# Facultative sex regulated by a prion-like switch

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## Abstract

Prions are proteins that can adopt multiple conformations, at least one of which is self-templating. Ensuing changes in protein activity and subsequent adaptive traits are heritable over long biological timescales. In budding yeast, transient overexpression of different ORFs can induce prion-like states associated with fitness benefits in various conditions. The induction of these prions influences cellular decisions to optimize growth, often in a manner sensitive to the environment through shifts in proteostasis. For budding yeast, mating is an important, well-characterized decision. Protein-based systems rooted in mechanisms of self-templating aggregation, in the case of Whi3, and cytosolic titration, in the case of Far1, inform this decision with memories of pheromone exposure. However, Whi3 aggregation is not transmitted trans-generationally, and the Far1 titration system does not benefit from the meso-scale stability afforded by self-templating. Overexpression of *SLI15*, a component of the chromosome passenger complex (CPC) regulator of mitosis, results in a prion-like state with an insensitivity to mating pheromone, referred to as Ste<sup>+</sup>. Acquisition of *Ste*<sup>+</sup> modulates histone patterning and global transcriptomic repression, downregulating the mating pathway. This novel behavior associated with a CPC component represents a molecular relationship between the decisions to reproduce sexually and asexually, delineated by a prion-like memory.

Overexpression of *SLI15* induces a novel state characterized by heritable sterility: Ste+

### Diploid growth on selective media



Post transient Hsp70 inhibition • *Ste*<sup>+</sup> cells do not form diploid progeny • *Ste*<sup>+</sup> sterility is chaperone

(Ssa1) dependent







• *Ste*<sup>+</sup> cells do not arrest and form mating projections in response to mating pheromone





Ste<sup>+</sup> x Naive Naive x Naive



STE2

STE4

STE6

STE12

STE18

FUS2

FUS3

KSS1

STE7

Mating Pathway

- Kss1 Ste7 Assay mating Far1 nucleus arrest Far11 polarization & fusion Fus2  $\bigcirc$  Significantly down (p < 0.05)  $\bigcirc$  Significantly up (p < 0.05) • No significant change (p > 0.05) Overexpression rescues mating
- *Ste*<sup>+</sup> cells have increased fitness in conditions predicted by transcriptomic analysis

Time (h)

48

• The transcriptional and phenotypic characteristics of the *Ste*<sup>+</sup> state

Ste<sup>+</sup>: ancestral

100 80

% Mating projected cells (2 hours in 20 μM α factor) 07 05 09 09 08 100-80 60-4(

20 HSP70 inhib: Independent Ste+ 0.001 10 0.01 inductants  $[\alpha \text{ factor}] (\mu M)$ 

Overexpression of *SLI15* induces a heritable change

*Ste*<sup>+</sup> cells maintain checkpoint related CPC activity

 Among mating pathway components, overexpresion of either STE7 or STE12 is sufficient to transiently rescue mating Mate -----

expr

0

Endogenous

24

-- Naive

100

--- Ste<sup>+</sup>

• *Ste*<sup>+</sup> cells display subtle

downregulation of several

mating pathway components





RED2)

Ste<sup>+</sup>



Residue

- Transient overexpression of *SLI15* results in isolates with altered Sli15-GFP distribution
  - These isolates are unable to mate, and referred to as Ste<sup>+</sup>





Ste<sup>+</sup> encompasses altered Sli15 distribution, histone modification, transcription, and mating dynamics



#### 11 0.125 -- Ste+ ਦ੍ਰ 0.0625· 50 100 Time (hours)

- Naive

## Ste<sup>+</sup> cells demonstrate altered histone patterning

0.5

0.25





• Working hypothesis: Altered CPC activity in *Ste*<sup>+</sup> cells

results in a distinct chromatin state via rewiring of

chromatin condensation pathways. This chromatin

state enforces a transcriptional profile underlying the

observed fitness and mating phenotypes.



