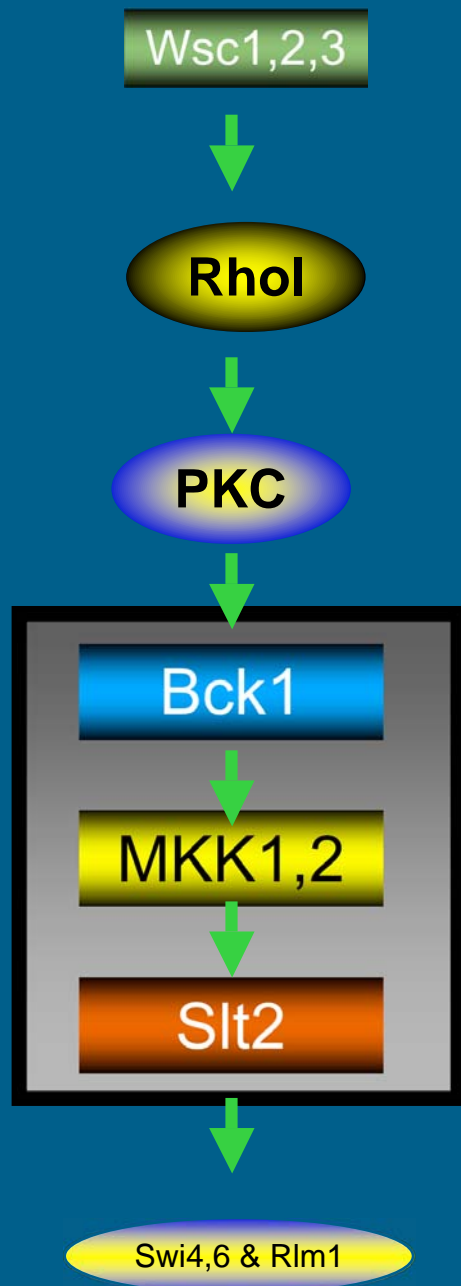
Compounds	MIC ($\mu\text{g.ml}^{-1}$)		Q value
	IPO323 ^a	IPO323 Δ MgSlt2 ^b	
Antibiotics			
Cycloheximide	500	500	1
Fungicides			
Kresoxim-methyl	>0.25	>0.25	1
Fenpiclonil	2.5	2.5	1
Trifloxim	> 0.05	> 0.05	1
Miconazole	0.025	0.005	2
Bifonazole	0.1	< 0.025	>4
Imazalil	0.5	0.1	5
Cyproconazole	0.5	0.05	10
Plant metabolites			
Berberine	>500	>500	1
Camptothecin	>500	>500	1
Other			
Rhodamine 6G	25	25	1

Conclusion (biological function of *MgSlt2*)

- Cell wall strengthening
- Dispensable for germination and penetration
- Required for colonization of mesophyll tissue
- The attenuated pathogenicity of *MgSlt2* mutants is probably due to an increased sensitivity to hitherto unknown plant defense compounds

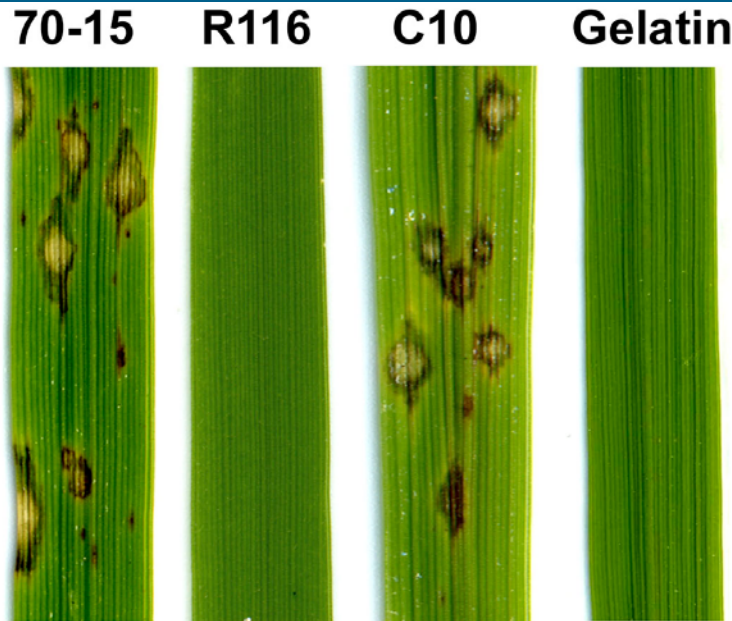


Dimorphic switch → Penetration → Colonization → Fructification



The *mig1* mutants of *Magnaporthe grisea* are non-pathogenic

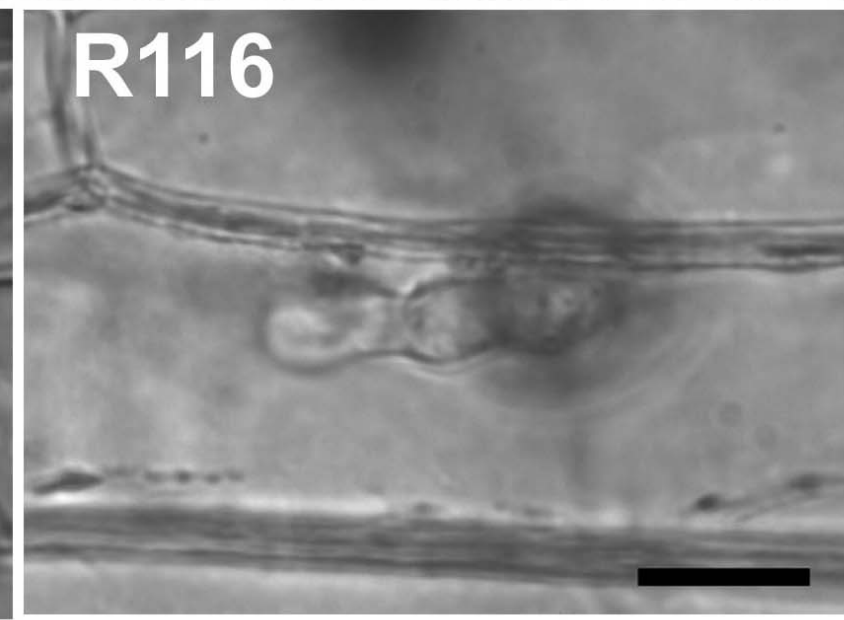
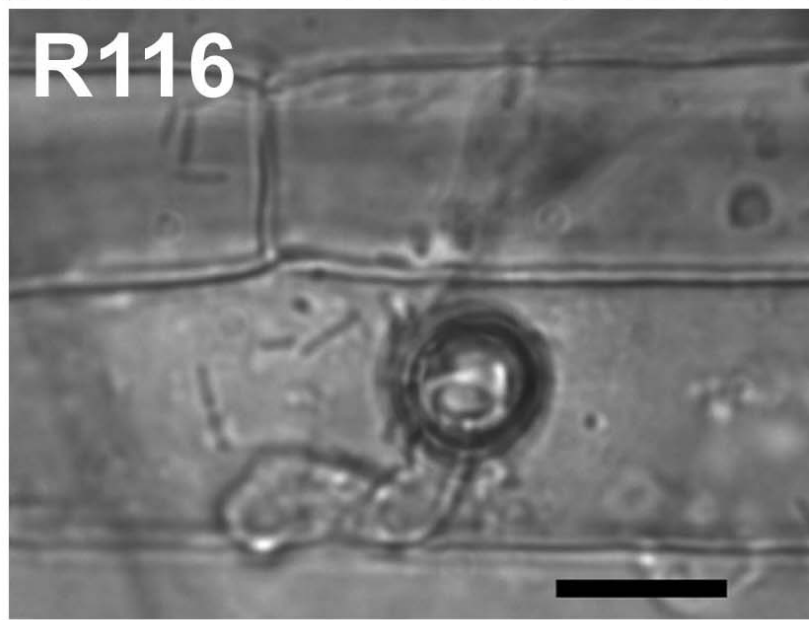
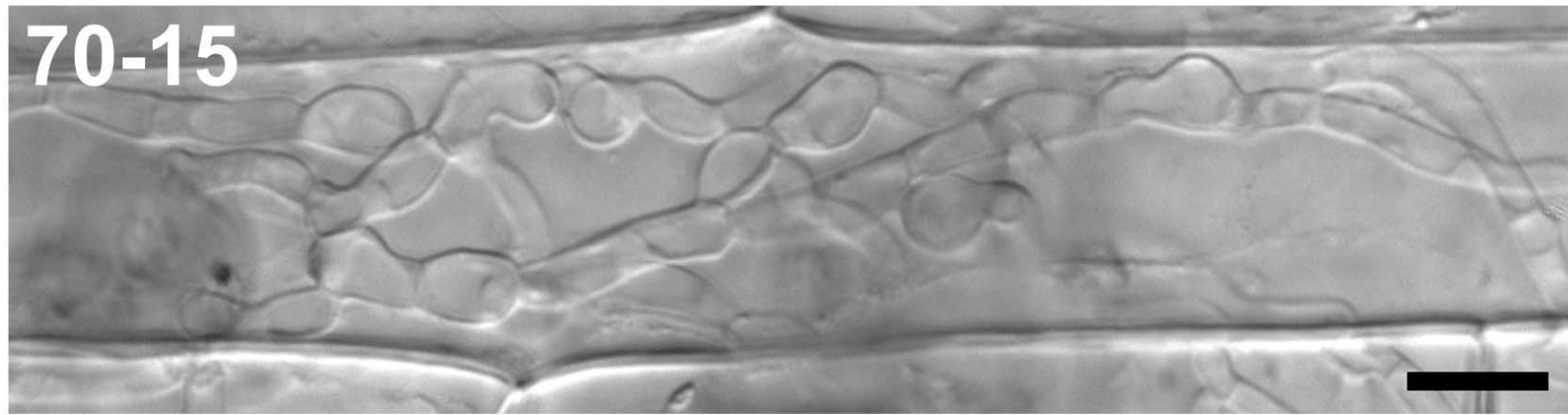
Rice



Barley

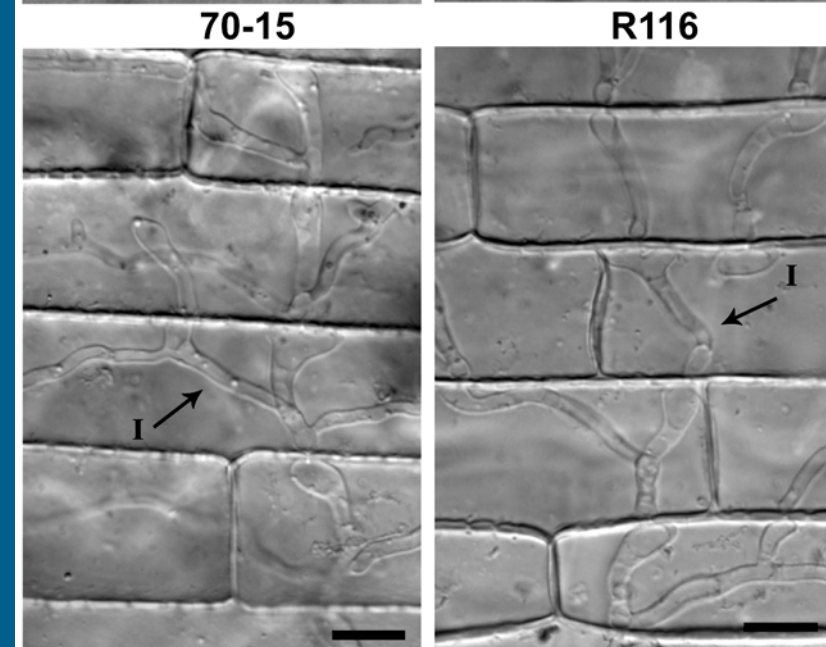
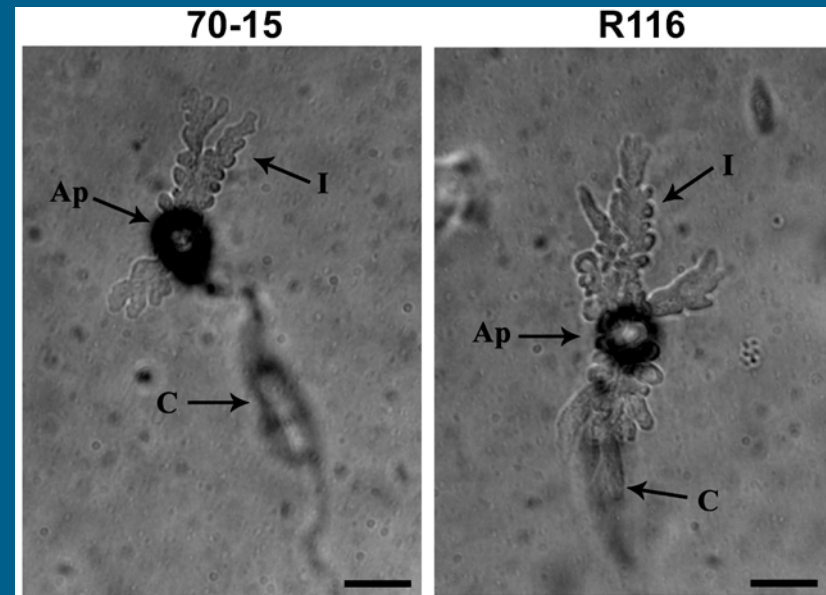


MIG1 is dispensable for appressorium formation but required for infectious growth



The *mig1* mutant might be defective in overcoming plant defense responses

Cellophane



Heat-killed rice epidermal cells

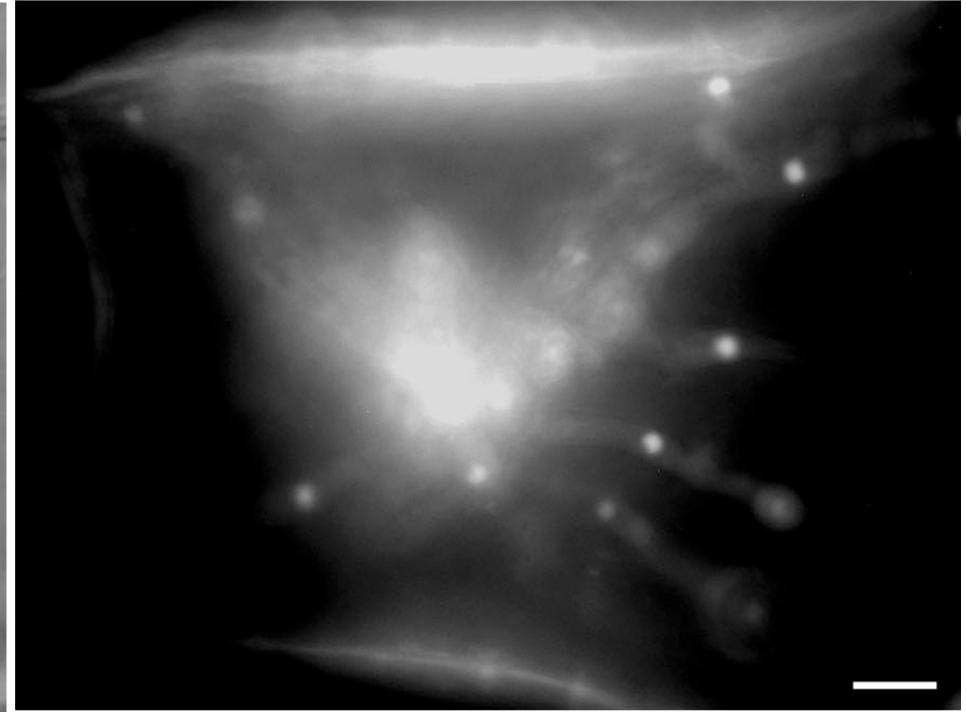
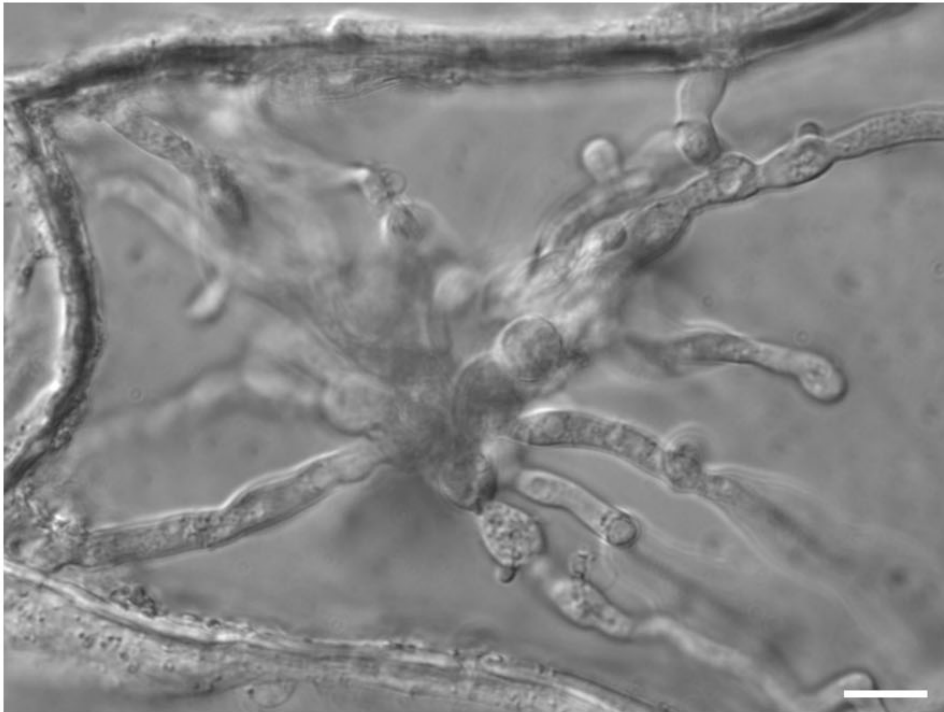
The Mig1-GFP fusion protein localizes to nucleus in infectious

hyphae

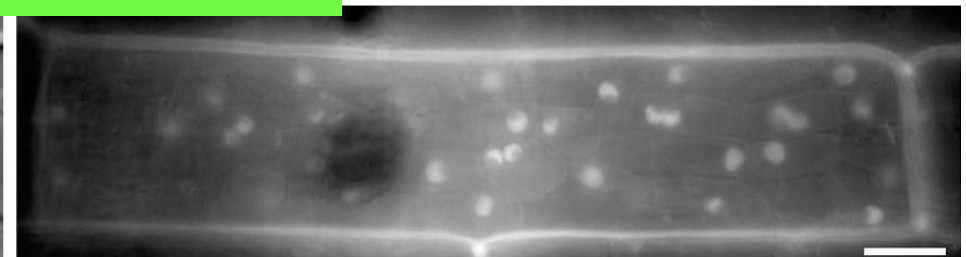
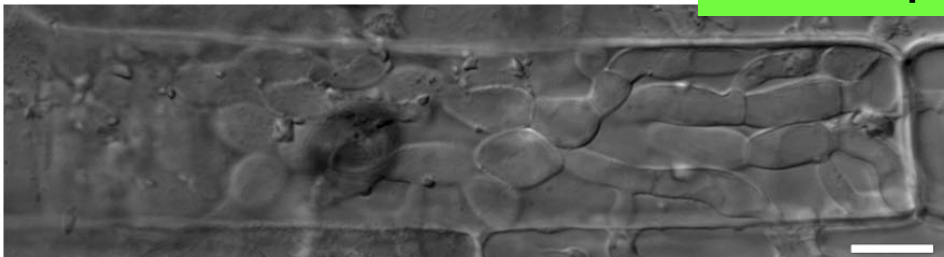
DIC

Onion epidermal cell

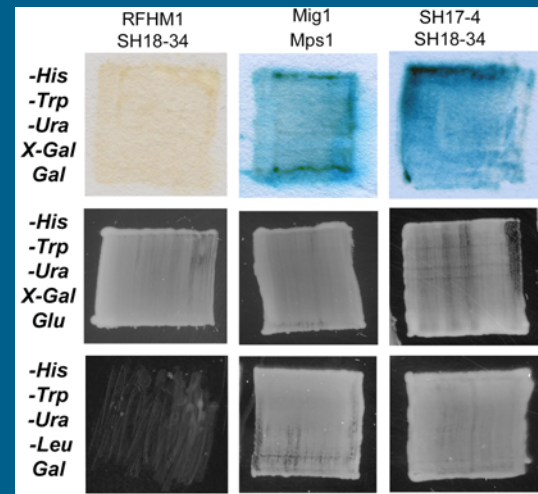
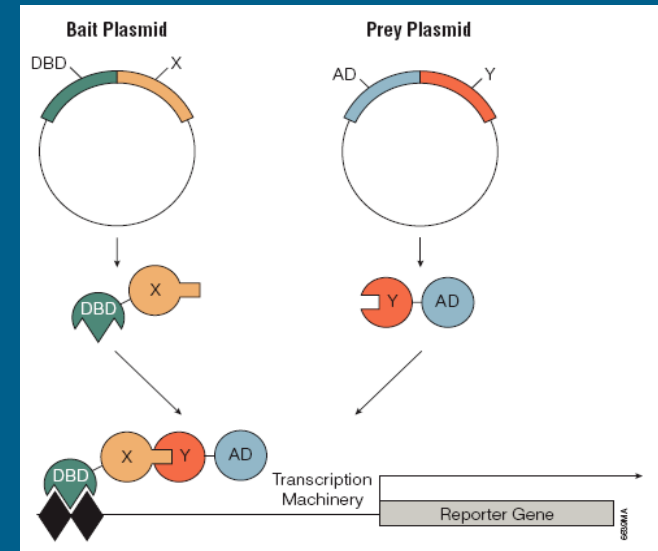
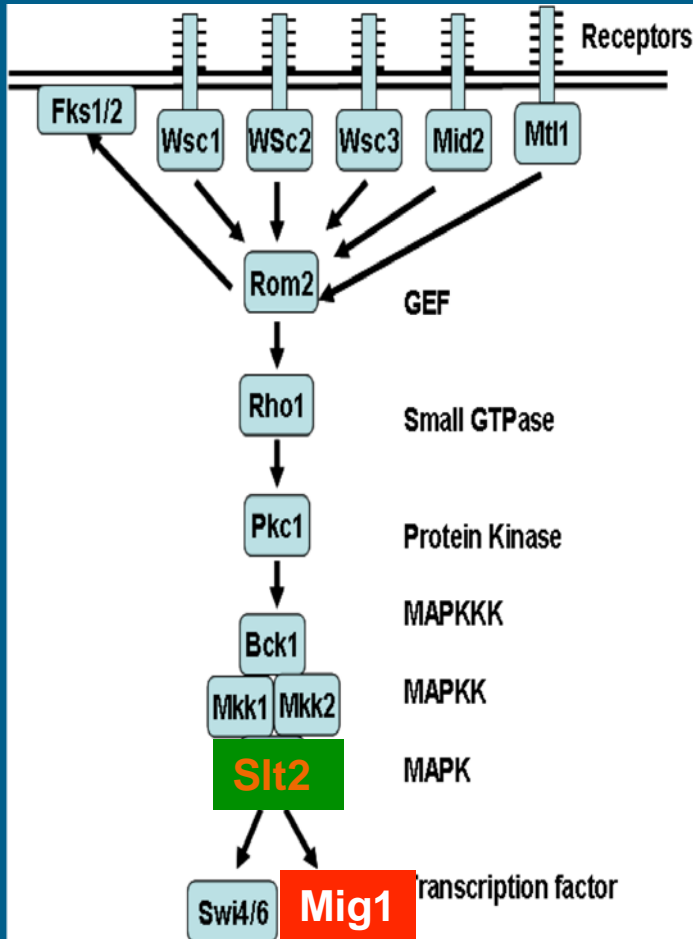
GFP



Rice Epidermal cell



Mig1 is downstream of the Slit2 MAPK



B-galactosidase

X-gal

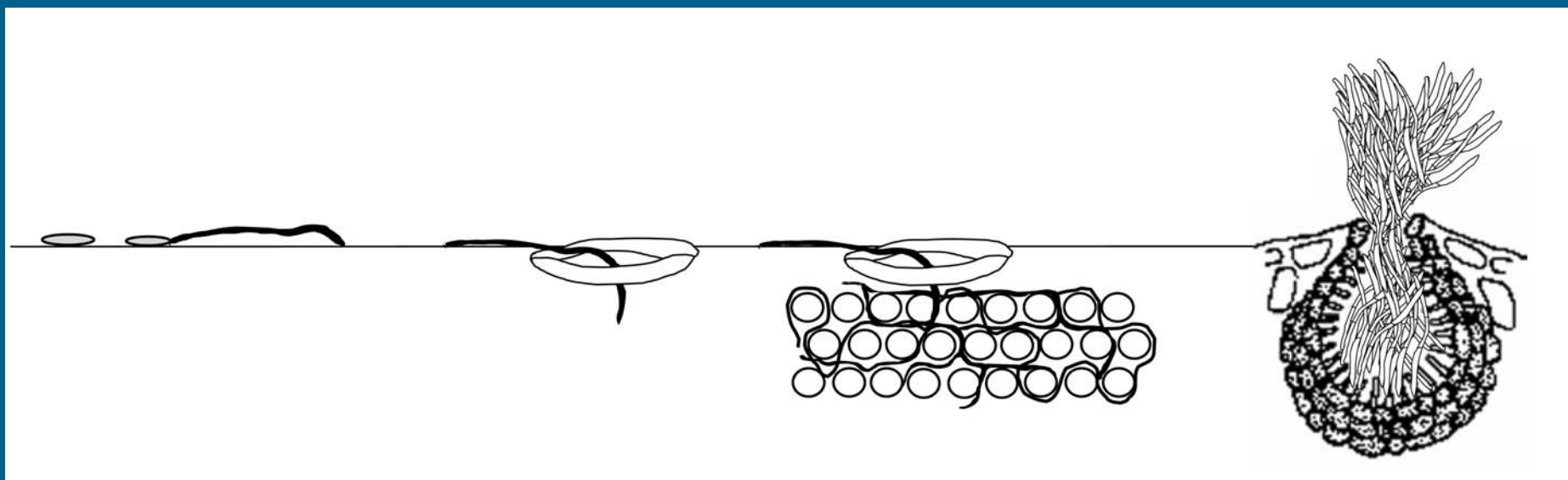
Infection Process

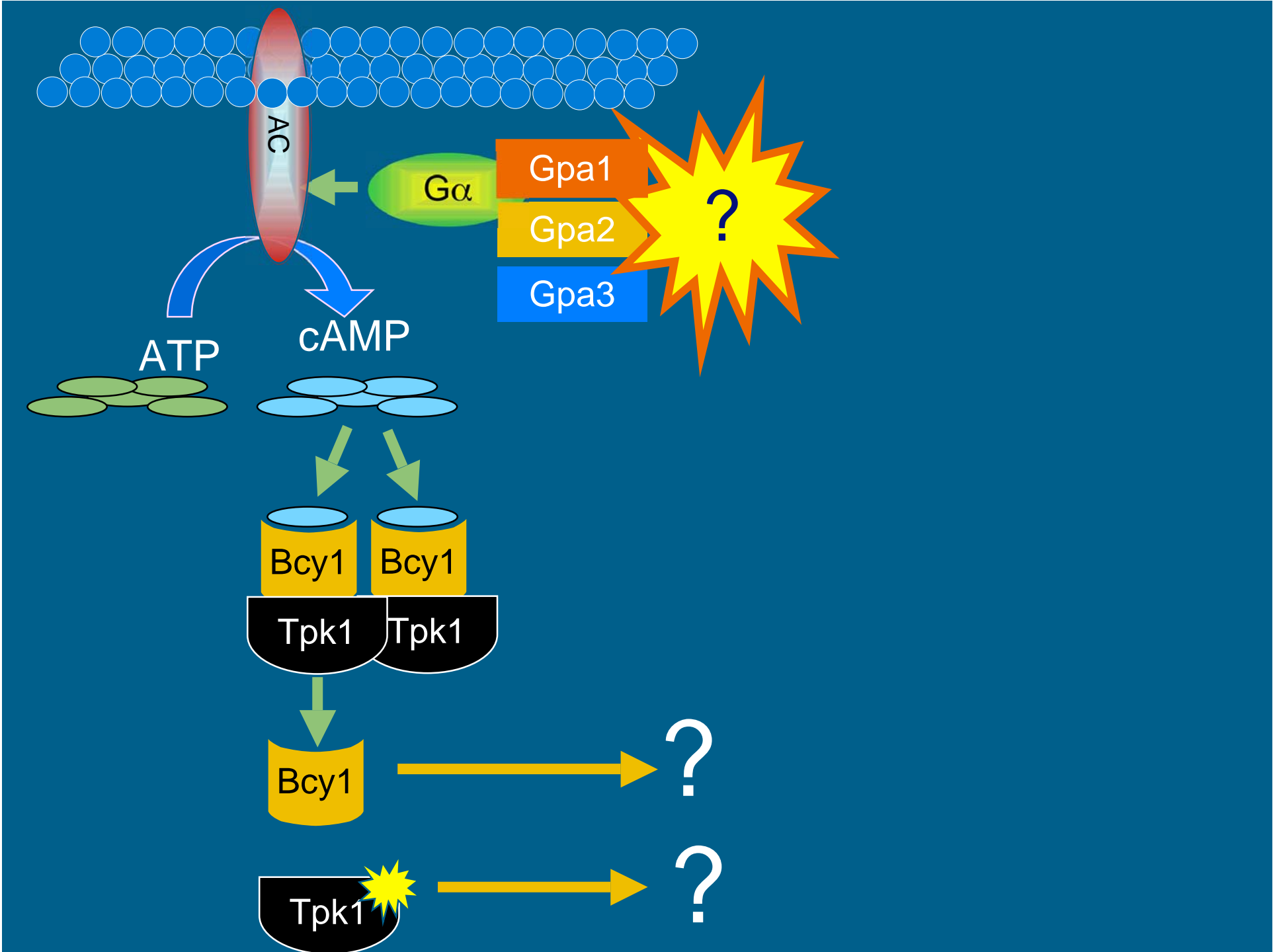
1- Transition

2- Penetration

3- Colonization

4- Fructification



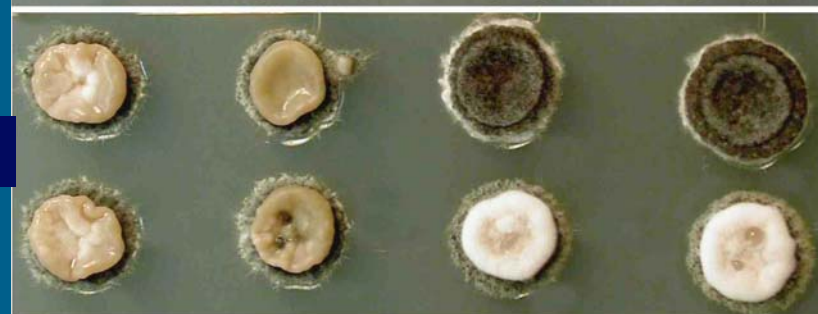


Morphological phenotype

- Mutation of *MgTpk2* facilitates melanization
- Mutation of *MgBcy1* hampers melanization
- Mutants of *MgBcy1* are osmosensitive
- *MgTpk2* mutants secrete dark pigment into YGB

WT	E	Δ MgTpk2-3	Δ MgTpk2-3
WT	E	Δ MgBcy1-3	Δ MgBcy1-6

PDA



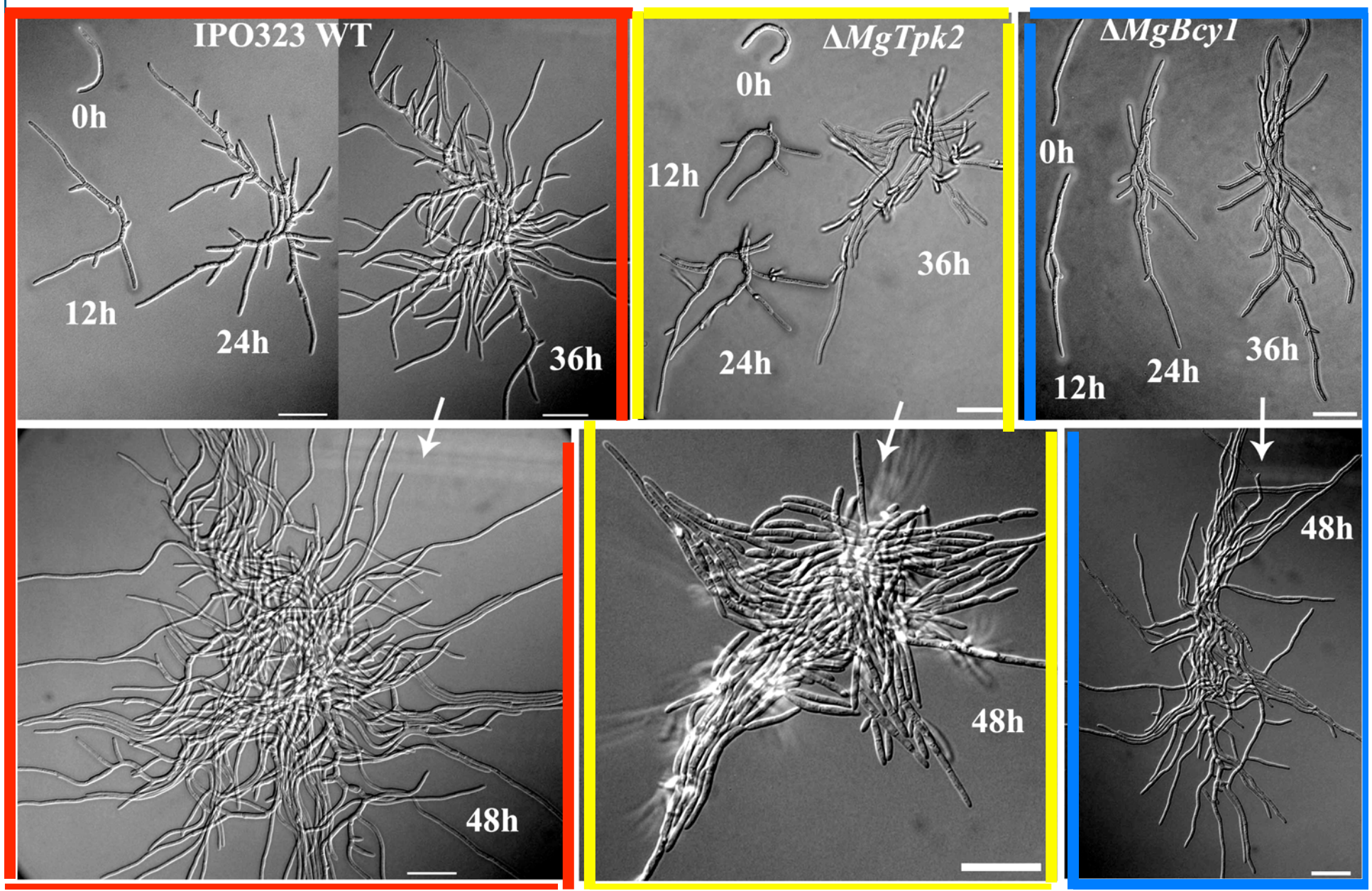
PDA+ Sorbitol



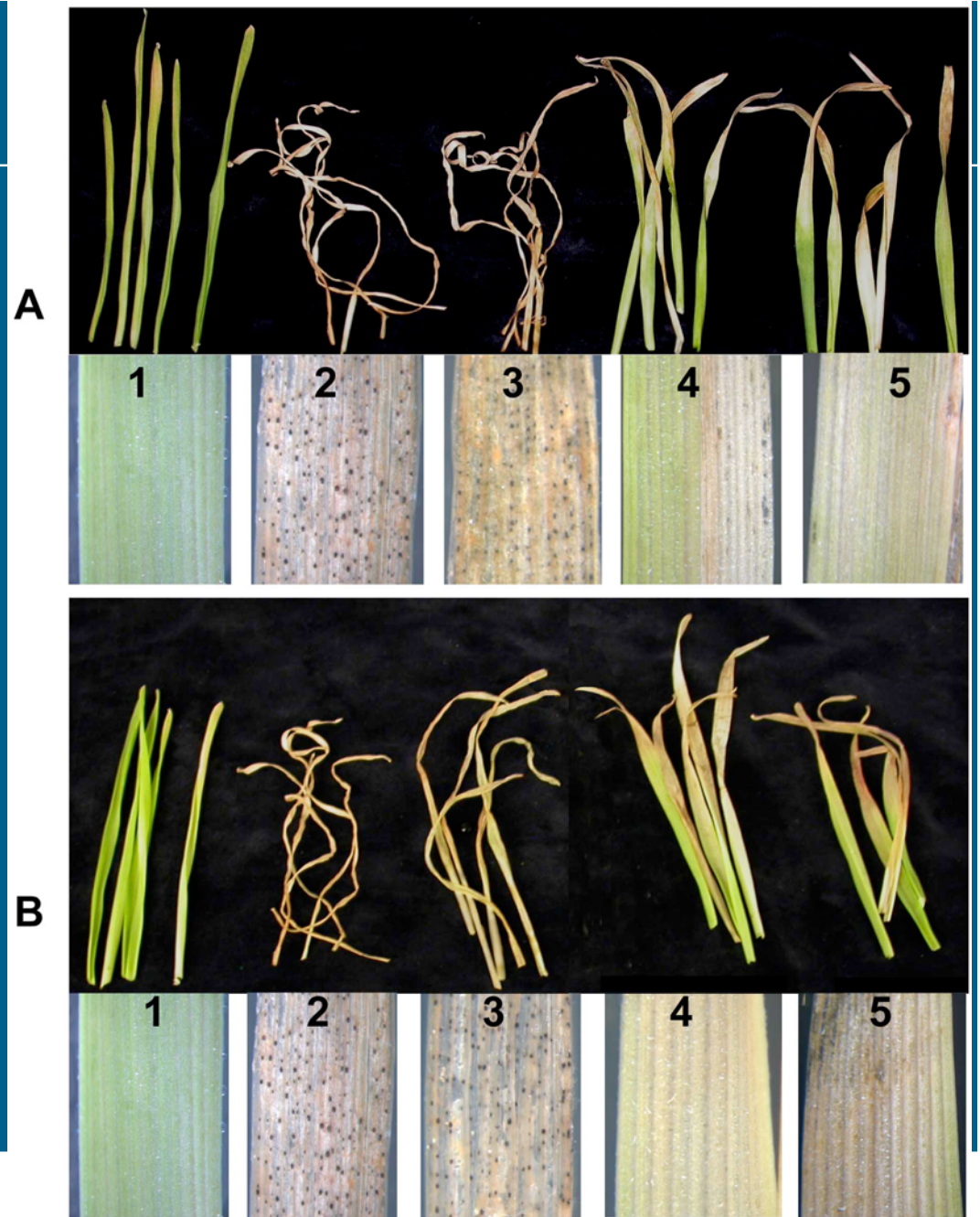
YGB



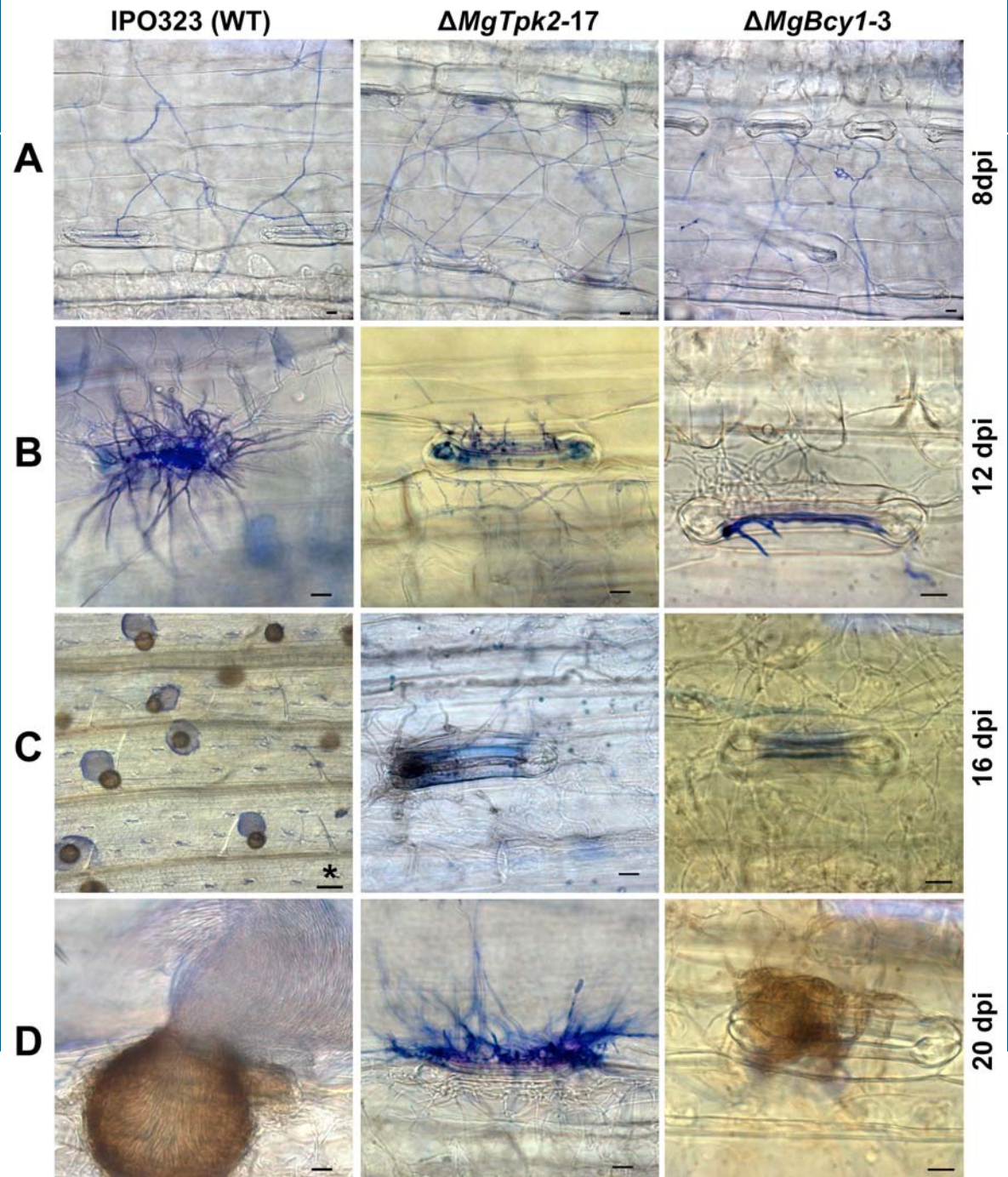
cAMP pathway regulates filamentation



- Proper regulation of cAMP pathway is required for virulence



- PKA subunits are involved in fructification



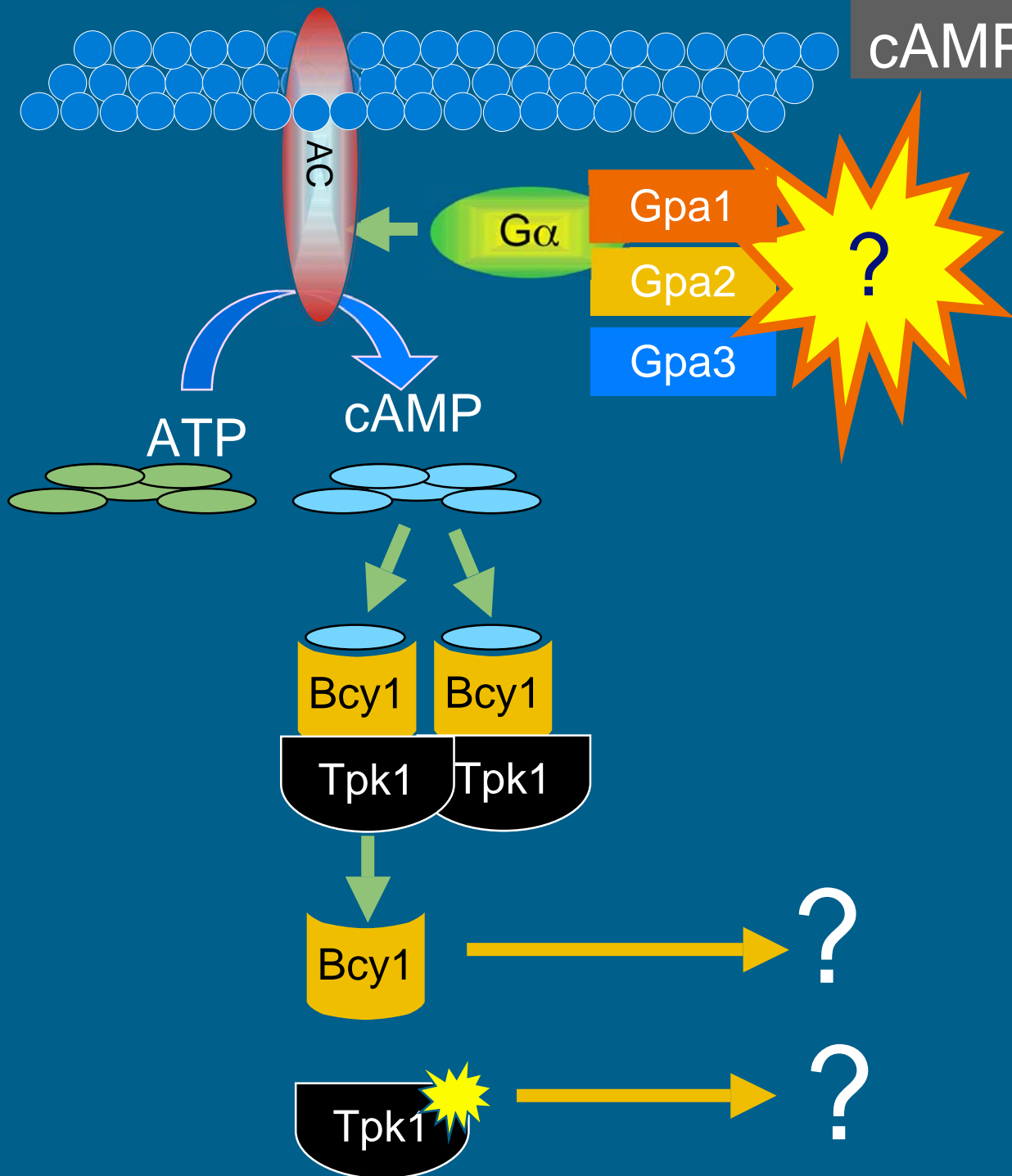
Conclusion (Biological function of PKA subunits)

- No role in dimorphic switch (*in planta*)
- Dispensable for stomatal penetration and colonization
- Involvement in later stages of infection (pycnidia differentiation)
- High PKA activity positively regulates filamentation but negatively regulates melanization and osmo-regulation

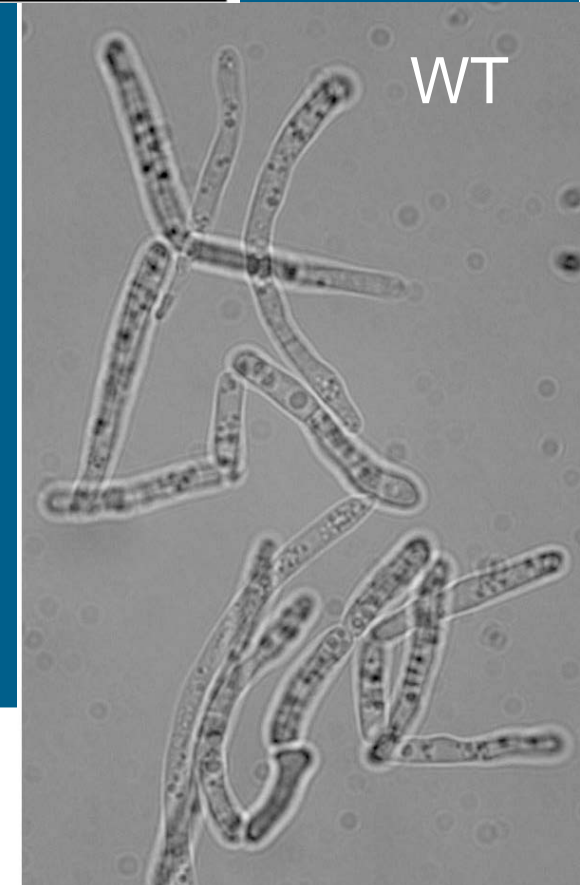
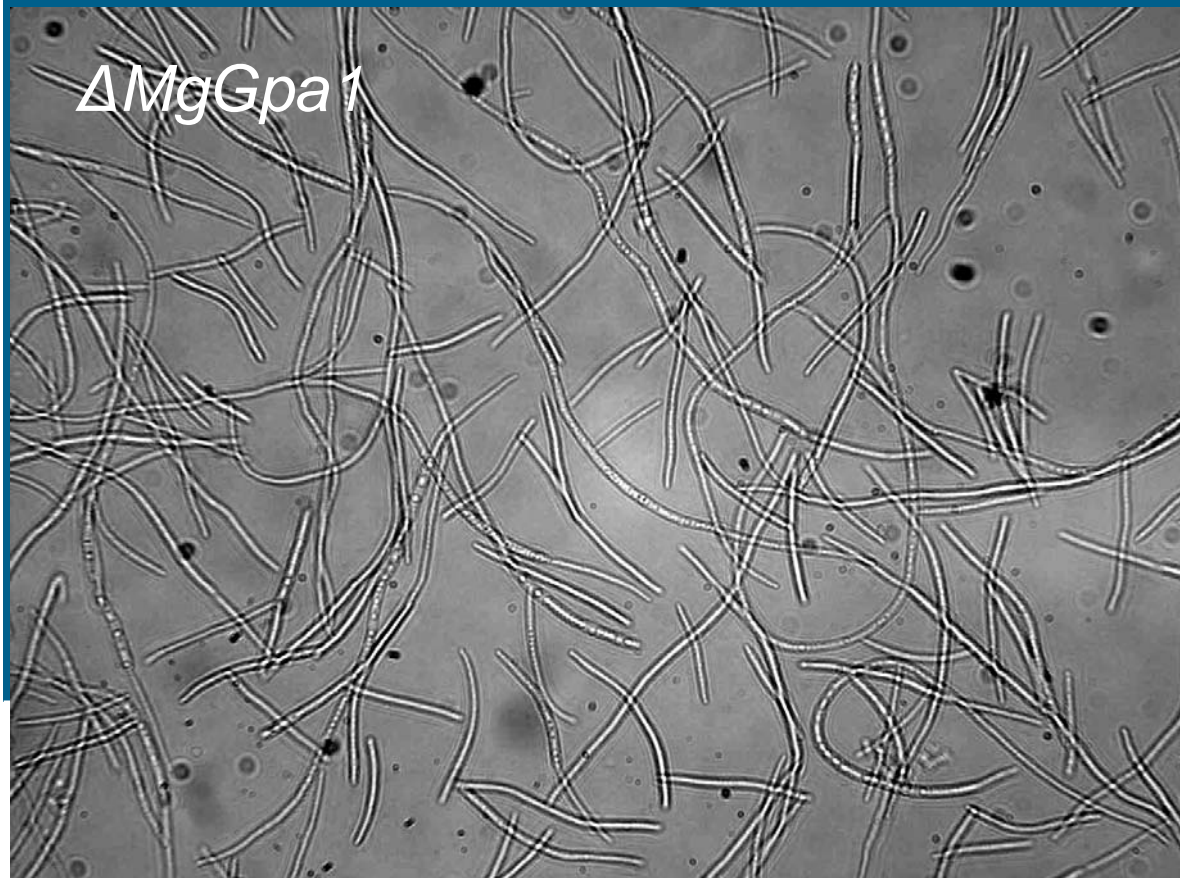
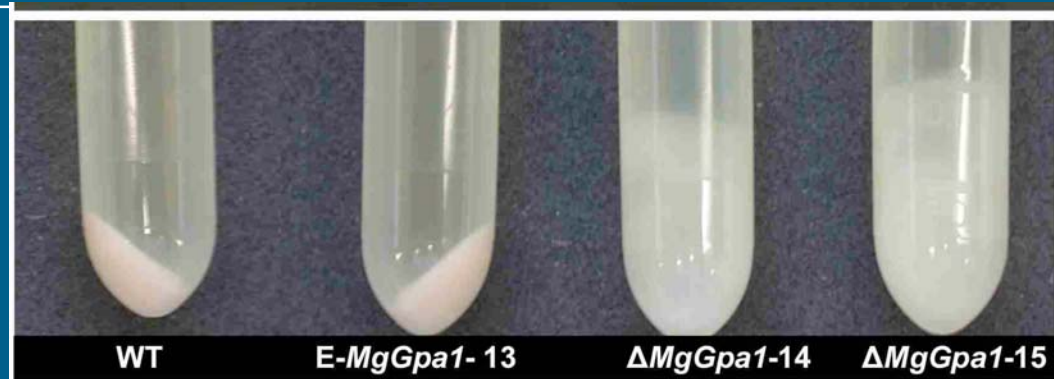


Dimorphic switch → Penetration → Colonization → Fructification

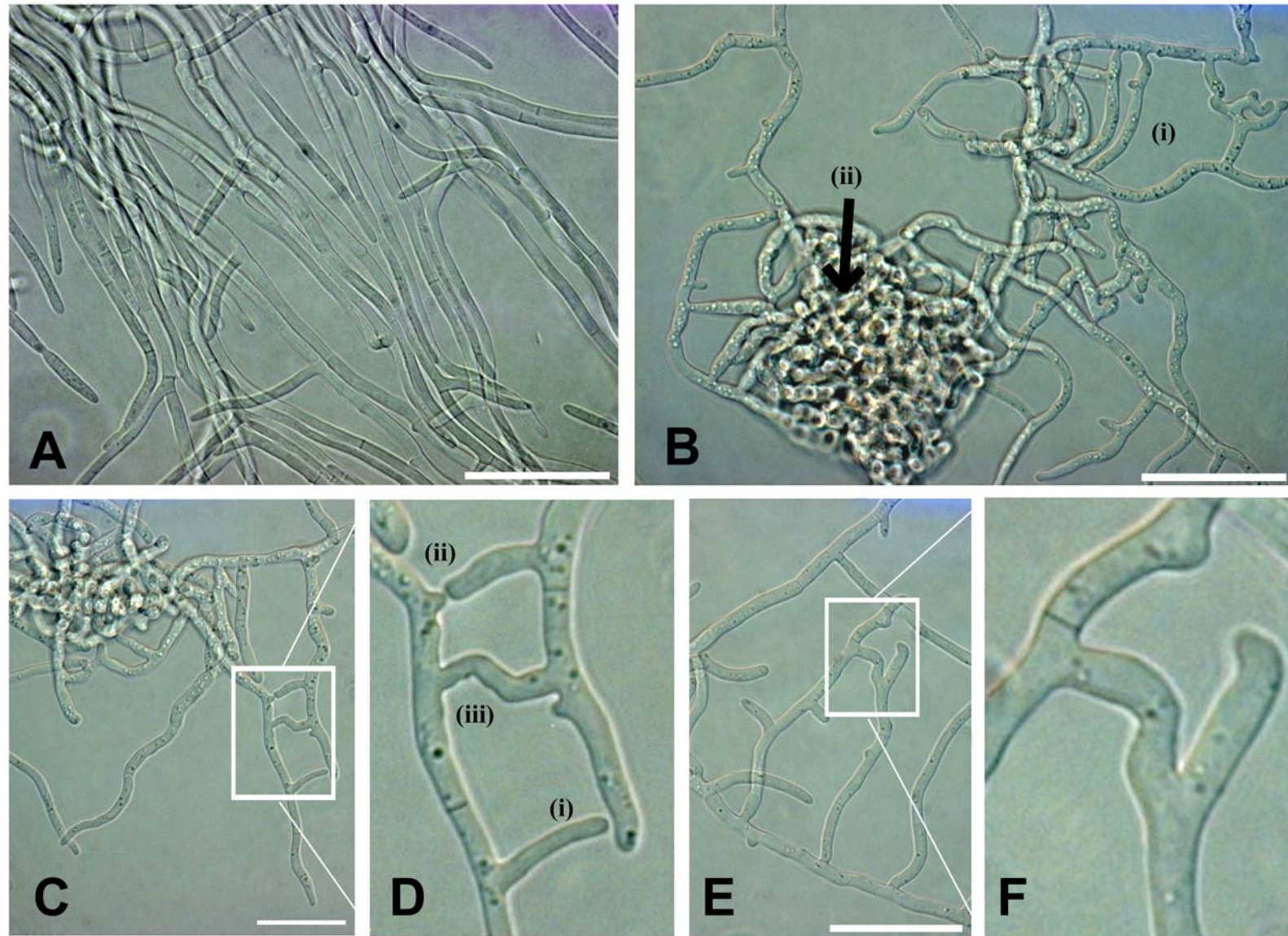
cAMP pathway



MgGpa1 negatively regulates filamentation

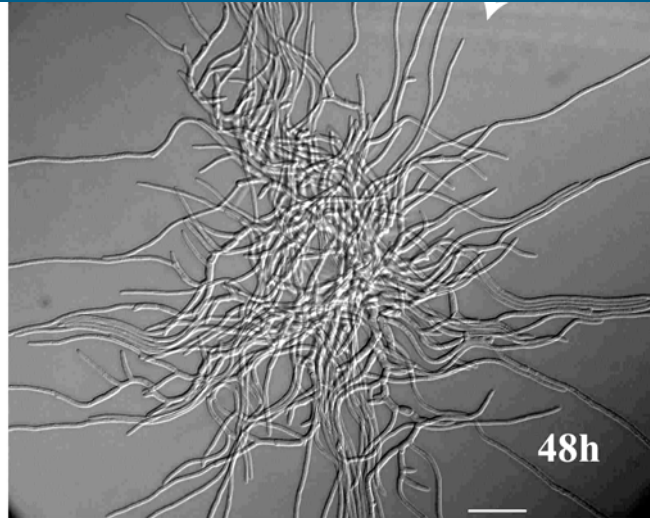


MgGpb1 negatively regulates cell fusion

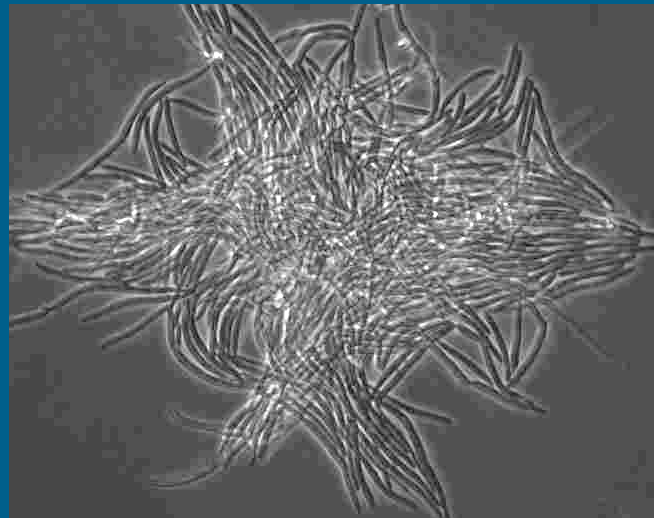


High phenotypic similarity of *MgTpk2* and *MgGpa3* mutants

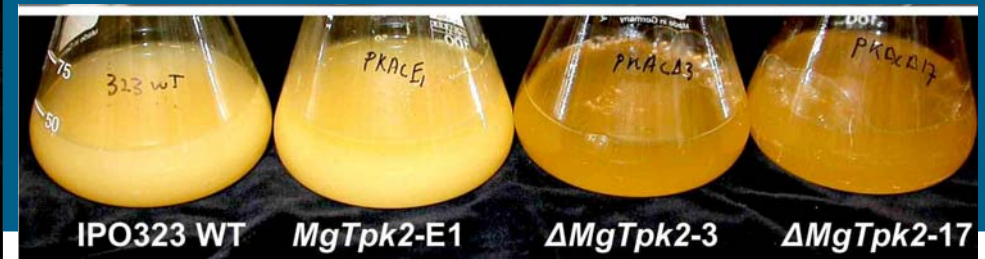
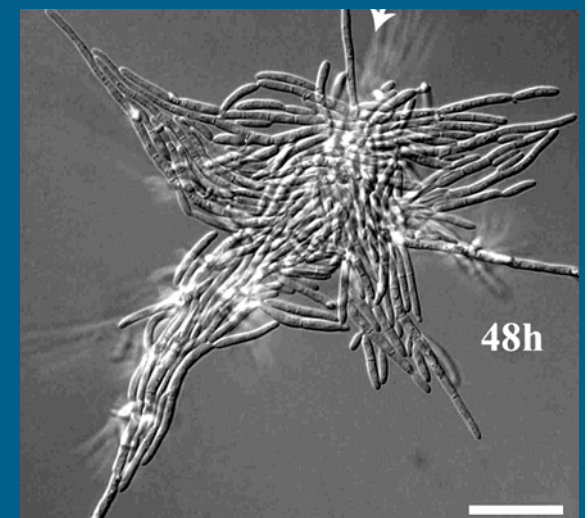
WT



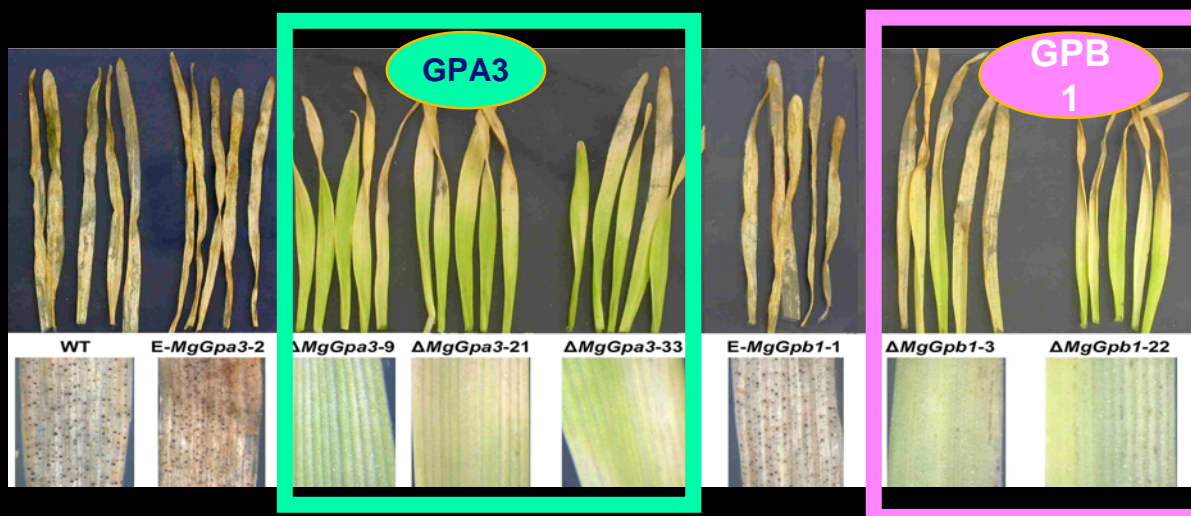
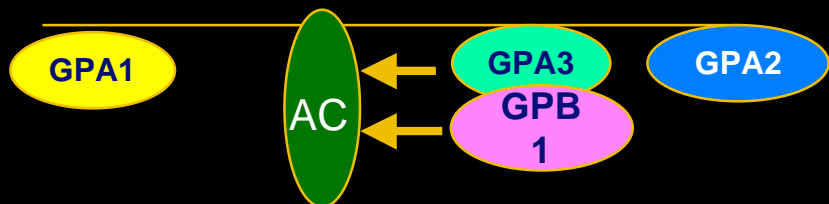
Δ *MgGpa3*



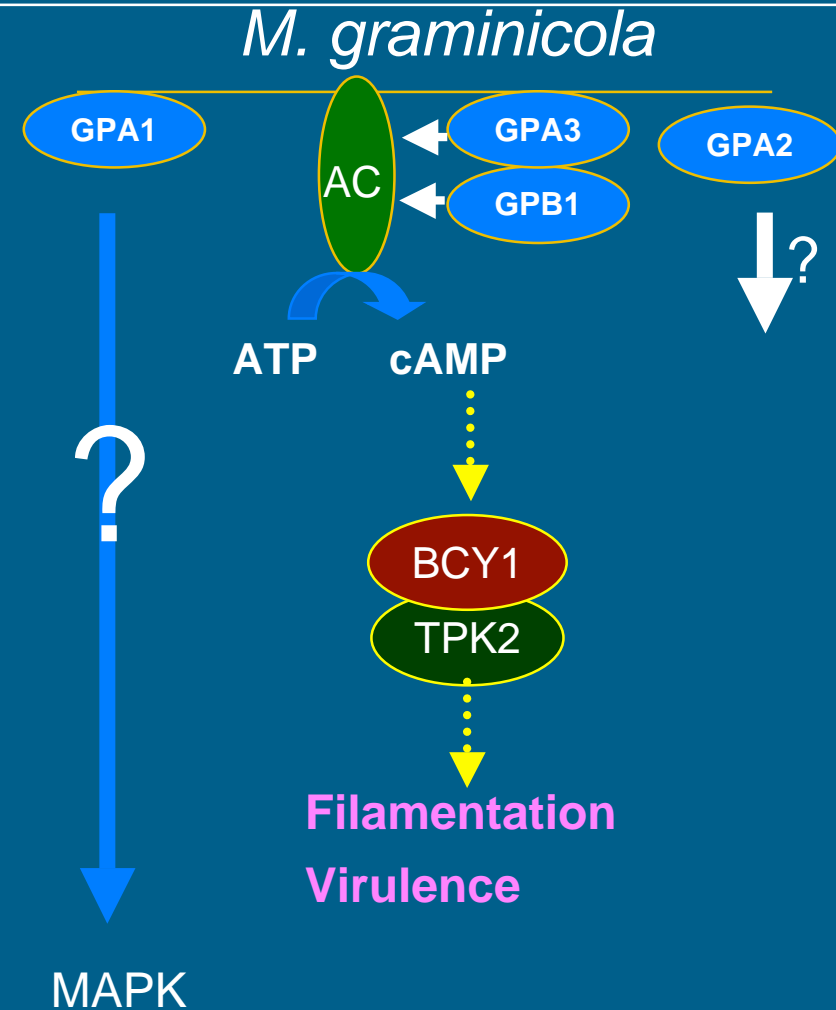
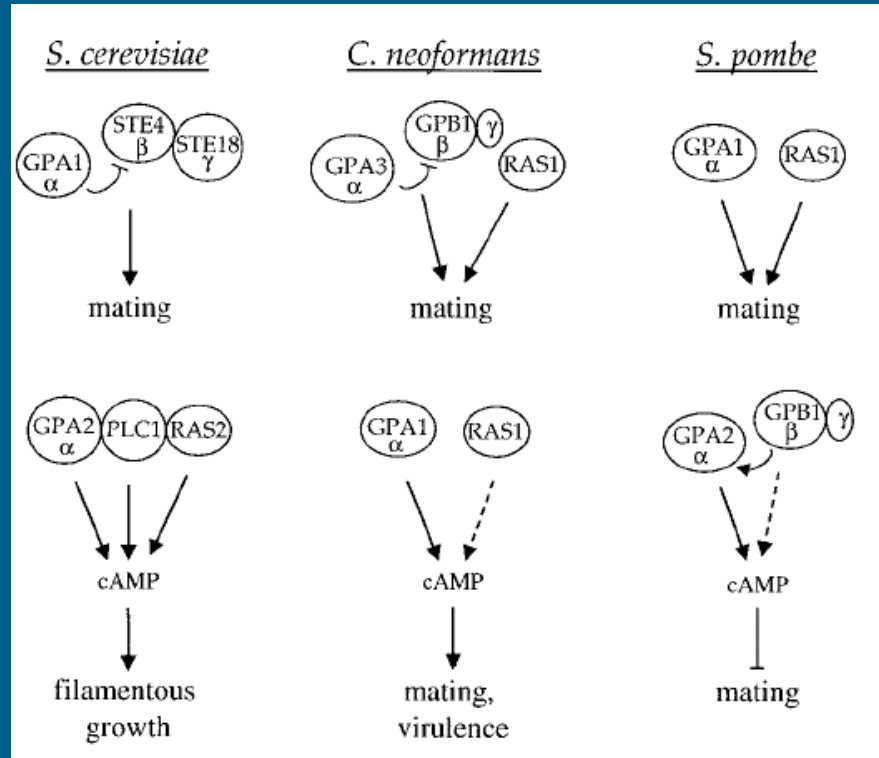
Δ *MgTpk2*

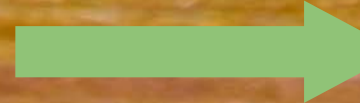


For quality of life



Regulation of the cAMP pathway by G proteins





3- initial Colonization

Biotrophic

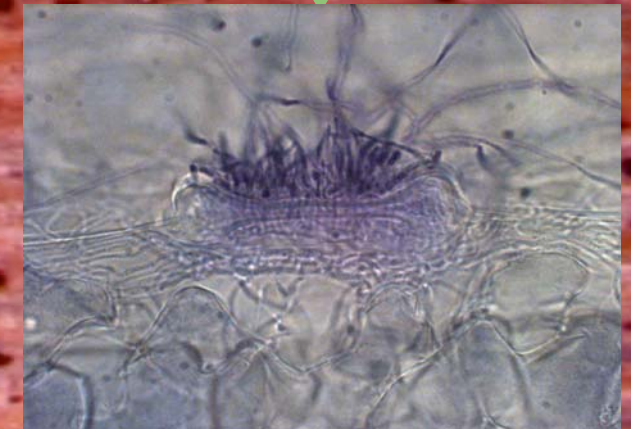
Necrotrophic

MgTpk2

MgBcy1



5-Pycnidia maturation



4-Pycnidia formation

Thanks

- Gert Kema
- Cees Wallwijk
- Theo van der Lee
- Maarten de Ward
- Pierre de Wit
- Sarrah Ben M'barak
- Jin-Rong Xu

The reaction of Iranian tetraploid wheat accessions for resistance to septoria tritici blotch pathogen

R. Mehrabi, M. Abrinbana, M. Zahravi and J. Mozafari

National Plant Gene Bank of Iran, Seed and Plant Improvement Institute, Karaj, Iran



Septoria tritici blotch (STB), caused by the fungus *Mycosphaerella graminicola* (Fuckel) Schroeter, is a major disease of wheat worldwide. Identification of new sources of resistance to this disease is important for sustainable management of the disease. The diploid and tetraploid wheats are the parents of commercial hexaploid wheats and they have provided valuable sources of many new resistance genes. Since Iran is one of the wheat origins, it could be useful to study on Iranian wheat landraces in order to identify new sources of resistance to STB.

Materials and Methods

Leaf samples showing STB symptoms were collected from different wheat growing areas of Iran and 11 strains were isolated. The fully unfolded primary leaves of wheat accessions were inoculated with a mixture of spores adjusted to 2×10^6 /ml. Disease severity was evaluated at 21 days after inoculation (dai) using percentage of lesions covered by pycnidia.



Fig1. The wheat seedlings were inoculated in the greenhouse and kept under humid conditions (left). The symptoms developed by STB after 21 dai (right).

In this study we screened different tetraploid wheat accessions to STB. Some 95 accessions of *Triticum turgidum* ssp. *turgidum*, 4 accessions of *T. turgidum* ssp. *polymicum*, 7 accessions of *T. turgidum* ssp. *dicoccum*, 21 accessions of *T. turgidum* ssp. *turanicum* were evaluated to a mixture of 11 *Septoria tritici* isolates, which were collected from different wheat-growing areas of Iran.

Results

The studied accessions showed different levels of pycnidia formation ranging from 0 to 90% of leaf areas. We found several resistant accessions including 28, 3, 1, and 10 accessions of *T. turgidum*

ssp. *turgidum*, *T. turgidum* ssp. *polymicum*, *T. turgidum* ssp. *dicoccum* and *T. turgidum* ssp. *turanicum*, respectively (Table 1 and Fig 2).

Table 1. The reaction of tetraploid wheats to STB. Disease severity below 5% is considered as resistance reaction.

Reaction:	Disease severity:	<i>Triticum turgidum</i> ssp.			
		<i>turgidum</i>	<i>turanicum</i>	<i>dicoccum</i>	<i>polymicum</i>
R	DS<5	25	10	1	3
MR	10>DS<5	14	1	0	0
MS	30>DS<10	22	3	4	0
S	DS>30	31	7	2	1
total		95	21	7	4

a: R=Resistant, MR= Moderately Resistant, MS=Moderately Susceptible, S=Susceptible
b: Percentage of lesions covered by pycnidia.

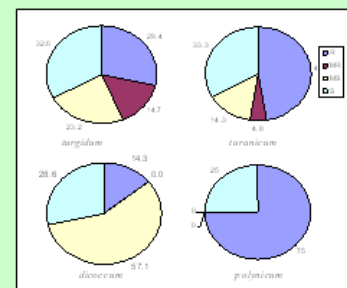


Fig. 2. Pie charts of different tetraploid wheat germplasm showing the percentage of each reaction types from resistant to susceptible.

Conclusion

Our results suggested that the local landraces, which possess resistance are valuable sources and may contain novel resistance genes and therefore are useful in breeding efforts to improve STB resistance in wheat. The specific reaction of the resistant accessions to different isolates is underway.