

Cell Biology Screens

Target of rapamycin screen 2: FK506 and rapamycin act through distinct mechanisms

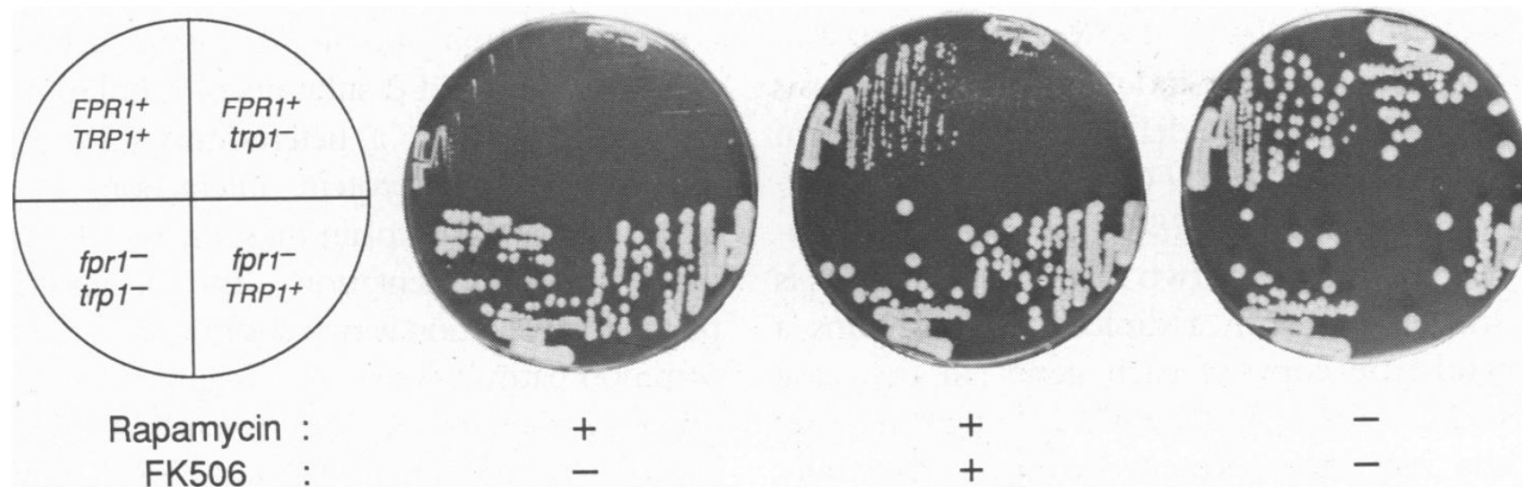
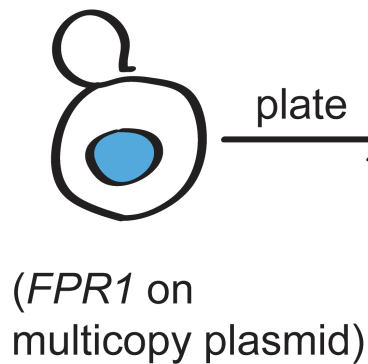


Fig. 3. Antagonism of rapamycin toxicity by FK506. Isogenic haploid derivatives of strain JK9-3d (17) were grown for 96 hours at 30°C on YEPD medium (32) that contained either rapamycin (0.1 µg/ml), rapamycin (0.1 µg/ml) plus FK506 (50 µg/ml), or neither drug (presence or absence indicated by + or -). Antagonism is seen with the *FPR1+* *TRP1+* strain JH6-1b (upper left quadrant); this is the only strain that is both sensitive to rapamycin (*FPR1+*) and resistant to the toxic effects of FK506 (*TRP1+*) (16, 19). All other strains are controls. The strains are JH6-1b (*FPR1+* *TRP1+*), JK9-3dα (*FPR1+* *trp1-*), JH10 (*fpr1-* *TRP1+*), and JH3-3b (*fpr1-* *trp1-*) (17).

Target of rapamycin screen 3: rapamycin toxicity requires functional *TOR* genes

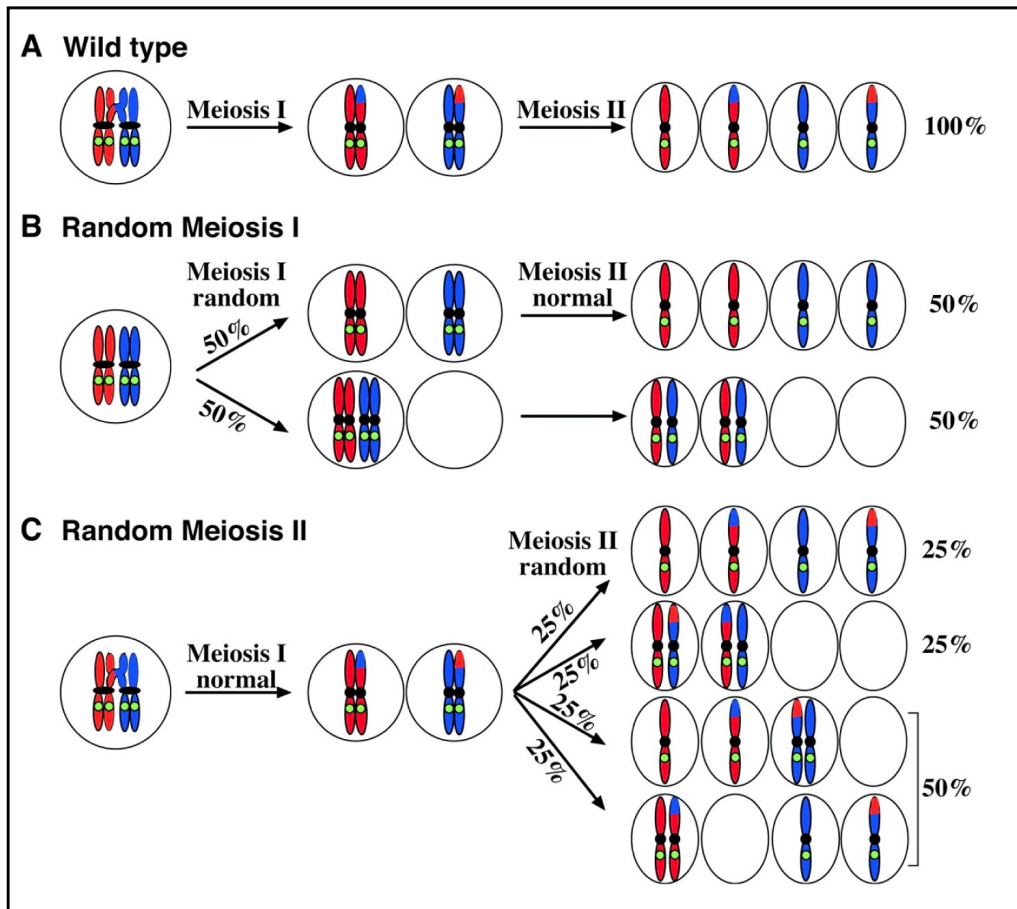


- cross to wild type
- complementation analysis

Allele	Growth on rapamycin (µg/ml)				FKBP sequence
	0	0.1	1	10	
<i>fpr1-4</i>	+	+	+	-	M11
<i>fpr1-5</i>	+	+	+	-	P23R
<i>fpr1-6</i>	+	+	+/-	-	H32P
<i>fpr1-7</i>	+	+	n.d.	n.d.	G35D
<i>fpr1-8</i>	+	+	+	+	G65D
<i>fpr1-9</i>	+	+	-/+	-	G65C
<i>fpr1-10</i>	+	+	+	-/+	G65V
<i>fpr1-11</i>	+	+	+/-	-	L81S
<i>fpr1-12</i>	+	+	+	+	E109ochre (UAA)
<i>tor1-1</i>	+	+	+	+	WT
<i>TOR1-2</i>	+	+/-	+/-	-/+	WT
<i>tor2-1</i>	+	+	+	+	n.d.
<i>fpr1-3</i>	+	+	+	+	<i>fpr1::URA3-3</i>
<i>FPR1</i>	+	-	-	-	WT

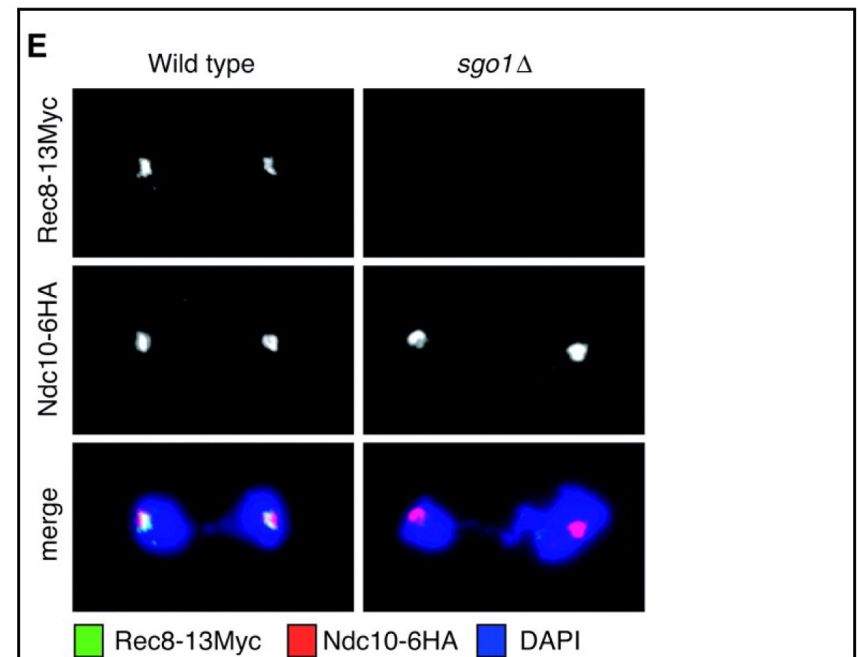
diploid	rap phenotype
<u><i>fpr1-3</i></u> <i>FPR1</i>	sensitive
<u><i>fpr1-6</i></u> <i>fpr1-3</i>	~ resistant
<u><i>fpr1-12</i></u> <i>fpr1-3</i>	resistant
<u><i>tor1-1</i></u> <i>fpr1-3</i>	sensitive
<u><i>TOR1-2</i></u> <i>fpr1-3</i>	resistant
<u><i>TOR1-2</i></u> <i>FPR1</i>	resistant
<u><i>tor1-1</i></u> <i>TOR1-1</i>	resistant (segregates 4R:0S)
<u><i>tor1-1</i></u> <i>tor2-1</i>	resistant (non-allelic non complementation)
<u><i>tor2-1</i></u> <i>fpr1-12</i>	resistant (non-allelic non complementation)

Phenotypic screens vs. selection screens

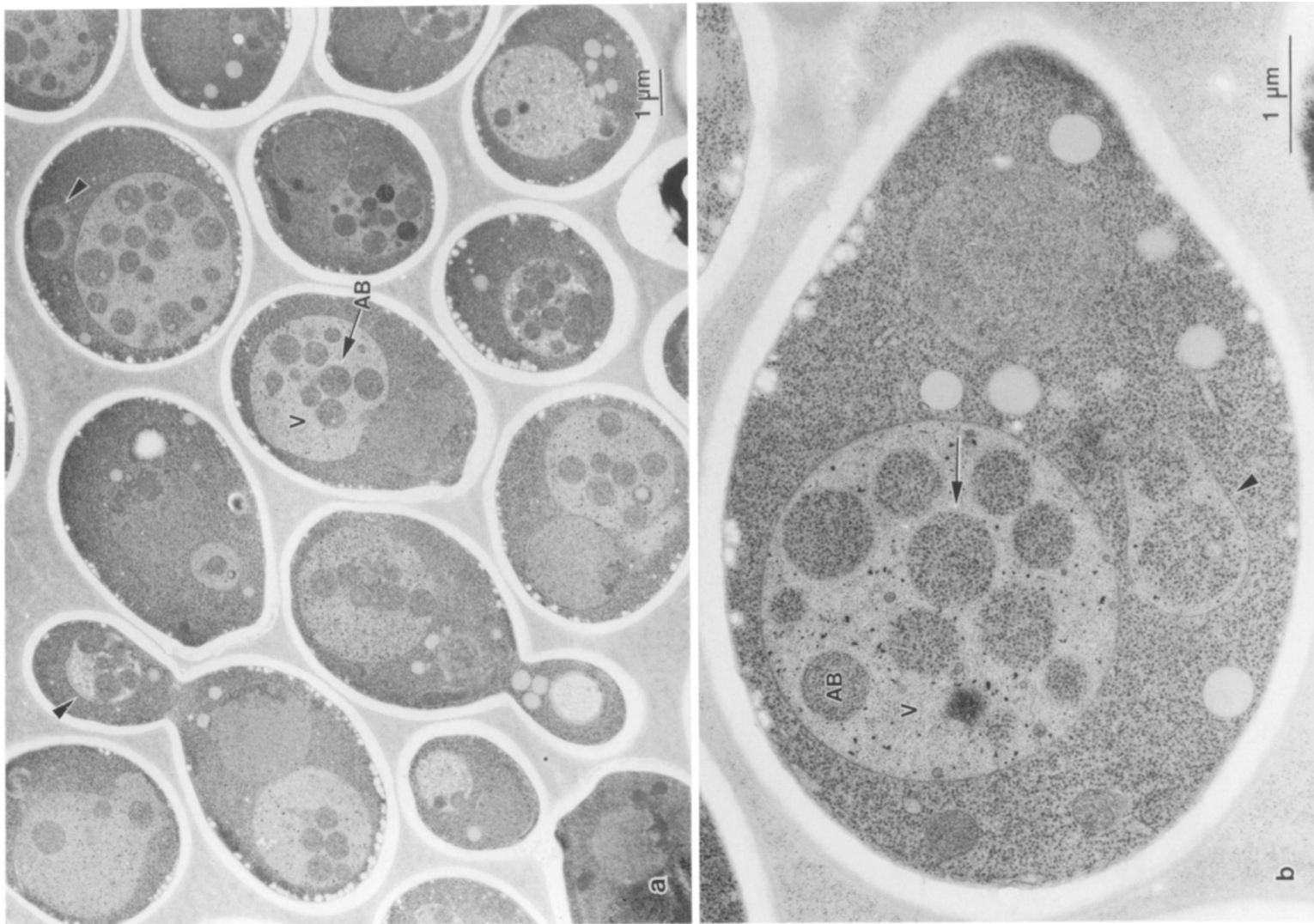


A

Genotype				other
Wild Type	99.5%	0.5%		
<i>sgo1Δ</i>	21.6%	43.1%	20.1%	15.2%
<i>iml3Δ</i>	60.5%	29.0%	10.5%	
<i>chl4Δ</i>	61.6%	29.3%	8.6%	0.5%



Autophagy screen 1: protease-deficient cells accumulate autophagic bodies



Autophagy screen 2: Isolation of the first autophagy mutant

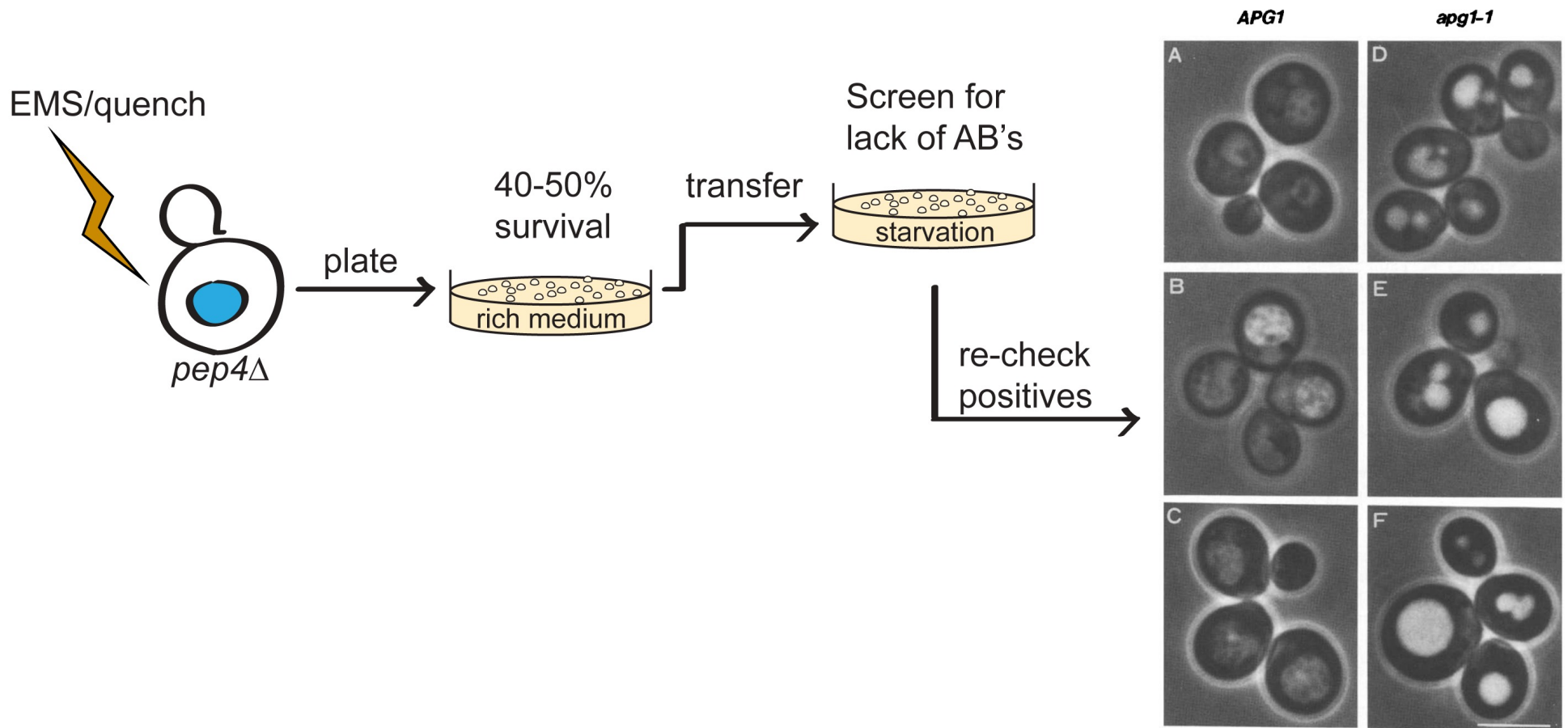


Fig. 1. Morphological changes of vacuoles during nitrogen starvation. Phase contrast microscopic images of cells of X2180-1A (*APG1*, left), and MT14-1B (*apg1-1*, right) incubated in SD (-N) medium containing 1 mM PMSF for 2 h (A,D), 4 h (B,E), and 8 h (C,F). Bar = 5 μ m.

Autophagy screen 3: Characteristics of autophagy mutants

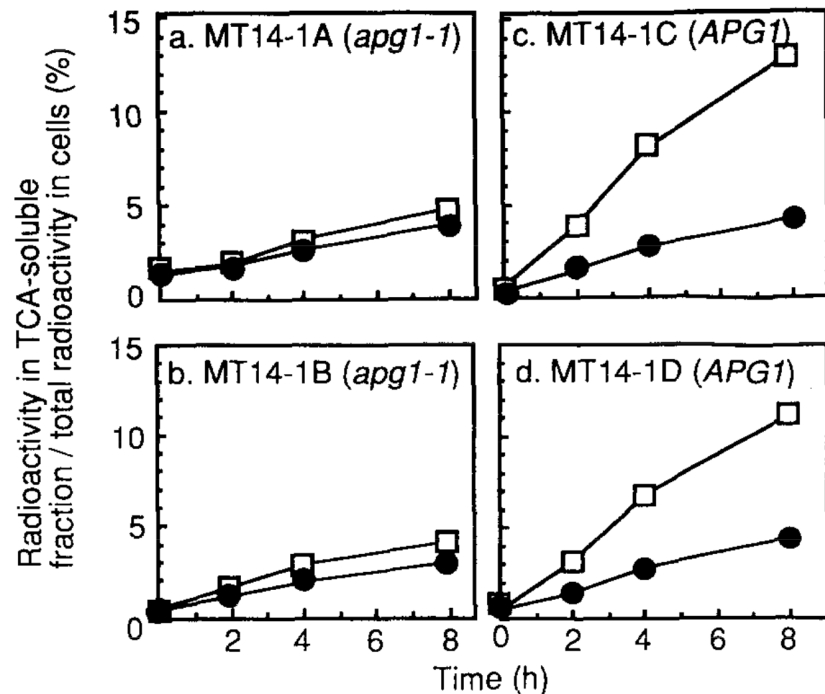


Fig. 2. Protein degradation in cells in nitrogen starvation medium. Radioactivities in the TCA-soluble fraction and in total cells were measured as described in section 2. With (●) and without 1 mM PMSF (□). (a) MT14-1A (*apg1-1*), (b) MT14-1B (*apg1-1*), (c) MT14-1C (*APG1*), and (d) MT14-1D (*APG1*) are segregants from X2180-1A/MT13-8C (*APG1apg1-1*).

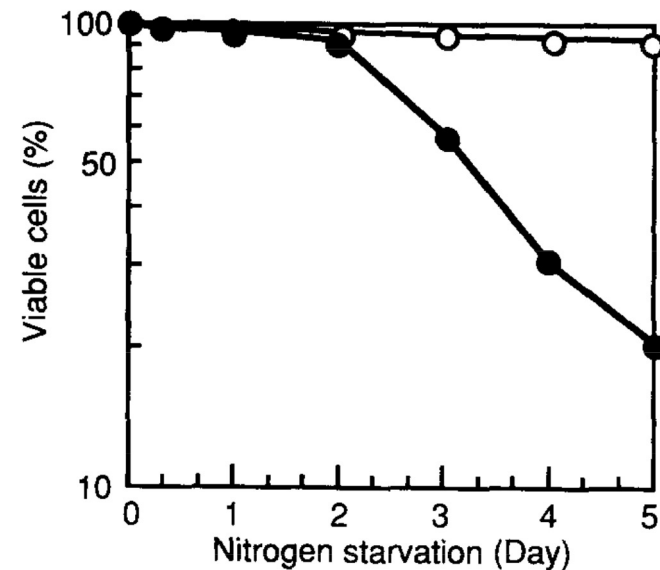
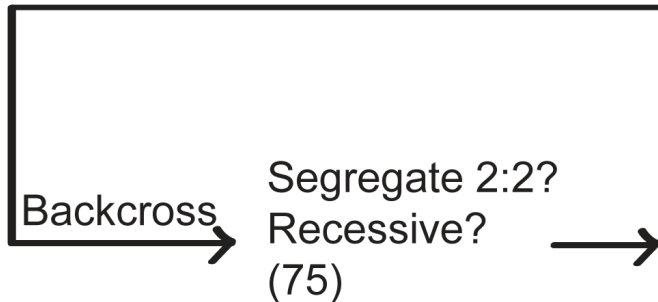
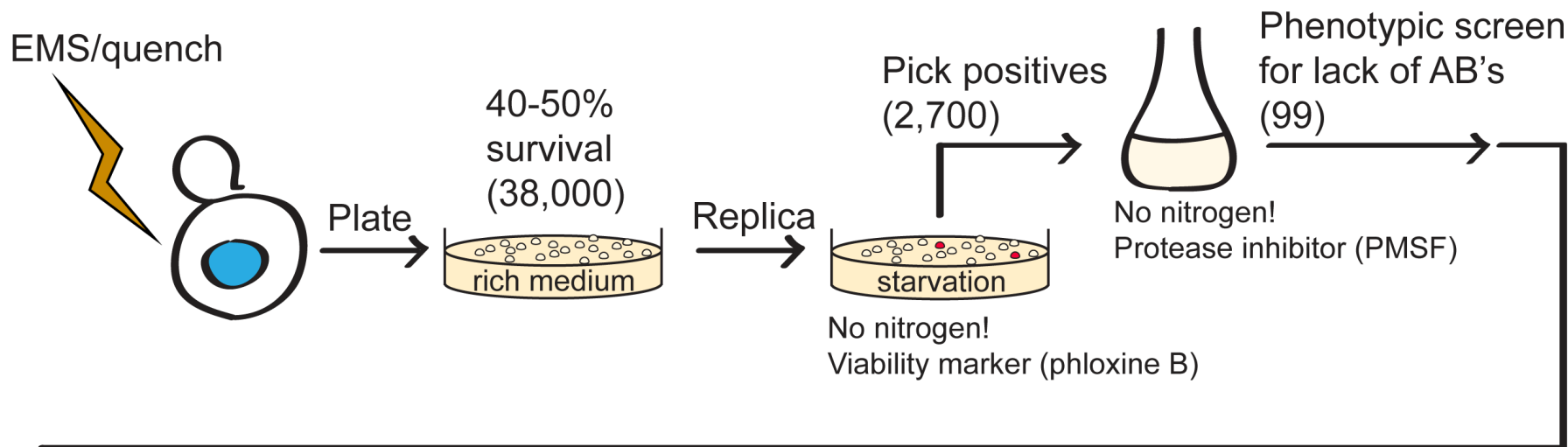


Fig. 3. Loss of viability of the *apg1* mutant in nitrogen starvation medium. Exponentially growing cells of X2180-1A (*APG1*, ○), and MT14-1B (*apg1-1*, ●) were transferred to SD (-N) medium. At the indicated times, viability was determined as described in section 2. 400–600 cells were counted at each time point. Data are averages of 3 determinations.

Autophagy screen 4: *E unum pluribus*: Isolation of 15 autophagy mutants



15 genes

Table I
Distributions of *apg* mutations in 15 complementation groups

<i>apg1</i>	15
<i>apg2</i>	13
<i>apg3</i>	10
<i>apg4</i>	9
<i>apg5</i>	5
<i>apg6</i>	4
<i>apg7</i>	4
<i>apg8</i>	4
<i>apg9</i>	4
<i>apg10</i>	3
<i>apg11</i>	2
<i>apg12</i>	1
<i>apg13</i>	1
<i>apg14</i>	1
<i>apg15</i>	1
Total	77

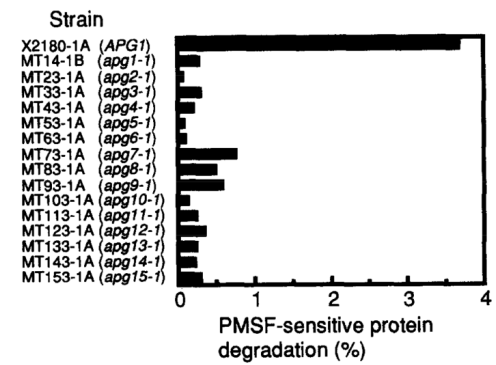


Fig. 4. PMSF-sensitive protein degradation of *apg* mutants in nitrogen starvation medium. PMSF-sensitive protein degradations in cells incubated in SD (-N) medium for 8 h are shown. PMSF-sensitive protein degradation was determined as described for Fig. 2. Total protein degradation in each *apg* mutants ranged to 28–36% of that in wild-type cells (see also Fig. 2). The strains used were representatives of each *apg* mutation.

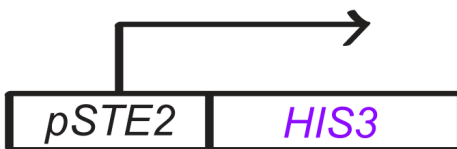
Using the yeast deletion collections

Gene disruption cassette

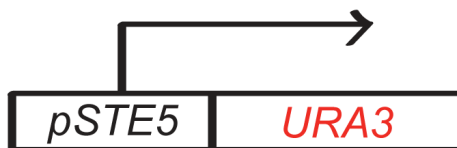


Each strain (~4,500 total) contains one gene disruption cassette

Useful selection cassettes



Allows for selection of particular mating types



Allows for selection of haploids/diploids

Plasmid Shuffle/rescue

