

1 **Stress-induced formation of cell wall-deficient cells in filamentous**
2 **actinomycetes**

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18 Keywords: hyperosmotic stress, morphogenesis, cell wall-deficient cells, S-cell, adaption

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28 ABSTRACT

29 The cell wall is a shape-defining structure that envelopes almost all bacteria. One of its main
30 functions is to serve as a protection barrier to environmental stresses. Bacteria can be forced
31 in a cell wall-deficient state under highly specialized conditions, which are invariably aimed
32 at interrupting cell wall synthesis. Therefore, the relevance of such cells has remained
33 obscure. Here we show that many filamentous actinomycetes have a natural ability to
34 generate a new, cell wall-deficient cell type in response to hyperosmotic stress, which we call
35 S-cells. This wall-deficient state is transient, as S-cells are able to switch to the canonical
36 mycelial mode-of-growth. Remarkably, prolonged exposure of S-cells to hyperosmotic stress
37 yielded variants that are able to proliferate indefinitely without their cell wall. This is the
38 first report that demonstrates the formation of wall-deficient cells as a natural adaptation
39 strategy and their potential transition into stable wall-less forms solely caused by prolonged
40 exposure to osmotic stress. Given that actinomycetes are potent antibiotic producers, our
41 work also provides important insights into how biosynthetic gene clusters and resistance
42 determinants may disseminate into the environment.

43 INTRODUCTION

44 All free-living bacteria are challenged by constant changes in their environment, and their
45 survival depends on the ability to adapt to sudden exposure to stressful conditions. For
46 instance, soil bacteria can encounter rapid osmotic fluctuations caused by rain, flooding, or
47 desiccation. Bacterial cells typically respond to osmotic changes by rapidly modulating the
48 osmotic potential within the cell, either by importing or exporting ions and compatible
49 solutes¹. While these responses typically occur immediately after cells have been exposed to
50 the changed environment, they are also able to tune the expression of metabolic pathways or
51 critical enzymes².

52 How such osmotic changes affect cellular morphology is not well known. The cells' shape
53 is largely dictated by the cell wall, which is a highly dynamic structure that acts as the
54 main barrier that provides osmotic protection³. The synthesis of its major constituent,
55 peptidoglycan (PG), involves the activity of large protein complexes that cooperatively build
56 and incorporate new PG precursors into the growing glycan strands at the cell surface⁴⁻⁷.
57 These strands are then cross-linked to form a single, giant sacculus that envelops the cell⁸.
58 The sites for the incorporation of new PG is a major difference between the planktonic
59 firmicutes that grow by extension of the lateral wall, and Actinobacteria, which grow via
60 apical extension and thereby incorporating new PG at the cell poles^{9,10}.

61 Actinobacteria display a wide diversity of morphologies, including cocci
62 (*Rhodococcus*), rods (*Mycobacterium* and *Corynebacterium*) and mycelia (*Streptomyces* and
63 *Kitasatospora*), or even multiple shapes (*Arthrobacter*)^{11,12}. Species belonging to these
64 genera are able to change their morphology to adapt to extreme environments. For example,
65 *Rhodococcus* species that are commonly found in arid environments are able to adapt to
66 desiccation by modulating their lipid content and form short-fragmented cells¹³.
67 *Arthrobacter* species also exhibit high resistance to desiccation and cold stresses. Upon
68 hyperosmotic stress, these cells can modulate the synthesis of osmoprotectants and switch
69 between rod-shaped and myceloid cells¹².

70 While the cell wall is considered an essential component of virtually all bacteria, most
71 species can be manipulated under laboratory conditions to produce so-called L-forms that are
72 able to propagate without their wall¹⁴⁻¹⁷. Typically, L-forms are generated by exposing
73 walled bacteria to high levels of lysozyme combined with antibiotics that target cell wall
74 synthesis in media containing high levels of osmolytes^{18,19}. Stable L-forms that can
75 propagate indefinitely without the cell wall require two mutations that fall in separate classes

76 ¹⁸. The first class of mutations leads to an increase in membrane synthesis, either directly by
77 increasing fatty acid biosynthesis, or indirectly by reducing cell wall synthesis ²⁰. The second
78 class of mutations reduces oxidative damage caused by reactive oxygen species, which are
79 detrimental to proliferation of L-forms ²¹. Notably, proliferation of L-forms is independent of
80 the FtsZ-based division machinery ^{15,22}. Instead, their proliferation can be explained solely by
81 biophysical processes, in which an imbalance between the cell surface area to volume ratio
82 leads to spontaneous blebbing and the subsequent generation of progeny cells ²⁰. Such a
83 purely biophysical mechanism of L-form proliferation is not species-specific. This
84 observation has led to the hypothesis that early life forms propagated in a similar fashion well
85 before the cell wall had evolved ^{15,20,23}. Whether L-forms have functional relevance in
86 modern bacteria, however, is unclear.

87 Here we present evidence that many filamentous actinobacteria have a natural ability
88 to extrude cell wall-deficient (CWD) cells when exposed to high levels of osmolytes. These
89 newly-identified cells, which we call S-cells, synthesize PG precursors and are able to switch
90 to the canonical mycelial mode-of-growth. Remarkably, upon prolonged exposure to
91 hyperosmotic stress conditions, S-cells can acquire mutations that enable them to proliferate
92 in the CWD state as so-called S-forms, which are morphologically similar to L-forms but not
93 originating from walled cells exposed to cell wall-targeting agents. These results demonstrate
94 that the extrusion of S-cells and their transition into proliferating S-forms is a natural
95 adaptation strategy in filamentous actinobacteria, solely caused by prolonged exposure to
96 osmotic stress.

97

98 **RESULTS**

99 **Hyperosmotic stress drives the formation of cell wall-deficient cells**

100 Recent work suggests that hyperosmotic stress conditions affects apical growth in
101 streptomycetes ²⁴. Consistent with these observations, we noticed that growth was
102 progressively disturbed in the filamentous actinomycete *Kitasatospora viridifaciens*, when
103 increasing amounts of sucrose were added to the medium (Fig. 1A). In liquid cultures
104 containing more than 0.5 M sucrose, initiation of growth was delayed by at least 5 h
105 compared to media with low levels of sucrose. A similar retardation in growth was observed
106 on solid medium supplemented with high levels of osmolytes, evident from the size decrease
107 of colonies (Fig. 1B, C). On average, their size decreased from 12.8 mm² to 1.4 mm² after 7
108 days of growth. Notably, the high osmolarity also reduced the number of colony forming

109 units (CFU) by 33%, from 9.3×10^8 CFU ml⁻¹ to 6.1×10^8 CFU ml⁻¹. In order to study the
110 morphological changes accompanying this growth reduction, we stained the mycelium after
111 48 h of growth with the membrane dye FM5-95 and the DNA stain SYTO-9 (Fig. 1D, E).
112 The high levels of osmolytes had a dramatic effect on mycelial morphology. The hyphae
113 showed indentations along the cylindrical part of the leading hyphae, reminiscent of initiation
114 of sporulation (see BF panel in Fig. 1E). In addition, the branching frequency increased by
115 more than three-fold in the presence of high levels of osmolytes (Extended Data Table 1 and
116 2, Student's T-test, *P*-value = 0,0010). Additionally, we noticed that these stressed hyphae
117 contained an excess of membrane (compare FM5-95 panels in Fig. 1D, E). The proportion of
118 the hyphae that were stained with FM5-95 increased from 10% to 21% in the presence of
119 0.64 M Sucrose (Extended Data Table 1 and 2, Student's T-test, *P*-value < 0,0001).
120 Simultaneously, the average surface area occupied by the nucleoid decreased from $2.59 \mu\text{m}^2$
121 to $1.83 \mu\text{m}^2$ (Extended Data Table 1 and 2, Student's T-test, *P*-value = 0.0074). Most
122 strikingly, we observed large DNA-containing vesicles surrounding the mycelial networks
123 (see arrowheads in Fig. 1E). High levels of NaCl had a similar effect on growth and
124 morphology (Fig. S1). *K. viridifaciens* was no longer able to grow when the NaCl
125 concentration was increased to more than 0.6 M (not shown). These results together indicate
126 that upon osmotic stress, the hyphae form a previously uncharacterized cell type, which we
127 hereinafter will refer to as S-cells, for stress-induced cells.

128 To distinguish S-cells from other cell wall-deficient (CWD) variants of *K.*
129 *viridifaciens*, we compared them to fresh protoplasts and L-form cells obtained after classical
130 induction with high levels of lysozyme and penicillin G (see Materials and Methods). Size
131 measurements from 2D images revealed that S-cells had an average surface area of $20.73 \mu\text{m}^2$
132 and were considerably larger than protoplasts and L-forms, which had an average
133 surface area of $4.01 \mu\text{m}^2$ and $7.06 \mu\text{m}^2$, respectively. Vancomycin-BODIPY staining (van^{FL},
134 Fig. S2A) revealed a heterogeneous pattern of nascent PG synthesis in these cells, while in L-
135 forms mostly detached wall material was observed. By contrast, no staining was detected
136 when freshly prepared protoplasts were used (Fig. S2A). When protoplasts were maintained
137 in LPB for 48 hours, their average surface area increased to $7.49 \pm 2.21 \mu\text{m}^2$, which is
138 considerably smaller than that of S-cells (Extended Data Table 3). Furthermore, protoplasts
139 regenerated a more uniform cell wall while S-cells showed a disordered, non-uniform pattern
140 of cell-wall assembly, whereby wall material was sometimes found to be detached from the
141 cell surface (Fig. S2B, Table Extended Data Table 3).

142

143 **Formation of S-cells is common in natural isolates**

144 To see how widespread the formation of S-cells is among natural isolates, we screened our
145 collection of filamentous actinomycetes, obtained from the Himalaya and Qinling mountains
146 ²⁵, using *Streptomyces coelicolor*, *Streptomyces lividans*, *Streptomyces griseus*, and
147 *Streptomyces venezuelae* as the reference strains. We used a cut-off diameter of 2 μ m to
148 distinguish small S-cells from spores. Spherical cells, similar to S-cells were evident in
149 hyperosmotic media in *S. venezuelae* and in 7 out of the 96 wild isolates (Fig. S3A). The cells
150 were variable in size within the same strains and between strains (Fig. 2A, Extended Data
151 Table 4) and showed differences in the organization of their DNA (Fig. 2A). No S-cells were
152 found in *S. coelicolor*, *S. griseus*, or *S. lividans* under the tested conditions. Phylogenetic
153 analysis based on 16S rRNA (Fig. S3B), or the taxonomic marker gene *ssgB* used for
154 classifying morphologically complex actinomycetes ²⁶ revealed that the formation of S-cells
155 is common in at least two genera (Fig. 2B). Moreover, the ability to form S-cells was not
156 restricted to strains that sporulate in liquid-grown cultures. This is based on the observation
157 that MBT86, which belongs to the *S. coelicolor* clade and is classified as a non-liquid
158 sporulating strain, also generates S-cells (Fig. 2C). Altogether, these results show the natural
159 ability to generate S-cells is widespread in filamentous actinomycetes.

160

161 **S-cells are viable cells with the ability to switch to the mycelial mode-of-growth**

162 To determine where S-cells are generated in the hyphae, we performed live imaging of
163 growing germlings of *K. viridifaciens* (Extended Data Video S1). Approximately 7 h after the
164 visible emergence of germ tubes, we detected a transient arrest in tip extension of the leading
165 hypha (Fig. 3A, t=400 mins). Shortly thereafter, small S-cells became visible, which were
166 extruded from the hyphal tip (see arrows in Fig. 3A). These cells rapidly increased in size and
167 number. After 545 min a narrow branch (Fig. 3A arrowhead) was formed in the apical region
168 from which the S-cells were initially extruded. Subapically, other branches became visible
169 approximately 210 minutes after the first appearance of these cells (Extended Data Video S1,
170 t= 770 min). Notably, such branches frequently also extruded S-cells, similarly to the leading
171 hypha (Extended Data Video S2). This showed that S-cells are produced at hyphal tips after
172 apical growth was arrested.

173 Further characterization of S-cells from *K. viridifaciens* revealed that these cells had a
174 granular appearance and membrane assemblies that stained with FM5-95 (Fig. 3B, arrows,
175 Supplementary Video S3). Notably, these assemblies often co-localized with DNA (Fig. 3B,
176 arrows). To study S-cells in more detail, we separated them after 7 days from the mycelia by

177 filtration (see Materials and Methods). In agreement with the previous findings, we also
178 detected agglomerates of membrane assemblies in close proximity of the DNA using electron
179 microscopy analysis (Fig. 3C). Additionally, we noticed that S-cells possessed a disorganized
180 surface, characterized by membrane protrusions that appeared to detach from the S-cells (Fig.
181 3D, 3E), and an apparent deficiency in normal cell-wall biogenesis (compare to the cell
182 surface of the hypha in Figs. 3F, 3G).

183 To establish if S-cells were truly viable cells, they were plated onto plates
184 supplemented with sucrose. After 7 days of growth, many mycelial colonies were found;
185 demonstrating that the cells indeed were viable, and that such cell are only transiently CWD
186 (Fig. 3H; $\pm 1.6 \times 10^4$ CFUs ml⁻¹ of the filtered culture). Time-lapse microscopy (Extended
187 Data Video S4) revealed that the cells (Fig. 3I, asterisk) initiated filamentous growth and
188 established mycelial colonies, which, in turn, also extruded new S-cells from the hyphal tips
189 (Fig. 3I, arrowheads). A switch to mycelial growth was also observed when S-cells were
190 inoculated in liquid medium, whether or not the media was supplemented with high levels of
191 sucrose (data not shown). We noticed that the viability of S-cells was reduced by 60%
192 (decreasing from 1.6×10^4 to 6.7×10^3 CFUs ml⁻¹) when these cells were diluted in water
193 before plating. Microscopy analysis indicated that the surviving S-cells were those that
194 showed abundant staining with WGA-Oregon (Fig. S4). Altogether, these results demonstrate
195 that *K. viridifaciens* generates S-cells that synthesize PG and are able to switch to the
196 mycelial mode-of-growth.

197

198 **S-cell formation frequently leads to loss of the linear megaplasmid KVP1**

199 When S-cells were allowed to switch to mycelium on MYM medium, we identified many
200 colonies with developmental defects (Fig. 4A). Most obvious was the frequent occurrence of
201 small, brown-colored colonies that failed to produce the white aerial hyphae or the grey-
202 pigmented spores. Non-differentiating colonies are referred to as bald, for the lack of the
203 fluffy aerial hyphae²⁷. To test if this aberrant phenotype was maintained in subsequent
204 generations, we selected three of these bald colonies (R3-R5) and two grey-pigmented
205 colonies with a near wild-type morphology (R1 and R2) for further analysis. The progeny of
206 the grey colonies developed similarly to the wild-type strain, and sporulated abundantly after
207 7 days of growth (Fig. 4B). In contrast, strains R3-R5 failed to sporulate after 7 days of
208 growth. This phenotype is reminiscent of the defective sporulation seen in colonies of
209 *Streptomyces clavuligerus* that have lost the large linear plasmid pSCL4 following protoplast
210 formation and regeneration²⁸. Given that *K. viridifaciens* contains a large megaplasmid

211 (KVP1²⁹), we reasoned that S-cell formation could increase the frequency of the loss of this
212 plasmid. To test this assumption, we performed quantitative real-time PCR using four genes
213 contained on the megaplasmid (*orf1*, *parA*, *tetR*, and *allC*). As a control, we included the two
214 house-keeping genes *infB* and *atpD*, both of which are located on the chromosome, and
215 which encode the translation initiation factor IF-2 and a subunit of the F₀F₁ ATP synthase,
216 respectively. Detectable amplification of *infB* and *atpD* was seen after 19 PCR cycles in
217 strains R3-R5, which was similar to the wild-type strain (Fig. 4C). The same was true for the
218 KVP1-specific genes *orf1*, *parA*, *tetR*, and *allC* in the wild-type strains. However,
219 amplification of these plasmid marker genes was only seen after 30 PCR cycles in strain R3-
220 R5 (Fig. 4D). This demonstrates that the KVP1-specific genes were only present in trace
221 amounts in the R3-R5 strains (at least 10⁴ times less abundant than the chromosomal genes
222 *infB* and *atpD*) (Fig. 4E), which is consistent with loss of KVP1 during formation of S-cells.
223

224 **Prolonged hyperosmotic stress is sufficient to convert S-cells into proliferating S-forms**
225 Although the switch to mycelial growth was exclusively observed when young S-cells were
226 cultured in fresh media, we noticed a dramatic change when S-cells had been exposed for
227 prolonged periods to the hyperosmotic stress conditions. In nine out of 15 independent
228 experiments, we found that S-cells switched to mycelial growth, while four times S-cells
229 failed to form a growing culture. Strikingly, however, were the two independent occasions
230 during which S-cells had proliferated in an apparent cell wall-deficient state. On solid
231 medium, these two independent cell lines, called M1 and M2 (for mutants 1 and 2,
232 respectively, see below), formed viscous colonies on LPMA medium, which were similar to
233 those formed by the L-form lineage induced with penicillin and lysozyme, but distinct from
234 the compact colonies formed by the wild-type strain (Fig. 5A). Liquid-grown cultures of M1
235 and M2 exclusively consisted of CWD cells when sucrose and MgCl₂ were added (Fig. 5B,
236 BF panels). Staining with WGA-Oregon Green showed these cell lines were indeed cell wall-
237 deficient, as nascent peptidoglycan was mainly found detached from the cell surface (Fig.
238 S5). The spherical cells produced by M1 and M2 were comparable in size to the PenG-
239 induced L-forms. Further microscopic analysis revealed that the cells from M1 and M2
240 contained inner vesicles (arrowheads in Fig 5B) and tubular protrusions emerging from the
241 cell surface (Fig. 5B, inlay). The vast majority of cells contained DNA, although some empty
242 vesicles were also evident in M1 and M2 (Fig. 5B, asterisks). Time-lapse microscopy
243 revealed that both strains proliferated, whereby smaller progeny cells were released following
244 deformation of the mother cell membrane by either vesiculation (Fig. 5C, taken from

245 Extended Data Video S5), blebbing (Fig. 5D, taken from Extended Data Video S6) or
246 tubulation (Fig. 5E, taken from Extended Data Video S7). Altogether these results inferred
247 that strains M1 and M2 closely resemble the previously described L-forms, both in the
248 inability to regain a cell wall as well as the ability to proliferate in the cell-wall-less state.
249 However, instead of originating from prolonged exposure to antibiotic and/or lysozyme
250 treatment, they originate from osmotically stress-induced cells, and we therefore will call
251 these cells S-forms.

252 The low frequency at which S-form cells formed made us wonder whether M1 and
253 M2 had acquired mutations that enabled these strains to proliferate without a proper cell wall.
254 Real-time qPCR studies revealed that M1 and M2, but also the PenG-induced L-form cell
255 line, had lost the megaplasmid (Fig. S6). However, loss of the megaplasmid is not sufficient
256 to drive the transition from S-cells to S-forms, as strains R3-R5, all of which had lost the
257 KVP1 megaplasmid, formed mycelia extruding S-cells under hyperosmotic stress conditions
258 (data not shown). Single nucleotide polymorphism (SNP) analysis following whole genome
259 sequencing showed that M1 and M2 had acquired several other mutations (Extended table 5
260 and 6). Interestingly, both strains carried a mutation in the gene BOQ63_RS21920, which
261 encodes a putative metal ABC transporter. Transporters are often used to cope with osmotic
262 stress conditions ³⁰. We also identified mutations in the PenG-induced L-form strain
263 (Extended table 7). These mutations, however, differed from those observed in the S-form
264 strains M1 and M2. Notably, the mutations in the PenG-induced L-form appeared to directly
265 relate to cell wall biogenesis, for example in the case of the mutation in *uppP*. The encoded
266 protein is involved in the recycling pathway of the carrier lipid undecaprenyl phosphate
267 (BOQ63_RS22750), which transports glycan biosynthetic intermediates for cell wall
268 synthesis. Altogether, these results demonstrate that prolonged exposures to hyperosmotic
269 stress conditions are apparently sufficient to convert a bacterium into an S-form strain that
270 proliferates without the cell wall.

271

272 **DISCUSSION**

273 Filamentous actinomycetes have been intensely studied for more than 50 years as a model for
274 bacterial development. Here, we provide compelling evidence that S-cells represent a natural
275 and previously unnoticed developmental stage in these organisms when they are exposed to
276 hyperosmotic stress conditions (Fig. 5F). These S-cells are extruded from the hyphal tips,
277 they contain DNA and are viable with the ability to grow into mycelial colonies.
278 Furthermore, upon prolonged exposure to hyperosmotic stress, S-cells may also accumulate

279 mutations that enable them to efficiently proliferate in the wall-deficient state we have
280 dubbed S-forms. Our data show that these S-forms can simply emerge as the product of
281 prolonged exposure of cells to hyperosmotic conditions, without directly requiring cell wall-
282 targeting agents. This work provides compelling evidence that such cells have an ecological
283 relevance.

284 Environmental fluctuations can dramatically influence the availability of water in
285 ecosystems and present osmotic shock conditions to organisms. For instance, microorganisms
286 living in hyperarid regions or hypersaline aquatic environments are frequently exposed to
287 desiccation or hypertonicity ³¹. Also, microbes in snow and ice habitats experience low water
288 availability and hypersaline or hyper-acidic environments ³². Bacteria can adapt to these
289 fluctuations by modulating fatty acid synthesis, accumulating or synthesizing
290 osmoprotectants, protecting their DNA, and secreting extracellular polymeric substance ^{31,33}.

291 Here, we focused on the adaptation of filamentous actinomycetes, which are common
292 in any soil, to extended periods of hyperosmotic stress. As expected, we detected that these
293 bacteria increased the amount of membrane in the hyphae and condensed their nucleoids.
294 Surprisingly though was the extrusion of S-cells. Together with sporulation and the recently
295 discovered explorative mode-of-growth ³⁴, the ability to form S-cells extends the repertoire
296 by which filamentous actinomycetes can thrive in changing environments. In addition to
297 switching to mycelial growth, these S-cells can have multiple fates. As these cells are wall-
298 deficient, they are prone to lysis due to influx of water. Indeed, exposure to water leads to a
299 steep decline in their ability to outgrow into colonies. However, even when S-cells lyse, the
300 DNA cargo will be released into the environment. Given the large number of biosynthetic
301 gene clusters (BGCs) that are present in the genomes of filamentous actinomycetes, including
302 their resistance determinants, this release of DNA may be a significant, and previously
303 unknown mechanism by which resistance genes are spread. In contrast to releasing DNA into
304 the environment, the S-cells may be able to take up DNA from the environment, similar to
305 other cell wall-deficient cell types such as protoplasts or L-forms ³⁵. This would enable the
306 cells to acquire genetic information that may help them to overcome the stressful conditions
307 to which they are exposed. In other organisms, this concept has been well characterized. For
308 instance, the bacterium *Bacillus subtilis* becomes naturally competent towards the end of the
309 exponential growth phase ³⁶. This allows the cells to pick up DNA from the environment,
310 with the prospect of withstanding the harsh conditions and improving the likelihood of
311 survival. Likewise, competence of *Streptococcus pneumoniae* is promoted by exposure to
312 antibiotics that target DNA replication ³⁷. This, in turn, enables the uptake of foreign DNA

313 (e.g. genes conferring antibiotic resistance). As such, maximizing survival by DNA uptake is
314 a proven strategy.

315 Our work shows that S-cells are extruded from hyphal tips into the environment,
316 coinciding with an arrest in tip growth. Following their release, the extruding hypha
317 reinitiates growth, indicating that the extrusion process occurs in a manner that apparently is
318 not lethal for the filament from which the cells are released. Tip growth in filamentous
319 actinomycetes is coordinated by the polarisome complex, of which the DivIVA protein is a
320 crucial member³⁸. Recent work revealed that hyperosmotic stress has a dramatic effect on the
321 polar growth machinery. Following osmotic upshift experiments, tip growth is arrested,
322 followed by relocation of the apical growth machinery to subapical sites. As a consequence,
323 lateral branches emerge from the leading hyphae²⁴. We hypothesize that an imbalance
324 between cell wall synthesis and cell wall turnover could locally lead to changes in the
325 thickness or structure of the cell wall, allowing S-cells to escape from the sacculus.

326

327 **Hyperosmotic stress-induced formation of S-forms**

328 L-forms have been studied for many decades, and only recently are we beginning to
329 understand their exciting biology, especially due to ground-breaking work from the Errington
330 lab. L-form cells have been artificially generated from many different bacteria in many
331 laboratories, invariably aimed at targeting the biosynthesis pathway of the cell wall. To that
332 end, cells are typically exposed to high levels of antibiotics, either or not combined with
333 lysozyme treatment^{18,23}. Our work expands on this research by providing for the first-time
334 evidence that CWD strains can emerge solely by exposure to hyperosmotic stress conditions
335 and implies an environmental relevance of this cell type. A crucial and limiting step in the
336 formation of L-forms in *B. subtilis*, as well as in other bacteria, is the escape of a protoplast
337 from the cell-wall sacculus. This process requires lytic activity, which usually comes from
338 lysozyme activity³⁹. Our data show that actinomycetes have a natural ability to release such
339 CWD cells when exposed to hyperosmotic conditions. Under prolonged exposure to osmotic
340 stress, some cells are able to acquire mutations allowing these cells to propagate as S-forms.
341 In line with these findings, recent work shows that *B. subtilis* and *S. aureus* both are able to
342 convert to wall-deficient cells. This has been shown in an animal infection model as well as
343 in macrophages, where lysozyme activity from the host converts walled bacteria into CWD
344 cells³⁹. Collectively, these results indicate that cell wall-deficient cells represent an adaptive
345 morphology allowing cells to overcome environmental challenges, such as antibiotic
346 treatment or hyperosmotic stress conditions.

347 In summary, our work provides evidence for a new, cell wall-deficient cell type in the
348 biology of filamentous actinomycetes. It further expands the large diversity in bacterial cell
349 types, and the plasticity that microorganisms employ to handle environmental stresses. It
350 remains to be elucidated how the ability to form S-cells improves fitness in these filamentous
351 actinomycetes, and how this morphogenetic switch is regulated.

352

353 MATERIALS AND METHODS

354 Strains and media

355 Bacterial strains used in this study are shown in Extended Data Table 8. To obtain
356 sporulating cultures, *Streptomyces* and *Kitasatospora* species were grown at 30°C for 4 days
357 on MYM medium ⁴⁰. To support growth of CWD cells, strains were grown on solid medium
358 L-Phase Medium (LPMA), containing 0.5% glucose, 0.5% yeast extract, 0.5% peptone, 20%
359 sucrose, 0.01% MgSO₄·7H₂O, 0.75% Iberian agar (all w/v). After autoclaving, the medium
360 was supplemented with MgCl₂ (final concentration of 25 mM) and 5% (v/v) horse serum.

361 L-Phase Broth (LPB) was used as liquid medium to support growth of wall-deficient
362 cells. LPB contains 0.15% yeast extract, 0.25% bacto-peptone, 0.15% oxoid malt extract,
363 0.5% glucose, 0.64 M sucrose, 1.5% oxoid tryptic soy broth powder (all w/v) and 25 mM
364 MgCl₂. To test the effect of different sucrose concentrations on mycelial growth and the
365 formation of S-cells, the amount of sucrose in LPB was changed to obtain final
366 concentrations of 0.0, 0.12, 0.18, 0.50 and 0.64 M. The influence of sodium chloride as an
367 osmolyte was analysed by replacing sucrose with NaCl. 50 ml cultures were inoculated with
368 10⁶ spores ml⁻¹ and grown in 250 ml flasks. Cultures were incubated at 30°C, while shaking
369 at 100 rpm.

370 To prepare protoplasts of *K. viridifaciens*, the wild-type strain was grown for 48 hours
371 in a mixture of TSBS and YEME (1:1 v/v) supplemented with 5 mM MgCl₂ and 0.5%
372 glycine. Protoplasts were prepared as described ⁴¹, with the difference that 10 mg ml⁻¹
373 lysozyme solution was used for three hours. Freshly-made protoplast were diluted and
374 immediately used for fluorescence microscopy.

375

376 Optical density measurements

377 The growth of *K. viridifaciens* was monitored with the Bioscreen C reader system (Oy
378 Growth Curves AB Ltd). To this end, aliquots of 100 µl of LPB medium with different
379 concentrations of sucrose were added to each well of the honeycomb microplate and
380 inoculated with 10⁶ spores ml⁻¹. Growth was monitored for 24 hours at 30°C, while shaking

381 continuously at medium speed. The OD wide band was measured every 30 min and corrected
382 for the absorbance of liquid medium without inoculum. In total, five replicate cultures were
383 used for each osmolyte concentration. The effect of sodium chloride as osmolyte was tested
384 using the same procedure, with the differences that the final volume of the cultures was 300
385 μl , and the experiment was run for 96 hours.

386

387 **Quantification of the number and size of colonies**

388 Serial dilutions of *K. viridifaciens* spores were plated in triplicates in LPMA (high
389 osmolarity) and LPMA without sucrose, MgCl_2 and horse serum (low osmolarity). After 7
390 days of incubation at 30°C the number of colonies was counted to determine the CFU ml^{-1} .
391 Quantification of the surface area of colonies was done with FIJI⁴².

392

393 **Screening for strains with the ability to release S-cells**

394 To identify strains that are able to release S-cells, strains from an in-house culture collection
395²⁵ were initially grown in flat-bottom polystyrene 96-well plates, of which each well
396 contained 200 μl LPB medium and 5 μl of spores. The 96-well plate was sealed with parafilm
397 and incubated at 30°C for 7 days. The cultures were then analysed with light microscopy, and
398 strains with the ability to release S-cells with a diameter larger 2 μm were selected. The
399 selected strains were then grown in 250 mL flasks containing 50 mL LPB medium (10^6
400 spores ml^{-1}) at 30°C while shaking at 100 rpm. After 7 days, aliquots of 50 μl of the bacterial
401 cultures were fluorescently stained with SYTO-9 and FM5-95. The surface area of the S-cells
402 was determined in FIJI⁴². Assuming circularity of these cells, the corresponding diameter D
403 was then calculated as
404 $D = 2 * [\text{SQRT}(\text{area}/\pi)]$.

405

406 **Filtration of S-cells from *K. viridifaciens***

407 50 ml LPB cultures of *K. viridifaciens*, inoculated with 10^6 spores ml^{-1} , were grown for 2 or 7
408 days at 30°C in an orbital shaker at 100 rpm. To separate the S-cells from the mycelium, the
409 cultures were passed through a sterile filter made from an EcoCloth™ wiper. A subsequent
410 filtration step was done by passing the S-cells through a 5 μm Isopore™ membrane filter.
411 The filtered vesicles were centrifuged at 1,000 rpm for 40 mins, after which the supernatant
412 was carefully removed with a 10 mL pipette to avoid disturbance of the S-cells.

413

414

415 **Viability and subculturing of S-cells from *K. viridifaciens***

416 To verify the viability of S-cells, the filtered cells were incubated in 10 mg ml⁻¹ lysozyme
417 solution for 3 hours at 30°C, while shaking at 100 rpm to remove residual hyphal fragments.
418 The filtered S-cells were then centrifuged at 1,000 rpm for 40 mins and resuspended in 1
419 volume of fresh LPB. Serial dilutions of the S-cells in LPB or water were then plated, in
420 triplicate, on LPMA or MYM medium. The plates were grown for 7 days at 30°C and the
421 CFU values were determined for each treatment.

422

423 **Generation of the PenG-induced L-form cell line**

424 Generation of the *K. viridifaciens* L-form lineage was performed by inoculating the wild-type
425 strain in 50 mL LPB medium, supplemented with lysozyme and/or penicillin G, in 250 mL
426 flasks in an orbital shaker at 100 rpm. Every week, 1 mL of this culture was transferred to
427 fresh LPB medium according to the cultivation regime previously described ¹⁹. After the 8th
428 subculture, the inducers were removed from the cultivation medium and the obtained lineage
429 did not revert back to the walled state on LPMA plates or in LPB medium. A single colony
430 obtained after the 8th subculture was designated as PenG-induced L-forms.

431

432 **Phylogenetic analysis**

433 The 16S rRNA sequences from strains of the in-house culture collection were previously
434 determined ²⁵. Homologues of *ssgB* in these strains were identified by BLAST analysis using
435 the *ssgB* sequence from *S. coelicolor* (SCO1541) as the input. For the *Streptomyces* and
436 *Kitasatospora* strains whose genome sequence was not available, the *ssgB* sequence was
437 obtained by PCR with the *ssgB* consensus primers (Extended Data Table 9). Geneious 9.1.7
438 was used to make alignments of *ssgB* and 16S rRNA, and for constructing neighbour-joining
439 trees.

440

441 **Quantitative real time PCR**

442 Filtered S-cells were allowed to regenerate on MYM medium, from which three regenerated
443 bald colonies (R3, R4, and R5) were selected. After two rounds of growth on MYM, bald
444 colonies of the three strains were grown in TSBS for 2 days at 30°C, and genomic DNA was
445 isolated from these strains as described ⁴¹. Primers were designed to amplify the *infB*
446 (BOQ63_RS18295) and *atpD* (BOQ63_RS18295) genes located in the chromosome, and
447 four genes located on the KVP1 megaplasmid: *allC* (BOQ63_RS01235), *tetR*
448 (BOQ63_RS09230), *parA* (BOQ63_RS03875) and *orf1* (BOQ63_RS04285) (Extended Data

449 Table 9). The PCR reactions were performed in triplicate in accordance with the
450 manufacturer's instructions, using 5 ng of DNA, 5% DMSO and the iTaq Universal SYBR
451 Green Supermix Mix (Bio-Rad). Quantitative real time PCR was performed using a CFX96
452 Touch Real-Time PCR Detection System (Bio-Rad). To normalize the relative amount of
453 DNA, the wild-type strain was used as a control, using the *atpD* gene as a reference.

454

455 **Isolation of the hyperosmotic stress-induced S-form cell lines M1 and M2**

456 Fifteen replicate cultures of *K. viridifaciens* were grown for 7 days in LPB medium. After
457 filtration, the S-cells were transferred to fresh LPB medium. The cultures that had not
458 switched to mycelium after 3 days of cultivation were kept for further analysis. Two cultures
459 turned dark green after 7 days, which after inspection with light microscopy contained
460 proliferating S-form cells. These cell lines were named M1 and M2.

461

462 **Microscopy**

463 Bright field images were taken with the Zeiss Axio Lab A1 upright Microscope, equipped
464 with an Axiocam MRc with a resolution of 64.5 nm/pixel.

465

466 *Fluorescence microscopy*

467 Fluorescent dyes (Molecular ProbesTM) were added directly to 100 µl aliquots of liquid-
468 grown cultures. For visualization of membranes, FM5-95 was used at a final concentration of
469 0.02 mg ml⁻¹. Nucleic acids were stained with 0.5 µM of SYTO-9 or 0.05 mg ml⁻¹ of Hoechst
470 34580. The detection of nascent peptidoglycan was done using 0.02 mg ml⁻¹ Wheat Germ
471 Agglutinin (WGA) Oregon Green, or 1 µg ml⁻¹ BOPIPY FL vancomycin. Prior to
472 visualization, cells and mycelium were applied on a thin layer of LPMA (without horse
473 serum) covering the glass slides. Confocal microscopy was performed using a Zeiss Axio
474 Imager M1 Microscope. Samples were excited using a 488-nm laser, and fluorescence
475 emissions for SYTO-9, and WGA Oregon Green were monitored in the region between 505–
476 600 nm, while a 560 nm long pass filter was used to detect FM5-95. Detailed fluorescence
477 microscopy pictures (i.e. those in Figures 1D-E, S1C-D, 5B) represent average Z-projections
478 of stacks.

479 The characterization of the membrane assemblies in S-cells was done on a Nikon
480 Eclipse Ti-E inverted microscope equipped with a confocal spinning disk unit (CSU-X1)
481 operated at 10,000 rpm (Yokogawa, Japan) using a 100x Plan Fluor Lens (Nikon, Japan) and
482 illuminated in bright-field and fluorescence. Samples were excited at wavelengths of 405 nm

483 and 561 nm for Hoechst and FM5-95, respectively. Fluorescence images were created with a
484 435 nm long pass filter for Hoechst, and 590-650 nm band pass for FM5-95. Z-stacks shown
485 in Extended Data Video S3 were acquired at 0.2 μ m intervals using a NI-DAQ controlled
486 Piezo element.

487 Visualization of stained CWD cells for size measurements were done using the Zeiss
488 Axio Observer Z1 microscope. Aliquots of 100 μ l of stained cells were deposited in each
489 well of the ibiTreat μ -slide chamber (ibidi®). Samples were excited with laser light at
490 wavelengths of 488, the green fluorescence (SYTO-9, BODIPY FL vancomycin, WGA-
491 Oregon) images were created with the 505-550 nm band pass, while a 650 nm long pass filter
492 was used to detect FM-595. An average Z-stack projection was used to make Fig. S2A.

493

494 *Time-lapse microscopy*

495 To visualize the emergence of S-cells, spores of *K. viridifaciens* were pre-germinated in
496 TSBS medium for 5 hours. An aliquot of 10 μ l of the recovered germlings was placed on the
497 bottom of an ibiTreat 35 mm low imaging dish (ibidi®), after which an LPMA patch was
498 placed on top of the germlings.

499 To visualize switching of S-cells, these cells were collected after 7 days by filtration
500 from a *K. viridifaciens* LPB liquid-grown culture. A 50 μ l aliquot of the filtrate was placed
501 on the bottom of an ibiTreat 35 mm low imaging dish (ibidi®) with a patch of LPMA on top.

502 To visualize the proliferation of M1 and M2, the strains were grown for 48 hours in
503 LPB. Aliquots of the culture were collected, and centrifuged at 9,000 rpm for 1 min, after
504 which the supernatant was removed, and the cells resuspended in fresh LPB. Serial dilutions
505 of the cells were placed in wells of a ibiTreat μ -slide chamber (ibidi®).

506 All samples were imaged for ~15 hours using an inverted Zeiss Axio Observer Z1
507 microscope equipped with a Temp Module S (PECON) stage-top set to 30°C. Z-stacks with a
508 1 μ m spacing were taken every five minutes using a 40x water immersion objective. Average
509 intensity projections of the in-focus frames were used to compile the final movies. Light
510 intensity over time was equalised using the correct bleach plugin of FIJI.

511

512 *Electron microscopy*

513 To visualize the vegetative mycelium of *K. viridifaciens* by transmission electron microscopy
514 (TEM), the strain was grown in TSBS medium for 48 hours. An aliquot of 1.5 ml of the
515 cultures was centrifuged for 10 mins at 1,000 rpm, after which the supernatant was carefully
516 removed with a pipette. The mycelium was washed with 1X PBS prior to fixation with 1.5%

517 glutaraldehyde for one hour at room temperature. The fixed mycelium was centrifuged with
518 2% low melting point agarose. The solid agarose containing the embedded mycelium was
519 sectioned in 1 mm³ blocks, which were post-fixed with 1% osmium tetroxide for one hour.
520 The samples were then dehydrated by passing through an ethanol gradient (70%, 80%, 90%
521 and 100%, 15 min per step). After incubation in 100% ethanol, samples were replaced in
522 propylene oxide for 15 minutes followed by incubation in a mixture of Epon and propylene
523 oxide (1:1) and pure Epon (each step one hour). Finally, the samples were embedded in Epon
524 and sectioned into 70 nm slices, which were placed on 200-mesh copper grids. Samples were
525 stained using uranyl-430 acetate (2%) and lead-citrate (0.4%), if necessary, and imaged at 70
526 kV in a Jeol 1010 transmission electron microscope.

527 To image S-cells, a culture of the wild-type *K.viridifaciens* strain that had been grown
528 in LPB medium for 7 days was immediately fixed for one hour with 1.5% glutaraldehyde.
529 Filtered S-cells (see above) were then washed twice with 1X PBS prior to embedding in 2%
530 low melting agarose. A post-fixation step with 1% OsO₄ was performed before samples were
531 embedded in Epon and sectioned into 70 nm slices (as described above). Samples were
532 stained using uranyl-430 acetate (2%) and lead-citrate (0.4%), if necessary, and imaged at 70
533 kV in a Jeol 1010 transmission electron microscope

534

535 *Image analysis*

536 Image analysis was performed using the FIJI software package. To describe the
537 morphological changes during hyperosmotic stress, we compared mycelium grown in LPB
538 with or without 0.64 M of sucrose (i.e. the concentration in LPB medium). After making
539 average Z-stack projections from mycelia, 10 hyphae derived from independent mycelia
540 projections were further analysed. For each hypha, the total length was measured using the
541 segmented line tool and the number of branches emerging from that hypha was counted. The
542 hyphal branching ratio was calculated as the number of branches per μm of leading hypha.

543 To calculate the surface area occupied by membrane in hyphae either or not exposed
544 to 0.64 M sucrose, we divided the total surface area that stained with FM5-95 by the total
545 surface area of the hypha. FIJI was also used to measure the average surface area of the
546 nucleoid (using SYTO-9 staining) in both growth conditions. Student's T-tests with two-
547 sample unequal variance were performed to calculate *P*-values and to discriminate between
548 the samples.

549 To determine the size of cell wall-deficient (CWD) cells, we compared cells of PenG-
550 induced L-form to fresh protoplasts and S-cells, all obtained or prepared after 48 hours of

551 growth. Cells were stained with FM5-95 and SYTO-9 and deposited in the wells of an
552 ibiTreat μ -slide chamber (ibidi®). The size of the spherical was determined as the surface
553 area enclosed by the FM5-95-stained membrane. For the particular case of L-forms, where
554 empty vesicles are frequent, only cells that contained DNA were measured. At least 200 cells
555 of each CWD variant were analysed. Proliferating L-forms in which the mother cell could not
556 be separated from the progeny, were counted as one cell.

557

558 **Genome sequencing and SNP analysis**

559 Whole-genome sequencing followed by *de novo* assembly (Illumina and PacBio) and variant
560 calling analyses were performed by BaseClear (Leiden, The Netherlands). The unique
561 mutations were identified by direct comparison to the parental strain *Kitasatospora*
562 *viridifaciens* DSM40239 (GenBank accession number PRJNA353578²⁹). The single and
563 multiple nucleotide variations were identified using a minimum sequencing coverage of 50
564 and a variant frequency of 70%. To reduce the false positives the initial variation list was
565 filtered, and the genes with unique mutations were further analysed. All variants were
566 verified by sequencing PCR fragments (primer sequence in Extended table S9).

567

568

569

570 **REFERENCES**

571

572 1 Sleator, R. D. & Hill, C. Bacterial osmoadaptation: the role of osmolytes in bacterial
573 stress and virulence. *FEMS Microbiol. Rev.* **26**, 49-71 (2002).

574 2 Poolman, B., Spitzer, J. J. & Wood, J. M. Bacterial osmosensing: roles of membrane
575 structure and electrostatics in lipid–protein and protein–protein interactions. *Biochim.
576 Biophys. Acta* **1666**, 88-104, doi:<https://doi.org/10.1016/j.bbamem.2004.06.013>
577 (2004).

578 3 Kysela, D. T., Randich, A. M., Caccamo, P. D. & Brun, Y. V. Diversity takes shape:
579 understanding the mechanistic and adaptive basis of bacterial morphology. *PLoS Biol.*
580 **14**, e1002565, doi:10.1371/journal.pbio.1002565 (2016).

581 4 Typas, A., Banzhaf, M., Gross, C. A. & Vollmer, W. From the regulation of
582 peptidoglycan synthesis to bacterial growth and morphology. *Nat. Rev. Microbiol.* **10**,
583 123-136, doi:10.1038/nrmicro2677 (2012).

584 5 Meeske, A. J. *et al.* SEDS proteins are a widespread family of bacterial cell wall
585 polymerases. *Nature* **537**, 634-638, doi:10.1038/nature19331 (2016).

586 6 Szwedziak, P. & Löwe, J. Do the divisome and elongasome share a common
587 evolutionary past? *Curr. Opin. Microbiol.* **16**, 745-751,
588 doi:10.1016/j.mib.2013.09.003 (2013).

589 7 Claessen, D. *et al.* Control of the cell elongation-division cycle by shuttling of PBP1
590 protein in *Bacillus subtilis*. *Mol. Microbiol.* **68**, 1029-1046, doi:10.1111/j.1365-
591 2958.2008.06210.x (2008).

592 8 Höltje, J. V. Growth of the stress-bearing and shape-maintaining murein sacculus of
593 *Escherichia coli*. *Microbiol. Mol. Biol. Rev.* **62**, 181-203 (1998).

594 9 Flärdh, K. & Buttner, M. J. *Streptomyces* morphogenetics: dissecting differentiation
595 in a filamentous bacterium. *Nat. Rev. Microbiol.* **7**, 36-49, doi:10.1038/nrmicro1968
596 (2009).

597 10 Claessen, D., Rozen, D. E., Kuipers, O. P., Søgaard-Andersen, L. & van Wezel, G. P.
598 Bacterial solutions to multicellularity: a tale of biofilms, filaments and fruiting bodies.
599 *Nat. Rev. Microbiol.* **12**, 115-124, doi:10.1038/nrmicro3178 (2014).

600 11 Barka, E. A. *et al.* Taxonomy, physiology, and natural products of *Actinobacteria*.
601 *Microbiol. Mol. Biol. Rev.* **80**, 1-43, doi:10.1128/MMBR.00019-15 (2016).

602 12 Chen, X. *et al.* A trehalose biosynthetic enzyme doubles as an osmotic stress sensor to
603 regulate bacterial morphogenesis. *PLoS Genet.* **13**, e1007062,
604 doi:10.1371/journal.pgen.1007062 (2017).

605 13 Alvarez, H. M. *et al.* Physiological and morphological responses of the soil bacterium
606 *Rhodococcus opacus* strain PD630 to water stress. *FEMS Microbiol. Ecol.* **50**, 75-86,
607 doi:10.1016/j.femsec.2004.06.002 (2004).

608 14 Klieneberger, E. The natural occurrence of pleuropneumonia-like organisms in
609 apparent symbiosis with *Streptobacillus moniliformis* and other bacteria. *J Pathol
610 Bacteriol* **40**, 93-105 (1935).

611 15 Leaver, M., Dominguez-Cuevas, P., Coxhead, J. M., Daniel, R. A. & Errington, J.
612 Life without a wall or division machine in *Bacillus subtilis*. *Nature* **457**, 849-853,
613 doi:10.1038/nature07742 (2009).

614 16 Frenkel, A. & Hirsch, W. Spontaneous development of L forms of Streptococci
615 requiring secretions of other bacteria or sulphhydryl compounds for normal growth.
616 *Nature* **191**, 728-730 (1961).

617 17 Studer, P. *et al.* Proliferation of *Listeria monocytogenes* L-form cells by formation of
618 internal and external vesicles. *Nat Commun* **7**, 13631, doi:10.1038/ncomms13631
619 (2016).

620 18 Errington, J., Mickiewicz, K., Kawai, Y. & Wu, L. J. L-form bacteria, chronic
621 diseases and the origins of life. *Philosophical Transactions of the Royal Society B:*
622 *Biological Sciences* **371**, doi:10.1098/rstb.2015.0494 (2016).

623 19 Innes, C. M. J. & Allan, E. J. Induction, growth and antibiotic production of
624 *Streptomyces viridifaciens* L-form bacteria. *J. Appl. Microbiol.* **90**, 301-308 (2001).

625 20 Mercier, R., Kawai, Y. & Errington, J. Excess membrane synthesis drives a primitive
626 mode of cell proliferation. *Cell* **152**, 997-1007, doi:10.1016/j.cell.2013.01.043 (2013).

627 21 Kawai, Y. *et al.* Cell growth of wall-free L-form bacteria is limited by oxidative
628 damage. *Curr. Biol.* **25**, 1613-1618, doi:10.1016/j.cub.2015.04.031 (2015).

629 22 Mercier, R., Kawai, Y. & Errington, J. General principles for the formation and
630 proliferation of a wall-free (L-form) state in bacteria. *eLife* **3**, doi:10.7554/eLife.04629
631 (2014).

632 23 Errington, J. L-form bacteria, cell walls and the origins of life. *Open Biol* **3**, 120143,
633 doi:10.1098/rsob.120143 (2013).

634 24 Fuchino, K., Flärdh, K., Dyson, P. & Ausmees, N. Cell-biological studies of osmotic
635 shock response in *Streptomyces* spp. *J. Bacteriol.* **199**, doi:10.1128/JB.00465-16
636 (2017).

637 25 Zhu, H. *et al.* Eliciting antibiotics active against the ESKAPE pathogens in a
638 collection of actinomycetes isolated from mountain soils. *Microbiology* **160**, 1714-
639 1725, doi:10.1099/mic.0.078295-0 (2014).

640 26 Girard, G. *et al.* A novel taxonomic marker that discriminates between
641 morphologically complex actinomycetes. *Open Biol* **3**, 130073,
642 doi:10.1098/rsob.130073 (2013).

643 27 Merrick, M. J. A morphological and genetic mapping study of bald colony mutants of
644 *Streptomyces coelicolor*. *J Gen Microbiol* **96**, 299-315 (1976).

645 28 Álvarez-Álvarez, R. *et al.* A 1.8-Mb-reduced *Streptomyces clavuligerus* genome:
646 relevance for secondary metabolism and differentiation. *Appl. Microbiol. Biotechnol.*
647 **98**, 2183-2195, doi:10.1007/s00253-013-5382-z (2014).

648 29 Ramijan, K., van Wezel, G. P. & Claessen, D. Genome sequence of the filamentous
649 actinomycete *Kitasatospora viridifaciens*. *Genome Announc* **5**,
650 doi:10.1128/genomeA.01560-16 (2017).

651 30 Kempf, B. & Bremer, E. Uptake and synthesis of compatible solutes as microbial
652 stress responses to high-osmolality environments. *Arch. Microbiol.* **170**, 319-330
653 (1998).

654 31 Lebre, P. H., De Maayer, P. & Cowan, D. A. Xerotolerant bacteria: surviving through
655 a dry spell. *Nat. Rev. Microbiol.* **15**, 285-296, doi:10.1038/nrmicro.2017.16 (2017).

656 32 Maccario, L., Sanguino, L., Vogel, T. M. & Larose, C. Snow and ice ecosystems: not
657 so extreme. *Res. Microbiol.* **166**, 782-795, doi:10.1016/j.resmic.2015.09.002 (2015).

658 33 De Maayer, P., Anderson, D., Cary, C. & Cowan, D. A. Some like it cold:
659 understanding the survival strategies of psychrophiles. *EMBO Rep* **15**, 508-517,
660 doi:10.1002/embr.201338170 (2014).

661 34 Jones, S. E. *et al.* *Streptomyces* exploration is triggered by fungal interactions and
662 volatile signals. *eLife* **6**, doi:10.7554/eLife.21738 (2017).

663 35 Kilcher, S., Studer, P., Muessner, C., Klumpp, J. & Loessner, M. J. Cross-genus
664 rebooting of custom-made, synthetic bacteriophage genomes in L-form bacteria. *Proc
665 Natl Acad Sci U S A* **115**, 567-572, doi:10.1073/pnas.1714658115 (2018).

666 36 Claverys, J. P., Prudhomme, M. & Martin, B. Induction of competence regulons as a
667 general response to stress in gram-positive bacteria. *Annu. Rev. Microbiol.* **60**, 451-
668 475, doi:10.1146/annurev.micro.60.080805.142139 (2006).

669 37 Slager, J., Kjos, M., Attaiech, L. & Veening, J. W. Antibiotic-induced replication
670 stress triggers bacterial competence by increasing gene dosage near the origin. *Cell*
671 **157**, 395-406, doi:10.1016/j.cell.2014.01.068 (2014).

672 38 Holmes, N. A. *et al.* Coiled-coil protein Scy is a key component of a multiprotein
673 assembly controlling polarized growth in *Streptomyces*. *Proc Natl Acad Sci U S A*
674 **110**, E397-406, doi:10.1073/pnas.1210657110 (2013).

675 39 Kawai, Y., Mickiewicz, K. & Errington, J. Lysozyme counteracts β -Lactam
676 antibiotics by promoting the emergence of L-form bacteria. *Cell* **172**, 1038-
677 1049.e1010, doi:<https://doi.org/10.1016/j.cell.2018.01.021> (2018).

678 40 Stuttard, C. Temperate phages of *Streptomyces venezuelae*: lysogeny and host
679 specificity shown by phages SV1 and SV2. *J Gen Microbiol* **128**, 115-121 (1982).

680 41 Kieser, T., Bibb, M. J., Buttner, M. J., Chater, K. F. & Hopwood, D. A. *Practical
681 Streptomyces genetics*. (The John Innes Foundation, 2000).

682 42 Schindelin, J. *et al.* Fiji: an open-source platform for biological-image analysis. *Nat.
683 Methods* **9**, 676-682, doi:10.1038/nmeth.2019 (2012).

684

685 **LEGENDS**

686 **Figure 1. High levels of sucrose affect growth and morphology of *K. viridifaciens*.** (A)
687 Growth curves of *K. viridifaciens* in LPB medium supplemented with increasing amounts of
688 sucrose. High levels of osmolytes reduce the number and size of colonies (B) in comparison
689 to media without osmolytes (C). Mycelial morphology *K. viridifaciens* grown in LPB without
690 sucrose (D) and with 0.64M of sucrose (E). Mycelium was stained with FM5-95 and SYTO-9
691 to visualize membranes and DNA, respectively. Please note the S-cells (arrowheads in E) and
692 indentations along the cylindrical part of the hypha (black arrowheads in BF panel) formed in
693 medium containing high levels of sucrose. Scale bars represent 10 mm (B, C), 10 μ m (left
694 panels in D, E) and 20 μ m (magnified section in D and E).

695

696 **Figure 2. Formation of S-cells is widespread in filamentous actinomycetes.** (A)
697 Morphology of S-cells released by *K. viridifaciens*, *S. venezuelae*, and a number of
698 filamentous actinomycetes from our culture collection (all referred to with the prefix MBT).
699 Cells were stained with FM5-95 (red) and SYTO-9 (green) to visualize membranes and
700 DNA, respectively. (B) Phylogenetic tree of filamentous actinomycetes based on the
701 taxonomic marker *ssgB*. Strains with the ability to form S-cells are indicated with an asterisk
702 (*). *Streptomyces* strains that are able to produce spores in liquid-grown cultures are referred
703 to as LSp (for Liquid Sporulation), while those unable to sporulate in liquid environments are
704 called NLSp (No Liquid Sporulation²⁶). This classification is based on amino acid residue
705 128 in the conserved SsgB protein, which is a threonine (T) or glutamine (Q) for LSp and
706 NLSp strains, respectively. Please note that an arginine (R) is present at this position in all
707 *Kitasatospora* strains (C). Scale bars represent 5 μ m

708

709 **Figure 3. S-cells represent a new cell type with the ability to switch to the mycelial**
710 **mode-of-growth.** (A) Time-lapse microscopy stills showing the extrusion of S-cells (arrows)
711 from hyphal tips. The arrow heads indicate new branches, while “S” designates the
712 germinated spore. Images were taken from Supplementary Video S1 (B) Z-stack projection
713 of filtered S-cells (taken from Supplementary Video 3). Cells were stained with Hoechst and
714 FM5-95 to visualize DNA and membranes, respectively. The intracellular membrane
715 assemblies are indicated with white arrows. (C) Transmission electron micrographs of S-cell
716 reveal the presence of agglomerates of membrane structures (white arrow) in close proximity
717 to the DNA. Contrary to filamentous cells (F, G), S-cells possess a disorganized cell surface
718 (D, E). (H) The S-cells are viable cells with the ability to form mycelial colonies on LPM

719 medium after 7 days of growth. (I) Time-lapse microscopy stills demonstrating the switch of
720 S-cells (asterisk, t=0 min) to filamentous growth. Please note that S-cells are also extruded
721 from newly-formed hyphal tips (arrowheads, t=600 min). Images were taken from
722 Supplementary Video 4. Scale bars represents 10 μ m (A, B), 5 μ m (magnified section in B),
723 2 μ m (C), 100 nm (D, E), 20 nm (F), 50 nm (G) and 20 μ m (I).

724

725 **Figure 4. S-cells switching to the mycelial mode-of-growth frequently leads to loss of the**
726 **megaplasmid KVP1.** The switch of S-cells to the mycelial mode-of-growth yields colonies
727 with different morphologies: besides grey-pigmented colonies (R1, R2), colonies are formed
728 that fail to develop efficiently, and which appear whitish or brown (R3-R5). (C) Subculturing
729 of R1 and R2 leads to the formation of grey colonies that appear similar to the wild type,
730 while subculturing of R3, R4 and R5 yield colonies that are unable to form a robust
731 sporulating aerial mycelium (brown and white colonies). Quantitative real time PCR of the
732 *infB* (C) and *allC* (D) genes using gDNA of the wild type and R3-R5 as the template. In all
733 strains, the *infB* gene located on the chromosome is amplified before the 20th cycle. However,
734 the *allC* gene, located on the KVP1 megaplasmid, is amplified in the wild type before the 20th
735 cycle, but in strains R3-R5 after the 30th cycle. (F) Quantitative comparison of the relative
736 abundance of four megaplasmid genes (*orf1*, *parA*, *tetR* and *allC*) and the *infB* gene (located
737 on the chromosome) between the wild type and strains R3-R5. The strong reduction in the
738 abundance of the megaplasmid genes are consistent with loss of this plasmid.

739

740 **Figure 5. Hyperosmotic stress conditions are sufficient to obtain strains that are able to**
741 **proliferate without the cell wall.** (A) Morphology of colonies of the *K. viridifaciens* wild-
742 type strain, the PenG-induced L-form strain and strains M1 and M2 on LPMA medium.
743 Please note that the wild-type strain forms compact, yellowish mycelial colonies, while the
744 other strains form mucoid green colonies. (B) Morphology of S-cells in comparison to cells
745 of the PenG-induced L-form strain and strains M1 and M2 grown for 48 hours in LPB
746 medium. Cells were stained with FM5-95 and SYTO-9 to visualize membranes and DNA,
747 respectively. Please note that the morphology of cells of strains M1 and M2 is similar to the
748 PenG-induced L-forms. The arrowheads indicate intracellular vesicles, while empty vesicles
749 are indicated with an asterisk. The inlay in M2 shows a proliferation-associated tubulation
750 event. (C-E) Frames from time-lapse microscopy show L-form-like proliferation involving
751 (C) vesiculation, (D) blebbing, and (E) membrane tubulation. (F) Formation of S-cells strains
752 upon prolonged exposure to hyperosmotic stress. Germination of spores under hyperosmotic

753 stress conditions generates germlings, which are able to extrude S-cells. These S-cells are
754 able to switch to the mycelial mode-of-growth, or sporadically acquire mutations that allow
755 them to proliferate like L-forms, which is characterized by tubulation, blebbing or
756 vesiculation. Scale bar represents 10 μ m (B), 2 μ m (inlay panel B) or 5 μ m (C, D, E).

757

758 **Figure S1. High levels of salt affect growth and morphology of *K. viridifaciens*.** (A)
759 Growth curves of *K. viridifaciens* in LPB medium supplemented with different amounts of
760 NaCl. (B) S-cells (arrowheads) are evident after 96 hours of growth in the presence of 0.3
761 (middle) or 0.6 M NaCl (bottom). Mycelial morphology of *K. viridifaciens* grown in the
762 presence of 0.6 M NaCl after 48 (C), and 96 hours (D). Mycelium was stained with FM5-95
763 and SYTO-9 to visualize membranes and DNA, respectively. After 48 hours in the presence
764 of NaCl, only small aggregates of spores and germlings were visible. Pellets obtained after 96
765 hours showed an excess of membrane and hypercondensation of DNA. Scale bars represent
766 10 μ m (B), or 20 μ m (C-D).

767

768 **Figure S2. Comparison between different types of cell wall-deficient cells of *K.***
769 ***viridifaciens*.** (A) Morphology of freshly made protoplasts (top panels), PenG-induced L-
770 forms (middle panels) and S-cells (bottom panels). Cells were stained with the membrane dye
771 FM5-95 or fluorescent vancomycin (van^{FL}) to detect nascent PG. (B) Morphology of
772 protoplasts (top panels) and S-cells (bottom panels) grown for 48 hours in LPB. Cells were
773 stained with the membrane dye FM5-95 or wheat germ agglutinin (WGA-Oregon) to detect
774 newly synthesized PG. Scale bars represents 10 μ m.

775

776 **Figure S3. Formation of S-cells is a natural adaptation in filamentous actinomycetes.**
777 (A) Microscopic analysis of strains grown for 7 days in liquid medium containing high levels
778 of osmolytes. Cells were stained with FM5-95 and SYTO-9 to visualize membranes and
779 DNA, respectively. Arrowheads indicate S-cells produced by the different strains. (B)
780 Phylogenetic tree of filamentous actinomycetes based on the 16S rDNA gene. Strains with
781 the ability to form S-cells are indicated with an asterisk (*). Scale bars represents 10 μ m.

782

783 **Figure S4. The presence of abundant peptidoglycan surrounding S-cells confers**
784 **resistance to water treatment.** (A) Filtered S-cells were stained with the membrane dye
785 FM5-95 and WGA-Oregon to stain nascent peptidoglycan. The inlay shows an S-cell
786 possessing abundant cell wall material surrounding the cell surface. (B) Morphology of S-

787 cells after exposing them to water. While many cells lyse, some S-cells remain intact, which
788 invariably have abundant cell wall material associated with their cell surface (see inlay).
789 Scale bars represents 10 μ m (A-B), and 5 μ m (inlays).

790

791 **Figure S5. The hyperosmotic stress-induced strains M1 and M2 are cell wall-deficient**
792 **variants.** Morphology of cells of strains M1 and M2 grown for 48 hours in LPB. Cells were
793 stained with WGA-Oregon to visualize nascent PG. The scale bar represents 10 μ m.

794

795 **Figure S6. Proliferation in the cell wall-deficient state leads to loss of the megaplasmid**
796 **KVPI.** Quantitative real time PCR of the *infB* (A) and *allC* (B) genes using gDNA of the
797 wild-type strain, the PenG-induced L-form strain, and strains M1 and M2. In all strains, the
798 *infB* gene located on the chromosome is amplified before the 20th cycle. However, the *allC*
799 gene, located on the KVPI megaplasmid, is only amplified in the wild type strain, but not in
800 any of the other strains. (F) Quantitative comparison of the relative abundance of four
801 megaplasmid genes (*orf1*, *parA*, *tetR* and *allC*) and the *infB* gene (located on the
802 chromosome) between the wild-type strain, the PenG-induced L-form strain, and strains M1
803 and M2.

804

805 **Extended Data Video S1. Apical extrusion of S-cells in *K. viridifaciens*.** S-cells are
806 extruded from the hyphal tip after 425 min, coinciding with a transient arrest in tip growth.
807 After extrusion of S-cells, a new tip is formed in the apical region of the hyphae after 540
808 min, while subapically new branches become visible after 620 min. The times are indicated
809 in min. The scale bar represents 10 μ m.

810

811 **Extended Data Video S2. Extrusion of S-cells from branches in *K. viridifaciens*.** S-cells
812 are extruded from the tips of branches that are formed subapically. The times are indicated in
813 min. Scale bar represents 10 μ m.

814

815 **Extended Data Video S3. S-cells of *K. viridifaciens* contain DNA and inner membrane**
816 **assemblies.** Z-stack projects of S-cells isolated after 48 hours, which were stained with
817 Hoechst (blue) and FM5-95 (red) to visualize DNA and membranes, respectively. The scale
818 bar represents 10 μ m.

819

820 **Extended Data Video S4. Switching of S-cells to the mycelial mode-of-growth.** Switching
821 of S-cells on solid LPMA medium yields colonies consisting of both hyphae and S-cells. The
822 times are indicated in min. The scale bar indicates 20 μ m.

823

824 **Extended Data Video S5. Example of vesiculation during proliferation of strain M2.**
825 Time-lapse microscopy showing proliferation of strain M2 on media containing high levels
826 of sucrose. Please note that vesiculation is evident in some cells. The times are indicated in
827 min. The scale bar indicates 5 μ m.

828

829 **Extended Data Video S6. Example of blebbing during proliferation of strain M2.** Time-
830 lapse microscopy showing proliferation of strain M2 on media containing high levels of
831 sucrose. Please note that blebbing is evident in some cells. The times are indicated in min.
832 The scale bar indicates 5 μ m.

833

834 **Extended Data Video S7. Example of membrane tubulation during proliferation of
835 strain M2.** Time-lapse microscopy showing membrane tubulation in strain M2 during
836 proliferation on media containing high levels of sucrose. The times are indicated in min. The
837 scale bar indicates 5 μ m.

Extended Data Table 1. Image analysis measurements on hyphae formed in the presence of low levels of osmolytes

Hyphae	Length (μm)	Number of branches	Branching frequency	Membrane fraction	Average nucleoid area (μm^2)
1	86,0180	1	0,01	0,10	2,53
2	90,377	3	0,03	0,09	2,01
3	72,3597	7	0,10	0,10	1,90
4	83,9838	0	0,00	0,10	3,02
5	79,0436	0	0,00	0,09	3,21
6	65,3853	1	0,02	0,17	4,18
7	80,7872	7	0,09	0,07	2,11
8	86,3086	2	0,02	0,10	3,05
9	76,4282	3	0,04	0,08	2,14
10	74,1033	2	0,03	0,12	1,71
Average	79,4795	2,6	0,03	0,10	2,59
SD	7,5857	2,5	0,03	0,03	0,77

Extended Data Table 2. Image analysis measurements on hyphae formed in the presence of high levels of osmolytes

Hyphae	length (μm)	Number of branches	Branching frequency	Membrane Fraction	Average nucleoid area (μm^2)
1	82,5308	11	0,13	0,22	1,35
2	90,9580	6	0,07	0,18	2,10
3	88,3428	8	0,09	0,16	1,82
4	60,4451	12	0,20	0,29	1,86
5	86,0180	9	0,10	0,24	2,08
6	76,7188	6	0,08	0,21	2,05
7	88,6334	6	0,07	0,22	2,34
8	53,4707	8	0,15	0,19	1,47
9	69,1631	7	0,10	0,20	2,04
10	70,3255	2	0,03	0,21	1,15
Average	76,6606	7,5	0,10	0,21	1,83
STDEVA	12,9242	2,8	0,05	0,03	0,38

Extended Data Table 3. Comparison between *K.viridifaciens* cell wall-deficient cells

Characteristic	Protoplast	L-form	S-cell
Origin	Osmoprotective conditions combined with lysozyme treatment	Osmoprotective conditions combined with prolonged exposure to lysozyme and PenG	Osmoprotective conditions
Area (μm^2)	4.01 \pm 1.93	7.06 \pm 5.87	20.73 \pm 11.53
Cell wall	Homogeneous regeneration. Wall material mostly associated with the cell surface	Not uniform, disordered assembly. Wall material often detached from the cell surface	Not uniform, disordered assembly. Wall material sometimes detached from the cell surface
Genotype	Wild type	Mutant	Wild-type

Extended Data Table 4. Calculated diameters (D) of S-cells released by different filamentous actinomycetes upon hyperosmotic stress. The diameters are indicated in μm .

Strain	D _{min}	D _{max}	D _{mean}	SD
<i>K. viridifaciens</i>	7,77	10,04	8,91	1,60
<i>S. venezuelae</i>	2,06	3,68	2,87	1,15
MBT13	2,62	4,49	3,56	1,32
MBT61	3,84	10,67	7,25	4,82
MBT63	2,52	5,21	3,86	1,91
MBT64	2,12	4,99	3,55	2,03
MBT66	2,56	6,78	4,67	2,99
MBT69	3,87	6,27	5,07	1,70
MBT89	2,01	6,05	4,03	2,86

Extended Data Table 5.

Mutations in the hyperosmotic stress-induced S-form strain M1

Variation	Position	Type	Reference	Allele	Locus	Protein	Effect in protein
1	4456932	SNV	C	G	BOQ63_RS28320	Acetyltransferase	Leu99Val
2	4876534	SNV	T	C	BOQ63_RS30295	Valine-tRNA ligase	Val319Ala
3	3219590	SNV	C	G	NCR		
4	3133612	SNV	G	A	BOQ63_RS21920	Metal ABC transporter ATPase	Asp504Asn

SNV: Single Nucleotide Variation

Extended Data Table 6. Mutations in the hyperosmotic stress-induced S-form strain M2

Variation	Position	Type	Reference	Allele	Locus	Protein	Effect in protein
1	2164717	SNV	A	G	NCR		
2	5054842	SNV	T	G	BOQ63_RS31145	XRE family transcriptional regulator	Glu332Ala
3	6460621- 6460623	Deletion	CCA	-	BOQ63_RS37840	Histidine kinase	Thr606del
4	3133753^ 3133754	Insertion	-	C	BOQ63_RS21920	Metal ABC transporter ATPase	Arg553fs

SNV: Single Nucleotide Variation, del: deletion, fs: frame shift

Extended Data Table 7. Mutations in the PenG induced L-form

Variation	Position	Type	Reference	Allele	Locus	Protein	Effect in protein
1	546832	SNV	C	A	NCR		
2	3549271	SNV	G	A	BOQ63_RS23890	Lysylphosphatidylglycerol synthetase-like protein	Thr203Ile
3	3297354	SNV	C	A	BOQ63_RS22750	Undecaprenyl-diphosphate phosphatase	Leu58Met

SNV: Single Nucleotide Variation

Extended Data Table 8. Strains used in this study

Strains	Genotype	Reference
<i>Streptomyces/Kitasatospora</i> strains		
<i>Streptomyces coelicolor</i> A3(2) M145	Wild-type	Lab collection
<i>Streptomyces lividans</i> 1326	Wild-type	Lab collection
<i>Streptomyces griseus</i>	Wild-type	Lab collection
<i>Streptomyces venezuelae</i> DIVERSA	Wild-type	Lab collection
<i>Kitasatospora viridifaciens</i> DSM40239	Wild-type	DSMZ, (Ramijan et al. 2017)
<i>Streptomyces</i> sp. MBT13	Wild-type	Lab collection (Zhu et al. 2014)
<i>Streptomyces</i> sp. MBT61	Wild-type	Lab collection (Zhu et al. 2014)
<i>Kitasatospora</i> sp. MBT63	Wild-type	Lab collection (Girard, 2014)
<i>Kitasatospora</i> sp. MBT64	Wild-type	Lab collection (Zhu et al. 2014)
<i>Kitasatospora</i> sp. MBT66	Wild-type	Lab collection (Girard, 2014)
<i>Kitasatospora</i> sp. MBT69	Wild-type	Lab collection (Zhu et al. 2014)
<i>Streptomyces</i> sp. MBT86	Wild-type	Lab collection (Zhu et al. 2014)
<i>K.viridifaciens</i> cell wall-deficient strains		
PenG-induced L-form	Mutant	This work
Hyperosmotic stress-induced S-form M1	Mutant	This work
Hyperosmotic stress-induced S-form M2	Mutant	This work

Extended Data Table 9: Primers used in this study

Primer	Sequence (5' – 3')
Consensus_ <i>ssgB</i> -Fw	ATGAACACCACGGTCAGCTG
Consensus_ <i>ssgB</i> -Rv	GCTCTCGGCCAGGATGTG
qPCR_ <i>infB</i> -Fw	GTCACGTCGACCACGGTAAG
qPCR_ <i>infB</i> -Rv	CACCGATGTGCTGGGTGATG
qPCR_ <i>atpD</i> -Fw	TTCGGACAGCTCGTCCATAC
qPCR_ <i>atpD</i> -Rv	ACATCGCGCAGAACCACTAC
qPCR_ <i>parA</i> -Fw	CGGTCGTACCCAGTACAAG
qPCR_ <i>parA</i> -Rv	TAACCGAGTTCGAGGGACAG
qPCR- <i>Orf1</i> -Fw	GAGGGAGCCAATCCGTATC
qPCR- <i>Orf1</i> -Rv	GGCTGTTGGACAGGACCATC
qPCR- <i>allC</i> -Fw	CGGCGATAGCGGAGACTAAG
qPCR- <i>allC</i> -Rv	CCACTGGTGGGACCAGAAAG
qPCR- <i>tetR</i> -Fw	TGCTCGACCAGCTGTTGAAG
qPCR- <i>tetR</i> -Rv	TGGCGAGCATGAAGTCGTAG
BOQ63_RS28320-Fw	CTAGGTCGAAGGACCGATGG
BOQ63_RS28320-Rv	CGGACGTGACGCTCTACAAC
Seq_RS28320-Rv	GAAATCGGCCAGCGGTAAG
Seq_RS30295-Fw	CTTCAAGCGCCTTTCGACG
Seq_RS30295-Rv	TGTCGACCCAGTCGAAGTAG
Seq_NCR-M1-Fw	CGTTGCGGATGTGGTTCTG
Seq_NCR-M1-Rv	GTTCGCTGGCCGAGATGTT
Seq_RS21920-Fw	TGATCGAGGCGATGCCCTTC
Seq_RS21920-Rv	CGTCGATGTTGCCGATCAC
Seq_NCR-M2-Fw	AGAGCAGCATGCCGAGCTTG
Seq_NCR-M2-Rv	CTTCCTGGTCGGGAAGTAG
Seq_RS31145-Fw	GTGGTGAATCCGTGCCACAG
Seq_RS31145-Rv	TGGAACGCCTACTCCATGGG
Seq_RS37840-Fw	GATCTCCACGCCGTTGAAAG
Seq_RS37840-Rv	GAGTTCGGTGGTTCGAAGG
Seq_NCR-L-form-Fw	GTGGCTATTCAAGGACTCTC
Seq_NCR-L-form-Rv	CGCCGCTTCATCTCTGATAC
Seq_RS23890-Fw	GAGAAGATCACCGCCTGTC
Seq_RS23890-Rv	ACAGGGCACCGCTCAACTAC
Seq_RS22750-Fw	CCGGTGACACCCGGAAATAC
Seq_RS22750-Rv	CCGGGATGGTGGAGATGATG

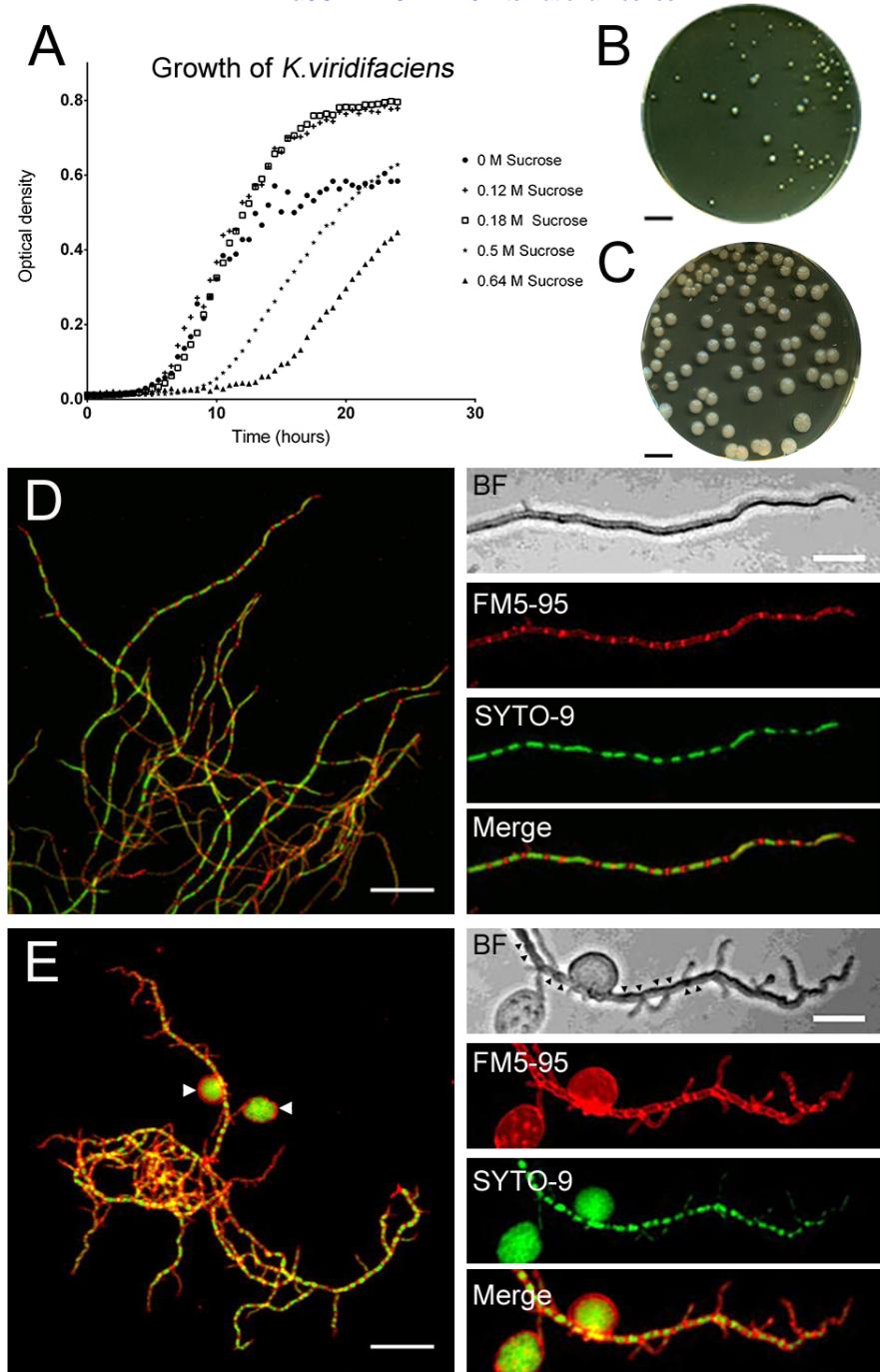


Figure 1. High levels of sucrose affect growth and morphology of *K. viridifaciens*. (A) Growth curves of *K. viridifaciens* in LPB medium supplemented with increasing amounts of sucrose. High levels of osmolytes reduce the number and size of colonies (B) in comparison to media without osmolytes (C). Mycelial morphology *K. viridifaciens* grown in LPB without sucrose (D) and with 0.64M of sucrose (E). Mycelium was stained with FM5-95 and SYTO-9 to visualize membranes and DNA, respectively. Please note the S-cells (white arrowheads in E) and indentations along the cylindrical part of the hypha (black arrowheads in BF section) formed in medium containing high levels of sucrose. Scale bars represent 10 mm (B, C), 10 μ m (left panels in D, E) and 20 μ m (magnified section in D and E).

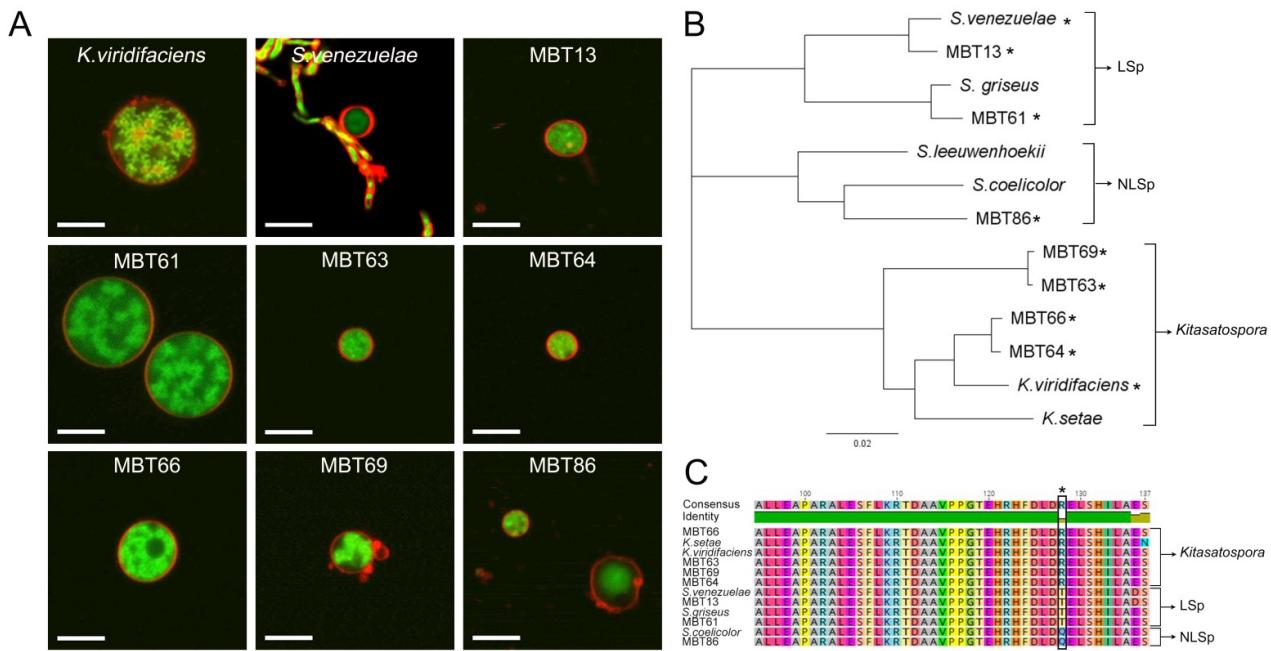


Figure 2. Formation of S-cells is widespread in filamentous actinomycetes. (A) Morphology of S-cells released by *K. viridifaciens*, *S. venezuelae*, and a number of filamentous actinomycetes from our culture collection (all referred to with the prefix MBT). Cells were stained with FM5-95 (red) and SYTO-9 (green) to visualize membranes and DNA, respectively. (B) Phylogenetic tree of filamentous actinomycetes based on the taxonomic marker *ssgB*. Strains with the ability to form S-cells are indicated with an asterisk (*). *Streptomyces* strains that are able to produce spores in liquid-grown cultures are referred to as LSp (for Liquid Sporulation), while those unable to sporulate in liquid environments are called NLSp (No Liquid Sporulation²⁶). This classification is based on amino acid residue 128 in the conserved SsgB protein, which is a threonine (T) or glutamine (Q) for LSp and NLSp strains, respectively. Please note that an arginine (R) is present at this position in all *Kitasatospora* strains (C). Scale bars represent 5 μ m

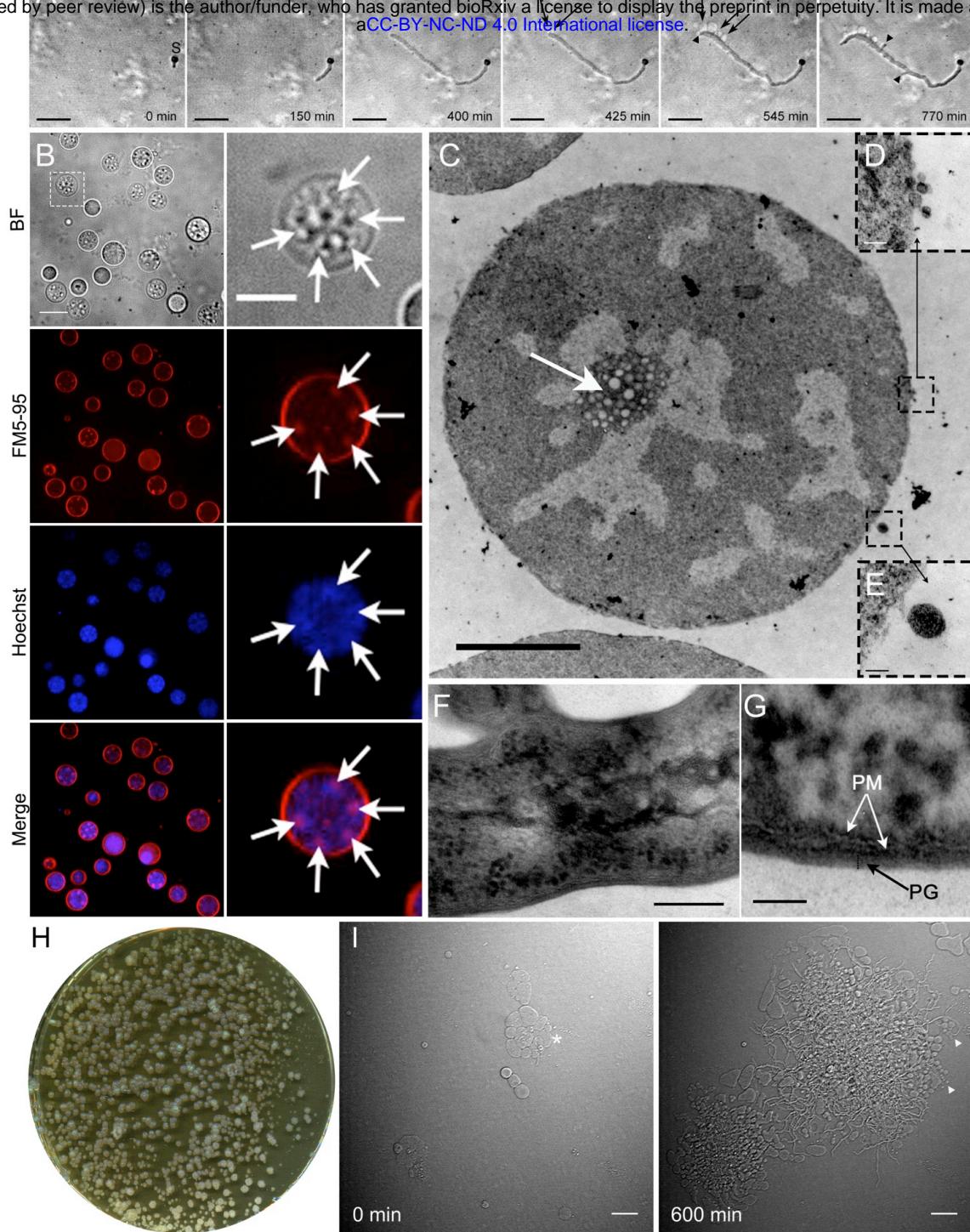


Figure 3. S-cells represent a new cell type with the ability to switch to the mycelial mode-of-growth. (A) Time-lapse microscopy stills showing the extrusion of S-cells (arrows) from hyphal tips. The arrow heads indicate new branches, while “S” designates the germinated spore. Images were taken from Supplementary Video S1 (B) Z-stack projection of filtered S-cells (taken from Supplementary Video 3). Cells were stained with Hoechst and FM5-95 to visualize DNA and membranes, respectively. The intracellular membrane assemblies are indicated with white arrows. (C) Transmission electron micrographs of S-cell reveal the presence of agglomerates of membrane structures (white arrow) in close proximity to the DNA. Contrary to filamentous cells (F, G), S-cells possess a disorganized cell surface (D, E). (H) The S-cells are viable cells with the ability to form mycelial colonies on LPM medium after 7 days of growth. (I) Time-lapse microscopy stills demonstrating the switch of S-cells (asterisk, $t=0$ min) to filamentous growth. Please note that S-cells are also extruded from newly-formed hyphal tips (arrowheads, $t=600$ min). Images were taken from Supplementary Video 4. Scale bars represents 10 μ m (A, B), 5 μ m (magnified section in B), 2 μ m (C), 100 nm (D, E), 20 nm (F), 50 nm (G) and 20 μ m (I).

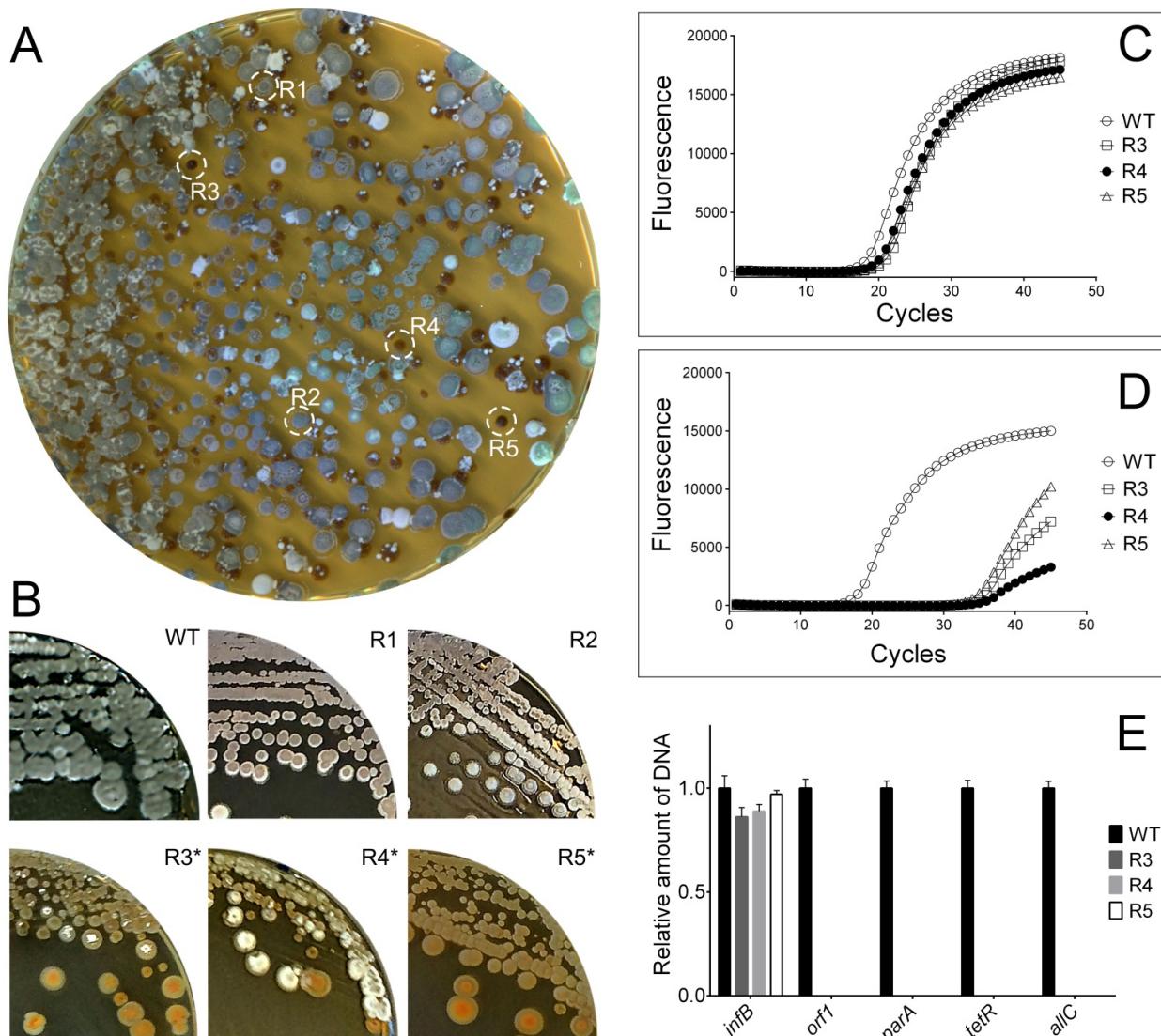


Figure 4. S-cells switching to the mycelial mode-of-growth frequently leads to loss of the megaplasmid KVP1. The switch of S-cells to the mycelial mode-of-growth yields colonies with different morphologies: besides grey-pigmented colonies (R1, R2), colonies are formed that fail to develop efficiently, and which appear whitish or brown (R3-R5). (C) Subculturing of R1 and R2 leads to the formation of grey colonies that appear similar to the wild type, while subculturing of R3, R4 and R5 yield colonies that are unable to form a robust sporulating aerial mycelium (brown and white colonies). Quantitative real time PCR of the *infB* (C) and *allC* (D) genes using gDNA of the wild type and R3-R5 as the template. In all strains, the *infB* gene located on the chromosome is amplified before the 20th cycle. However, the *allC* gene, located on the KVP1 megaplasmid, is amplified in the wild type before the 20th cycle, but in strains R3-R5 after the 30th cycle. (F) Quantitative comparison of the relative abundance of four megaplasmid genes (*orf1*, *parA*, *tetR* and *allC*) and the *infB* gene (located on the chromosome) between the wild type and strains R3-R5. The strong reduction in the abundance of the megaplasmid genes are consistent with loss of this plasmid.

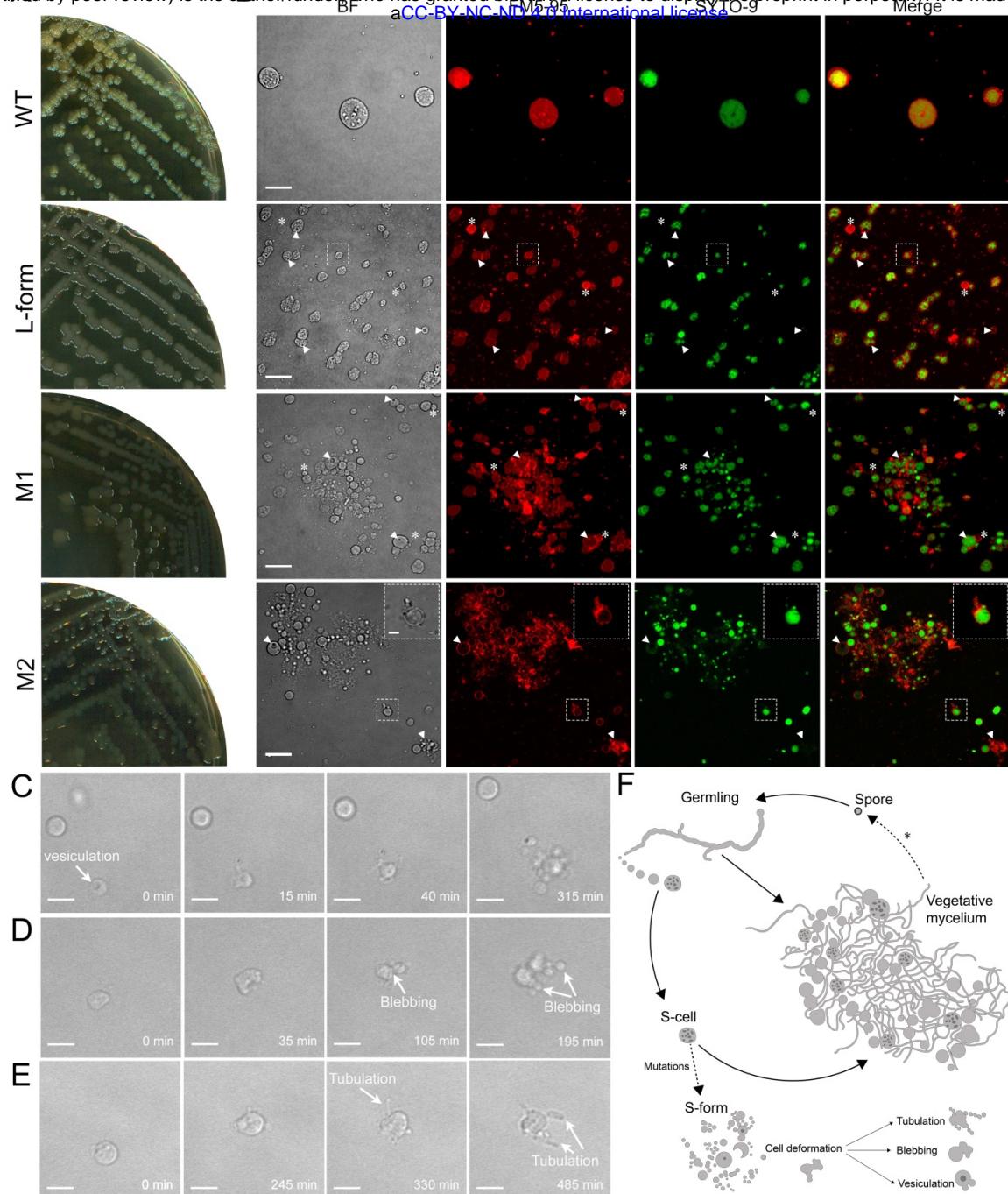


Figure 5 . Hyperosmotic stress conditions are sufficient to isolate strains that are able to proliferate without the cell wall. (A) Morphology of colonies of the *K. viridisaciens* wild-type strain, the PenG-induced L-form strain and strains M1 and M2 on LPMA medium. Please note that the wild-type strain forms compact, yellowish mycelial colonies, while the other strains form mucoid green colonies. (B) Morphology of S-cells in comparison to cells of the PenG-induced L-form strain and strains M1 and M2 grown for 48 hours in LPB medium. Cells were stained with FM5-95 and SYTO-9 to visualize membranes and DNA, respectively. Please note that the morphology of cells of strains M1 and M2 is similar to the PenG-induced L-forms. The arrowheads indicate intracellular vesicles, while empty vesicles are indicated with an asterisk. The inlay in M2 shows a proliferation-associated tubulation event. (C-E) Frames from time-lapse microscopy show L-form-like proliferation involving (C) vesiculation, (D) blebbing, and (E) membrane tubulation. (F) Formation of S-cells strains upon prolonged exposure to hyperosmotic stress. Germination of spores under hyperosmotic stress conditions generates germlings, which are able to extrude S-cells. These S-cells are able to switch to the mycelial mode-of-growth, or sporadically acquire mutations that allow them to proliferate like L-forms, which is characterized by tubulation, blebbing or vesiculation. Scale bar represents 10 μ m (B), 2 μ m (inlay panel B) or 5 μ m (C, D, E).