

**Regulation of cellular morphogenesis during  
development in *Aspergillus nidulans***

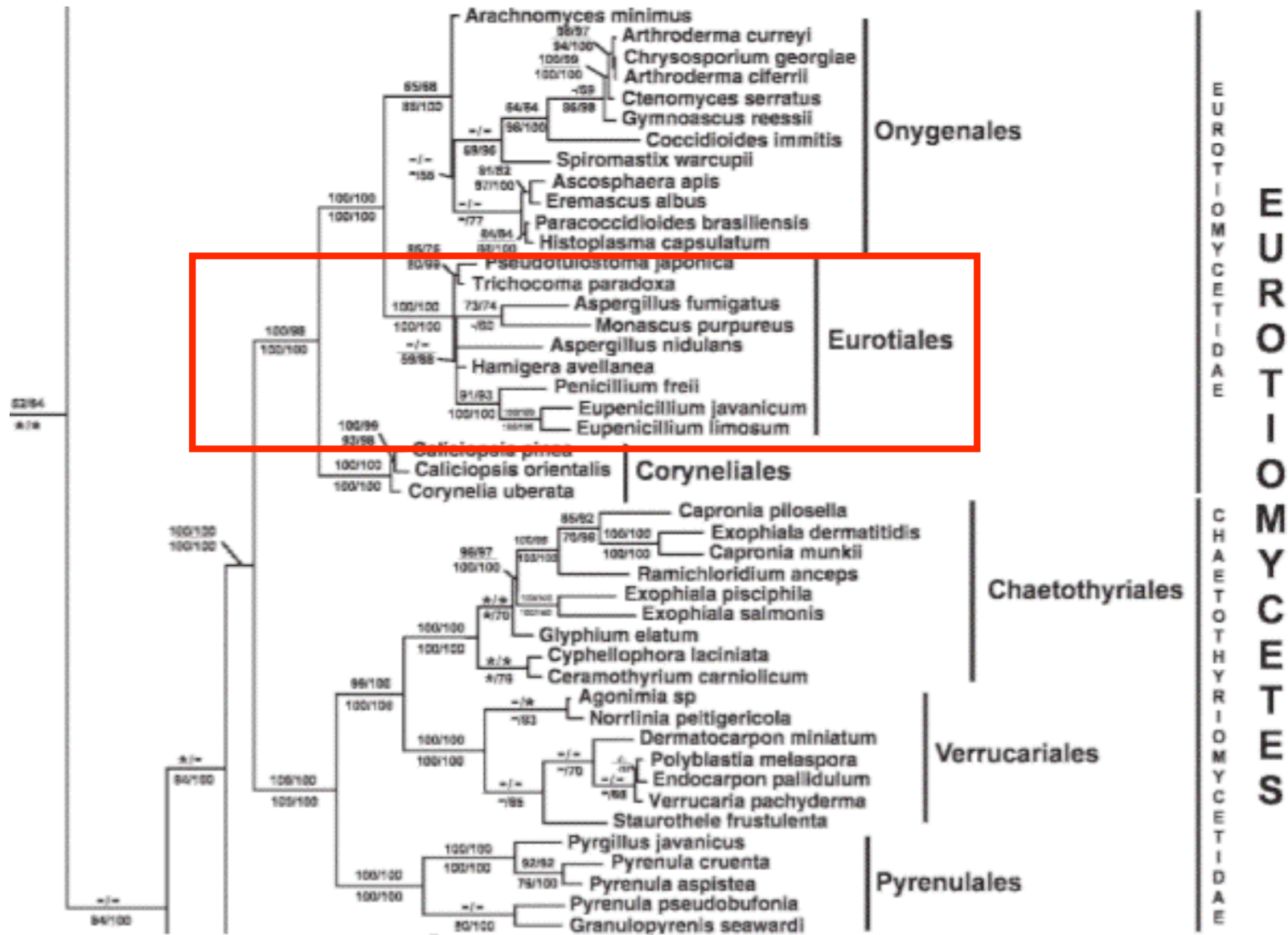
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Pathology**

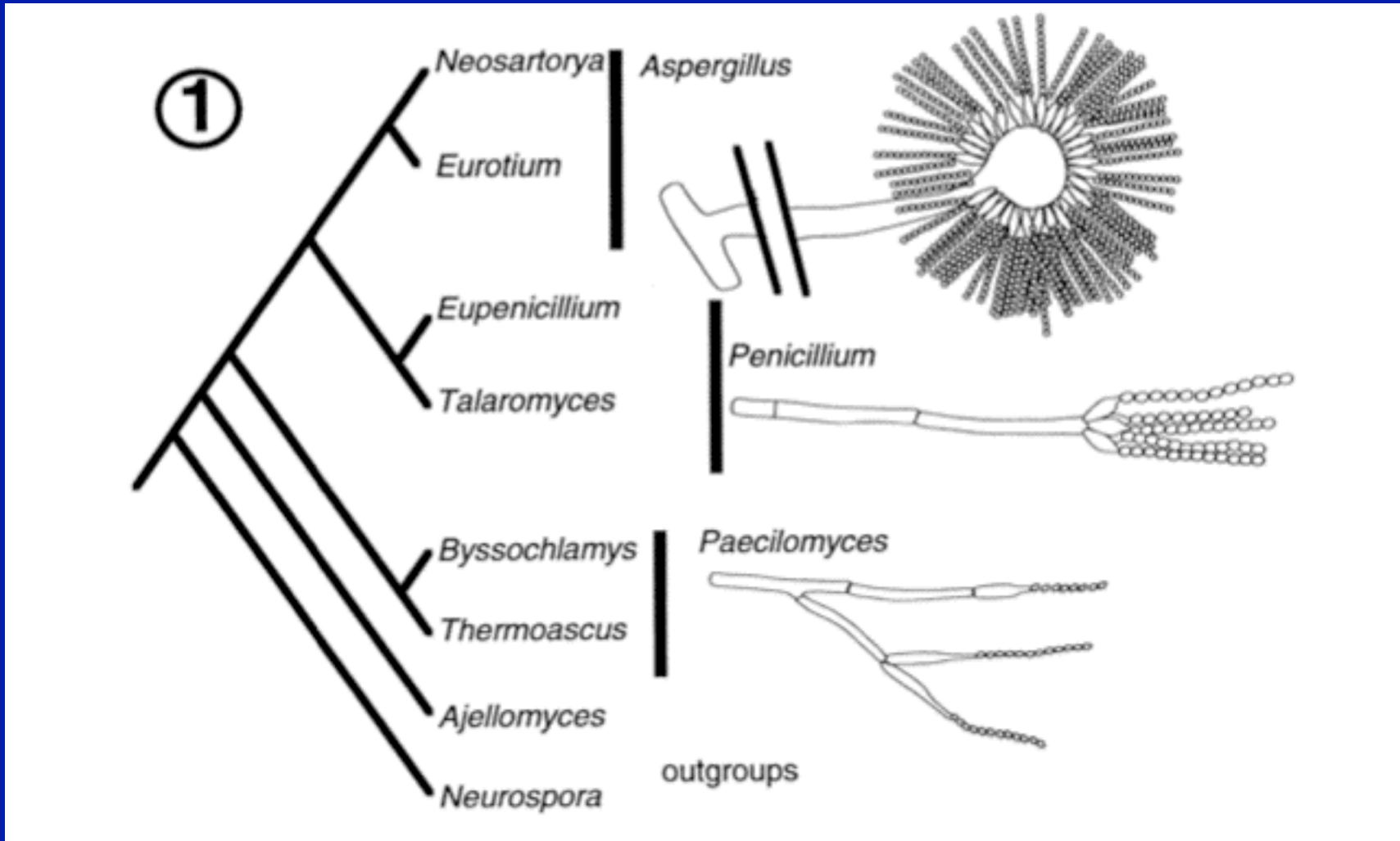
**University of Nebraska**

**Lincoln, NE**

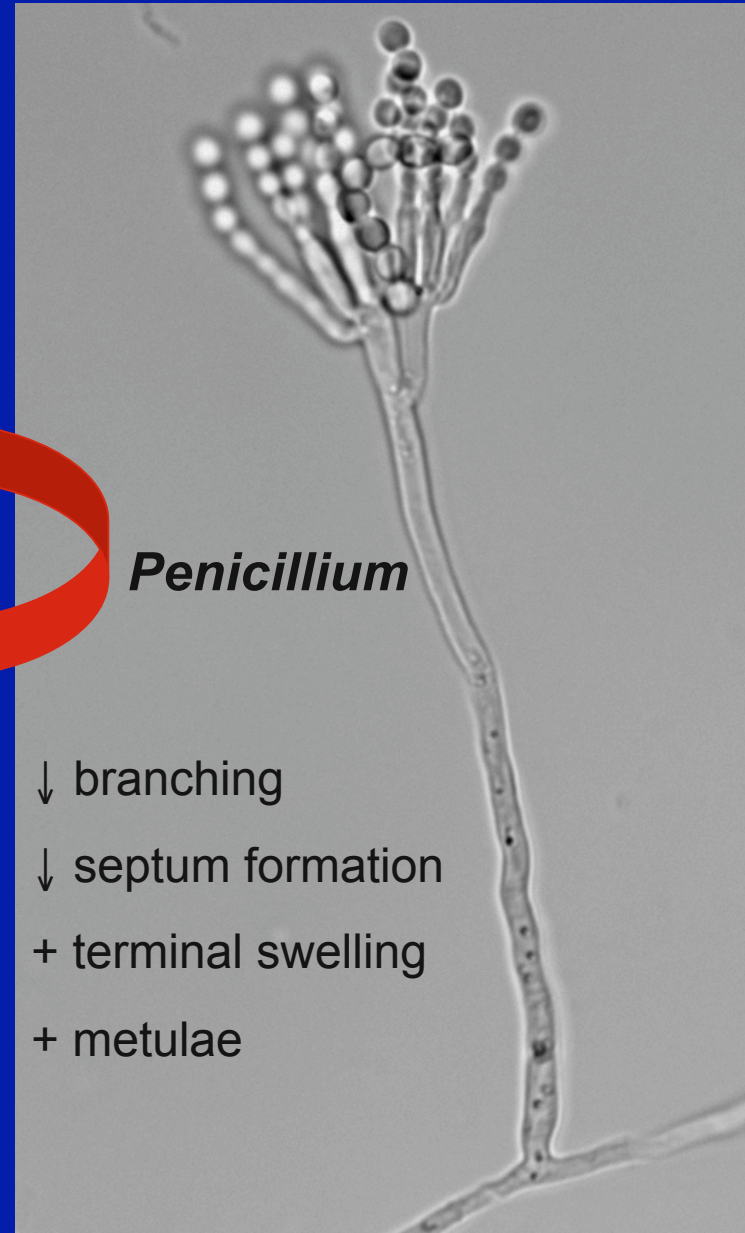
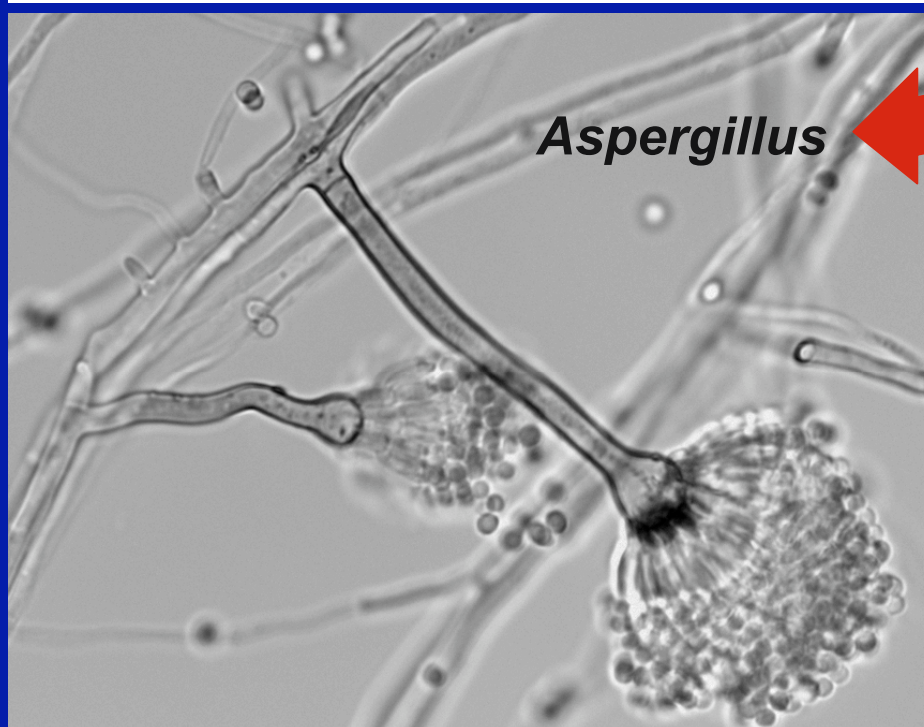
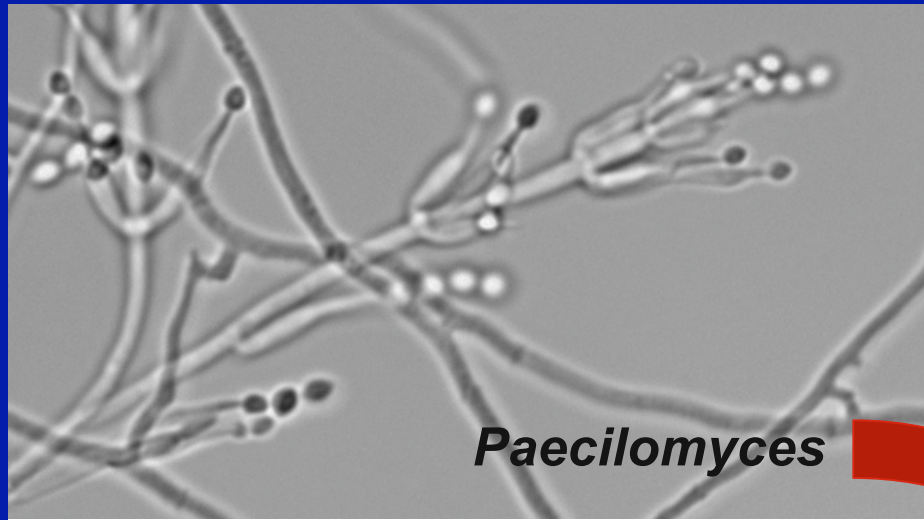
# Evolution of conidiophore morphology in the Eurotiales



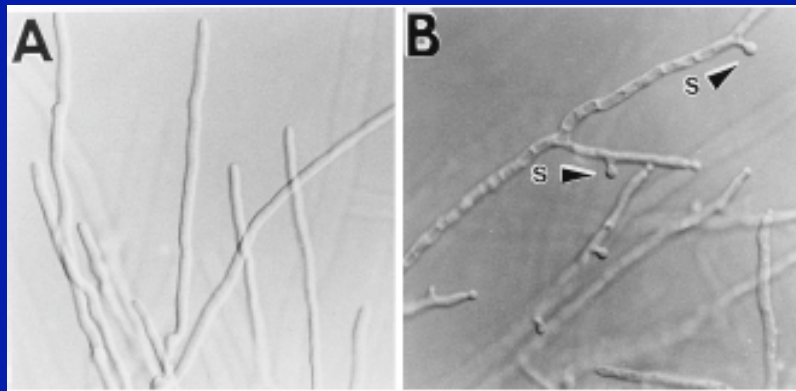
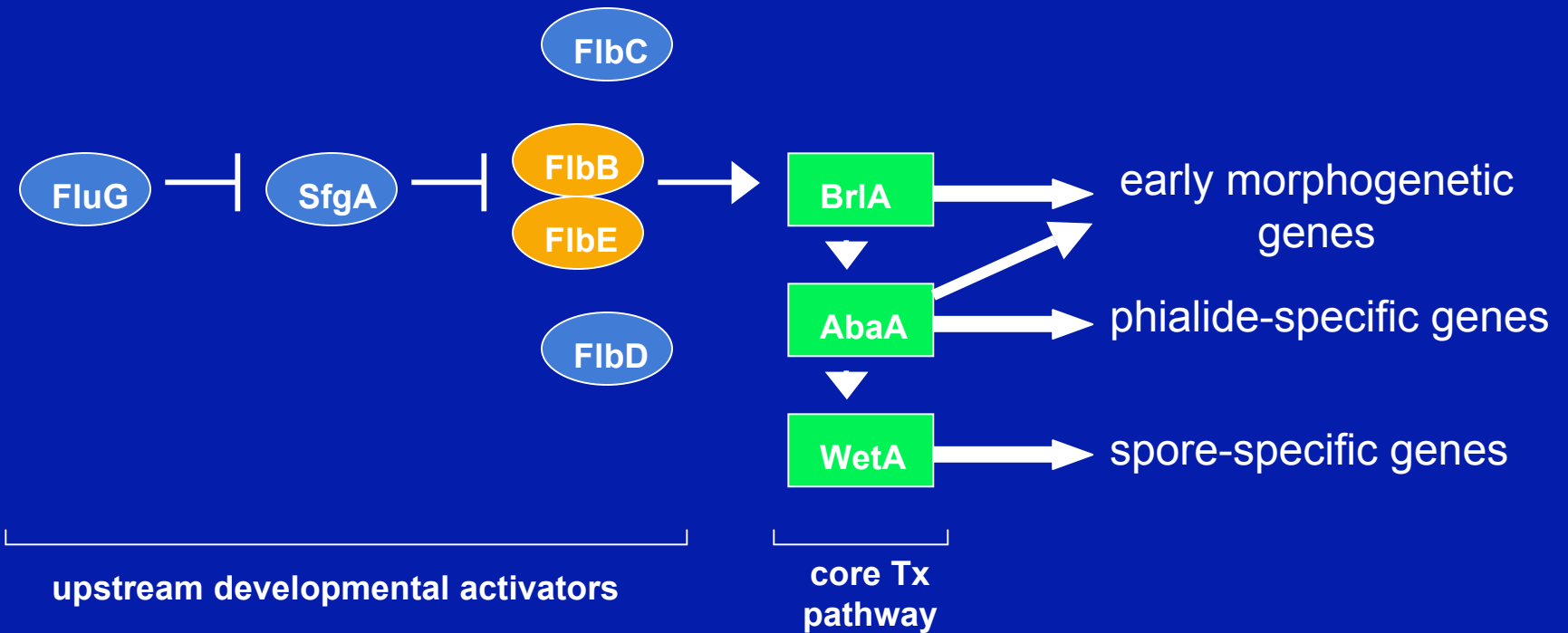
# Evolution of conidiophore morphology in the Eurotiales



# Increasing complexity of conidiophore architecture



# Regulation of conidiophore development in *A. nidulans*



expression of *alcA(p)::brlA*  
drives formation of spores in  
submerged hyphae

How are cell cycle and morphogenetic functions integrated within this regulatory network?

# Potential factors underlying the evolution of conidiophore morphology

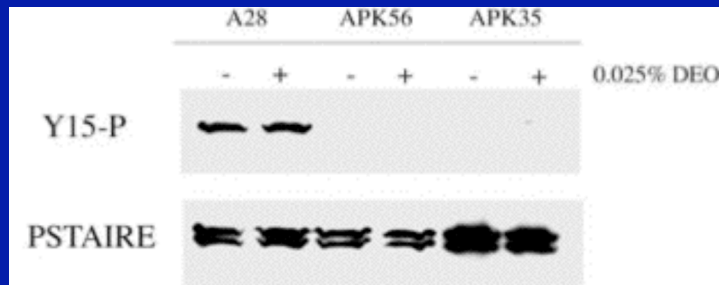
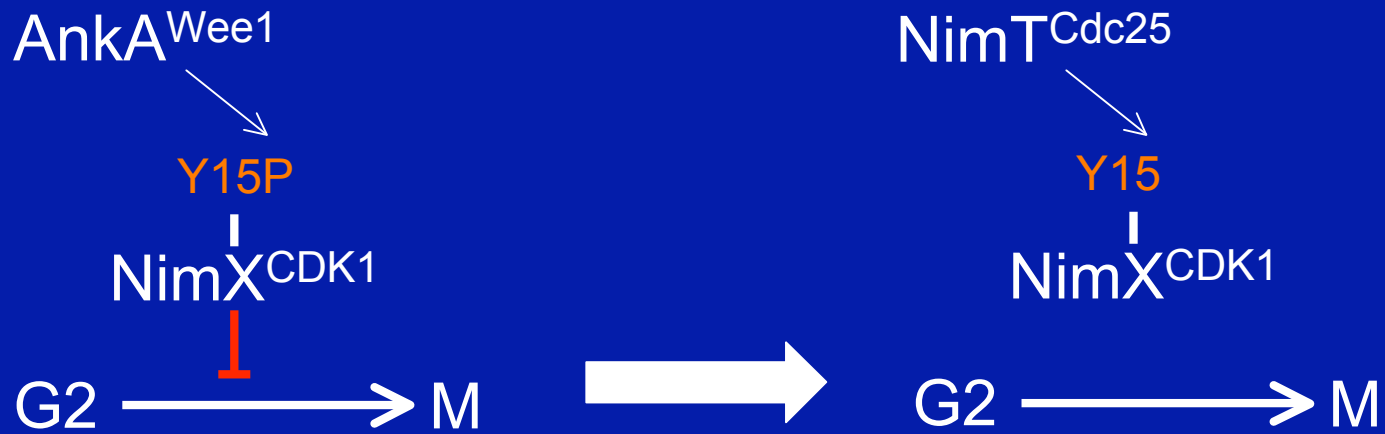
1. Cell cycle regulation  
Wee1 tyrosine kinase; Ace2/Swi5 C2H2 transcription factor
2. Spatial regulation of cellular morphogenesis  
Cdc42 GTPase module
3. Integration with UDAs and core transcriptional regulatory network  
BrlA; AbaA

Why?

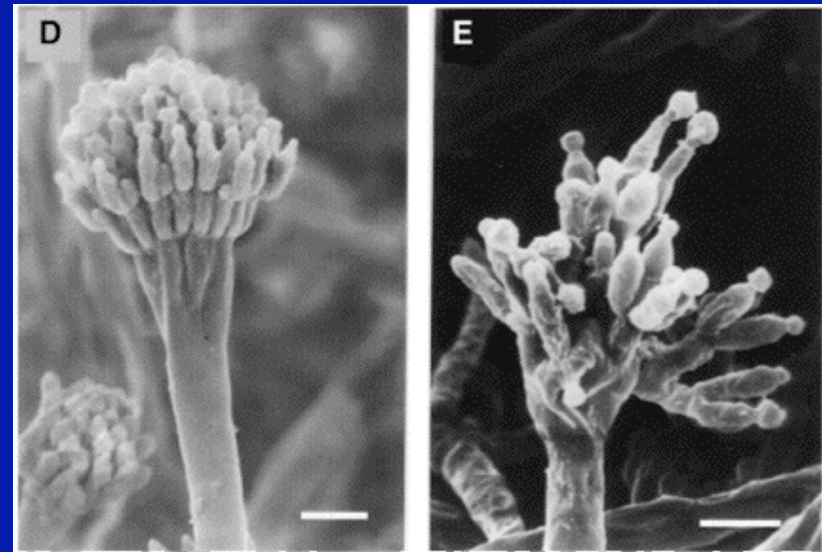
- improved understanding of conidiophore morphogenesis
- understand the molecular events involved in the evolution of conidiophore morphology
- identification of potential strategies for the control of sporulation

Progress →

# Cell cycle regulation: Wee1



Kraus and Harris, 2001

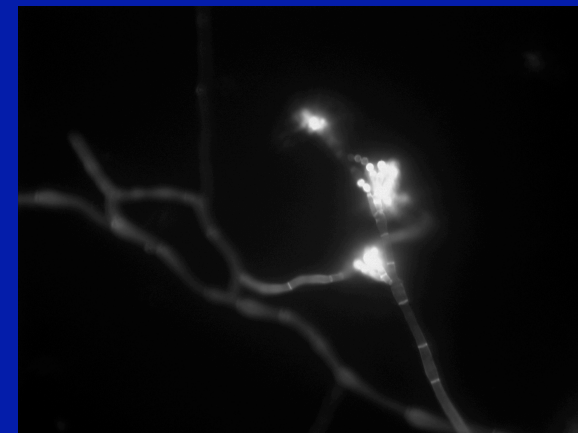
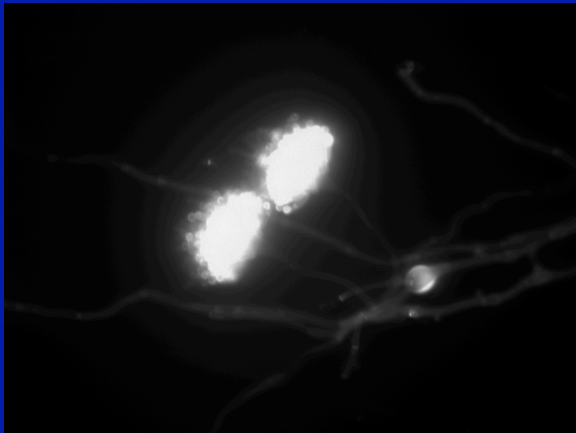
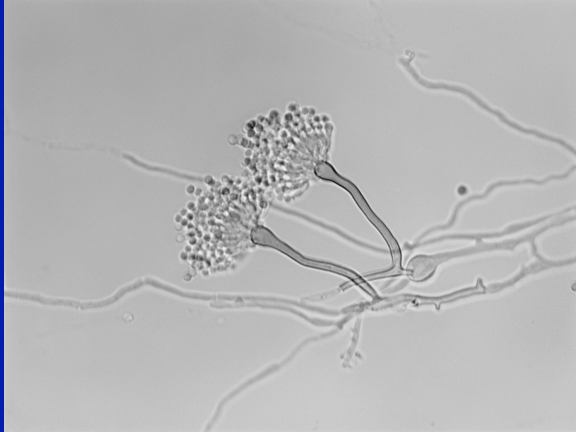


Ye et al., 1999

# Cell cycle regulation: Wee1

wildtype

*ankA2* (formerly *sntA1*)



Loss of Wee1 function (i.e., NimX<sup>CDK1Y15</sup> Pn) causes;

septum formation in stalk, loss of vesicle, spurious branch formation,  
defective hyphal → budding transition



# Cell cycle regulation: Ace2/Swi5

Ace2 and Swi5 = paralogous C2H2 transcription factors in yeast

Ace2 → septum degradation following cytokinesis

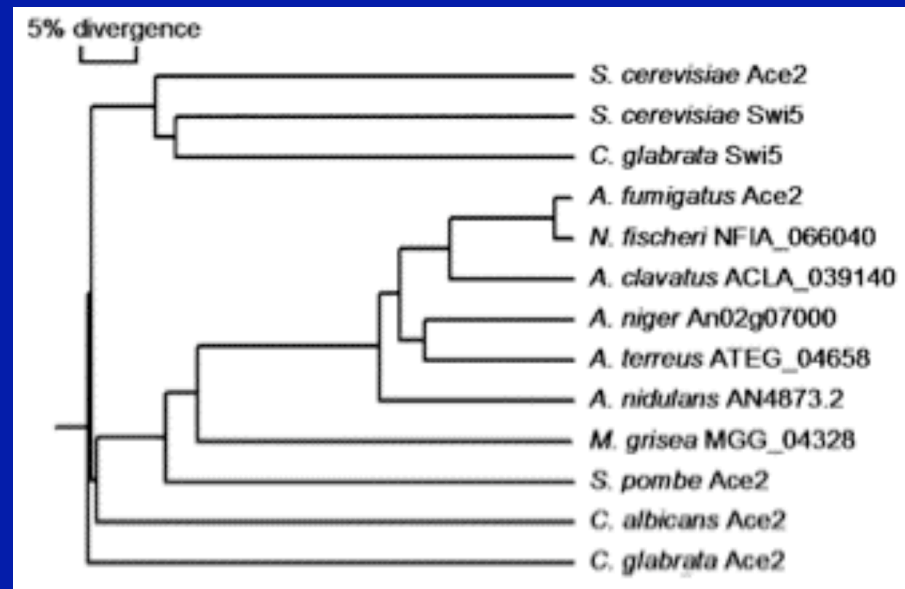
Swi5 → transcription of genes expressed at M/G1 transition and in G1

Afum Ace2 (Afu3g11250) required for phialide formation, cell wall architecture, and virulence (Ejzykowicz et al., 2009)

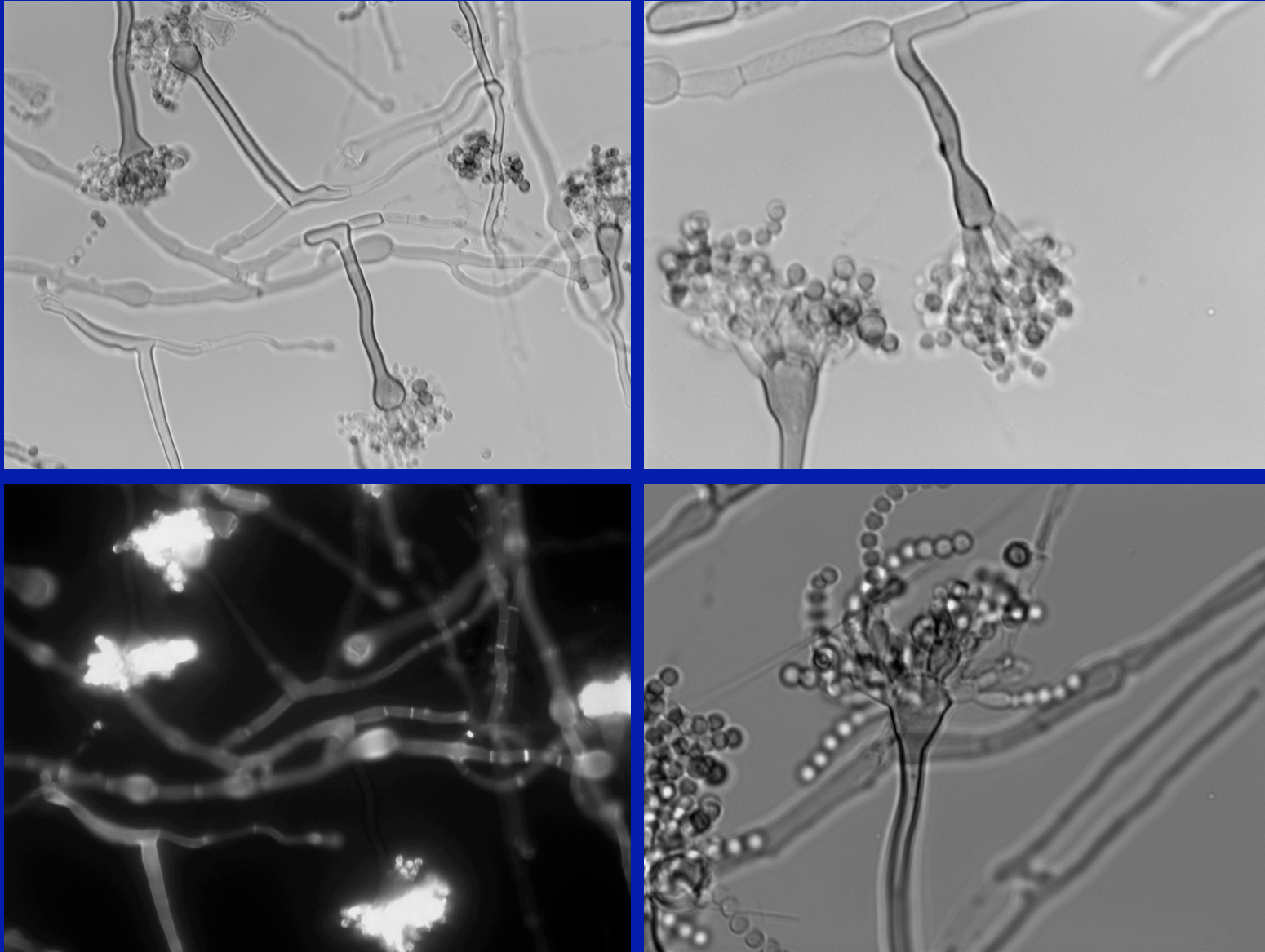
## ANID\_04873.1

51%ID/71%S over 781 AA – Afum  
55%ID/65%S over 110 AA – Swi5

generated  $\Delta ace2::pyroA$  mutants  
and screened for conidiation  
defects

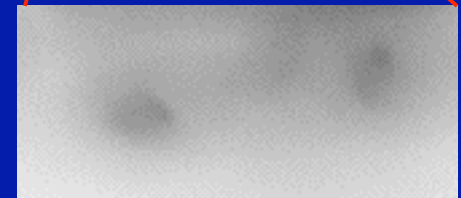
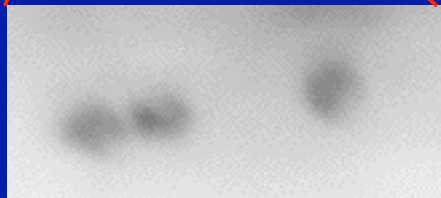
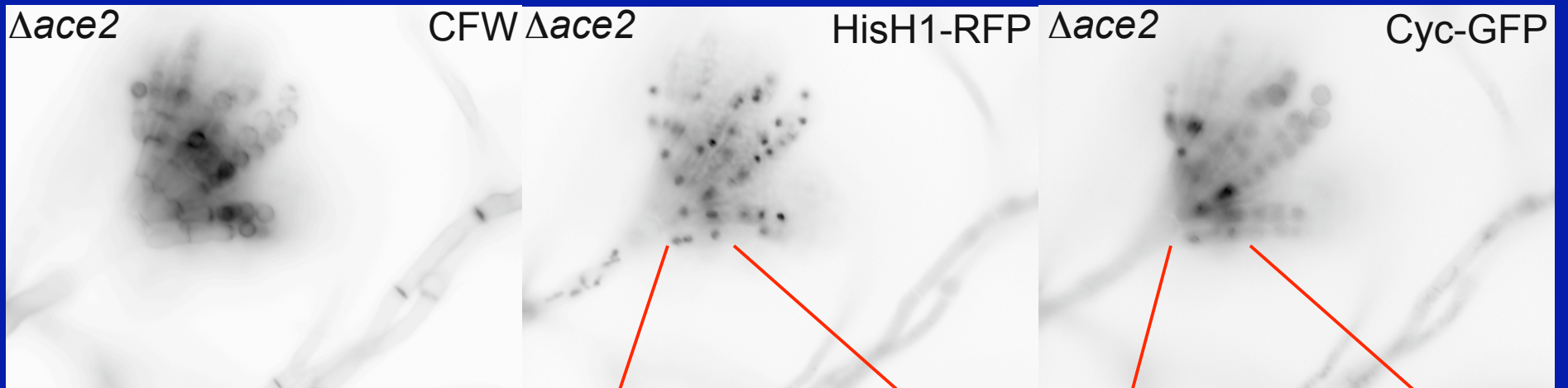
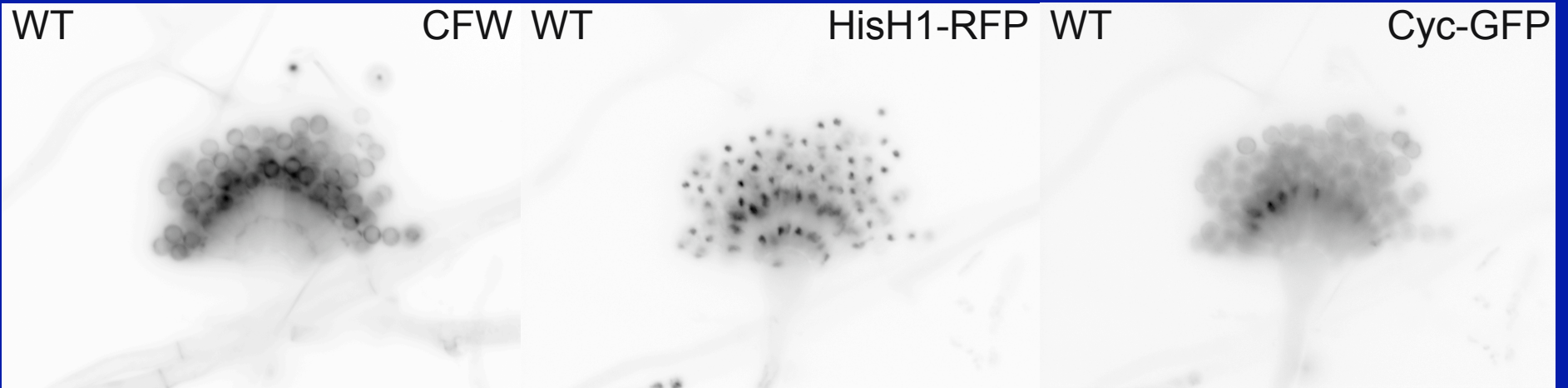


## Cell cycle regulation: Ace2/Swi5

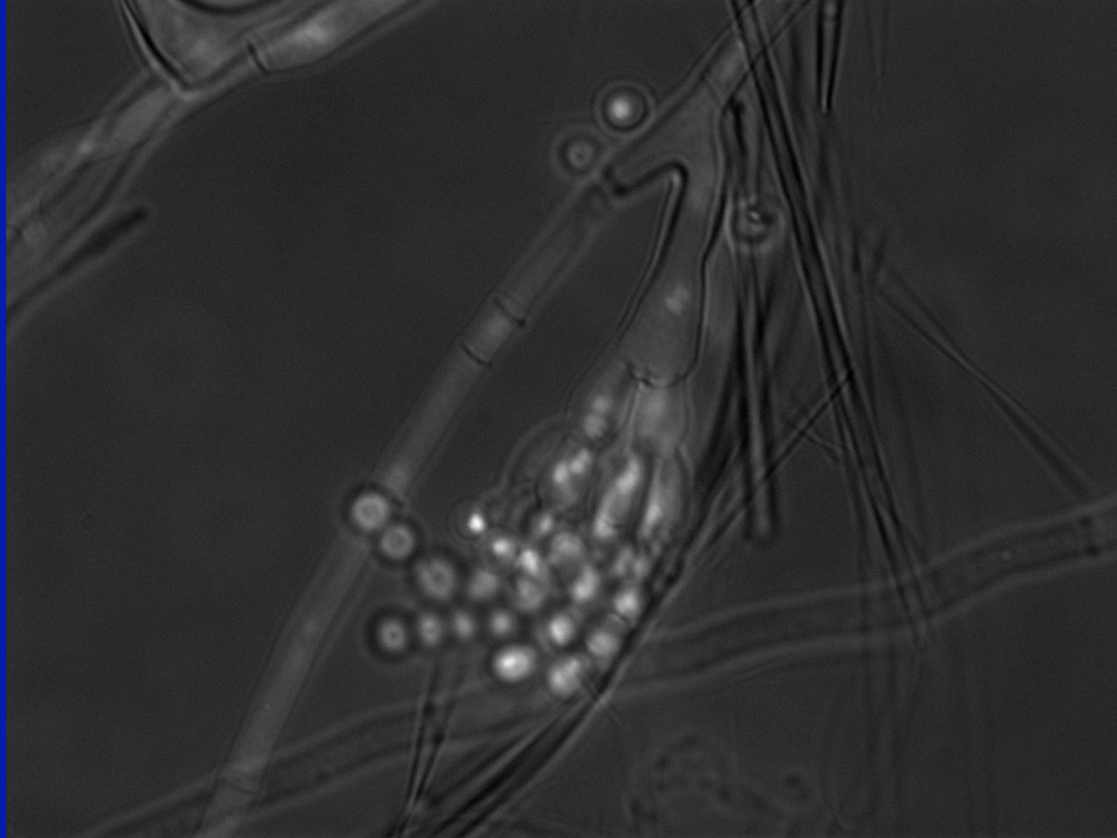


normal stalk + vesicle; defective transition from vesicle to metulae (hyphal → budding)

# Cell cycle regulation: *Ace2*/*Swi5*



## Cell cycle regulation: Ace2/Swi5

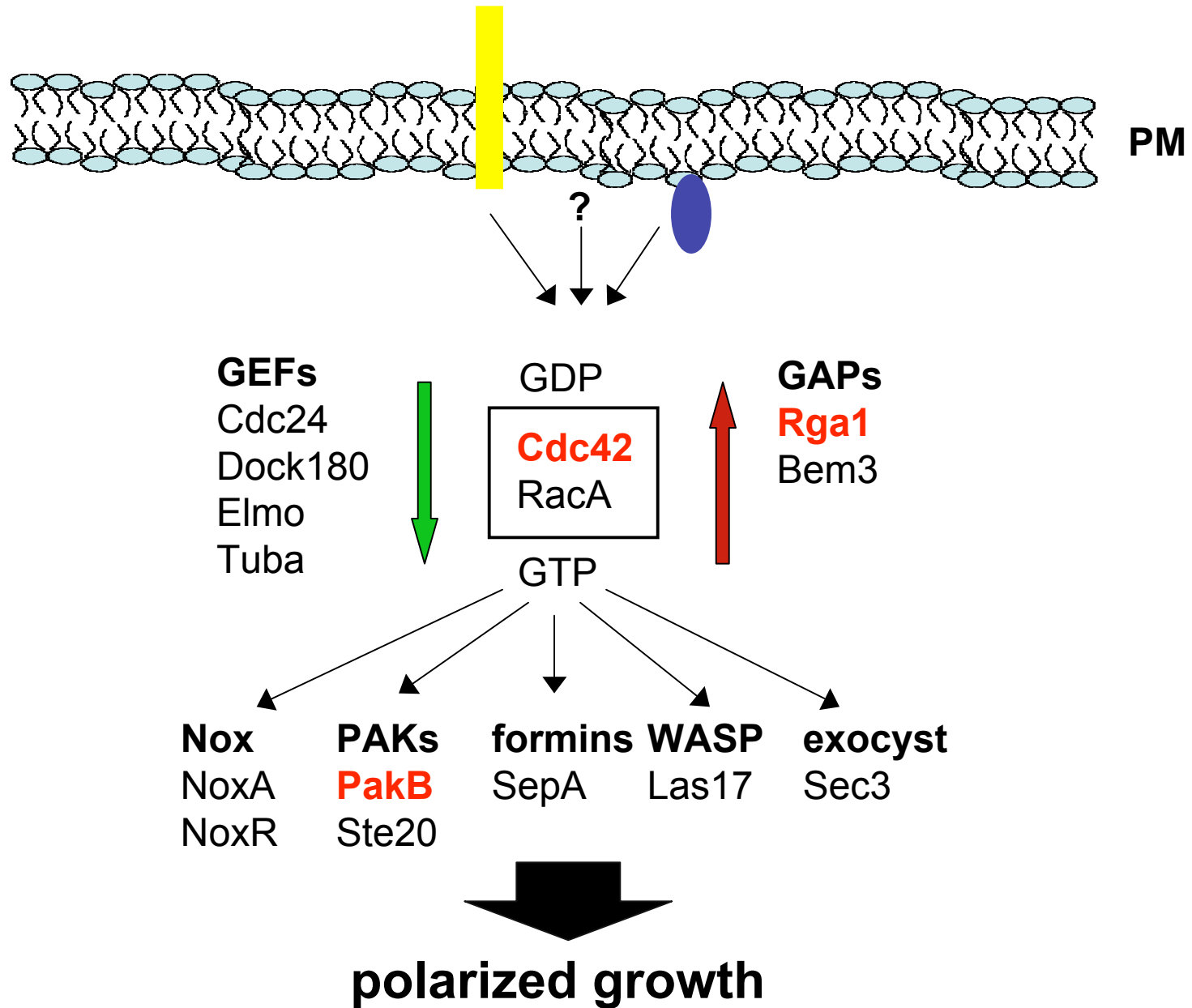


Ace2/Swi5 is required for orderly transition from vesicle → metulae

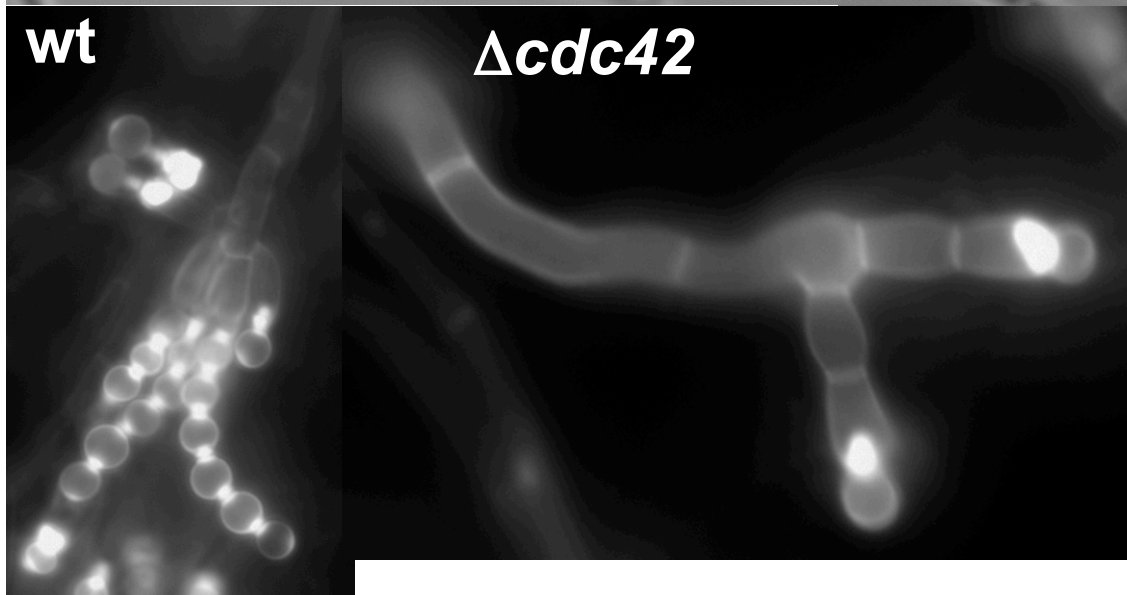
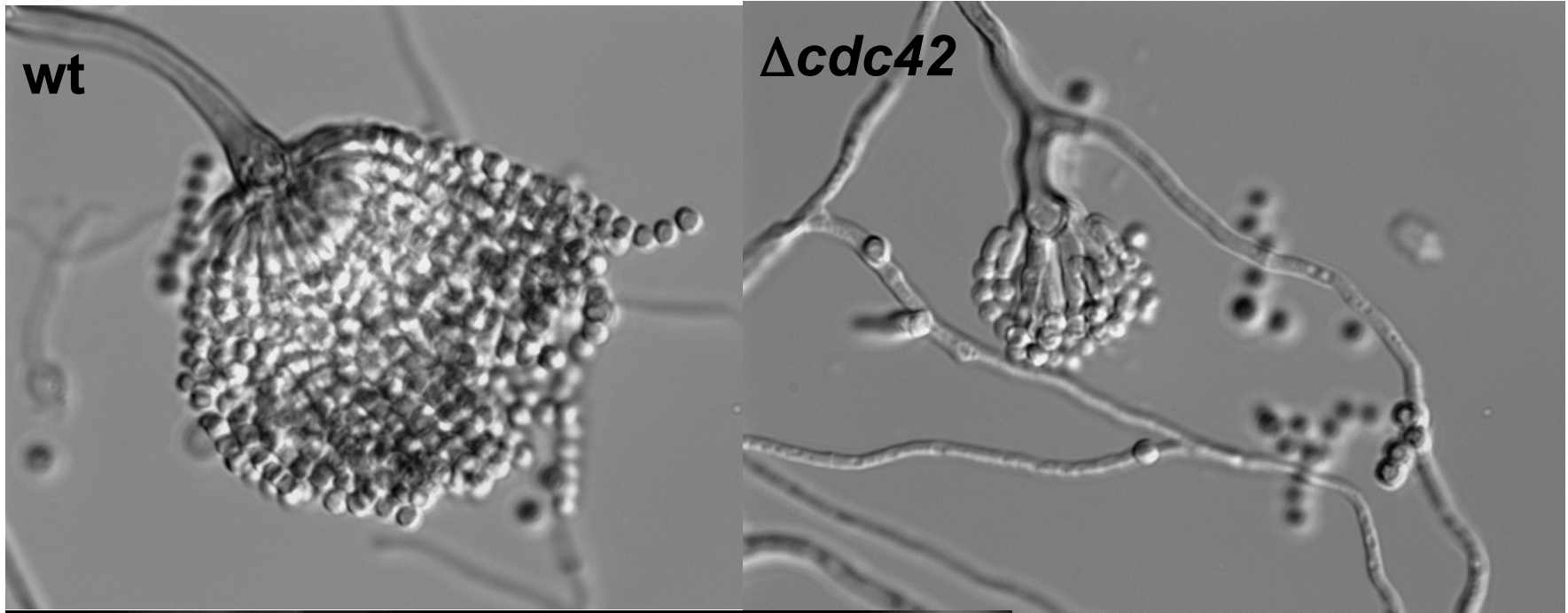
absence results in multinucleate hybrid cells that appear to undergo asynchronous mitosis

**coordinated cell cycle regulation underlies morphological transitions**

# Cdc42/Rac GTPase module

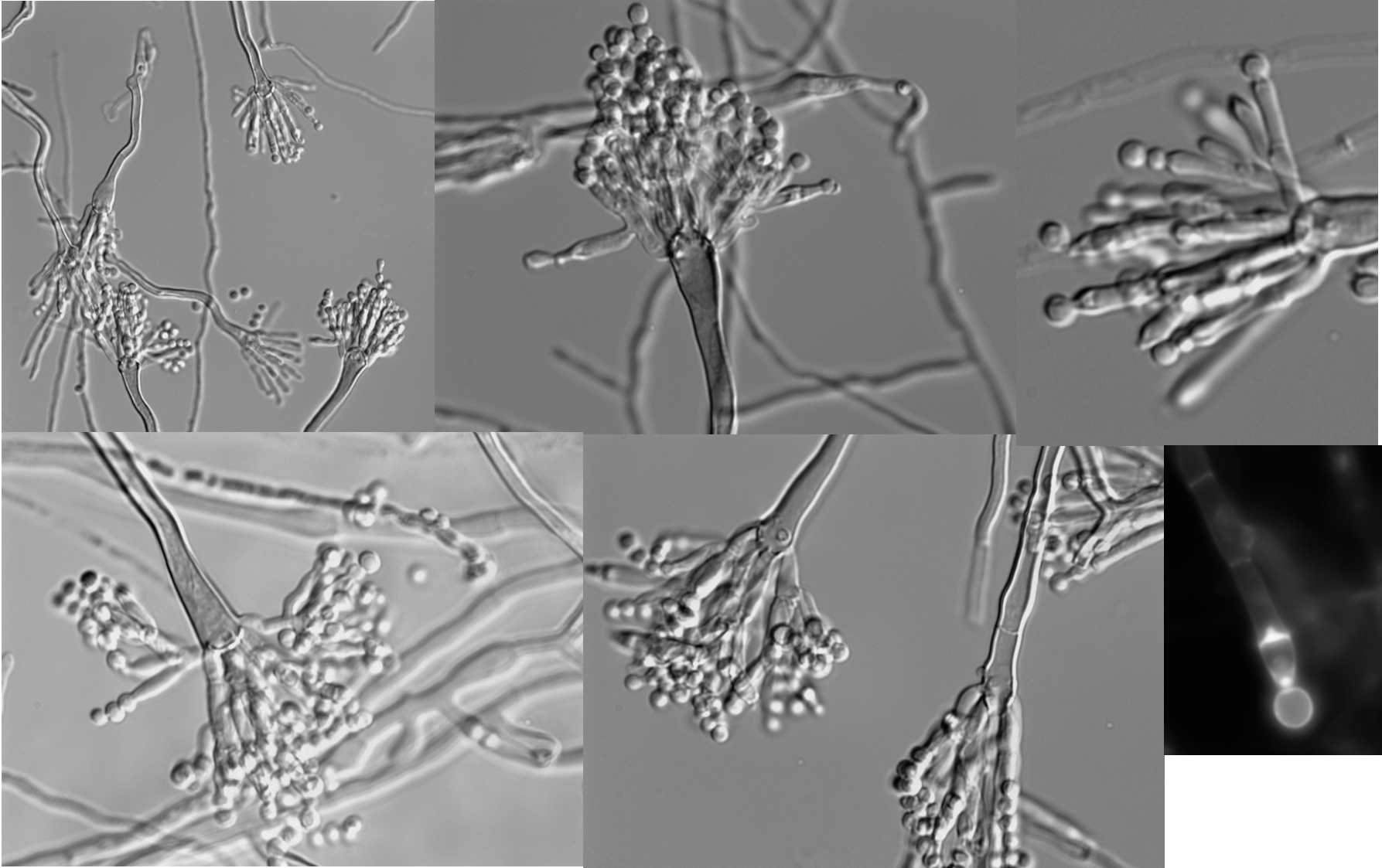


# Conidiophore development: Cdc42



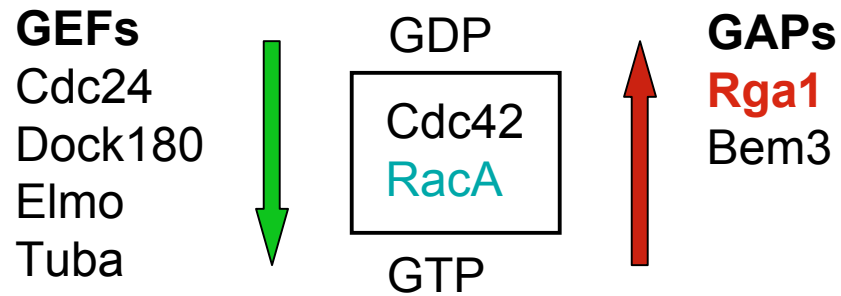
shorter conidiophores  
wider cells  
abnormal phialide-  
spore junctions

## Conidiophore development: Rga1



$\Delta rga1$  -- no obvious vesicles; elongated metulae and phialides; random branching of metulae

## Conidiophore development: Rga1



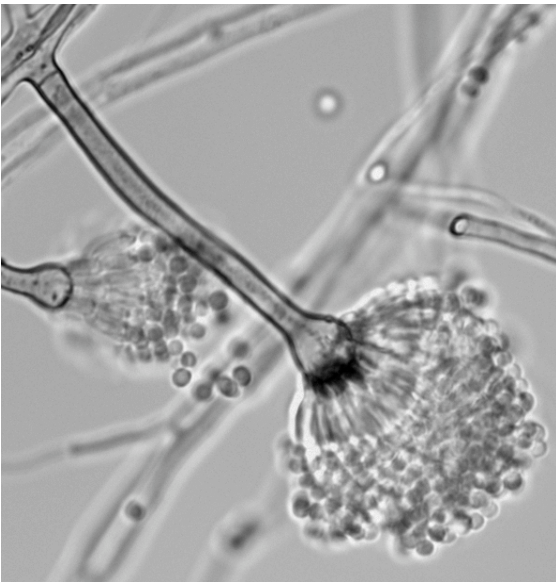
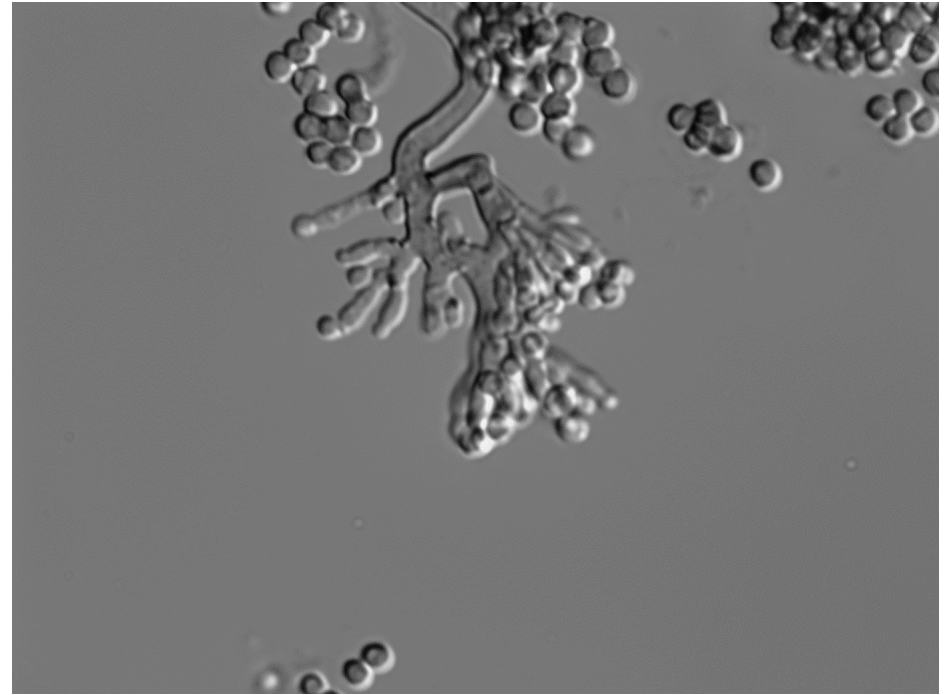
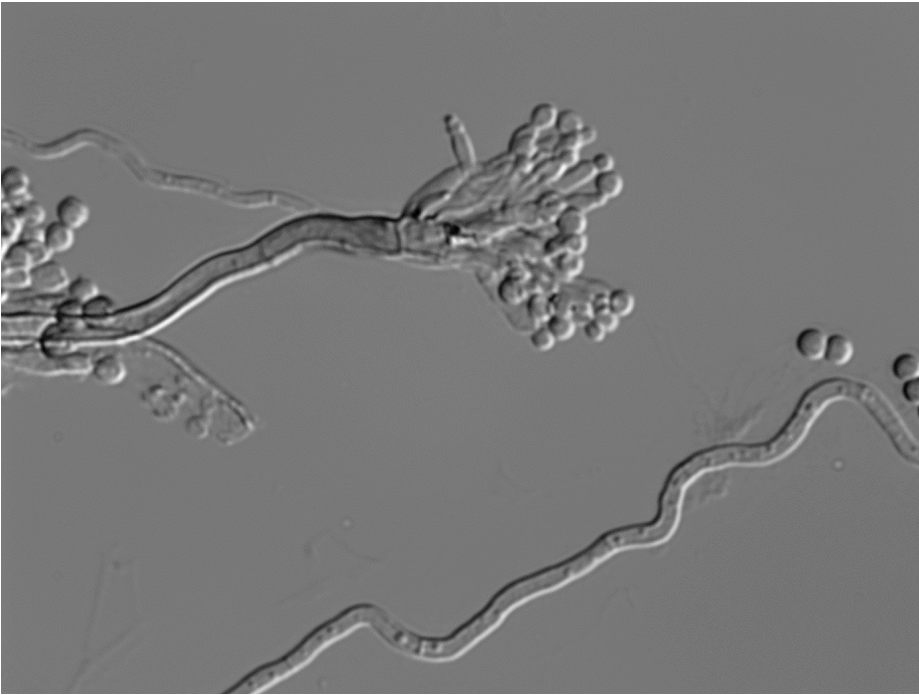
Does the  $\Delta rga1$  phenotypes reflect activation of Cdc42 or Rac1?



Deletion of *cdc42* suppresses  $\Delta rga1$  conidiophore defects. Thus, at least during conidiation, the primary target of Rga1 is Cdc42 (and  $\Delta rga1$  defects are due to abnormally active Cdc42)



## Conidiophore development: PakB



**PakB;**

suppresses conidiophore branching, formation of vesicle

## Cdc42/Rac GTPase module

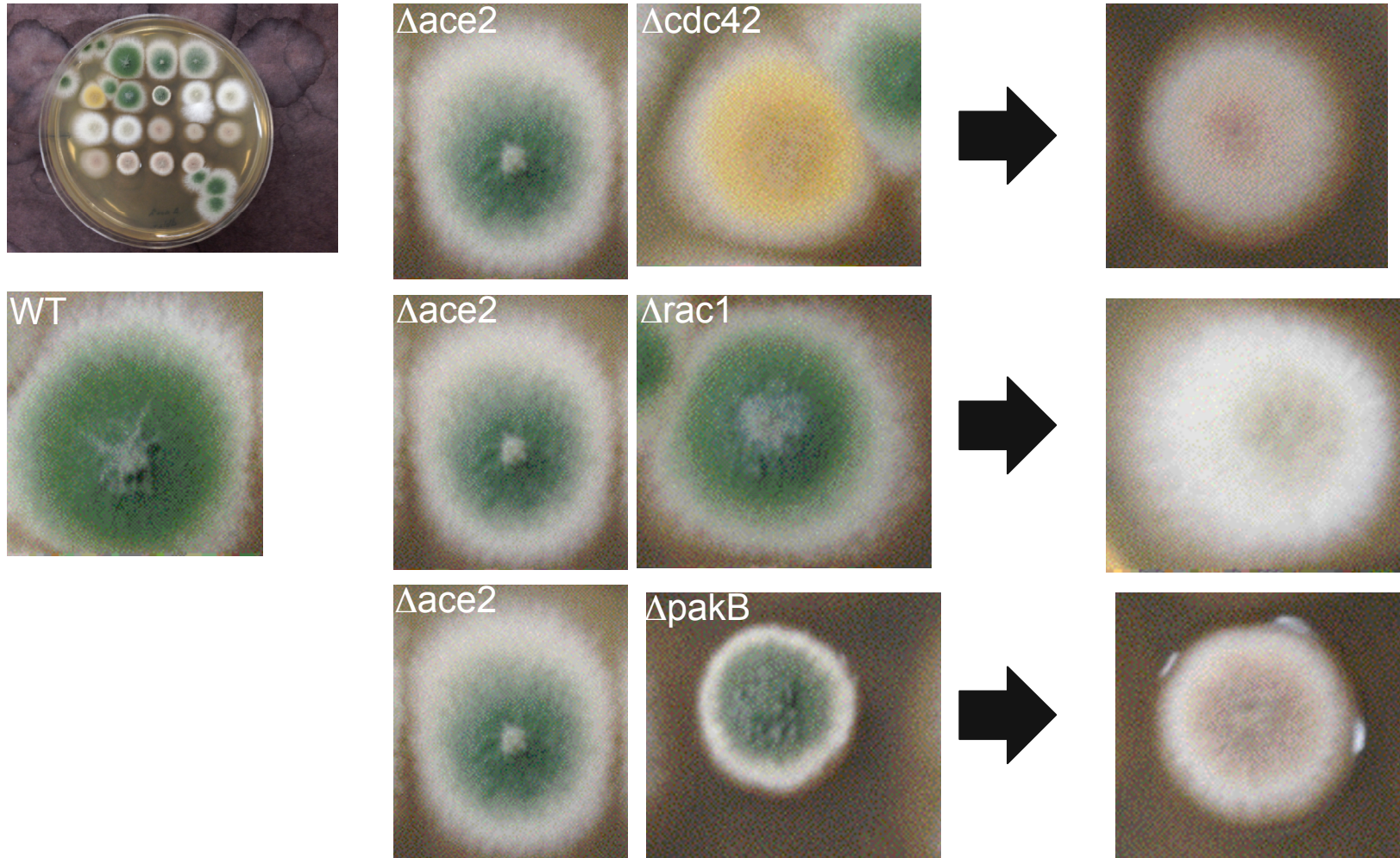
Rga1 and PakB suppress lateral branching during stalk formation --- proper spatial control of Cdc42 activation confines growth to tip and enables vesicle formation?

Rga1 is required for normal transition from hyphal to budding growth --- Cdc42 activity must be down-regulated to enable budding of metulae from vesicle?

Do cell cycle regulation and the Cdc42/Rac GTPase modules function in the same pathway?

Test double mutants for epistasis

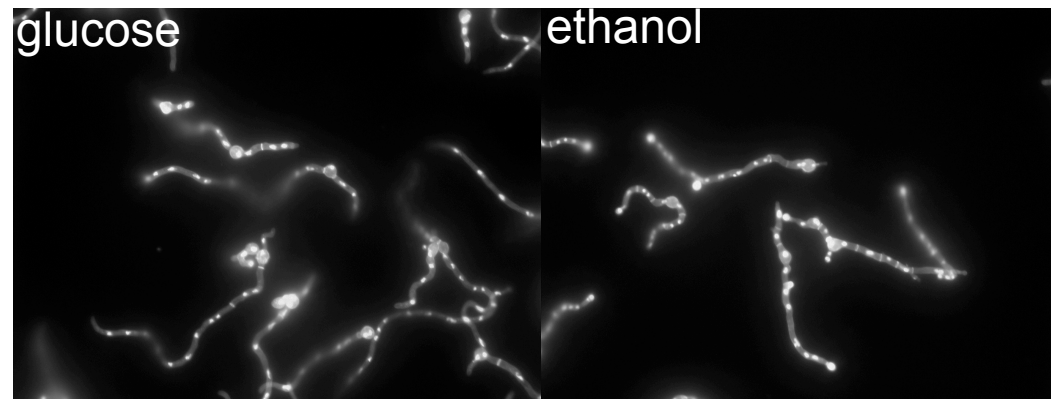
# Genetic interaction analysis



Enhanced conidiation defects imply that Ace2/Swi5 and the Cdc42/Rac1 GTPase module act via different pathways to regulate development

# Integration of cell cycle functions and Cdc42/Rac GTPase module with the core transcription pathway (BrlA)

Forced expression of *brlA* triggers formation of conidia (Adams and Timberlake, 1988)



*alcA(p)::brlA*

RNA-Seq was used to examine transcript profiles following *brlA* induction;

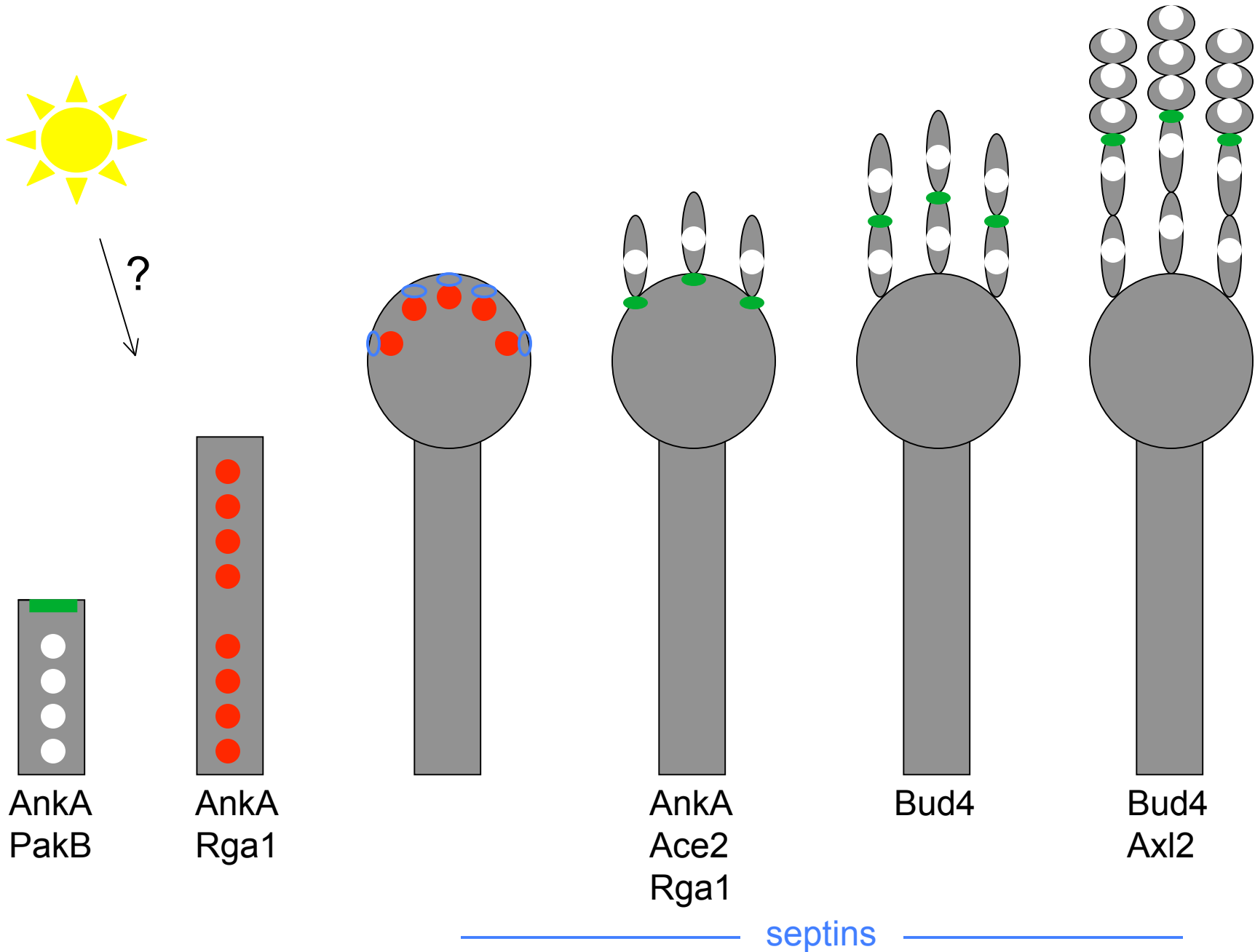
cell cycle	nimX (CDK1)	↑2.5x
	ankA (Wee1)	↑2.2x
	nimE (G2 cyclin)	↑5.4x
	cln1 (G1 cyclin)	↑2.2x
	pclA (G1 cyclin)	↑4.9x
	ace2/swi5	↑3.8x

Suggests that expression of cell cycle functions is regulated by BrlA → AbaA

stronger induction in response to *abaA* induction

Cdc42/Rac1 GTPase module – no response; post-transcriptional?

# Model for conidiophore morphogenesis in *A. nidulans*



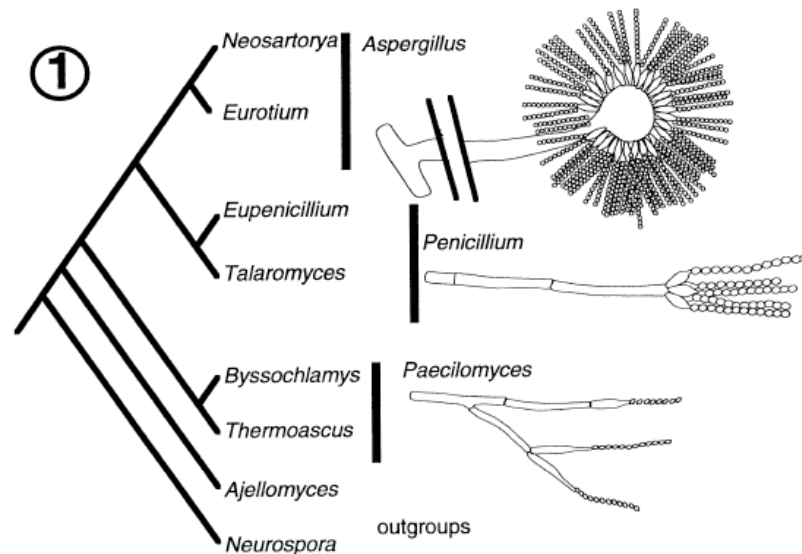
# Evolution of conidiophore morphology

- suppression of branching and septum formation in stalk
- termination of polarized growth to form vesicle
- switch to budding growth

Targets of selection?

expression of *ankA*, *ace2/swi5*, cyclins, or other cell cycle regulators?

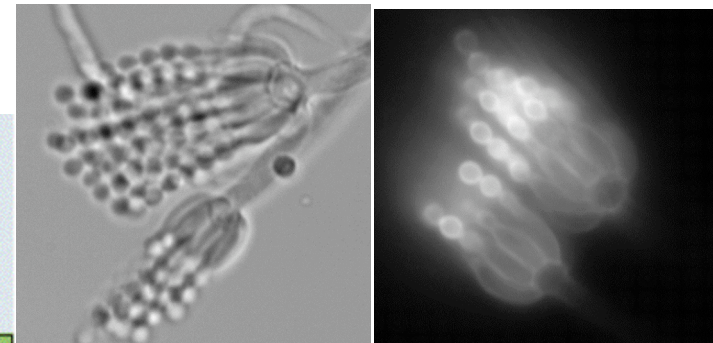
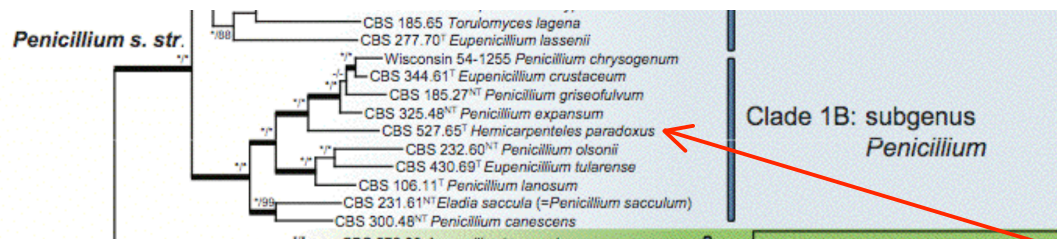
post-transcriptional control of Cdc42 GTPase activity (phosphorylation of GEFs, GAPs)?



# Evolution of conidiophore morphology

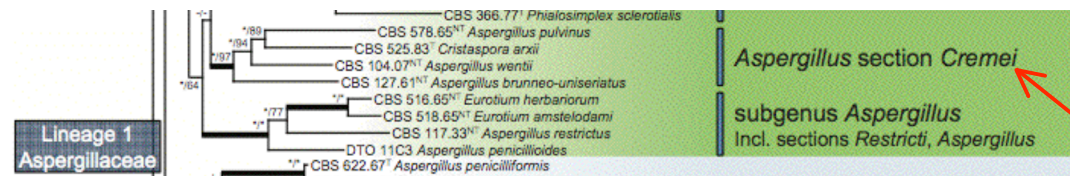
Test by;

1. Comparative gene expression analysis (e.g., *A. nidulans* vs. *P. chrysogenum*) during staged conidiation
2. Examine morphologically aberrant/transitional species



an "aspergillioid" *Penicillium*?

*Penicillium paradoxus*



a "penicillioid" *Aspergillus*?

*Penicillium inflatum*

**Aleks Virag**

**Haoyu Si**

**Bill Rittenour**

**Brad Downs**

**Rennes Nassrat**

**Lakshmi Yerra**



**IOS-0920504**  
**BDI-0743873**

