Constraints on the G1/S transition pathway may favor selection of multicellularity as a passenger phenotype

Selection of multicellularity as a passenger phenotype

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Abstract

Multicellularity has emerged in the three branches of the tree of life. The formation of simple multicellular entities can either result from cells aggregating or staying together after mitosis. However, it is not yet fully understood how, once formed, these simple multicellular entities could be maintained or even selected for. Here, using the *ace2* yeast snowflake model of simple multicellularity, we aimed at identifying genetic conditions favoring its maintenance. Growth-competition experiments revealed that, while the *ace2* mutation by itself does not provide any fitness advantage or disadvantage, the *ace2* snowflakes were strongly selected when combined to conditions affecting regulators of the G1/S transition of the cell cycle, such as Cln3 or Whi5. We show that this selection results from a faster exit from quiescence of the *ace2* snowflake cells. Importantly, this advantage is not dependent on the multicellular phenotype, but rather on the *ace2* genotype itself. We found that the *ace2* selective advantage in the *cln3* background fully depends on the *KSS1* gene, a target of the Ace2 transcription factor. Finally, we show that phenotypes observed for *ace2* mutants are phenocopied by the $AMN1^{368D}$ allelic form found in "non-laboratory" yeast strains, hence adding physiological relevance to these observations. Altogether, our results support the hypothesis that simple multicellularity could persist, not because it provides a direct selective advantage due to multicellularity itself, but rather as a "passenger" phenotype that is maintained alongside other selected traits.

28 # Introduction

29 Multicellularity has evolved repeatedly and independently in distinct lineages within bacteria, archaea
30 and eukaryotes (1). This evolutionary process firstly involves the selection of simple forms of
31 multicellularity such as clusters of cells. Several selective drivers of simple multicellularity have been
32 proposed (2) that are generally associated to changes in geometry allowing access to new resources
33 (faster sedimentation, increased mobility, foraging, dispersal), as well as other advantages associated
34 with size increase (predation avoidance, stress resistance, improved extracellular metabolism) and
35 finally, chimerism: the capacity to combine different cellular phenotypes in a single entity, allowing the
36 establishment of intra-organism division of labor.

37 Many forms of multicellularity are facultative and their formation is triggered by external signals. One
38 of the best studied case is that of the slime mold *Dictyostelium discoideum*, which cells, in response to
39 resource limitation, aggregate to form a fruiting body that favors dispersal of spores (3,4). Another
40 example comes from *Saccharomyces cerevisiae* cells that, under poor nitrogen conditions, can become
41 highly polarized and stay attached, thereby favoring foraging, a phenomenon known as pseudohyphal
42 growth (5,6). In such cases, multicellularity provides alternative options to the non-proliferation
43 observed in unicellular organisms in response to local nutritional starvation (7). These multicellularity-
44 specific responses are triggered by nutritional cues and, some of them may have evolved by functional
45 recruitment of unicellular pre-existing sensors and pathways. It is hence likely that some actors of
46 nutritional control of cell cycle progression should modulate facultative multicellularity. Indeed, there
47 are several experimental evidences connecting the regulators of G1/S transition in the cell cycle to
48 multicellularity. This mostly concerns two major regulators, retinoblastoma (RB) and Cyclin D. RB is a
49 negative regulator of E2F, a transcription factor critical for G1/S progression, while cyclin D is a negative
50 regulator of RB (8).

51 Several experimental evidences connect regulators of G1/S transition, and notably RB, to
52 multicellularity. First, when RB from the simple multicellular volvocine *Gonium pectorale* was

53 expressed in its close unicellular relative *Chlamydomonas*, the C*hlamydomonas* cells behaved as a
54 simple multicellular colonial entity (9). This points to an important role for RB in triggering uni- to
55 multicellular transition. Second, in the aggregative multicellular slime mold, *Dictyostelium discoideum*,
56 the RB orthologue, RblA, was found to be involved in the stalk *vs* spore cell-fate preference (10). Finally,
57 another key regulator of G1/S transition, namely Cyclin D, has also been associated to uni- to
58 multicellular transition in two different yeast species, *Candida albicans* and *Saccharomyces cerevisiae*.
59 Depending on environmental conditions, *Candida albicans* can grow either as a yeast unicellular
60 planktonic form, or as a multicellular hyphal form. The transition from one form to the other is
61 associated with invasion and virulence. Strikingly, the knock-down of the *C. albicans* cyclin D
62 orthologue Cln3 resulted in hyphal growth suggesting that the G1 phase of the cell cycle is important
63 in the transition from uni- to multicellular development in *C. albicans* (11). Similarly, in *S. cerevisiae*
64 deletion of *CLN3*, the budding yeast cyclin D homolog, enhanced pseudohyphal growth (12).
65 Interestingly, *CLN3* encodes an inhibitor of Whi5 which is the yeast functional equivalent of RB. It hence
66 seems that, during evolution, uni- to multicellularity transitions have repeatedly used pre-existing
67 regulators of the G1/S transition, such as RB and cyclin D. These intriguing observations, from
68 phylogenetically distant organisms, connecting G1/S transition regulators to multicellularity led us to
69 ask the following question. Could the evolution of the G1/S regulation pathway itself have somehow
70 favored multicellularity emergence and/or maintenance?

71 In this work we used *S. cerevisiae* to question the complex relationship between G1/S cell cycle
72 regulators and multicellularity. We took advantage of the snowflake model (13,14) in which
73 multicellularity is due to a genetic defect in cell separation caused by the deletion of Ace2 a
74 transcription factor that control the expression of chitinases and endoglucanases required for cell wall
75 degradation after cytokinesis completion (15,16). When planktonic *ACE2* and snowflake *ace2* cells
76 were co-cultured and their fitness compared, we observed that *CLN3* deletion, as well as *WHI5*
77 overexpression, favored the *ace2* snowflake form. We showed that exit from quiescence is the critical
78 stage leading to the *ace2 cln3* snowflakes selection. Importantly we demonstrated that the *ace2*

79 mutation, but not the snowflake phenotype, was responsible for the *cln3* faster quiescence exit
80 phenotype. Finally, we show that phenotypes observed for *ace2* mutants are phenocopied by the
81 *AMN1*^{368D} allele found in "non-laboratory" yeast strains. Our results point to the possibility that
82 evolution of cell cycle control could promote the evolution of multicellularity as a passenger
83 phenotype.

84

85 Results

86 The *ace2 cln3* snowflake strain is selected over the *ACE2 cln3* planktonic strain.

87 In order to investigate the relationship between the G1/S cell cycle regulators and multicellularity, we
88 used the yeast snowflake model in which the absence of Ace2, a transcription activator of several
89 chitinase and endoglucanases genes (17–19), results in the lack of separation of the daughter cell from
90 the mother cell after cytokinesis. It ensues that *ace2* mutant yeasts form cell clusters that grow and
91 end-up breaking most probably due to mechanical constraints (20). A major advantage of studying
92 snowflakes rather than inducible forms of multicellularity, such as pseudo-hyphae, is that unicellular
93 (planktonic, PK) and multicellular (snowflake, SF) yeast, differing only by one mutation in the *ACE2*
94 gene, can be co-cultivated and their fitness compared. We hence grew isogenic diploid *ACE2*/*ACE2* and
95 *ace2*/*ace2* cells of the BY (S288c-derived) background in minimal enriched medium (SD casa WAU).
96 Cultures of both genotypes were mixed to obtain a 50/50 ratio of *ace2* SF and *ACE2* PK strains, either
97 at the phenotype level (number of entities observed by microscopy, a SF being an entity with 4 or more
98 cells, Figure 1-figure supplement 1) or at the cell genotype level (by monitoring the *ace2::kanMX*
99 disruption using qPCR) (Figure 1A). The mixtures were then repeatedly grown to saturation and diluted
100 every 2 days, resulting in a total of more than 100 generations. Interestingly, the *ace2* strain showed
101 no selective advantage or disadvantage over the *ACE2* strain, both at the SF phenotype level (Figure
102 1B, black bars) and the genotype level (Figure 1C, black bars). This indicates that, under these growth

103 conditions, the *ace2* mutation and its multicellular phenotype have no effect on fitness. Strikingly,
104 when similar experiments were performed with *ace2* or *ACE2* strains carrying a deletion of the *CLN3*
105 gene, a deletion known to lengthen the G1 phase and to significantly increase cell volume (21), the
106 *ace2* snowflake strains rapidly took over the population (red bars, Figure 1B and 1C). A similar result
107 was obtained when *WHI5,* encoding the major downstream target of *CLN3*, was overexpressed (red
108 bars, Figure 1D). These results strongly suggest that the observed effect on population fitness takes
109 place through the *CLN3/WHI5* G1/S transition regulatory pathway. Together our results reveal a robust
110 phenotypic interaction between the G1/S transition major players, *CLN3* and *WHI5*, and the *ace2*
111 snowflakes.

112

113 *ace2 cln3* cells exit faster from quiescence than *ACE2 cln3*

114 In our competition experimental setup (Figure 1A), cultures alternate phases of active cell division with
115 stationary phases during which cells are in a quiescent state (Figure 2-figure supplement 1A).
116 Theoretically, the fitness advantage of the *ace2 cln3* strain over its *ACE2 cln3* isogenic counterpart
117 could be due to a faster doubling time during exponential growth, to a higher biomass yield of the
118 population, to a better survival in stationary phase or to a faster exit from stationary phase, each of
119 these possibilities (schematized Figure 2-figure supplement 1A) acting either alone or in combination.
120 We tested these four possibilities separately. First, we found that the population doubling times of the
121 two sets of strains was not significantly different (Figure 2-figure supplement 1B). In addition, *ace2* and
122 *ACE2* cell populations led to similar biomass accumulation indicating that the yield of carbon utilization
123 was not significantly modified by the *ace2* and/or the *CLN3* mutation (Figure 2-figure supplement 1C).
124 We then estimated cell survival in stationary phase by staining 2 days-old cells with methylene blue, a
125 dye that specifically accumulates in dead cells. No significant differences in dead cell percentages were
126 observed between *ace2* and *ACE2* cells should they be *cln3* or *CLN3* (Figure 2-figure supplement 1D).

127 From these experiments, we conclude that neither the doubling time, nor the biomass yield, or the cell
128 death rate could explain the selective advantage of the *ace2 cln3* cells over their *ACE2 cln3* counterpart.

129 We then compared the time required for *ace2 cln3* and *ACE2 cln3* quiescent-cell populations to exit
130 stationary phase. We found that the time required for population to resume proliferation after
131 refeeding, referred to as lag-time, was not significantly different between *ace2 CLN3* and *ACE2 CLN3*
132 cells (grey and black dots, Figure 2A). In addition, we confirmed that the lag-time was significantly
133 longer for the *ACE2 cln3* (light red dots) than for *ACE2 CLN3* cell population (black dots) (Figure 2A), as
134 previously described (22,23). Indeed, after refeeding of stationary phase cultures, *CLN3* transcription
135 is increased by 5- to 10-fold within five minutes (23). Cln3 is hence likely to play an important role for
136 quiescent cells to move out from G1 and reenter proliferation. Importantly, this difference was
137 partially but significantly suppressed in *ace2 cln3* (red dots) cell populations (Figure 2A) suggesting that
138 the *ace2* mutation genetically suppresses the *cln3* strain lag-time defect. We then re-fed quiescent
139 cells on microscope agarose pads containing new medium and addressed cell ability to emit a new bud
140 *i.e.* to exit quiescence. While the time required by cells to exit quiescence was not significantly different
141 between *ace2 CLN3* and *ACE2 CLN3* strains (Figure 2-figure supplement 1E), it was significantly lower
142 for the *ace2 cln3* cells than for the *ACE2 cln3* cells (Figure 2C). Importantly, similar observations were
143 made with haploid *ace2 cln3* cells (Figure 2D) for which snowflakes are much smaller (Figure 2-figure
144 supplement 1G-K). Indeed, not only haploid cells display a smaller cell volume than diploid cells, but
145 their proximal budding pattern make haploid snowflakes much more globular than diploid snowflakes
146 that are rather elongated (24). This observation confirmed the robustness of the observed initial *cln3*
147 phenotype and its suppression by *ace2*. Altogether these results point to quiescence exit as the key
148 step accounting for the competition outcomes.

149 A simple prediction from these results is that a competition experiment ran under conditions where
150 the cells are always maintained in proliferation should not result in any fitness difference between for
151 *ace2 cln3* and *ACE2 cln3* cells. This is what was observed when maintaining these two strains in

152 proliferation for 94hrs (corresponding to at least 70 generations, Figure 2E, left panel), by contrast to
153 an equivalent number of generations obtained by alternating proliferation and stationary phases
154 (Figure 2E, right panel). Reciprocally, as described previously (25), increasing the duration of stationary
155 phase caused an increase of the lag phase length at the population level (Figure 2F). Importantly, it
156 also increased the fitness advantage of *ace2 cln3* over *ACE2 cln3* cells (red and pink bars Figure 2G),
157 while there was still no difference between *ace2 CLN3* and *ACE2 CLN3* cells (black and grey bars Figure
158 2G). Altogether, our results pinpoint exit from quiescence as the critical stage in which the *ace2 cln3*
159 snowflakes are positively selected.

160

161 The advantage of *ace2 cln3* during quiescence exit is independent of the 162 snowflake phenotype

163 Why do *ace2 cln3* cells exit quiescence faster than *ACE2 cln3* cells? This could be due to some specificity
164 associated with *cln3* mutation that would modify the snowflake properties. Alternatively, it could be
165 dependent on the specific *ace2 cln3* mutation combination independently of the snowflake
166 phenotype. To answer this question, we dissociated the snowflake phenotype from the *ace2* mutation
167 and vice versa.

168 First, we asked whether the snowflake phenotype was sufficient, independently of the *ace2* mutation,
169 to rescue the quiescence-exit default associated with *cln3*. Ace2 is a transcription factor that induces
170 the expression of several chitinases and endoglucanases necessary for the septum digestion and cell
171 separation. To mimic the *ace2* snowflake phenotype, we constructed a quintuple chitinase and
172 endoglucanase mutant (*cts1, dse2 dse4, egt2, scw11*), hereafter "quintuple mutant", that results in a
173 snowflake phenotype comparable to that of the *ace2* mutant (Figure 3-figure supplement 1) while
174 carrying the wild-type *ACE2* allele. When combined with the *cln3* mutation, the five deletions have no
175 effect on quiescence exit efficiency (Figure 3A). Accordingly, the *cln3 ace2* strain exited quiescence

176 much more efficiently than the *cln3* quintuple mutant (Figure 3B). This indicates that the *ace2* mutation
177 itself, and not multicellularity, suppresses the quiescence exit defect of the *cln3* mutant. Finally,
178 competition experiments in co-cultures initially containing equal proportion of quintuple mutant and
179 WT cells confirmed that the snowflake phenotype is not sufficient to give the *cln3* mutant a
180 phenotypical advantage (Figure 3C).

181 Reciprocally, we asked whether the *ace2* mutation itself, independently of the snowflake phenotype,
182 could be sufficient to rescue the quiescence-exit default associated with *cln3*. We thus examined
183 whether planktonic cells obtained in an *ace2* mutant background would still behave as their snowflake
184 counterparts. To obtain planktonic *ace2* cells, we used sonication to physically break the snowflakes,
185 before triggering quiescence exit. Mild sonication resulted in an increased proportion of planktonic
186 cells in the *ace2 cln3* cell population (up to 50%, Figure 4-figure supplement 1A) with no defect in cell
187 survival (Figure 4-figure supplement 1B). After sonication, isolated cells, small and large cell clusters
188 displayed a similar quiescence exit efficiency (Figure 4A). Furthermore, the sonicated and non-
189 sonicated cells had the same quiescence exit efficiency, indicating that sonication *per se* had no
190 significant impact (Figure 4-figure supplement 1C). Still, after sonication, *cln3 ace2* isolated cells exited
191 quiescence faster than their *cln3 ACE2* counterpart (Figure 4B). These results show that the snowflake
192 phenotype is not necessary for the ability of the *ace2 cln3* mutant to exit quiescence faster than *ACE2*
193 *cln3* cells. Altogether our data establish that the *ace2* mutation, but not the snowflake phenotype, is
194 responsible for the *cln3* fast quiescence exit phenotype.

195

196 The *ace2 cln3* fast quiescence exit phenotype is dependent on the Kss1 MAP 197 kinase

198 As previously mentioned, a delay of *cln3* mutants to exit quiescence was already documented (23).
199 Why is this phenotype suppressed by the *ace2* deletion? Among Ace2 well-established targets , *AMN1*,

200 *BUD9, CHS7, CTS1, DSE2, DSE4* and *SCW11* are activated, while *KSS1* is down regulated by Ace2 (17).
201 Four of those, namely *CTS1, DSE2, DSE4* and *SCW11*, are not involved in suppressing the delay
202 phenotype since they are mutated in the quintuple mutant that, in combination with *cln3*, has the
203 same delay as a single *cln3* mutant (Figure 3D). We focused on Kss1, a MAP kinase involved in
204 filamentous growth and mating (26,27), because the Kss1 pathway was previously found to positively
205 regulate *CLN1,* a G1 cyclin encoding gene that is partially redundant to *CLN3* (28). We hypothesize that
206 deletion of *ACE2* would result in higher *KSS1* expression (17) that in turn, could lead to higher *CLN1*
207 expression and thereby be responsible for the *cln3* mutation suppression. We hence tested whether
208 suppression of *cln3* by *ace2* was dependent on *KSS1* by comparing quiescence exit efficiency of *ace2*
209 *cln3 KSS1* and *ace2 cln3 kss1* cells. Clearly, the knock-out of *KSS1* totally abolished the phenotypic
210 suppression of *cln3* by *ace2* (Figure 5A). Further, *CLN1* expression upon quiescence exit was
211 significantly higher in the *ace2 cln3* than in the *ACE2 cln3* strain (Figure 5B), this difference of
212 expression being entirely abolished in the absence of *KSS1* (Figure 5C). We conclude that the
213 competitive advantage of the *ace2* mutant over its *ACE2* wild-type counterpart is most likely due to
214 higher expression of *CLN1* that, at least partially, compensates for the absence of *CLN3*. Importantly,
215 this transcriptional effect of Ace2 on *CLN1*, *via* Kss1, is independent of the role of Ace2 on
216 multicellularity.

217

218 The *AMN1*^{368D} allelic-form found in the wild, phenocopies the *ace2* deletion

219 In laboratory strains, the Ace2 protein level is constant throughout the cell cycle, while it is not always
220 the case in non-laboratory strains (24). This is due to the presence of the recessive *amn1*^{368V} allelic
221 form in laboratory strains (hereafter *amn1-368V*), which was probably initially selected to avoid
222 "unwanted" cell clusters. In non-laboratory strains, the Amn1-368D protein induces the proteolysis of
223 Ace2 through the ubiquitin proteasome pathway (24). It thus appears that the Amn1/Ace2 tandem has
224 an important physiological role associated with optional post-mitotic cell separation. We first observed

225 that expression of *AMN1*^{368D} (hereafter *AMN1*) in the BY background resulted in a snowflake
226 phenotype comparable to that of *ace2* mutant strains (Figure 6-figure supplement 1). We then asked
227 whether *AMN1* allelic form could suppress the quiescence exit delay of the *cln3* mutant. Indeed, the
228 *cln3 AMN1* strain exited quiescence much more rapidly than the *cln3 amn1-368V* strain (Figure 6A).
229 Finally, we found that *AMN1* strain was strongly enriched in competition experiments when associated
230 with a *cln3* mutation (Figure 6B) or with *WHI5* overexpression (Figure 6C). We conclude that, in haploid
231 yeast, the *AMN1* allelic-form phenocopies both the multicellularity and the suppression phenotypes
232 of the *ace2* mutant.

233

234 Discussion

235 In this work, we took advantage of the snowflake model of multicellularity that is genetically
236 determined, by *ace2* or *AMN1* and is hence not triggered by external cues, as it is often the case for
237 facultative multicellularity. This experimental design allows direct fitness measurements between uni-
238 and multicellular entities. Importantly, in a wild-type background, multicellularity was neither selected
239 nor counter-selected, even following a substantial period of co-culture. Such a neutral effect of
240 multicellularity on fitness could easily result in phenotypical *aller-retours* between unicellularity and
241 multicellularity during evolution. In fact, such *aller-retours* are observed during the life cycle of non-
242 laboratory strains in which diploids are planktonic while haploid strains form clusters (29). Here we
243 show that the evolution of the cell cycle regulation may interfere with this neutral effect on fitness.
244 We indeed revealed a genetic connection between major G1/S regulators and the *AMN1* and *ACE2*,
245 key actors modulating cell cohesion at the end of mitosis (Figure 7). Interestingly, this connection
246 operates differently in laboratory strains carrying the *amn1-368V* allele (Figure 7A) and strains carrying
247 the *AMN1* allele (Figure 7B). We established that this genetic interaction is due to the pleiotropy of the
248 *ace2* mutation, affecting not only the chitinases and endoglucanases that are critical for septum
249 digestion and cell separation, but also the Kss1 MAP kinase which contributes to the activation of Cln1,

250 one of the G1 cyclins. This phenotypical link between *CLN1* expression and multicellularity, achieved
251 by Ace2 function, is particularly important during quiescence exit, a situation that is likely to happen
252 very often under ecological conditions. We propose that in some instances, multicellularity may have
253 evolved as a side effect, named here "passenger phenotype", of another phenotype that was the one
254 selected (Figure 7B). Since transcription factors often have multiple targets, an alteration in their
255 expression or function leading to the selection of a phenotype due to one of the targets could easily
256 lead to the selection of additional phenotypes due to other targets. This could be a common feature
257 involved in evolutionary processes.

258 Connections between G1/S regulators and multicellularity have been repeatedly observed in
259 phylogenetically distant species (see introduction section), suggesting a propitious genetic interplay
260 for co-evolution. Olson and co-workers have shown that RB could have played a role in early steps of
261 multicellularity evolution *via* a cooption mechanism favoring the appearance of simple multicellular
262 entities (9). Our work further supports a role for G1/S regulators in evolution of multicellularity, but
263 the mechanism appears different and affects selection of multicellularity rather than its initial
264 appearance. We show that the *ace2* or *AMN1* allelic forms are sufficient to counteract a negative
265 fitness effect of the overexpression of the RB functional orthologue Whi5 (Figure 1D, Figure 6F).
266 Importantly we have shown that this phenotypic suppression is independent of the multicellular
267 phenotype associated with the *ace2* or *AMN1* allelic forms. This observation led us to propose that
268 some regulatory effects on the G1/S transition could be alleviated by Amn1 degradation of Ace2 and
269 thereby associated with multicellularity. In this hypothesis the selective pressure applies on G1/S
270 transition efficiency and not on multicellularity itself. It is hence different from the cooption hypothesis
271 in which the RB protein acquired new functionalities leading to multicellularity that would result in
272 some directly selectable fitness advantage. Both scenarios imply co-evolution of cell cycle regulation
273 and multicellularity, which could therefore be a much more general feature than first thought. It could
274 have started very early in the evolution of eukaryotic cells or alternatively could be a case of
275 convergent evolution as suggested by the fact that it may involve distinct mechanisms. Importantly

276 regulator genes of the G1/S transition are among the most frequent drivers of cancer, the RB gene
277 being generally mutated while cyclin D being overexpressed through various means (30,31). Because
278 the link between cancer and multicellularity is regularly questioned (32,33), understanding the role of
279 these G1/S regulators in multicellularity in parallel to their role in cancer is particularly relevant.

280 More generally, our results prompted us to reconsider whether simple multicellularity, which
281 appeared multiple times in evolution, was always selected for the new physical and physiological
282 properties it provides (2). Alternatively, it is possible that multicellularity was initially selected as a
283 byproduct, allowing it to be maintained although not necessarily increasing fitness as such. This would
284 contribute to disconnect the initial selection of simple multicellularity from the selection of further
285 associated advantages, such as division of labor, that would require time and necessitate that the
286 multicellularity phenotype would not be counter-selected in the first place. Such a passenger selection
287 of multicellularity would make it independent of physical constraints such as size or shape that could
288 restrain its further evolution. The work presented here provides a proof of concept that such a scenario
289 is plausible and may have contributed to the multiple appearance of multicellularity in the tree of life.

290

291 Materials and methods

292

293 Yeast media and strains, plasmids and oligonucleotides

294 Yeast cells were grown in liquid or solid media at 30 °C. SD is a synthetic minimal medium containing
295 0.5% ammonium sulfate, 0.67% yeast nitrogen base (Difco), 2% glucose. SDcasaWAU is an SD medium
296 supplemented with 0.2% casamino acids (Difco) tryptophan (0.2 mM), adenine (0.3 mM) and uracil
297 (0.3 mM). Unless specified, cells were grown in SDCasaWAU medium. When indicated, medium was
298 depleted in uracil, resulting in a medium named SDCasaWA, allowing the selection of cells expressing
299 a vector carrying *URA3* marker. SC medium was prepared as described by Sherman (34) and was

300 supplemented by histidine (0.06 mM), leucine (0.5 mM), lysine (0.07 mM), tryptophan (0.2 mM),
301 adenine (0.3 mM), and uracil (0.3 mM). The medium obtained by the depletion of both uracil and
302 leucine, called SC-U-L medium, allows the selection of cells expressing both *URA3* and *LEU2* markers.
303 The YPD medium contained 1% yeast extract, 2% peptone, and 2% glucose.

304 Yeast strains (listed in Table 1) are derived from both FY4 and FY5 prototrophic strains and from
305 disrupted strains isogenic to BY4741 or BY4742 purchased from Euroscarf (Frankfurt, Germany). Strains
306 described in Table 1 were either obtained by crossing, sporulation, and micromanipulation of meiosis
307 progeny or by transformation of cells with a DNA fragment of interest (plasmid, PCR product). Yeast
308 strains were transformed using the lithium acetate method (35).

309 **Table 1: Strains**

Strain name	Genotype
FY4	
Y12580, Y12581, Y12582	*cln3::URA3/cln3::URA3 ura3Δ0/ura3Δ0 leu2Δ0/leu2Δ0*
Y12584, Y12585, Y12586	*ace2::KanMX4/ace2::KanMX4 cln3::URA3/cln3::URA3 ura3Δ0/ura3Δ0 leu2Δ0/leu2Δ0*
Y12606, Y12607, Y12608	*leu2Δ0/leu2Δ0*
Y12973, Y12974, Y12975	*ace2::KanMX4/ace2::KanMX4 leu2Δ0/leu2Δ0*
Y12575 + p5314	*ace2::KanMX4/ace2::KanMX4 ura3Δ0/ura3Δ0* carrying empty plasmid 2µ
(Y11418xY12599) + p5314	*ura3Δ0/ura3Δ0* carrying empty plasmid 2µ
Y12575 + p4726	*ace2::KanMX4/ace2::KanMX4 ura3Δ0/ura3Δ0* carrying plasmid 2µ *WHI5*
(Y11418xY12599) + p4726	*ura3Δ0/ura3Δ0* carrying plasmid 2µ *WHI5*
Y12512	*ace2::KanMX4/ace2::KanMX4 HTB1-3xCFP-LEU2/HTB1-3xCFP-LEU2 ura3Δ0/ura3Δ0 his3Δ1/HIS3*
Y12565, Y12566, Y12958	*ace2::KanMX4 cln3::URA3 ura3Δ0 leu2Δ0*
Y12567, Y12568, Y12959	*cln3::URA3 ura3Δ0 leu2Δ0*
Y12408, Y12595, Y12596	*ace2::KanMX4 leu2Δ0*
Y11417, Y12571	*leu2Δ0*
Y12709, Y12710, Y12711	*cln3::URA3/cln3::URA3 ura3Δ0/ura3Δ0 leu2Δ0/leu2Δ0*
Y12716, Y12717, Y12718	*dse2::KanMX4/dse2::KanMX4 cts1::KanMX4/cts1::KanMX4 scw11::KanMX4/scw11::KanMX4 egt2::KanMX4/egt2::KanMX4 dse4::KanMX4/dse4::KanMX4 cln3::URA3/cln3::URA3 ura3Δ0/ura3Δ0 leu2Δ0/leu2Δ0*

Y12976, Y12977, Y12978	*dse2::KanMX4/dse2::KanMX4 cts1::KanMX4/cts1::KanMX4 scw11::KanMX4/scw11::KanMX4 egt2::KanMX4/egt2::KanMX4 dse4::KanMX4/dse4::KanMX4 leu2Δ0/leu2Δ0*
Y12967, Y12968	*kss1::KanMX4 ace2::KanMX4 cln3::URA3 ura3Δ0 leu2Δ0*
Y12969, Y12970	*kss1::KanMX4 cln3::URA3 ura3Δ0 leu2Δ0*
Y12838, Y12839, Y12840	*AMN1368D-URA3-AMN1368V ura3Δ0 leu2Δ0*
Y12935, Y12936, Y12937	*AMN1368V-URA3-AMN1368V ura3Δ0 leu2Δ0*
Y12942, Y12943, Y12944	*AMN1368D-URA3-AMN1368V cln3::KanR ura3Δ0 leu2Δ0 his3Δ1*
Y12946, Y12947, Y12949	*AMN1368V-URA3-AMN1368V cln3::KanR ura3Δ0 leu2Δ0 his3Δ1*
Y12838 + p338	*AMN1368D-URA3-AMN1368V ura3Δ0 leu2Δ0* carrying empty plasmid 2µ
Y12935 + p6053	*AMN1368D-URA3-AMN1368V ura3Δ0 leu2Δ0* carrying plasmid 2µ *WHI5*
Y12838 + p338	*AMN1368D-URA3-AMN1368V ura3Δ0 leu2Δ0* carrying empty plasmid 2µ
Y12935 + p6053	*AMN1368D-URA3-AMN1368V ura3Δ0 leu2Δ0* carrying plasmid 2µ *WHI5*
GN-1C	*HO:NatR AMN1368D FLO8+*

All plasmids and oligonucleotides are listed in Table 2 and Table 3, respectively. To construct the plasmids allowing the overexpression of *WHI5* in yeast strains, the open reading frame of the *WHI5* gene was amplified using the genomic DNA of the FY4 strain as a template. The PCR product was then cloned into two 2µ vectors, YEpLac195 and YEpLac181, carrying respectively *URA3* and *LEU2* markers. Two plasmids carrying respectively two different alleles of the *AMN1* gene were also constructed. The open reading frame of the *AMN1* gene was amplified using either the FY4 strain genomic DNA (*amn1*^{368V} PCR product) or the GN-1C strain genomic DNA (*AMN1*^{368D} PCR product). The GN-1C strain was a generous gift from Pr. Marullo. The PCR products were cloned into YIpLac211, that allowed integration of the cloned *AMN1* allele at the yeast *AMN1* locus.

S2 Table: Plasmids

Plasmid Name	Description	
p5314	YEpLac195: 2µ *URA3* AmpR	(36)
p4726	*WHI5* in YEpLac195	lab collection
p338	YEpLac181 : 2µ *LEU2* AmpR	(36)
p6053	*WHI5* in YEpLac181	This study
p6164	YIpLac211 : integrative plasmid *URA3* AmpR	(36)

p6165	*AMN1-368D* in YIpLac211	This study
p6167	*AMN1-368V* in YIpLac211	This study

321

322 **S3 Table: Oligonucleotides**

Oligonucleotide name	Sequence 5'-3'
qPCR locus ACE2 -26 forward	GGACCAAAAACGGTGTTAATACAATC
qPCR KanMX4 specific reverse	CTGGCGCGCCTTAATTAACC
qPCR ACT1 forward (coding)	CCCCAGAAGAACACCCTGTTC
qPCR ACT1 reverse (coding)	CGTAGAAGGCTGGAACGTTG
qPCR CLN1 coding forward	ATCGATCAGCAACCGGAGAT
qPCR CLN1 coding reverse	AACCTGACAGCGTGGAAGAA
KanB reverse	CTGCAGCGAGGAGCCGTAAT
ACE2 promoter forward	CGTCACTCCATTAGAATCCC
CLN3 promoter forward	TCCTCATTCGGTTTAACTCC
CLN3 terminator reverse	TGACTAGAGGAAGTAAGGAG
DSE2 promoter forward	CAGTAGAGCTAACCACAGTC
CTS1 promoter forward	ACTGTCGCTCGTTTCACAAC
SCW11 promoter forward	CAGTTACGCAACAAAGACAG
DSE4 promoter forward	ACTACAAGCGAGGGTAAAGG
EGT2 promoter forward	GATGCTGGTTTGATGCTAAG
CLN3 promoter -500 forward	TGAGGAAAGAGGACTATACC
CLN3 terminator +500 reverse	TAGGTAGCGATGAAGATTGG
URA3 promoter -500 forward	TCATCATCTCATGGATCTGC
URA3 terminator +500 reverse	TACGCCAGTACACCTTATCG
CLN1 promoter -200 forward	CCAAGGAGTTCTTCGTTCGC
CLN1 terminator +200 reverse	TCGCGTCATCTTTTCCGTTC
AMN1 promoter -75 forward	GTTTAATATCCATCCATTCC
AMN1 +459 forward	CCTTTGACTGCTCAACATCAG
AMN1 +882 forward	CATCAAGTAACACAACCAG
AMN1 +1269 forward	GGTTGTGATGTTGATGATG
AMN1 terminator +169 reverse	GTTTCTTCGGCCCTTCTGGA
AMN1 +1269 reverse	CATCATCAACATCACAACC
AMN1 +882 reverse	CTGGTTGTGTTACTTGATG
AMN1 +376 reverse	GAAAGACTGGATGCAGAAAC
Mat a and alpha forward	AGTCACATCAAGATCGTTTATGG
Mat a specific reverse	CTCCACTTCAAGTAAGAGTTTG
Mat alpha specific reverse	GCACGGAATATGGGACTACTTCG
WHI5 BamHI forward	CGCGGATCCCAAATCGGATATGAGCAGCTG
WHI5 PstI reverse	ACGTCTGCAGGCTCGAGGCGATCTGTCGC

M13 reverse	CAGGAAACAGCTATGACC
AMN1 BamHI forward	GTTGGATCCATGAAACTAGAACGCG
AMN1 PstI reverse	AACCTGCAGCTAGTCCACATTATTCTCTATTTCG

323

324 ## Description of a Snowflake population

325 Snowflake populations or co-culture between Snowflake and Planktonic strains were observed in a
326 Kova Glasstic slide (Kova international, 87144F). The proportion of the Snowflake phenotype in these
327 populations was determined by counting entities formed by four or more cells. To characterize the size
328 of Snowflakes within a population, the population was observed between slide and coverslip separated
329 by a layer of double-sided adhesive tape. The longest segment of the Snowflake entity was measured,
330 as well as the longest segment perpendicular to the first segment and lying in the same Z plane.

331

332 ## Competitions experiment in co-culture

333 Snowflake strains (either *ace2* or quintuple mutant or $AMN1^{368D}$) and planktonic strains were grown in
334 monocultures to stationary phase, for 2 days unless specified. Snowflake and planktonic strains were
335 then mixed in indicated proportion and co-cultured. Unless specified, every 2 days, co-cultures, after
336 they reached stationary phase, were diluted by a factor of 1000 into fresh liquid medium.

337 To set up the co-cultures for which the proportion of Snowflake phenotype was monitored, the entity
338 (Snowflake entity or single-cell entity) concentrations in each of the monocultures were determined.
339 The volumes of the 2 monocultures in the mix were accordingly determined and then adjusted to
340 obtain 50% of Snowflake entity in the mix. The proportion of Snowflakes in the co-culture was
341 determined every two days before dilution in fresh medium.

342 To set up the co-cultures for which the proportion of *ace2* genotype was monitored, the two strains
343 were mixed to obtain a 50/50 cell ratio. Every 2 days, the genomic DNA of the stationary phase co-

344 cultures was extracted by phenol-chloroform protocol. Quantitative PCR amplifications were then
345 performed with GoTaq® qPCR Master Mix (Promega, A6001), using 50ng of DNA extracted from co-
346 cultures. The first set of primers was designed to amplify the *ace2::KanMX4* locus with the first primer
347 targeting the region directly upstream of the ATG of the *ACE2* gene, and the second primer targeting
348 a region specific to the *KanMX4* marker (Supplemental Table 3). The second set of primers targeted a
349 region of *ACT1* gene (Supplemental Table 3).

350 For competitions in which the co-cultures were maintained in proliferation phase for 94 hours, the co-
351 cultures were diluted every 8 hours to ensure that the OD_{600nm} was always maintained below 0.5.

352

353 Population measurement

354 To determine the population doubling time of yeast strains, cells were kept in exponential proliferation
355 phase ($OD_{600nm} \leq 1.0$) for at least 24 hours by successive dilutions before any measurement. Population
356 doubling time was then determined by following the optical density at 600 nm during 5 hours on at
357 least three independent exponential growth culture. Population doubling time was then determined
358 by exponential growth regression of the proliferation curves using GraphPad Prism 8 (GraphPad
359 Software, Inc. La Jolla, USA).

360 To determine cell viability, the cells were stained with a solution containing 0.2% of methylene blue
361 (Sigma-Aldrich, Saint Louis, MI, USA) and 2% sodium citrate pH7. After 5 minutes of incubation, the
362 proportion of blue-stained dead cells was scored.

363 The biomass yield of cultures was determined by filtration of 2-day stationary phase cultures on 0.45
364 µm polyamide pre-weighted filters (25006–47-N; Sartorius). The filter was washed twice with 10 mL of
365 miliQ water and then dried with successive 30 seconds cycles in a microwave oven at 800 W until the
366 mass of the filter and cells was constant.

367

368 ## Refeeding of stationary phase cultures

369 Unless the age of cultures is otherwise specified, 2-day stationary phase liquid monocultures were
370 refed either on liquid or solid fresh SDcasaWAU medium.

371 Stationary phase cultures were refed by dilution into liquid fresh SDcasaWAU medium at
372 approximately 0.05 OD_{600nm}. The OD_{600nm} was monitored upon refeeding for at least 7 hours covering
373 both 'lag' and exponential phases (until at least a 5-fold increase of the OD_{600nm} compared to the initial
374 point). To quantify the duration of the 'lag' phase, we normalized all the OD_{600nm} values of each
375 individual growth curve to their respective initial OD_{600nm} value and then applied the logarithmic
376 function to all the normalized OD_{600nm} values of the growth curve. We next performed a linear
377 regression on the points corresponding to the proliferation phase of the growth curve using GraphPad
378 Prism 8 (GraphPad Software, Inc. La Jolla, USA). The time value for which the linear regression
379 intersects the Time-X axis corresponds to the end of the 'lag' phase and the beginning of the
380 proliferation phase, and is referred as 'the duration of lag phase'.

381 Quiescent cells from stationary phase cultures were also refed onto solid medium. Cells were spread
382 onto half a 3% agarose microscope pad made of fresh SDcasaWAU. Bright field images of individual
383 cells were then captured every 15 minutes for up to 4 hours. The cells forming an unequivocal new
384 bud upon refeeding were scored.

385 When indicated, an aliquot of stationary phase culture can be sonicated before a refeeding experiment
386 on microscope agarose pad. Cycles of 30 seconds in a sonication bath were carried out until the
387 proportion of single-cell entities in the *ace2* SF culture increased to a desired proportion
388 (approximately 40%).

389

390 ## Determination of *CLN1* mRNA level upon refeeding by Reverse transcriptase-
391 ## PCR.

392 To determine the level of *CLN1* mRNA upon refeeding of 2-day stationary phase cultures, 15 mL of a
393 2-day culture was diluted in 85 mL of fresh medium. Fifteen minutes upon refeeding, 25 mL of culture
394 was sampled and centrifuged at 4000 rpm at 4°C for 3 min. The pellet was washed in 1 mL of RNase-
395 free H2O, and centrifuged at 12,000 g at 4°C for 30 seconds. A Tri-Reagent (Sigma, T9424) protocol
396 was then performed to extract total RNA. A reverse-transcription of 200ng of total RNA using the 'High
397 Capacity cDNA Reverse Transcription' Kit (ThermoFisher, 4368813) was then performed. The cDNA was
398 diluted to 1/25 and amplified with a Quantitative-PCR protocol, using the GoTaq® qPCR Master Mix
399 (Promega, A6001) and primers specific to the coding region of *CLN1* or the coding region of *ACT1*
400 (Supplemental Table 3).

401

402 **Microscopy**

403 The refeeding experiments on microscope pad, as well as the Snowflake size-measurement
404 experiments were carried out using a Zeiss 200M inverted microscope (Carl Zeiss, Thornwood, NY,
405 USA) with the additional equipment : a MS-2000 stage (Applied Scientific Instrumentation, Eugene,
406 OR, USA), a Lambda LS 300 W xenon light source (Sutter, Novato, CA, USA), a 5 positions filter turret, a
407 100X 1.4NA Plan-Apochromat objective and a CoolSnap HQ camera (Roper Scientific, Tucson, AZ, USA).
408 The filters are from Chroma Technology Corp. The microscope and additional equipment were
409 controlled by SlideBook software 5.0. (Intelligent Imaging Innovations, Denver, CO, USA). The images
410 were analyzed with Image J. All other microscopy experiments were carried out using Zeiss Primo Star
411 microscope, equipped with a 40X/0.65 Plan-Achromat objective.

412

413 **Statistical analysis**

414 All experiments were carried out at least three times on independent biological samples. The exact
415 number of independent samples is indicated in the figure legends. Data are presented as mean ± SD.

All the statistical analyses were done using GraphPad Prism 8 (GraphPad Software, Inc. La Jolla, USA). The proportion of SF in competition experiments, the refeeding experiments on microscope pad and the proportion of dead cells were analyzed by Fisher's exact test on a contingency table. Other experiments are analyzed by Welch's unpaired t-test. p-values below 0.05 are represented by *; p values inferior to 0.005 are represented by **; and p values inferior to 0.001 are represented by ***. p-values superior to 0.05 were considered non-significant and are represented by 'ns'.

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Author contributions

T.L.D., D.L. and B.D.-F. designed research; T.L.D. performed research; T.L.D., D.L. and B.D.-F. analyzed data; and T.L.D. and B.D.-F. wrote the paper.

Competing interests

The authors declare no competing interest.

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521 # Figures

Figure 1

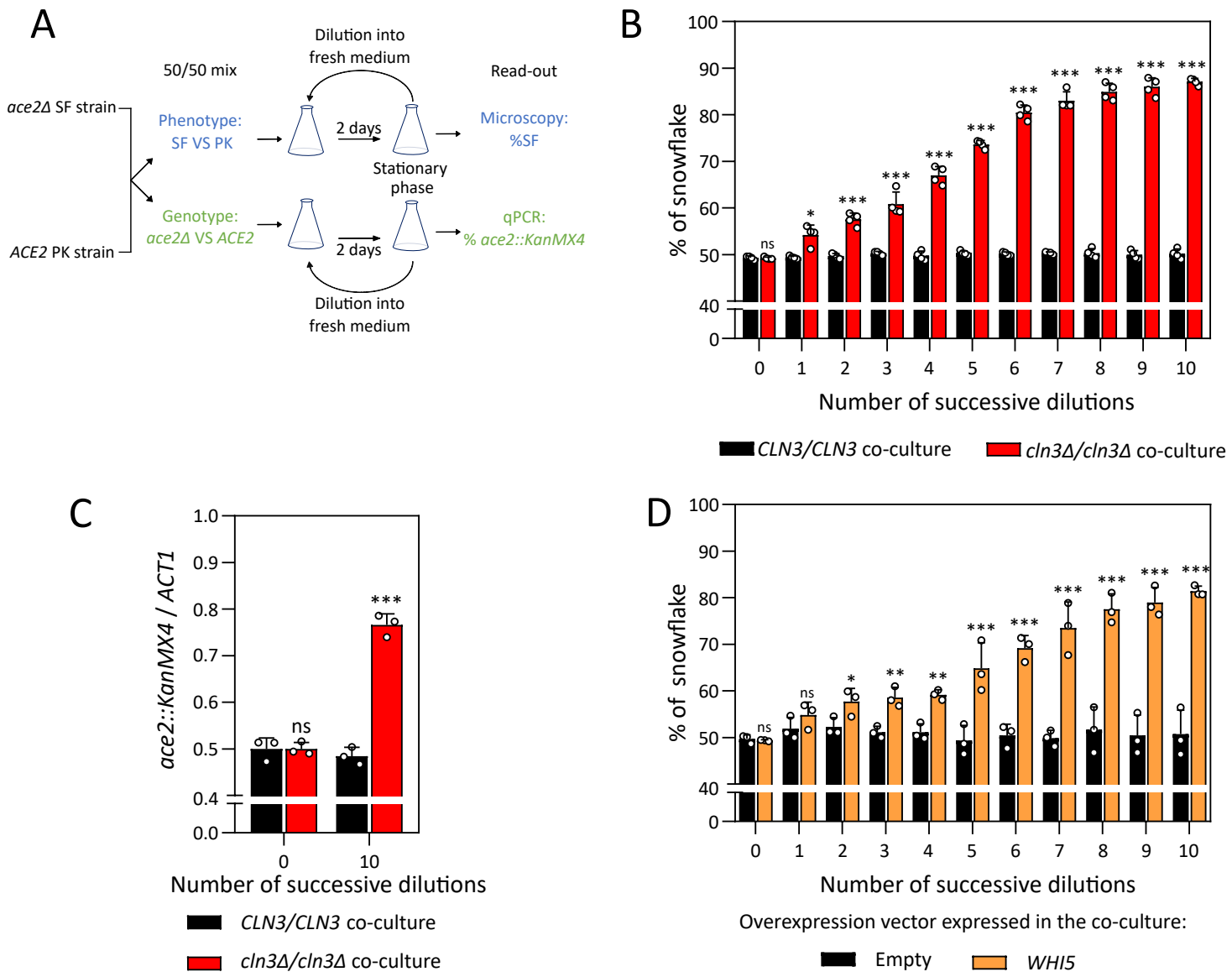
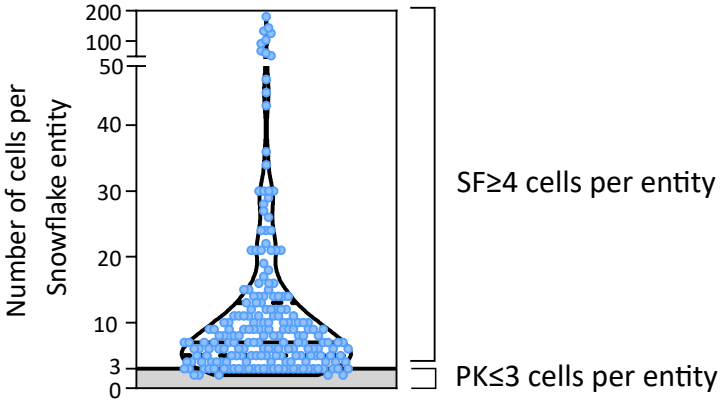

A
50/50 mix
Dilution into fresh medium
Read-out
ace2Δ SF strain
Phenotype: SF VS PK
2 days
Microscopy: %SF
Stationary phase
Genotype: ace2Δ VS ACE2
2 days
qPCR: % ace2::KanMX4
ACE2 PK strain
Dilution into fresh medium
B
% of snowflake
Number of successive dilutions
CLN3/CLN3 co-culture
cln3Δ/cln3Δ co-culture
C
ace2::KanMX4 / ACT1
Number of successive dilutions
CLN3/CLN3 co-culture
cln3Δ/cln3Δ co-culture
D
% of snowflake
Number of successive dilutions
Overexpression vector expressed in the co-culture:
Empty
WHI5

Figure 1 - figure supplement 1



522 **Figure 1. Competition experiments. (A)** Experimental set-up of the co-culture competition
523 experiments between *ace2/ace2* and *ACE2/ACE2* strains. A 50/50 mix of the two strains based either
524 on phenotype (snowflake vs planktonic, microscopy) or on genotype (*ace2* vs *ACE2,* qPCR) was
525 inoculated in SDcasaWAU liquid medium. The resulting co-culture was grown for 2 days until stationary
526 phase was reached and then diluted in new SDcasaWAU medium. For each dilution step, the
527 proportion of the snowflake phenotype or *ace2* genotype was determined (by microscopy or qPCR
528 respectively). **(B)** Evolution of the percentage of snowflake entities during independent co-culture
529 competitions between *ace2/ace2* and *ACE2/ACE2* strains, either *cln3/cln3* (red bars) or *CLN3/CLN3*
530 (black bars) (N=4, n>250, mean ± SD, ns p>0.05, *p<0.05, ***p<0.001). The percentage of snowflakes
531 is statistically compared between *CLN3/CLN3* and *cln3/cln3* co-cultures at each dilution round, using a
532 Fisher's exact test. **(C)** The proportion of *ace2/ace2* genotype was monitored by qPCR in independent
533 competitions in *cln3/cln3* (red bars) and *CLN3/CLN3* (black bars) backgrounds. The *ACT1* locus,
534 amplified in all the cells of the population, was used to normalize the proportion of *ace2* cells in the
535 co-culture cell population (N=3, mean ± SD, unpaired t-test, Welch correction, ns p>0.05, ***p<0.001).
536 **(D)** Evolution of the percentage of snowflake entities during independent co-culture competitions
537 between *ace2/ace2* and *ACE2/ACE2* strains overexpressing *WHI5* (orange bars) or not (black bars)
538 (N=3, n>235, mean ± SD, Fisher's exact test, ns p>0.05, *p<0.05, **p<0.005, ***p<0.001).

539 **Figure supplement 1.** Number of cells per Snowflake entity determined by counting the number of
540 *HTB1-CFP* positive nuclei per Snowflake entity.

Figure 2

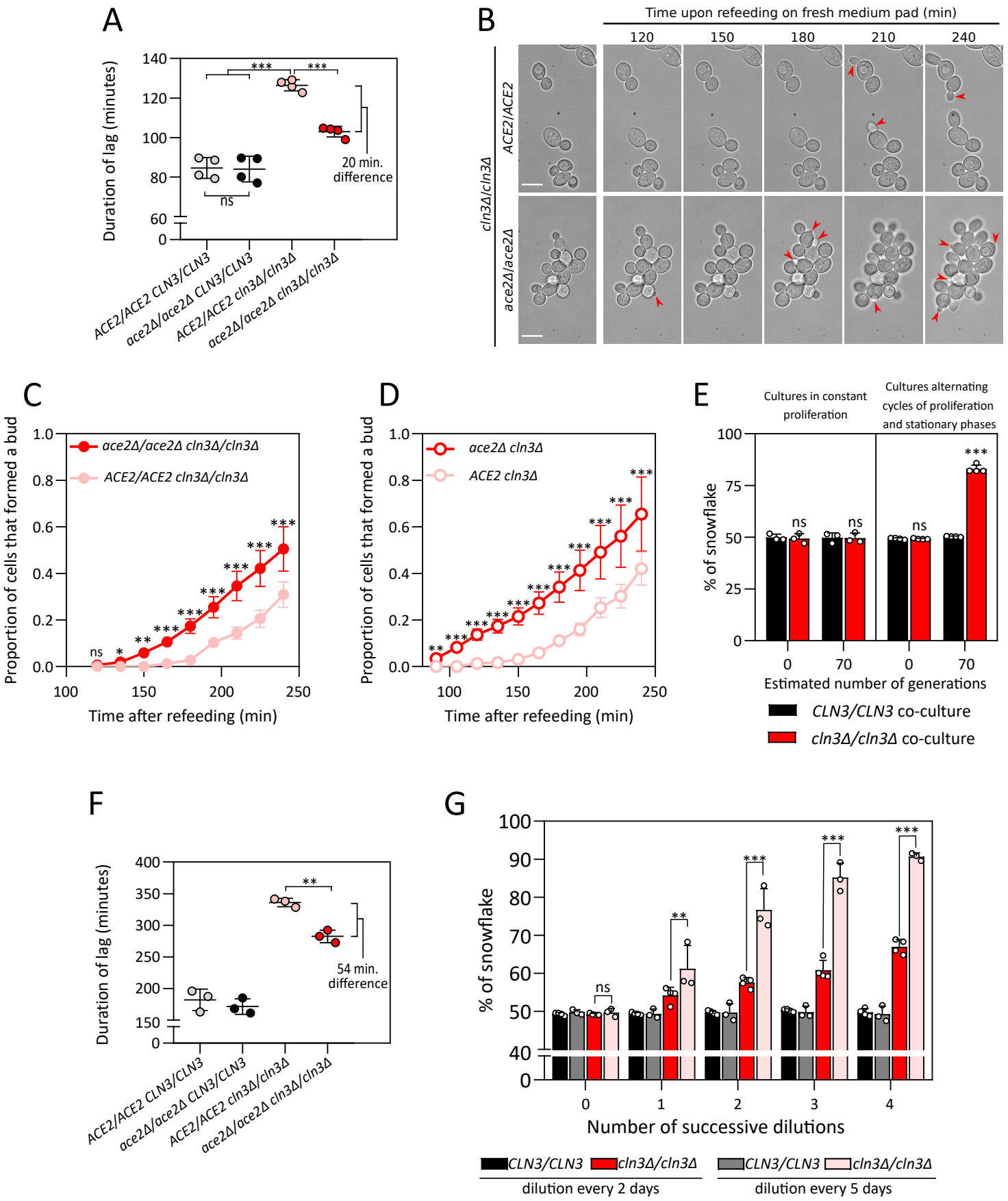
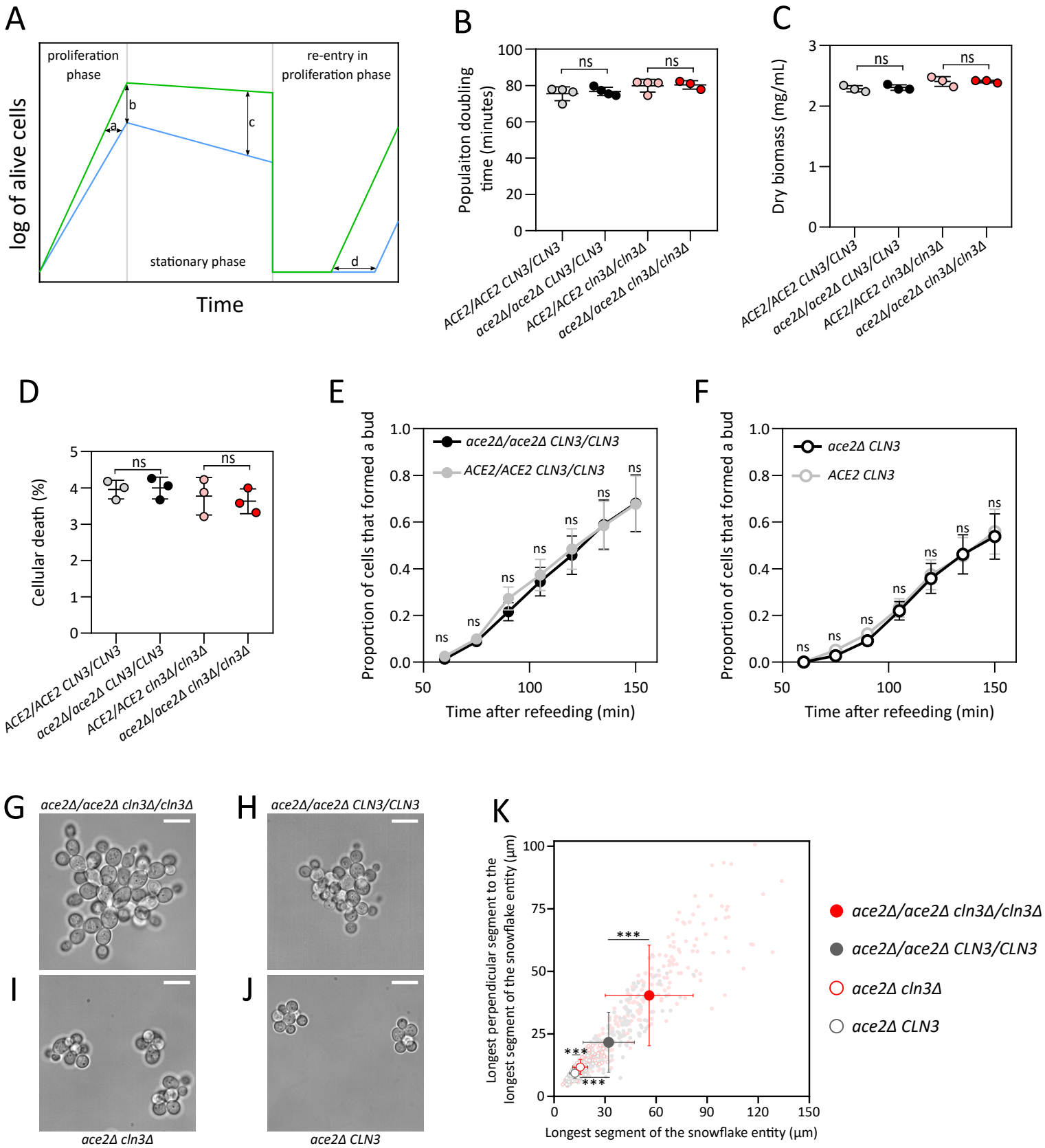

A
Duration of lag (minutes)
140
120
100
80
60
0
***
***
ns
20 min. difference
ACE2/ACE2 CLN3/CLN3
ace2Δ/ace2Δ CLN3/CLN3
ACE2/ACE2 cln3Δ/cln3Δ
ace2Δ/ace2Δ cln3Δ/cln3Δ
B
Time upon refeeding on fresh medium pad (min)
120
150
180
210
240
ACE2/ACE2
cln3Δ/cln3Δ
ace2Δ/ace2Δ
C
Proportion of cells that formed a bud
ace2Δ/ace2Δ cln3Δ/cln3Δ
ACE2/ACE2 cln3Δ/cln3Δ
Time after refeeding (min)
D
Proportion of cells that formed a bud
ace2Δ cln3Δ
ACE2 cln3Δ
Time after refeeding (min)
E
Cultures in constant proliferation
Cultures alternating cycles of proliferation and stationary phases
% of snowflake
Estimated number of generations
CLN3/CLN3 co-culture
cln3Δ/cln3Δ co-culture
F
Duration of lag (minutes)
**
54 min. difference
ACE2/ACE2 CLN3/CLN3
ace2Δ/ace2Δ CLN3/CLN3
ACE2/ACE2 cln3Δ/cln3Δ
ace2Δ/ace2Δ cln3Δ/cln3Δ
G
% of snowflake
Number of successive dilutions
CLN3/CLN3
cln3Δ/cln3Δ
dilution every 2 days
dilution every 5 days

Figure 2 - figure supplement 1



541 **Figure 2. Quiescence exit efficiency explains the results of competition experiments. (A)** Lag phase
542 duration after cell 2-day old population refeeding with SDCasaWAU medium. The optical density at
543 600nm was followed after population refeeding for 4 independent experiments. The mean and the SD
544 are indicated together with an unpaired t-test, Welch correction, ns p>0.05, ***p<0.001. **(B)**
545 Representative image series of *cln3/cln3* cells either *ace2/ace2* or *ACE2/ACE2* after refeeding of 2 days
546 cultures on a SDCasaWAU medium containing microscope pad. Arrows point to emerging buds. Bars
547 are 10µm. **(C)** Proportion of *cln3/cln3* cells that have formed a new bud after refeeding on a
548 SDCasaWAU medium containing microscope pad of either *ace2/ace2* or *ACE2/ACE2* 2 days cultures
549 (N=3, n>101, Fisher's exact test, mean ± SD, ns p>0.05, *p<0.05, **p<0.005, ***p<0.001). **(D)** Same as
550 C in a *cln3* haploid background (N=3, n>100, mean ± SD, Fisher's exact test, **p<0.005, ***p<0.001).
551 **(E)** Percentage of snowflake entities observed in independent co-cultures of *ace2/ace2* and *ACE2/ACE2*
552 strains. Cultures either went through cycles of proliferation and stationary phase as described in Fig1A
553 (right panel), or maintained in constant exponential phase (left panel) (N>3, n>208, mean ± SD, Fisher's
554 exact test, ns p>0.05). **(F)** Same as A except that the refeeding was done after a culture of 5 days (N=3,
555 mean ± SD, unpaired t-test, Welch correction, **p<0.005). **(G)** Percentage of snowflake entities
556 observed in independent co-cultures of *ace2/ace2* and *ACE2/ACE2* strains diluted every two days (red
557 and black bars) or every five days (grey and pink bars) (N≥3, n>700, mean ± SD, Fisher's exact test, ns
558 p>0.05, **p<0.005, ***p<0.001).

559 **Figure supplement 1**. **(A)** Theoretical diagram showing the various phenomena that can explain, either
560 alone or combined, how one subpopulation can outcompete another subpopulation in a co-culture.
561 One subpopulation may divide more rapidly in exponential phase (a), may have a higher yield (b), may
562 undergo less cell death during stationary phase (c) or may re-enter proliferation phase faster after
563 refeeding (d). **(B)** Doubling time of populations in proliferation phase. Independent cultures (N>3) were
564 maintained in constant proliferation phase for more than 24 hours, then the optical density at 600 nm
565 was measured every 15 minutes for 8 hours (mean ± SD, unpaired t-test, Welch correction, ns p>0.05).
566 **(C-D)** The dry biomass determined by filtration (**C**, N=3, mean ± SD, unpaired t-test, Welch correction,

567 ns p>0.05) and the percentage of dead cells stained with ethylene blue (**D**, N=3, n>280, mean ± SD,
568 Fisher's exact test, ns p>0.05,) were also measured for 2 days stationary phase cultures. **(E)** Proportion
569 of *CLN3/CLN3* cells that have formed a new bud after refeeding on a SDCasaWAU medium containing
570 microscope pad of either *ace2/ace2* or *ACE2/ACE2* 2 days cultures (N=3, n>101, Fisher's exact test,
571 mean ± SD, ns p>0.05). **(F)** Proportion of *CLN3* cells that have formed a new bud after refeeding on a
572 SDCasaWAU medium containing microscope pad of either *ace2* or *ACE2* 2 days cultures (N=3, n>91,
573 Fisher's exact test, mean ± SD, ns p>0.05). **(G-J)** Representative images of diploid *ace2/ace2* snowflakes
574 either *cln3/cln3* (**G**) or *CLN3/CLN3* (**H**), and haploid *ace2* snowflakes either *cln3* (**I**) or *CLN3* (**J**). Bars are
575 10 µm. **(K).** Size distribution of snowflakes in haploid (empty circles) or diploids (plain circles)
576 backgrounds, either *CLN3* (black) or *cln3* (red). Size is estimated by measuring both the longest
577 segment of the snowflake entity and the longest segment perpendicular to the first one (N=3, n>72).
578 We compared the length of each segment independently with an unpaired t-test with a Welch
579 correction (error bars ± SD, unpaired t-test, Welch correction, ***p<0.001, account for both segment).

Figure 3

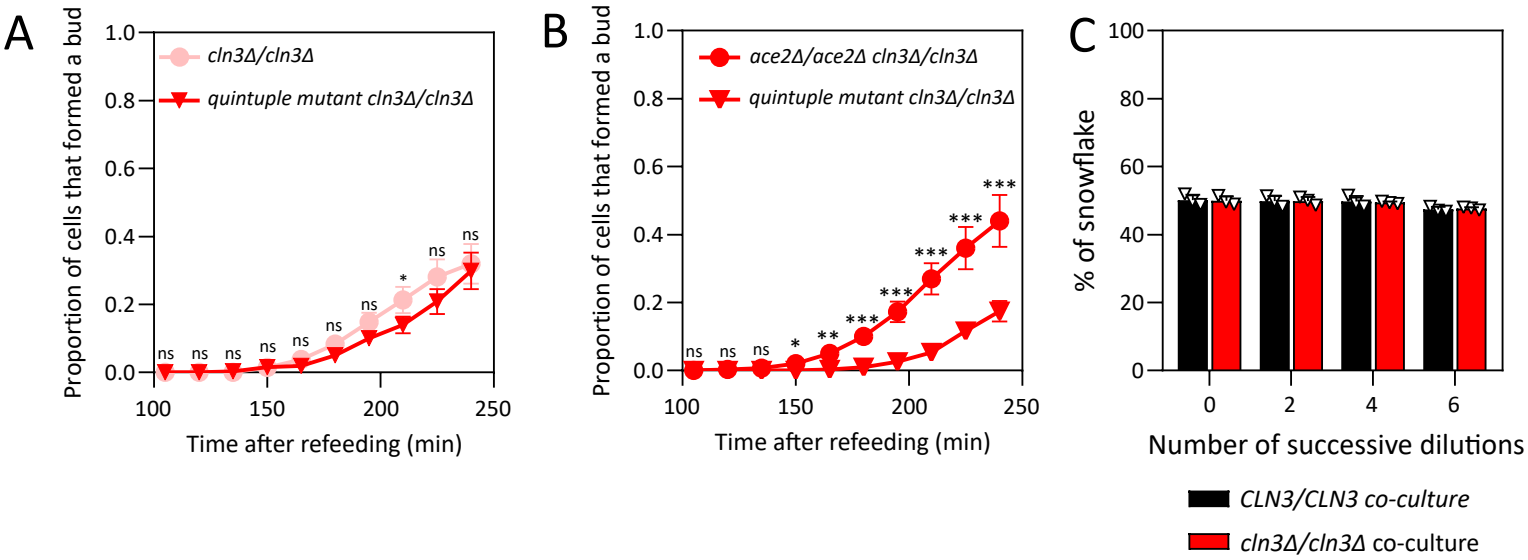
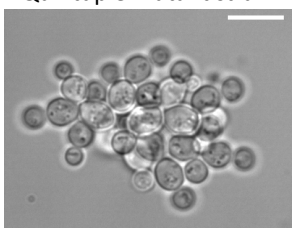

A
Proportion of cells that formed a bud
1.0
0.8
0.6
0.4
0.2
0.0
cln3Δ/cln3Δ
quintuple mutant cln3Δ/cln3Δ
ns
*
100
150
200
250
Time after refeeding (min)
B
Proportion of cells that formed a bud
ace2Δ/ace2Δ cln3Δ/cln3Δ
quintuple mutant cln3Δ/cln3Δ
ns
*
**
***
Time after refeeding (min)
C
% of snowflake
100
80
60
40
20
0
0
2
4
6
Number of successive dilutions
CLN3/CLN3 co-culture
cln3Δ/cln3Δ co-culture

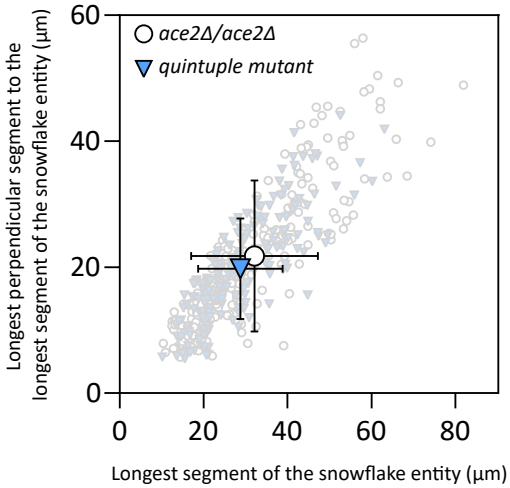
Figure 3 - figure supplement 1

A

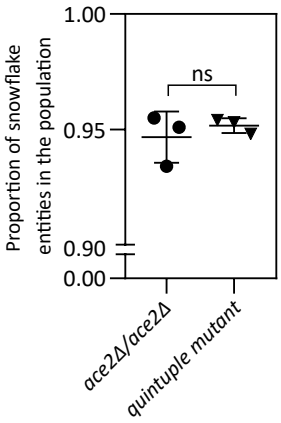
Quintuple mutant strain



B



C



580 **Figure 3. Quintuple mutant strains do not rescue the quiescence-exit default associated with *cln3***
581 **and are not selected in competition experiments. (A)** Proportion of *cln3/cln3* cells, either quintuple
582 mutant or WT, that formed a new bud after refeeding of 2 days cultures on a SDCasaWAU medium
583 containing microscope pad (N=3, n>102, mean ± SD, Fisher's exact test, ns p>0.05, *p<0.05). **(B)**
584 Proportion of *cln3/cln3* cells, either quintuple mutant or *ace2/ace2*, that formed a new bud after
585 refeeding of 2 days cultures on a SDCasaWAU medium containing microscope pad (N=3, n>75, mean
586 ± SD, Fisher's exact test, ns p>0.05, *p<0.05, **p<0.005, ***p<0.001). **(C)** Evolution of the percentage
587 of snowflake entities during independent co-culture competitions between quintuple mutant and WT
588 strains either *cln3/cln3* (red bars) or *CLN3/CLN3* (black bars) (N=3, n>250, mean ± SD, Fisher's exact
589 test).

590 **Figure supplement 1. Snowflake characterization of quintuple mutant strains. (A)** Representative
591 image of the quintuple mutant strain. Bar is 10µm. **(B)** Size distribution of quintuple mutant (triangles)
592 or *ace2/ace2* (circles) snowflakes. Size is estimated by measuring both the longest segment of the
593 snowflake entity and the longest segment perpendicular to the first one. We compared the length of
594 each segment independently with an unpaired t-test with a Welch correction (N=3, n>60, mean ± SD).
595 **(C)** Proportion of snowflake entities in a population of quintuple mutant or *ace2/ace2* strains (N=3,
596 n>201, mean ± SD, Fisher's exact test, ns p>0.05).

Figure 4

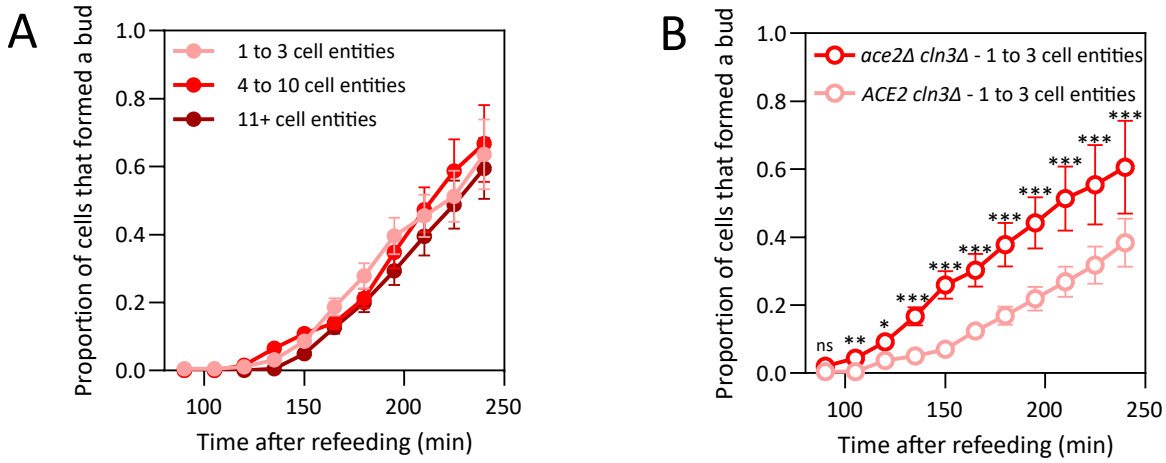
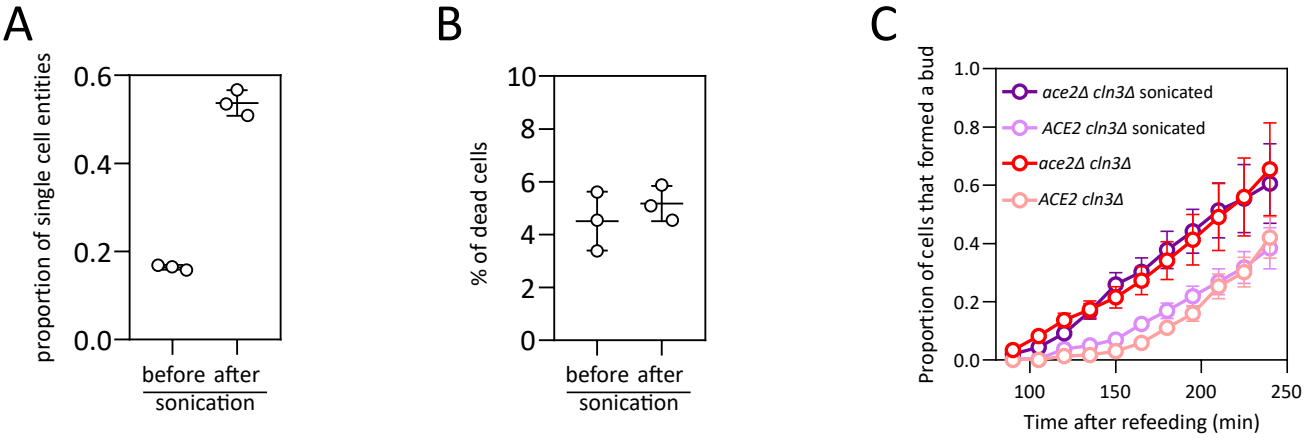

A
Proportion of cells that formed a bud
1.0
0.8
0.6
0.4
0.2
0.0
1 to 3 cell entities
4 to 10 cell entities
11+ cell entities
100
150
200
250
Time after refeeding (min)
B
Proportion of cells that formed a bud
1.0
0.8
0.6
0.4
0.2
0.0
ace2Δ cln3Δ - 1 to 3 cell entities
ACE2 cln3Δ - 1 to 3 cell entities
ns
**
*
***
***
***
***
***
***
100
150
200
250
Time after refeeding (min)

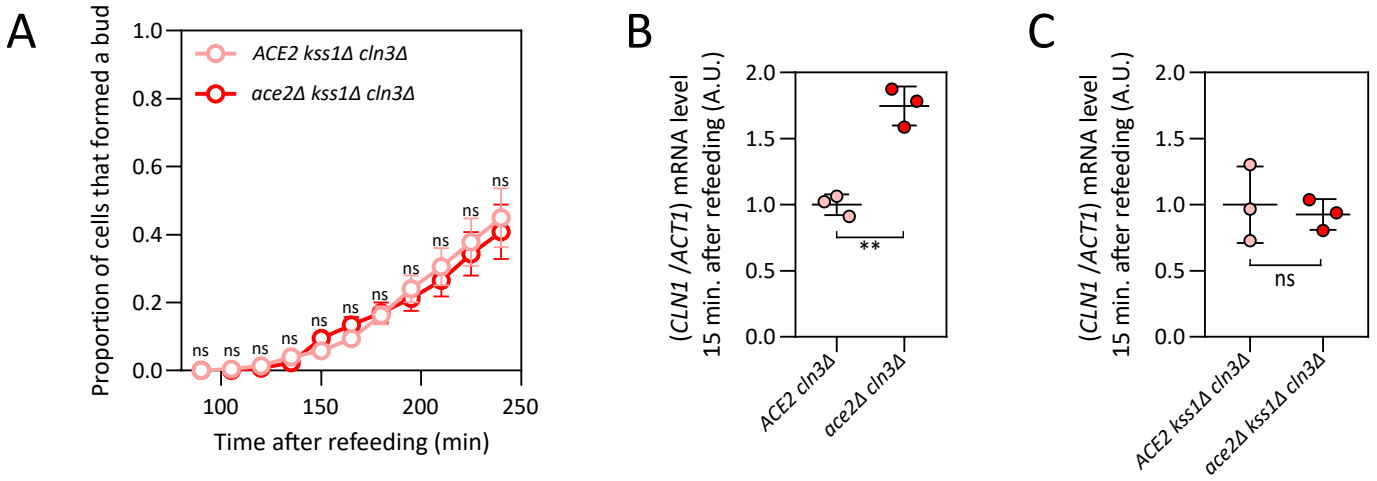
Figure 4 - figure supplement 1



597 **Figure 4. Rescue of the quiescence-exit default associated with *cln3* depends on the *ace2* mutation**
598 **and not on the Snowflake phenotype. (A)** A 2-day *ace2/ace2 cln3/cln3* culture was sonicated and refed
599 onto a fresh SDCasaWAU microscope pad. The proportion of cells that formed a new bud after
600 refeeding on a SDCasaWAU medium containing microscope pad was assessed within different
601 multicellular size ranges (N=3, n>184, mean ± SD, Fisher's exact test). **(B)** 2-day *cln3* cultures, either
602 *ace2* or *ACE2*, were sonicated and refed onto a fresh SDCasaWAU microscope pad. Within entities
603 formed of 1 to 3 cells, the proportion of cells that formed a new bud after refeeding on a SDCasaWAU
604 medium containing microscope pad was assessed (N=3, n>63, mean ± SD, Fisher's exact test, ns p>0.05,
605 *p<0.05, **p<0.005, ***p<0.001).

606 **Figure supplement 1**. **Effect of sonication on SF phenotype, cell death and quiescence exit**. **(A-B)** The
607 effect of sonication bath on an *ace2* culture was assessed by measuring the proportion of single cell
608 entities (**A**, N=3, n>212) and the percentage of dead cells (**B**, N=3, n>207) in the population before and
609 after the culture was sonicated. **(C)** Proportion of *cln3* cells, either *ace2* or *ACE2*, and either sonicated
610 or not, that formed a new bud after refeeding of 2 days cultures on a SDCasaWAU medium containing
611 microscope pad (N=3, n>63, Fisher's exact test, mean ± SD).

Figure 5


A
Proportion of cells that formed a bud
1.0
0.8
0.6
0.4
0.2
0.0
ACE2 kss1Δ cln3Δ
ace2Δ kss1Δ cln3Δ
ns
100
150
200
250
Time after refeeding (min)
B
(CLN1 /ACT1) mRNA level
15 min. after refeeding (A.U.)
2.0
1.5
1.0
0.5
0.0
**
ACE2 cln3Δ
ace2Δ cln3Δ
C
(CLN1 /ACT1) mRNA level
15 min. after refeeding (A.U.)
ns
ACE2 kss1Δ cln3Δ
ace2Δ kss1Δ cln3Δ

612 **Figure 5. Rescue of the quiescence-exit default associated with *cln3* is dependent on the Kss1 MAP**
613 **kinase, which favors transcription of the *CLN1* cyclin gene. (A)** Proportion of *cln3 kss1* cells, either
614 *ace2* or *ACE2*, that formed a new bud after refeeding of 2-day cultures on a fresh SDCasaWAU medium
615 containing microscope pad (N=3, n>86, mean ± SD, Fisher's exact test, ns p>0.05). **(B)** Ratio of *CLN1*
616 mRNA level and *ACT1* mRNA level, determined by RT-qPCR, 15 minutes after refeeding of 2 days *cln3*
617 cultures, either *ace2* or *ACE2* (N=3, mean ± SD, unpaired t-test, Welch correction, **p<0.005). **(C)** Ratio
618 of *CLN1* mRNA level and *ACT1* mRNA level, determined by RT-qPCR, 15 minutes after refeeding of 2-
619 day *kss1 cln3* cultures, either *ace2* or *ACE2* (N=3, mean ± SD, unpaired t-test, Welch correction, ns
620 p>0.05).

Figure 6

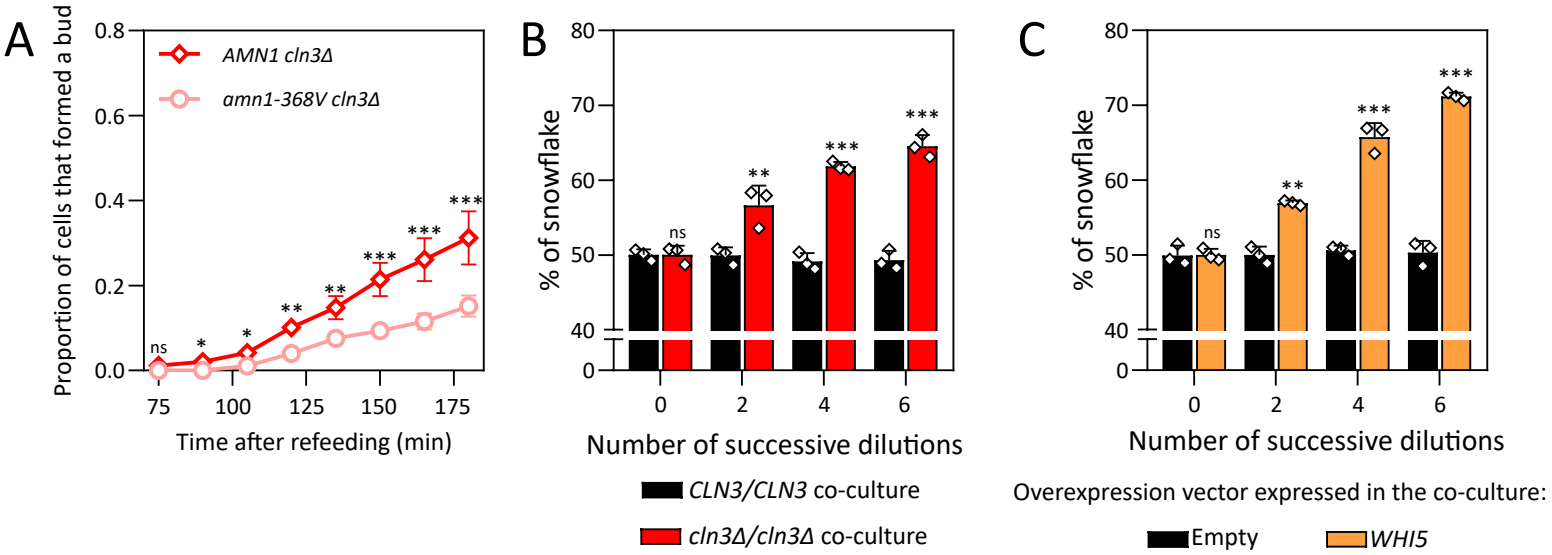
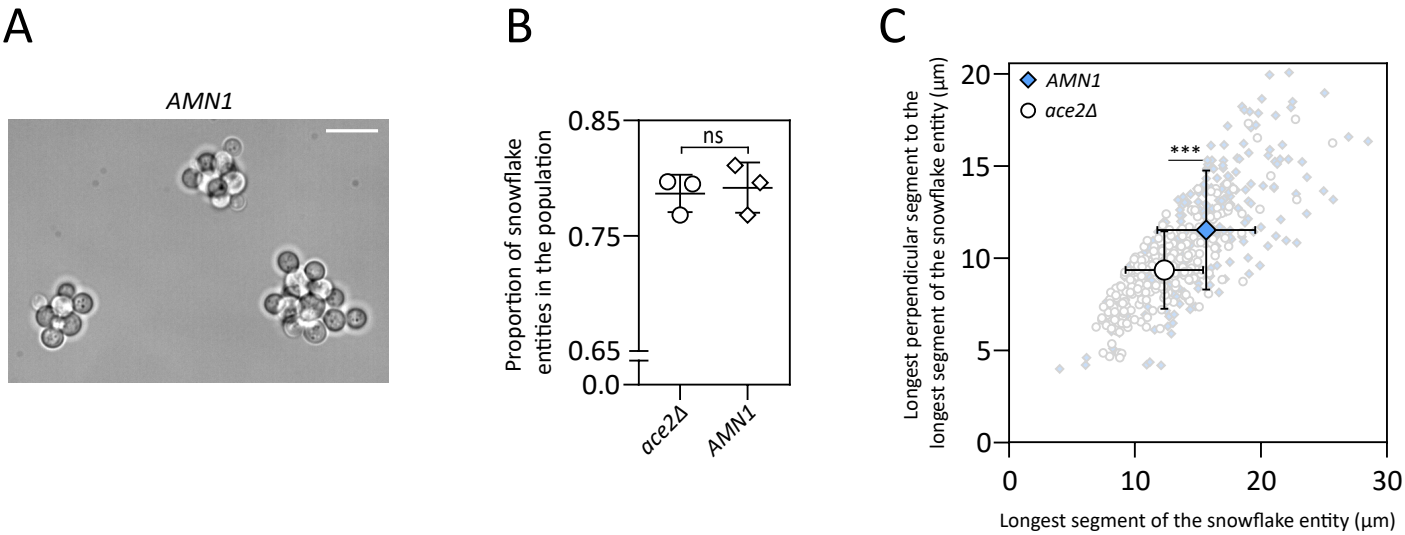

A
Proportion of cells that formed a bud
0.8
0.6
0.4
0.2
0.0
AMN1 cln3Δ
amn1-368V cln3Δ
ns
*
*
**
**
***
***
***
75
100
125
150
175
Time after refeeding (min)
B
% of snowflake
80
70
60
50
40
0
ns
**
***
***
0
2
4
6
Number of successive dilutions
CLN3/CLN3 co-culture
cln3Δ/cln3Δ co-culture
C
% of snowflake
80
70
60
50
40
0
ns
**
***
***
0
2
4
6
Number of successive dilutions
Overexpression vector expressed in the co-culture:
Empty
WHI5

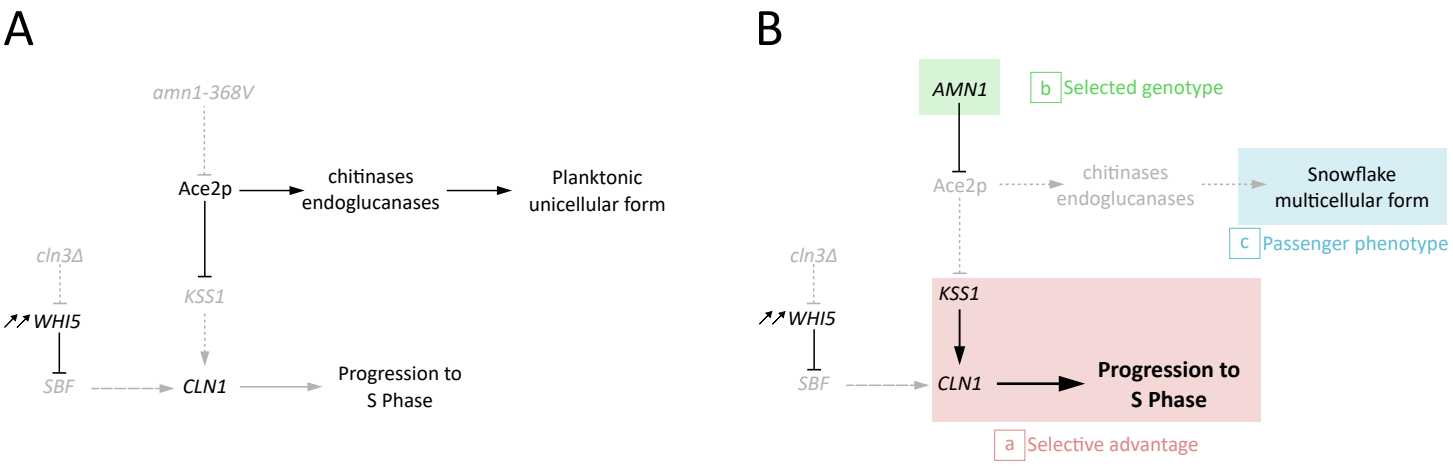
Figure 6 - figure supplement 1



621 **Fig 6. Quiescence exit efficiency and selection in competition experiments of Snowflake *AMN1***
622 **strains. (A)** Proportion of *cln3* cells, either *AMN1* or *amn1-368V*, that formed a new bud after refeeding
623 of 2 days cultures on a fresh SDCasaWAU medium containing microscope pad (N=3, n>77, mean ± SD,
624 Fisher's exact test, ns p>0.05, *p<0.05, **p<0.005, ***p<0.001). **(B)** Evolution of the percentage of
625 snowflake entities during independent co-culture competitions between *AMN1* and *amn1-368V*
626 strains, either *cln3/cln3* (red bars) or *CLN3/CLN3* (black bars) (N=3, n>252, mean ± SD, Fisher's exact
627 test, ns p>0.05, **p<0.005, ***p<0.001). **(C)** Evolution of the percentage of snowflake entities during
628 independent co-culture competitions between *AMN1* and *amn1-368V* strains overexpressing *WHI5*
629 (orange bars) or not (black bars) (N=3, n>302, Fisher's exact test, ns p>0.05, **p<0.005, ***p<0.001).

630 **Figure supplement 1. Snowflake characterization of *AMN1* strains. (A)** Representative image of the
631 *AMN1* strain. Bar is 10µm. **(B)** Proportion of snowflake entities in populations of *AMN1* or *ace2* haploid
632 strains (N=3, n>219, mean ± SD, Fisher's exact test, ns p>0.05). **(C)** Size distribution of *AMN1* (diamond)
633 or *ace2* (circle) snowflakes. Size is estimated by measuring both the longest segment of the snowflake
634 entity and the longest segment perpendicular to the first one (N=3, n>74, mean ± SD, unpaired t-test,
635 Welch correction, ***p<0.001, account for both segment).

Figure 7


A
amn1-368V
Ace2p
chitinases
endoglucanases
Planktonic
unicellular form
cln3Δ
KSS1
↗↗WHI5
SBF
CLN1
Progression to
S Phase
B
AMN1
b Selected genotype
Ace2p
chitinases
endoglucanases
Snowflake
multicellular form
c Passenger phenotype
cln3Δ
KSS1
↗↗WHI5
SBF
CLN1
Progression to
S Phase
a Selective advantage

636 **Fig 7. Model explaining the selection of the Snowflake phenotype as a passenger phenotype.** In
637 strains expressing the non- functional *amn1-368V* allele **(A)**, a default in quiescence exit after refeeding
638 was observed in a *cln3* mutant. In non-laboratory strains **(B)**, the functional *AMN1* allele leads to
639 degradation of Ace2p, which can no longer repress the expression of the Kss1 Map kinase. Kss1p favors
640 the transcription of *CLN1*, which would favor progression to S phase and partially suppress the default
641 in quiescence exit associated with the *cln3* mutation. This observed selective advantage (a) leads to
642 the selection of *AMN1* genotype (b), and because of the pleiotropy of Ace2p transcription factor, to
643 the selection of the Snowflake multicellular phenotype as a passenger phenotype (c).