

Impact of spatial organization on a novel auxotrophic interaction among soil microbes.

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Running title: Impact of spatial organization on a novel auxotrophic interaction

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Keywords: Auxotrophy, soil microbial communities, *Serendipita indica*, *Bacillus subtilis*, endophytic fungi, thiamine, vitamins, metabolic interaction, precision farming.

1 **Abstract**

2 A key prerequisite to achieve a deeper understanding of microbial communities and to engineer
3 synthetic ones is to identify the individual metabolic interactions among key species and how
4 these interactions are affected by different environmental factors. Deciphering the
5 physiological basis of species-species and species-environment interactions in spatially
6 organized environment requires reductionist approaches using ecologically and functionally
7 relevant species. To this end, we focus here on a specific defined system to study the metabolic
8 interactions in a spatial context among a plant-beneficial endophytic fungus *Serendipita indica*,
9 and the soil-dwelling model bacterium *Bacillus subtilis*. Focusing on the growth dynamics of
10 *S. indica* under defined conditions, we identified an auxotrophy in this organism for thiamine,
11 which is a key co-factor for essential reactions in the central carbon metabolism. We found that
12 *S. indica* growth is restored in thiamine-free media, when co-cultured with *B. subtilis*. The
13 success of this auxotrophic interaction, however, was dependent on the spatial and temporal
14 organization of the system; the beneficial impact of *B. subtilis* was only visible when its
15 inoculation was separated from that of *S. indica* either in time or space. These findings describe
16 a key auxotrophic interaction in the soil among organisms that are shown to be important for
17 plant ecosystem functioning, and point to the potential importance of spatial and temporal
18 organization for the success of auxotrophic interactions. These points can be particularly
19 important for engineering of minimal functional synthetic communities as plant-seed
20 treatments and for vertical farming under defined conditions.

21 **Introduction**

22 Higher-level functions and population dynamics within microbial communities are
23 underpinned by the interactions among the composing species within the community and their
24 environment (Falkowski *et al.*, 2008; Sañudo-Wilhelmy *et al.*, 2014). Deciphering these
25 interactions is a pre-requisite to understand and manage complex natural communities (Abreu
26 and Taga, 2016; Widder *et al.*, 2016) and to achieve community-level synthetic engineering
27 (Großkopf and Soyer, 2014; Hays *et al.*, 2015; Lindemann *et al.*, 2016). To this end, increasing
28 numbers of experimental studies and (meta)genomic surveys have shown that auxotrophic
29 interactions, involving vitamins and amino acids, are wide-spread in many microbial natural
30 communities (Sañudo-Wilhelmy *et al.*, 2014; Morris *et al.*, 2012; Helliwell *et al.*, 2013) and
31 can also be engineered genetically to create synthetic communities (Mee *et al.*, 2014; Pande *et*
32 *al.*, 2014). Specific auxotrophic interactions among microbes are shown to influence ecosystem
33 functioning; e.g. infection outcomes within higher organisms (Wargo and Hogan, 2006),
34 ecological population dynamics in the oceans (Sañudo-Wilhelmy *et al.*, 2014), and the level of
35 biodegradation of organic matter under anoxic conditions (Schink, 1997; Embree *et al.*, 2015).

36
37 It has been suggested that auxotrophies can result from reduced selective pressures for
38 maintaining biosynthesis capabilities under stable metabolite availability due to abiotic or
39 biotic sources (Morris *et al.*, 2012; Helliwell *et al.*, 2013). This proposition is supported by the
40 observed independent evolution of vitamin and amino acid auxotrophies in different, unrelated
41 taxa (Helliwell *et al.*, 2011; Rodionova *et al.*, 2015), and points to a direct linkage between
42 ecological dynamics and evolution of auxotrophies (Embree *et al.*, 2015). The possible
43 fluctuations in a metabolite's availability in time and space would be expected to impact both
44 the emergence of auxotrophies and the population dynamics of resulting auxotrophic species.
45 For example, in the marine environment, where the observed auxotrophies relate mostly to the
46 loss of biosynthesis capacity for vitamins and amino acids, population dynamics of auxotrophic
47 species are believed to be directly linked to those of 'provider' species (Helliwell *et al.*, 2013;
48 Hom and Murray, 2014; Sañudo-Wilhelmy *et al.*, 2014). The ecological influences of
49 auxotrophic species on community structure and population dynamics can also be exerted by

51 abiotic fluctuations or directly by the abundances and actions of higher organisms within the
52 system.

53
54 These ecological influences on microbial population dynamics can increase significantly in
55 spatially organized systems. Yet, the spatial context of microbial interactions is under-studied.
56 Considering that each species can display multiple metabolic actions that all affect a common
57 environment, it is not clear if auxotrophic interactions can always be successfully established
58 even if genetic/metabolic complementarity is present. For example, changes in environmental
59 pH upon growth of one species can affect its subsequent interactions with other microbes
60 (Vylkova, 2017; Ratzke and Gore, 2017). Similarly, extensive oxygen depletion upon
61 microbial colony growth plates (Peters and Wimpenny, 1987; Dietrich *et al.*, 2013; Kempes
62 and Okegbé, 2014) can directly influence subsequent or simultaneous growth of different
63 species or their interactions. These possible interplays between species-species and species-
64 environment interactions are currently not well-understood and only explored in few studies,
65 which used either synthetically engineered interactions (Shou *et al.*, 2007; Mee *et al.*, 2014) or
66 enriched microbial communities (Embree *et al.*, 2015). This lack of understanding, however,
67 causes a particular challenge for the engineering of novel applications of microbial
68 communities with inherent spatial organisation, such as seen in agriculture and involving for
69 example closed-ecosystem production, seed treatment and microbe-based biofertilisation
70 (Gòdia *et al.*, 2002; Lucy *et al.*, 2004; Richardson *et al.*, 2011).

71
72 Towards addressing this challenge, we focus here on identifying potential metabolic
73 interactions among plant-beneficial endophytic fungus *Serendipita indica* (previously called
74 *Piriformospora indica* (Weiss *et al.*, 2016)) and the common soil microbe *Bacillus subtilis*.
75 Identifying a defined media for *S. indica*, we found it to be auxotrophic for the vitamin B1,
76 thiamine. To study the potential auxotrophic interactions of *S. indica*, we then created a co-
77 culture system using *Bacillus subtilis*. We found that *S. indica* thiamine auxotrophy can be
78 satisfied and its growth is restored in the presence of *B. subtilis*. The success of this auxotrophic
79 interaction, however, is strongly dependent on temporal and spatial organization in the system.
80 These findings and the established synthetic co-culture can act as a basis to develop a more
81 complete functional synthetic community, as advocated for biotechnological applications and
82 for gaining insights into community function (Mee and Wang, 2012; Großkopf and Soyer, 2014;
83 Widder *et al.*, 2016; Lindemann *et al.*, 2016). With the inclusion of a plant, such a synthetic
84 community can allow further insights into microbe-microbe, and microbe-plant interactions
85 and development of new agricultural technologies such as in seed coating and vertical farming
86 in controlled environments.

87
88 **Results**
89 ***S. indica* is auxotrophic for thiamine.** *S. indica* is an endophytic fungus that can colonize
90 roots of a wide range of plants and can confer a range of beneficial effects, including enhancing
91 plant growth, resistance to biotic and abiotic stresses (Waller *et al.*, 2005; Sherameti *et al.*,
92 2008; Vadassery *et al.*, 2009), promotion of adventitious root formation in cuttings (Druge *et*
93 *al.*, 2007), and assisting phosphate assimilation (Yadav *et al.*, 2010). Despite its broad host
94 range, *S. indica* also has the ability to grow in the absence of host plants (Kumar *et al.*, 2011).
95 Exploiting this ability, we attempted to create a fully defined growth medium that was based
96 on previous physiological studies on *S. indica* (Zuccaro *et al.*, 2011; Kumar *et al.*, 2011; Jacobs
97 *et al.*, 2011; Varma *et al.*, 2012; Qiang *et al.*, 2012). Using our defined media, we tested the
98 effect of the vitamins on growth by cultivating *S. indica* in a series of vitamin-free media each
99 supplemented by a specific vitamin (Figure 1). The analyses showed that *S. indica* is
100 auxotrophic for thiamine; while none of the other individual vitamin additions supported

101 growth, thiamine and full vitamin addition did. This finding was further confirmed by growing
102 *S. indica* on plates supplemented with an additional agar block only containing a defined
103 amount of thiamine. In this case, growth of *S. indica* resulted in expansion towards the thiamine
104 agar block, suggesting that growth occurs on a thiamine gradient or is linked with an active
105 chemotaxis towards thiamine source (Figure S1). We also quantified the growth of *S. indica*
106 with different concentrations of thiamine and found that hyphae growth and spore formation
107 showed a positive, but saturating, dependency on thiamine levels (Figure S2). At zero
108 concentration of thiamine in the media, we still observe germination and very little hyphal
109 growth (Figure S2), possibly supported by thiamine stored in spores. Besides these
110 measurements, we also observed thiamine effect on *S. indica* growth using time-lapse
111 microscopy (see further discussion below and supplementary videos 1 and 2).

112
113 ***S. indica* auxotrophy is reflected in its genomic enzyme content.** To support and better
114 understand these physiological results, we analyzed the *S. indica* genome for the presence of
115 genes associated with thiamine use, biosynthesis, and transport. Bioinformatics analysis
116 revealed that *S. indica* lacks most of the genes of the thiamine-biosynthesis pathway (Table S1,
117 Figure 2a). In particular, we were not able to find any homologs of the genes *thi5* and *thi6*. The
118 former encodes the enzyme involved in the synthesis of the thiamine-precursor
119 hydroxymethylpyrimidine (HMP), while the later encodes the bifunctional enzyme acting as
120 thiamine phosphate pyrophosphorylase and hydroxyethylthiazole kinase. A homolog of the
121 gene *thi4*, the product of which also relates to mitochondrial DNA damage tolerance (Machado
122 *et al.*, 1997; Hohmann and Meacock, 1998; Wightman, 2003), is present. We also found that
123 *S. indica* contains a homolog of the *thi7* (or alternative name *thi10*) that encodes a thiamine
124 transporter, and a homolog of the *pho3* gene, whose product catalyzes dephosphorylation of
125 thiamine phosphate to thiamine, thereby increasing its uptake (Wightman, 2003). These
126 findings suggest that *S. indica* is unable to synthesize thiamine, but can acquire thiamine from
127 the environment, as also suggested for other microbes that encode thiamine salvage pathways
128 (Jenkins *et al.*, 2007) . The utilization of thiamine in physiology is evidenced by the presence
129 of homologs of the *thi80* gene, which encodes a thiamine pyrophosphokinase involved in the
130 catalysis of thiamine into thiamine pyrophosphate (ThPP), the presence of at least one gene
131 encoding a ThPP binding domain-containing protein, and the role of ThPP as a key co-factor
132 involved in central metabolic reactions (see Figure 2b). The last point involves key metabolic
133 reactions such as pyruvate fermentation and conversion for entry into the citric acid cycle
134 (TCA), oxo-glutarate to succinyl-CoA conversion in the TCA cycle, transketolase reactions in
135 the pentose phosphate pathway, and biosynthesis reactions for leucine, isoleucine and valine
136 (Michal and Schomburg, 1999)

137
138 ***B. subtilis* complements *S. indica*'s auxotrophy for thiamine and promotes its growth.**
139 Given the crucial role of thiamine-derived co-factors in central metabolism, *S. indica* growth
140 in nature apparently depends on environment-derived thiamine. Indeed, thiamine can be
141 synthesized by various bacteria, fungi and plants (Begley *et al.*, 1999; Jenkins *et al.*, 2007;
142 Jurgenson *et al.*, 2009). Among these, *B. subtilis*, a bacterium commonly found in soil (Hong
143 *et al.*, 2009), is an established model organism (Mader *et al.*, 2011), and well-studied for
144 thiamine biosynthesis (Schyns *et al.*, 2005; Begley *et al.*, 1999). Combined with the fact that
145 *B. subtilis* is normally a plant-beneficial microbe (Castillo *et al.*, 2013), this motivated us to
146 explore the possibility that the identified *S. indica* auxotrophy for thiamine could be satisfied
147 upon co-culturing with *B. subtilis*. We created co-cultures of these two species on agar plates
148 using our defined media and two common nitrogen sources to evaluate possible auxotrophic
149 interaction under these conditions. We found that *B. subtilis* could indeed stimulate *S. indica*

150 growth under thiamine-free conditions and that *S. indica* growth followed a spatial pattern with
151 significant growth in the vicinity of the *B. subtilis* colony (Figure 3a).

152 We used time-lapse microscopy to quantify this spatial growth pattern of *S. indica* and
153 found that growth (as approximated by image density) happened faster at the side closer to the
154 *B. subtilis* colony compared to the far side of the plate (see Figure 3b and Supplementary
155 Videos 3 and 4). This could be explained by the presence of an increasing thiamine gradient
156 towards the *B. subtilis* colony that facilitates *S. indica* hyphal growth. While these findings
157 strongly suggest a *B. subtilis*-linked thiamine provision, which then promotes *S. indica* growth,
158 our attempts to quantify thiamine from agar plate co-cultures has failed, presumably due to a
159 combination of thiamine consumption and sensitivity limitations of available thiamine assays
160 (50 µg/L) (Lu and Frank, 2008). We were, however, able to detect thiamine from concentrated
161 *B. subtilis* and found the concentration in liquid culture supernatants to be approximately 7.56
162 µg/l.

163 While the above findings strongly suggest that the growth enabling of *S. indica* by *B. subtilis* is due to thiamine supply, another theoretical possibility is that *B. subtilis* provides
164 metabolites other than thiamine, that allow bypassing of central reactions requiring thiamine
165 as a co-factor. In other words, provision of metabolites that are downstream of pyruvate in the
166 TCA cycle (Figure 2b). To rule out this possibility, we have analyzed growth of *S. indica* in
167 the absence of thiamine but supplemented with organic and amino acids that link to the central
168 carbon metabolism. We found that none of the 17 amino acids or 8 organic acids tested or their
169 combinations allowed for *S. indica* growth in the absence of thiamine (Figure S3). This finding
170 further confirmed that *B. subtilis* facilitated growth of *S. indica* in thiamine-free medium is
171 linked directly to thiamine.

172
173
174 **Metabolic profiling shows additional metabolic interactions between *S. indica* and *B. subtilis*.** To analyse the basis of metabolic interactions between the two organisms and to
175 collect more evidence for thiamine-based auxotrophy, we grew each organism in liquid culture
176 on its own and then cross-cultured the other organism on the supernatant of the first one. As
177 with agar plates, we found that in the absence of thiamine, the *S. indica* growth was limited to
178 spore germination (Figure 4). When supplemented with *B. subtilis* supernatant, however, *S. indica*
179 showed significantly increased growth in liquid culture (Figure 4). Consistent with this,
180 there was also a growth enhancement of *S. indica* by the *B. subtilis* supernatant when cultured
181 in the presence of thiamine.

182 To better understand the metabolic basis of these physiological observations, we
183 repeated these experiments and quantified the concentrations of the key organic acids linking
184 to the TCA cycle (lactate, acetate, pyruvate, and formate) in the supernatant of each organism
185 before and after cross-cultivation using ion chromatography. We found that the supernatant
186 from *B. subtilis* monoculture contained significantly higher amounts of acetate and some
187 formate and pyruvate, and that the extracellular levels for these compounds did not change in
188 the presence or absence of thiamine in the media (Figure S4). When *S. indica* was grown in the
189 *B. subtilis* supernatant and in the absence of thiamine, it consumed both acetate and formate
190 and produced pyruvate. In the presence of both thiamine and the *B. subtilis* supernatant, the
191 consumption of acetate and formate was also observed, but there was also production of lactate
192 in addition to pyruvate (Figure S4). These findings, in particular acetate and formate cross-
193 feeding from *B. subtilis* to *S. indica*, explain the positive impact of *B. subtilis* supernatant on
194 growth irrespective of thiamine availability. They also provide further support that the *B. subtilis*-associated
195 growth of *S. indica* relates to thiamine provision rather than organic acids,
196 since acetate and formate alone did not enable *S. indica* growth in thiamine-free media (Figure
197 S3). We further found that *S. indica* secreted an unidentified organic acid in thiamine-media,

199 that showed an IC profile overlapping with that of glutamine, and that was consumed by *B. subtilis*
200 in the reverse experiment design (of growing *B. subtilis* in *S. indica* supernatant).

201
202 **The successful co-existence of *S. indica* and *B. subtilis* depends on spatiotemporal**
203 **organization in the system.** The above findings show that *B. subtilis* can support the growth
204 of *S. indica* in thiamine-free medium either through its supernatant or when co-cultured at a
205 distance on an agar plate. Both experimental setups were geared towards identifying possible
206 interactions among the two species through utilization of the excretions of one species by the
207 other, but did not necessarily consider the spatiotemporal factors on such interaction. Thus, a
208 remaining question was whether both species could still co-exist and establish a successful
209 interaction under different conditions regarding the spatial proximity or size of initial
210 inoculation, or the actual growth phase that the different species are in at the time of
211 introduction onto the agar. While addressing these questions is experimentally challenging, we
212 attempted here to analyse the impact of spatial-temporal factors on the outcome of the *S. indica*
213 – *B. subtilis* auxotrophic interaction by changing inoculation time and location on agar plates.
214 In particular, we separated the inoculation of *S. indica* spores from *B. subtilis* inoculation either
215 in time (by inoculating spores 3 days before *B. subtilis* colony inoculation) or space (by
216 inoculating *S. indica* and *B. subtilis* at certain distance to each other). Alternatively, we
217 inoculated *S. indica* spores after mixing with *B. subtilis*. These experiments mimic a scenario
218 commonly found in agri-technology practices when using pre-mixed cultures or spores of
219 different microbes as soil biofertilizers or plant seed pre-treatments (Turner, 1991). We found
220 that with temporal or spatial separation, both species could successfully grow in the absence of
221 thiamine, indicating a positive auxotrophic interaction (Figure 5). In contrast, direct co-
222 inoculation of *B. subtilis* with *S. indica* significantly hampered co-existence of the two species,
223 particularly reducing *S. indica* growth (Figure 5). These findings indicate the significance of
224 the spatiotemporal organization on microbial co-existence for the formation of stable
225 interactions and, hence, on higher order microbial community structures. Our observations
226 either reflect competition for resources upon co-inoculation, or alteration of the micro-
227 environment by one species so that the other cannot establish itself, as discussed further below.
228

229 **Conclusion**

230 Here, we report the discovery of a novel auxotrophy for thiamine in the endophytic fungus *S.*
231 *indica* and how this thiamine requirement can be satisfied by *B. subtilis*. Our findings suggest
232 that *S. indica* possesses thiamine transporters but lacks necessary thiamine biosynthesis genes,
233 and its growth in thiamine-free medium cannot be supported by any other vitamin or relevant
234 organic and amino acids. In contrast, co-culturing with *B. subtilis* in thiamine-free media allows
235 *S. indica* growth, indicating a successful auxotrophic interaction between the two organisms.
236 In addition, we have identified several cross-feeding interactions between the two organisms
237 involving overflow and consumption of organic acids. We found that the auxotrophic
238 interaction can only be achieved under conditions where the inoculation (and germination) of
239 the two species is separated in time or space.

240
241 These findings have implications both for the study of *S. indica*, as an important plant-
242 supporting soil fungus (Qiang *et al.*, 2012), and for the engineering and application of minimal
243 synthetic communities that aim to establish plant supporting soil communities. In the former
244 direction, future metabolic and physiological studies of *S. indica* will be enabled by the defined
245 media conditions and identified thiamine auxotrophy in this study. A key suggestion from a
246 biotechnological perspective, for example, is to consider thiamine as an important factor in the
247 commercial mass production of *S. indica* (Singhal *et al.*, 2017). In the latter direction, the
248 presented results point to the importance of the role of spatiotemporal dynamics on the outcome

249 of microbial interactions. The failure of establishment of auxotrophic interactions between *S.*
250 *indica* and *B. subtilis*, when co-cultured in the same place and time suggest that additional
251 ecological factors can override naïve expectations from complementary metabolic interactions.
252 This interplay between ecological forces, abundance, and interactions of auxotrophic species
253 is currently not well-understood and only explored in a few studies, which used either
254 synthetically engineered interactions (Shou *et al.*, 2007; Mee *et al.*, 2014) or enriched microbial
255 communities (Embree *et al.*, 2015). Thus, our defined synthetic co-culture represents a
256 powerful system towards understanding this new emerging axis of the molecular ecology of
257 species interactions.

258
259 The observed failure to establish a successful auxotrophic interaction when co-cultured at the
260 same time and space could be related to several factors. At the simplest level of explanation, *S.*
261 *indica* and *B. subtilis* could be competing for and depleting the local carbon source. This is an
262 unlikely explanation for our experiments, where carbon levels were relatively high. An
263 alternative explanation would be that changes in ecological conditions caused by one species,
264 would prevent the other species from establishing itself. In this ecological explanation, both
265 the changes in local pH and in oxygen availability could be relevant. Changes in pH upon
266 microbial growth were highlighted recently as affecting the subsequent microbial interactions
267 and growth (Vylkova, 2017; Ratzke and Gore, 2017). Similarly, extensive oxygen depletion
268 upon microbial colony growth on agar plates has been shown in several studies (Peters and
269 Wimpenny, 1987; Dietrich *et al.*, 2013; Kempes and Okegbé, 2014) and can directly influence
270 subsequent or simultaneous growth of different species or their interactions. This explanation
271 could be particularly relevant in our experiments, where we expect *S. indica* germination and
272 initial growth to require substantial oxygen (Tacon *et al.*, 1983).

273
274 The finding that the success of auxotrophic interactions relates to spatiotemporal effects
275 suggest that consideration should be given to inoculation timing when designing or applying
276 biofertilizers or bio-control agents to the soil. Indeed, microbial interactions and synergisms
277 are suggested to be crucial for soil fertility, bioproduction and ecosystem functioning (Perotto
278 and Bonfante, 1997; Bulgarelli *et al.*, 2013; Pérez-Jaramillo *et al.*, 2016). Plants significantly
279 benefit from symbioses with soil microbes, with benefits ranging from nutrient supply, growth
280 promotion to elevating plant stress resistance (Vessey, 2003; Esser, 2013; Davison, 1988;
281 Castillo *et al.*, 2013; Yurgel *et al.*, 2014). At the same time, soil microbes can interact among
282 themselves or alter each other's interactions with the plants (Veresoglou *et al.*, 2012; Lareen
283 *et al.*, 2016) (Fitter and Garbaye, 1994; Kohlmeier *et al.*, 2005). The biochemical basis of these
284 potential multi-level interactions in the soil has remained mostly elusive to date, with few
285 documented cases of amino acid auxotrophies in specific soil bacteria and vitamin-provision
286 from plants relating to their root colonization (Nagae *et al.*, 2016; diCenzo *et al.*, 2015; Streit
287 *et al.*, 1996). The presented synthetic community of *S. indica* and *B. subtilis* shows for the first
288 time that metabolic auxotrophy can directly underpin microbial interactions and growth, and
289 that the success of interaction can be determined by spatiotemporal organization in the system.
290 In to the future, this synthetic system allows controlled investigation (and potential
291 optimization) of fungal-bacteria interactions and can be further extended with additional
292 microbes and a plant. The resulting minimalist synthetic eco-system can provide a platform to
293 analyze and control cross-kingdom relationships between plants and their growth promoting
294 fungi and bacteria, and enable new applications for vertical farming and crop production in the
295 field.

296
297 **Materials and methods**

298 **S. indica cultures, growth media and conditions.** The defined basic medium for testing *S.*
299 *indica* growth with ammonium as nitrogen source contained per liter; 15g agar, 20g glucose,
300 1.32 g $(\text{NH}_4)_2\text{SO}_4$, 0.89 g $\text{Na}_2\text{HPO}_4 \cdot 2\text{H}_2\text{O}$, 0.68 g KH_2PO_4 , 35 mg $\text{Na}_2\text{MoO}_7 \cdot 2\text{H}_2\text{O}$, 5.2 mg
301 MgSO_4 , 2.5 mg $\text{FeSO}_4 \cdot 7\text{H}_2\text{O}$, 0.74 mg $\text{CaCl}_2 \cdot 2\text{H}_2\text{O}$, 0.0043 mg $\text{ZnSO}_4 \cdot 7\text{H}_2\text{O}$, 0.004 mg
302 $\text{CuSO}_4 \cdot 5\text{H}_2\text{O}$. Growth experiments for testing effects of different vitamins were performed in
303 24-well plates (Ref: 353226, Falcon), where each well contained 2 ml of the basic medium,
304 supplemented with either 200 $\mu\text{g/l}$ of single vitamin solution, 1 g/l yeast extract, 200 $\mu\text{g/l}$
305 mixture of all eight vitamins tested, or equivalent amount of water. Each well was then
306 inoculated with 1 μl of *S. indica* spore suspension (approximately 500,000 spores/ml, counted
307 with Neubauer counting chamber), where spores were harvested from 6-8 weeks old *S. indica*
308 agar plates. In the ‘non-inoculated’ control treatment, 1 μl of water was used instead. Each
309 treatment condition was prepared in three technical replicates. 24-well plates were then sealed
310 with parafilm and placed in a 30 °C static incubator for 2 weeks. Images were taken with a gel
311 doc system (Syngene) at the end of this period.
312

313 **Experiments on agar plates, growth media and conditions.** The defined (basic) medium for
314 testing *S. indica* growth on agar plates contained per liter; 15 g agar, 20 g glucose, 0.89 g
315 $\text{Na}_2\text{HPO}_4 \cdot 2\text{H}_2\text{O}$, 0.68 g KH_2PO_4 , 35 mg $\text{Na}_2\text{MoO}_7 \cdot 2\text{H}_2\text{O}$, 5.2 mg MgSO_4 , 2.5 mg $\text{FeSO}_4 \cdot 7\text{H}_2\text{O}$,
316 0.74 mg $\text{CaCl}_2 \cdot 2\text{H}_2\text{O}$, 0.0043 mg $\text{ZnSO}_4 \cdot 7\text{H}_2\text{O}$, 0.004 mg $\text{CuSO}_4 \cdot 5\text{H}_2\text{O}$. When the chosen
317 nitrogen source was ammonium, 1.32 g/l $(\text{NH}_4)_2\text{SO}_4$ was added to this basic recipe. When the
318 chosen nitrogen source was glutamine, 1.46 g/l glutamine was added to this basic recipe. For
319 experiments with thiamine, 150 $\mu\text{g/l}$ thiamine was added to the basic media after autoclaving.
320

321 Experiments were carried out on 60 mm dishes, filled with 6ml of agar medium given
322 above. A 500,000 spores/ml *S. indica* spore suspension, with spores harvested from 6-8 weeks
323 old *S. indica* agar plates, was inoculated with 2 μl (on the left side of the plates). At
324 approximately 2 cm distance to the right of the inoculum, either a ‘mock’ solution, a thiamine
325 block, or a *B. subtilis* inoculum were placed. The ‘mock’ solution was 2 μl of sterile water. The
326 thiamine blocks were made by pouring 6 ml of 1.5% agar solution containing 150 $\mu\text{g/l}$ thiamine
327 into a 60 mm plate, and then punching a block out using a sterile pipette tip with a diameter of
328 4.7 mm. Therefore, each agar block used contained approximately 5.6 ng thiamine. The *B.*
329 *subtilis* inoculum was a 2 μl sample harvested from a culture, grown in 5ml liquid Lysogeny
330 broth (LB) (Bertani, 1951) to an $\text{OD}_{600} \approx 0.5$ measured by spectrophotometer (Spectronic 200,
331 Thermo Fisher Scientific), then washed and re-suspend to $\text{OD}_{600} 0.5$ with 10 mM MgCl_2 . The
332 plates were incubated in 30 °C for 2 weeks. Images were taken with gel doc system (Syngene)
333 at the end of this period.

334 **Time-lapse microscopy and image analysis.** Time-lapse microscopy was performed on agar-
335 medium cultures that were prepared using the same basic medium described above. A 6-well
336 tissue culture plate (Ref: 353046, Falcon) was used and 1 μl of *S. indica*, *B. subtilis* or mock
337 solution prepared as described above were inoculated on each well accordingly to experiment
338 design. An Olympus IX83 microscope, UPlanFLN 4 \times objective and cellSens software were
339 used for recording the growth. Okolab stage top incubator (H301-T-UNIT-BL-Plus system,
340 and H301-EC chamber) were used for incubation, with a temperature sensor and lens heater
341 set to 30 °C and stabilized for at least 2 hours prior to the experiment. Different fields of view
342 were chosen at interior and periphery of each colony and images from those fields were
343 recorded using the automated microscope stage and Olympus cellSens software. Images were
344 taken in 1 hour intervals and put together as image series. ImageJ (Fiji) (Schindelin *et al.*, 2012)
345 was used for measuring the mean intensity on each field of view over time, normalized against
346 the intensity value of the first frame from each view point (as shown in Figure 3).
347

348 **Spatial and temporal separation experiments.** *S. indica* (500,000 spores/ml, determined by
349 counting with Neubauer counting chamber) and *B. subtilis* ($OD_{600} \approx 0.5$, determined by
350 spectrophotometer (Spectronic 200, Thermo Fisher Scientific)) were cultivated on thiamine-
351 free synthetic medium containing ammonium as sole nitrogen source. 6-well tissue culture
352 plates (Ref: 353046, Falcon). On each plate, 1 μ l of *S. indica* and 1 μ l of *B. subtilis* were
353 inoculated on 5 of the wells; one well was intentionally left non-inoculated as a blank. In the
354 “no separation” case, *S. indica* and *B. subtilis* were pre-mixed at 1:1 volume ration, and
355 inoculated on the center of each well. For “spatial separation” case, *S. indica* was inoculated
356 7.5 mm left to the center of a well and *B. subtilis* 7.5mm right to the center, leaving 15 mm
357 distance in between. For “temporal separation” case, *S. indica* was inoculated on each well, the
358 plates were then incubated for 3 days and *B. subtilis* was inoculated after this time. All the
359 plates were incubated in 30°C for 2 weeks (starting from the time of *S. indica* inoculation).
360 Images were taken by scanning each well under a microscope (Olympus IX83) using the same
361 exposure time under bright field.

362 ImageJ was used for measuring the biomass by integration of the total colony density.
363 An image of each colony was manually outlined using the selection tool. The selected area was
364 compared with the same location on a blank well from the same plate. The area and relative
365 intensity were recorded (using “measure” function) and used for calculating the colony growth.
366

367 **Supernatant cross-feeding experiments.** Axenic cultures of *S. indica* and *B. subtilis* were
368 cultivated in 50 ml basic medium described above, with or without thiamine. For *S. indica* an
369 inoculum of 50 μ l of a 500,000 spores/ml spore suspension, harvested from 6-8 weeks old *S.*
370 *indica* agar plates, was used. For *B. subtilis*, an inoculum of 50 μ l, sampled from a culture grown
371 in LB to an $OD_{600} \approx 0.5$ determined by spectrophotometer (Spectronic 200, Thermo Fisher
372 Scientific), and washed with 10 mM MgCl₂, was used. After one week incubation in 30°C and
373 at 150 rpm, *S. indica* cells were harvested by centrifugation at 18,000 g for 20 minutes. The
374 supernatant was collected and filtered through a 0.2 μ m polyethersulfone (PES) filter (Ref:
375 WHA67802502, Whatman), while biomass was washed with 40 ml MilliQ water, dried using
376 a centrifugal evaporator (EZ-2 Elite, Genevac), and then weighted. The growth of *B. subtilis*
377 liquid cultures was monitored daily by taking 1 ml samples and measuring OD_{600} by
378 spectrophotometer (Spectronic 200, Thermo Fisher Scientific). At the end of 1 week, the
379 remaining liquid culture was centrifuged at 18,000 g for 10 min. The supernatant was collected
380 and filtered through a 0.2 μ m PES filter, while biomass was discarded.

381 Both supernatants were mixed with fresh basic medium in a 1:1 ratio to set up new
382 axenic cultures of *S. indica* and *B. subtilis*. 1 ml liquid samples were collected from these
383 cultures after one week by filtering through a 0.2 μ m nylon membrane (Ref: WHA7402004,
384 Whatman). Samples were transferred into polypropylene vials (Ref: 079812, Thermo Fisher
385 Scientific) for Ion Chromatography, which was performed using Dionex ICS-500⁺ and column
386 Dionex IonPac AS11-HC-4 μ m (2 x 250 mm).

387
388 **Sequence analysis and BLAST search.** Sequences of key thiamine biosynthesis enzyme
389 genes (Table S1) from *Saccharomyces cerevisiae* S288c were compared with available *S.*
390 *indica* genome homologues using Position-Specific Initiated BLAST
391 (<https://blast.ncbi.nlm.nih.gov/Blast.cgi>), to identify the putative functions of the
392 corresponding genes. An e-value of 1e-6 was chosen as cut-off to identify homologous
393 sequences (Altschul, 1997). The results of the analysis using blastx are shown in Table S1,
394 while blastn and tblastx did not return any results with the chosen cut-off.
395

396 **Thiamine measurements on *B. subtilis* liquid cultures.** Axenic cultures of *B. subtilis* were
397 cultivated in 50ml synthetic medium containing glutamine as sole nitrogen source without

398 thiamine. *B. subtilis* inoculum of 50 μ l, sampled from a culture grown in LB to $OD_{600} \approx 0.5$
399 determined by spectrophotometer (Spectronic 200, Thermo Fisher Scientific), and washed with
400 10 mM MgCl₂ was used. After one week of incubation in 30 °C and at 150 rpm, *B. subtilis*
401 cultures were harvested by centrifugation at 18,000 g for 10 minutes. The supernatant was
402 collected and filtered through a 0.2 nm PES membrane filter (Ref: WHA67802502, Whatman).
403 The supernatant of 250 μ l from each culture was transferred to a clean 1.5 ml Eppendorf tube,
404 followed by sequentially adding 10 μ l 1% K₃[Fe(CN)₆], 150 μ l 15% NaOH solution and 150 μ l
405 isobutanol. The tubes were shaken vigorously for 1 minute, followed by 2 minutes of
406 centrifugation at 13,000 g. The upper isobutanol layer of each tube was transferred to a new
407 1.5 ml Eppendorf tube, containing approximate 0.2g Na₂SO₄. The tubes were mixed well and
408 centrifuged for 1 minute at 13,000 g for solids to settle. 100 μ l of supernatant from each tube
409 were transferred to 96-well plates (Ref: 3916, black flat bottom, Corning) and the fluorescence
410 was measured using a plate reader (CLARIOstar, BMG Labtech) at 365 nm excitation and 450
411 emission. The concentration of thiamine was determined with a series of known concentration
412 standard thiamine solutions under the same treatment.
413

414 ***S. indica* growth under different thiamine concentrations.** Synthetic medium containing
415 ammonium as sole nitrogen source was used for testing *S. indica* growth in different thiamine
416 concentrations. Media containing final thiamine concentrations of 0 μ g/l, 1.5 μ g/l, 15 μ g/l, 150
417 μ g/l and 1500 μ g/l were prepared, and distributed in a 6-well tissue culture plate (Ref: 353046,
418 Falcon). Each 6-well plate contained one concentration condition, with 3ml medium in each
419 well. On each plate, 1 μ l of *S. indica* (500,000 spores/ml) were inoculated on the center of five
420 wells, while one well was intentionally left non-inoculated as a blank. Plates were incubated at
421 30 °C for 2 weeks. Afterwards, lids were removed and OD_{600} and fluorescence at 365 nm for
422 excitation and 450 nm for emission were measured using a plate reader (CLARIOstar, BMG
423 Labtech) and the plate scan function to get an overall reading of each well. Images of plates
424 were taken using a gel doc system (Syngene).
425

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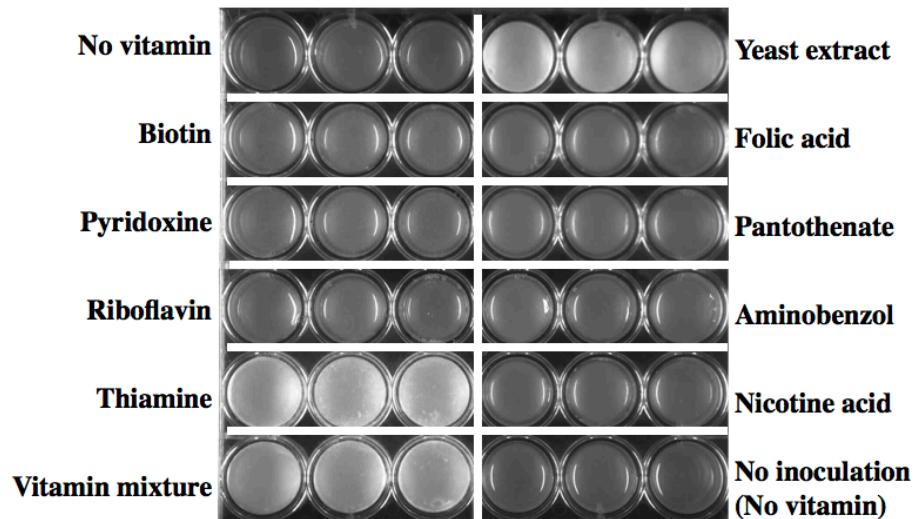
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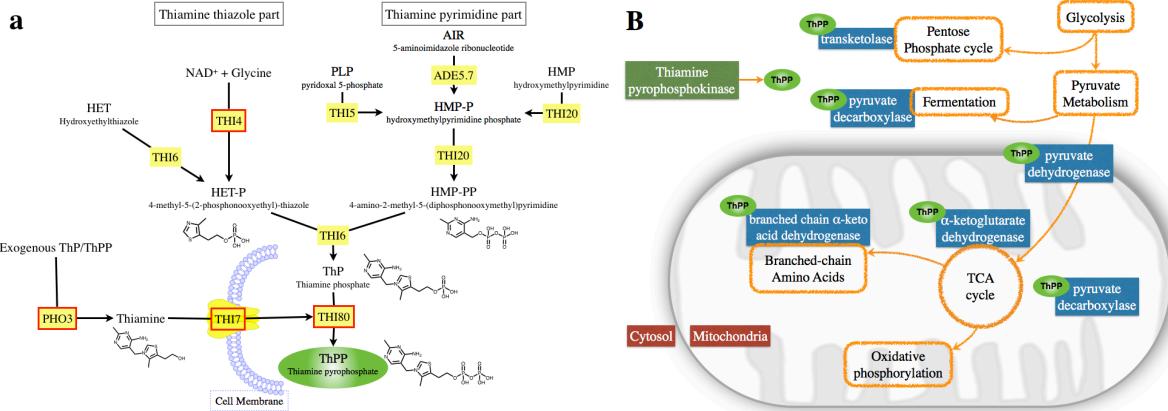
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599 **FIGURES & TABLES**

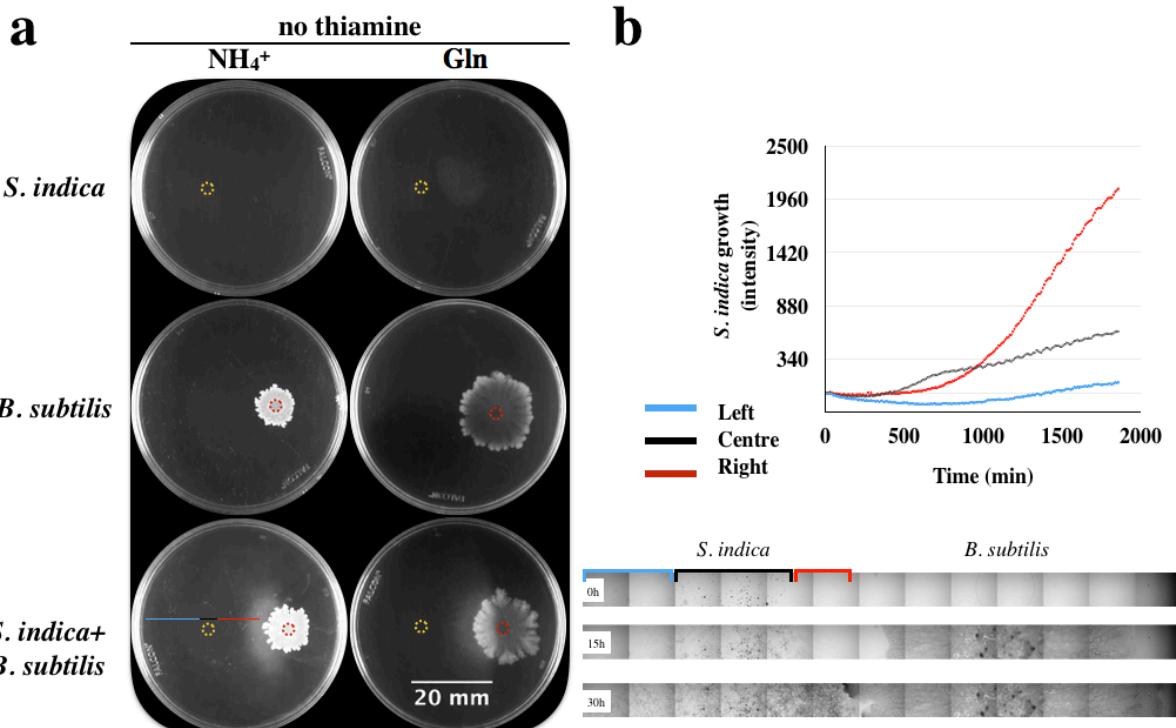


600
601 **Figure 1. *S. indica* growth under different conditions.** Growth on agar plates with defined
602 medium supplemented with different vitamins as shown on each row and column. Each
603 treatment has three replicates presented in 3 adjacent wells. *S. indica* grows in white colonies.
604 Images were taken after two weeks of growth.
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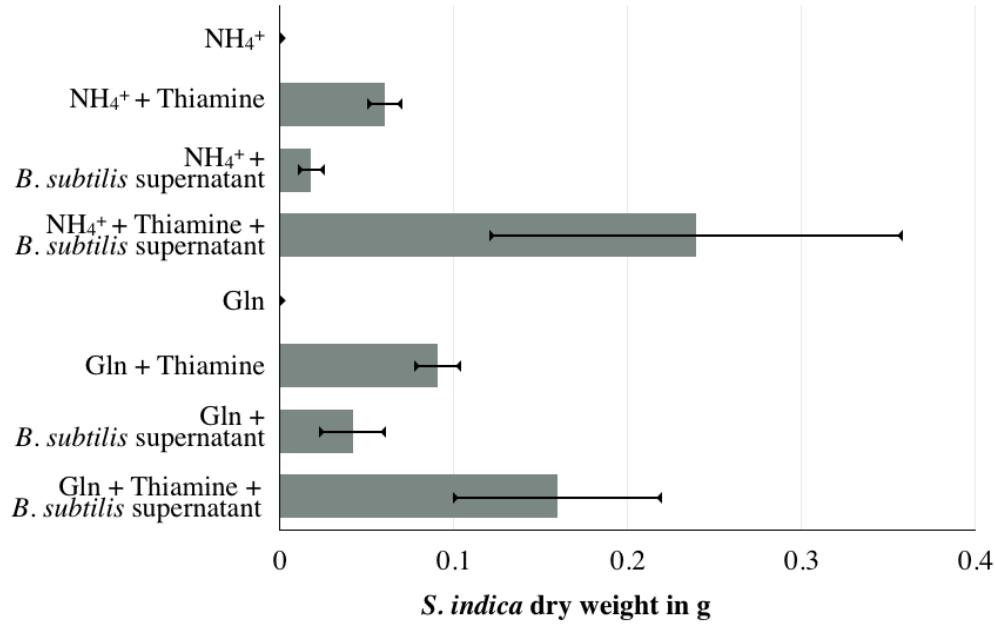


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Figure 2. Thiamine related genes and reactions. a. Overview of the thiamine biosynthesis pathway in *Saccharomyces cerevisiae* based on (Wightman, 2003), and as included in the KEGG metabolic pathways (Pathway: sce00730) (Kanehisa and Goto, 2000). Yellow squares indicate genes encoding for the enzymes in the corresponding reactions. Red borders indicate genes for which there are *S. cerevisiae* homologues in *S. indica* (see Methods). **b.** Simplified schematic of central metabolism in eukaryotic cells with cytosol and mitochondria compartments indicated. Orange enclosures show reactions of the central metabolism, while blue squares show essential enzymes catalyzing these reactions and requiring ThPP as a co-factor (shown in green).

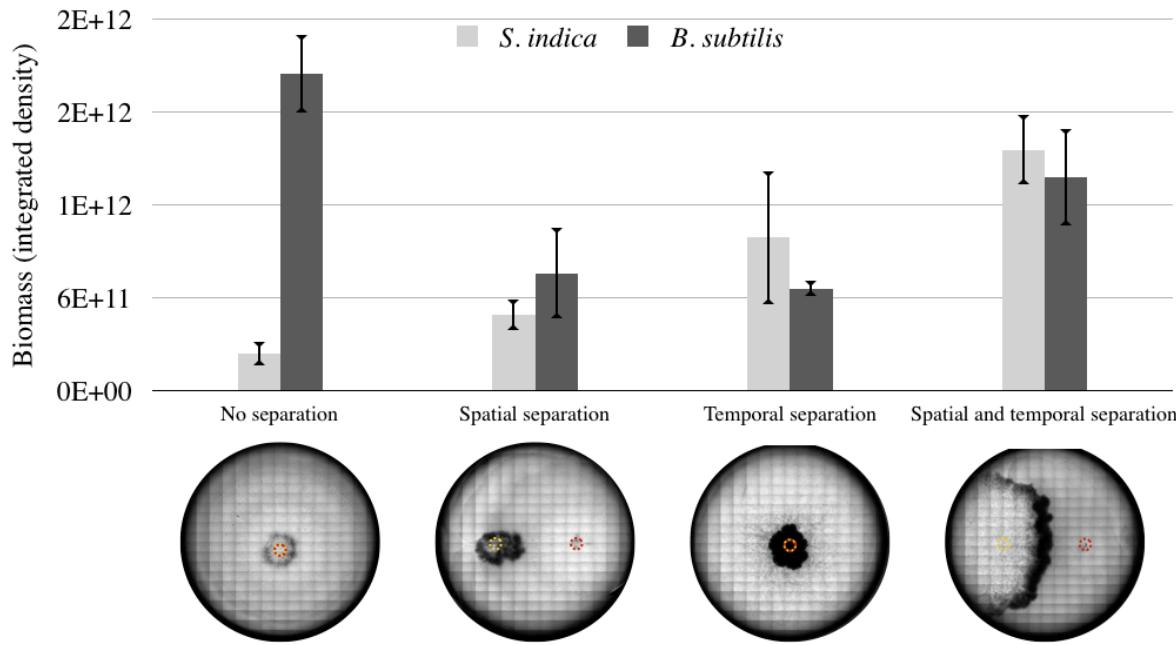


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619 **Figure 3. *S. indica* and *B. subtilis* interactions on agar plates.** **a.** Rows from top to bottom
620 showed growth of monocultures of *S. indica*, *B. subtilis*, and their co-culture respectively under
621 the absence of thiamine. The yellow dotted circle on the images indicates the *S. indica*
622 inoculation point. Red dotted circle indicates *B. subtilis* inoculation point. The left and right
623 columns show growth on plates after two weeks, using ammonium and glutamine as nitrogen
624 sources respectively. When both organisms were cultured together (bottom row), *B. subtilis*
625 and *S. indica* were inoculated on the right and left of the plate respectively. Plates shown are
626 representative of at least 3 replicates for each condition. We performed 2 biological replicates
627 of this experiment, with qualitatively similar results. **b.** Bottom: Time lapse image series of *S.*
628 *indica* and *B. subtilis* growth on agar plates in the absence of thiamine and with ammonium as
629 nitrogen source. Each image strip is composed of microscopy images of the same horizontal
630 section from the middle of the plate through the inoculation point of *S. indica* and *B. subtilis*,
631 at 0 h, 15 h and 30 h after inoculation. *S. indica* growth across defined parts of this horizontal
632 section (blue, black, and red lines – also compare bottom left plate in 3a) was quantified by
633 measuring image density and plotted over time (upper chart). The sections correspond to the *S.*
634 *indica* colony side closer to *B. subtilis* (red), the middle of the colony (black), and the colony
635 side far from *B. subtilis* (blue).
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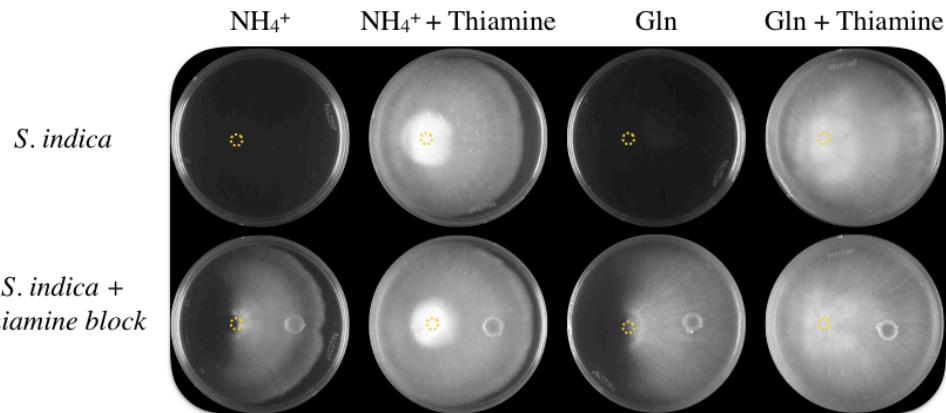
Figure 4. *S. indica* growth under different media compositions. Growth using either ammonia or glutamine and supplemented with thiamine or *B. subtilis* supernatant, as indicated on the y-axis. The x-axis shows *S. indica* growth approximated by total dry weight after one week of growth (see *Methods*).



646
647 **Figure 5. Biomass of *B. subtilis* and *S. indica* under different spatiotemporal culturing**
648 **cases.** “No separation” refers to *B. subtilis* culture and *S. indica* spores being pre-mixed at 1:1
649 volume ratio, and then inoculated as a single solution. “Spatial separation” refers to
650 approximately 1.5 cm separation of *S. indica* (left) and *B. subtilis* (right) inoculation points.
651 “Temporal separation” refers to inoculation of *S. indica* 3 days prior to *B. subtilis* inoculation.
652 The yellow dotted circle on the images indicates the *S. indica* inoculation point. Red dotted
653 circle indicates *B. subtilis* inoculation point. Growth of the different species was approximated
654 by tracing their respective colonies on the plate and measuring the image intensity from the
655 engulfing areas 2 weeks after *S. indica* inoculation. Measurements are from 3 replicate agar
656 plates, with a representative plate image shown at the bottom. These images show microscopic
657 scans of each plate at 2 weeks of growth. For the “no separation” case, there was no observable
658 *S. indica* colony expansion after 1 week. We performed 2 biological repetitions of this
659 experiment, with qualitatively similar results.
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663 **SUPPLEMENTARY FIGURES**

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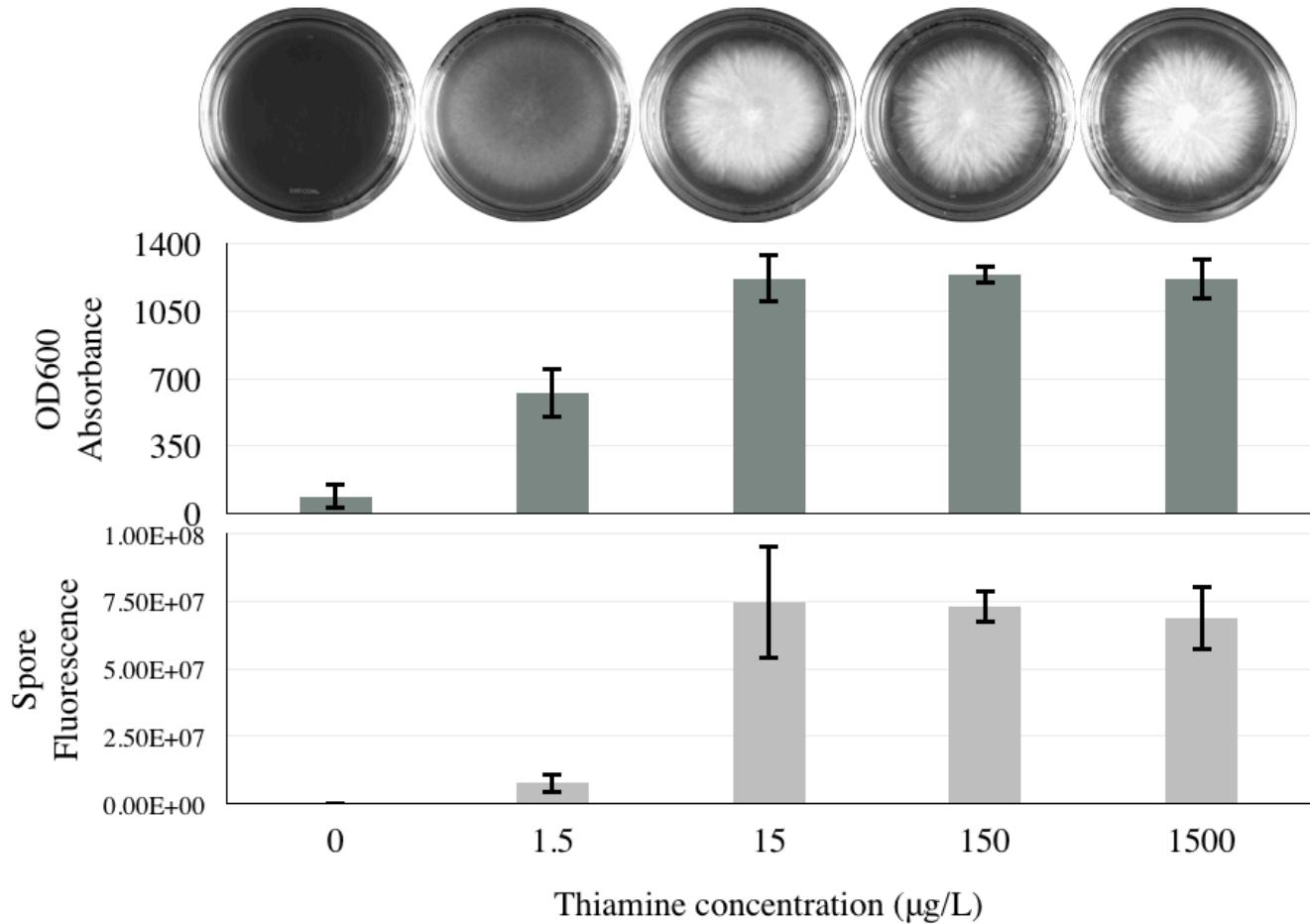
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666 **Supplementary Figure 1.** *S. indica* growth on agar plates after two weeks. Columns show
667 different media containing thiamine or not and using ammonium and glutamine as nitrogen
668 sources (shown as “NH₄⁺” or “Gln” on the panels). The top and bottom rows show the images
669 of agar plates without or with an additional agar block containing thiamine, placed ~1.5 cm to
670 the right side of *S. indica* inoculation point, which is indicated with a yellow circle.

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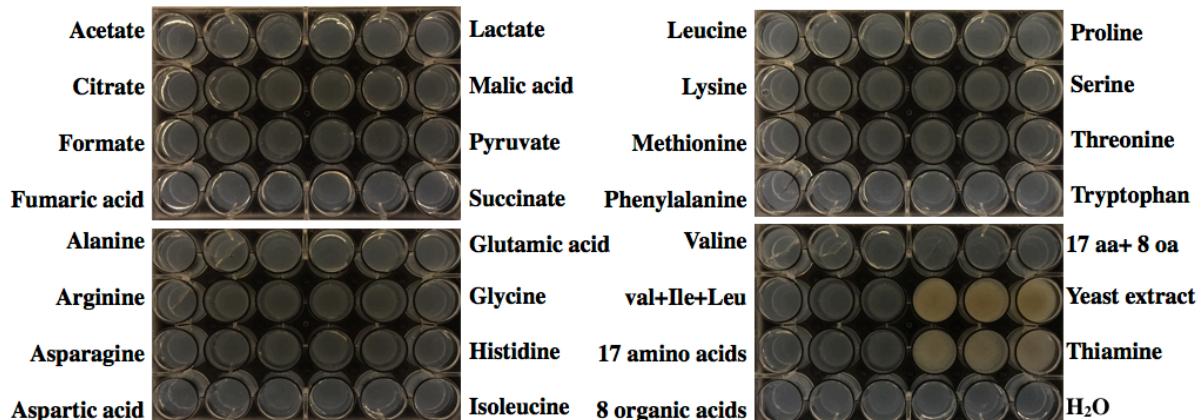
675 **Supplementary Figure 2.** *S. indica* growth on medium containing different concentrations of
676 thiamine and ammonium as nitrogen source. Images at top show two weeks growth of *S. indica*
677 on agar plates, and at different concentrations of thiamine as shown below on the bottom x -
678 axis. Each condition was repeated 6 times and images shown here are representatives for each
679 condition. Upper and lower bar-plots show plate absorbance at OD₆₀₀ and fluorescence
680 intensity (measured at 390 excitation and 470 emission for detection of *S. indica* spores)
681 respectively.

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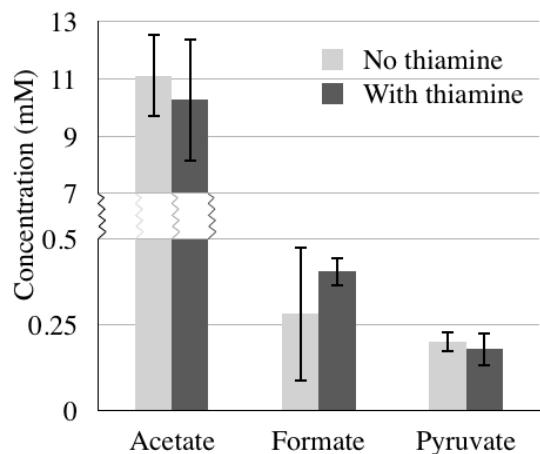


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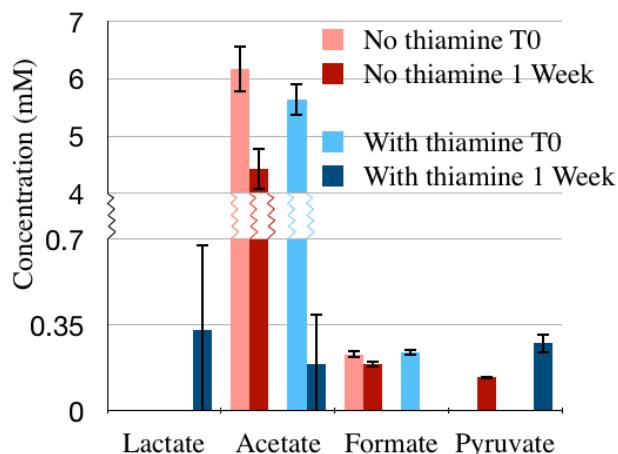
Supplementary Figure 3. *S. indica* amino acid and organic acid screen. *S. indica* growth on the media containing different amino acid or organic acid as supplement. Each treatment has three replicates presented in 3 adjacent wells. *S. indica* growth is visible as white-yellow colonies on the surface of a well. Images were taken after two weeks of growth.

693

B. subtilis supernatant



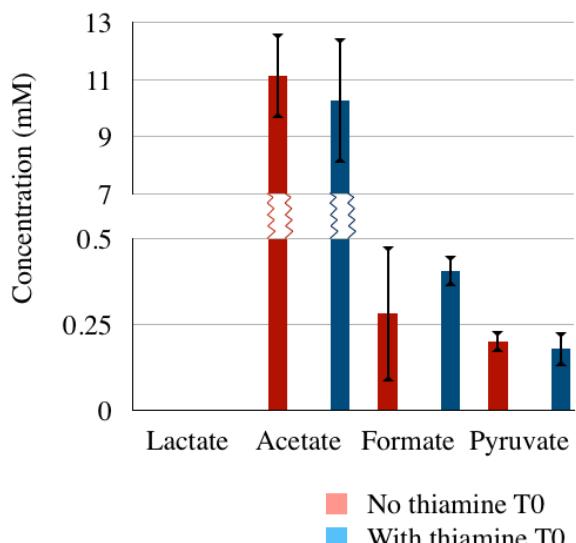
S. indica in *B. subtilis* supernatant



694

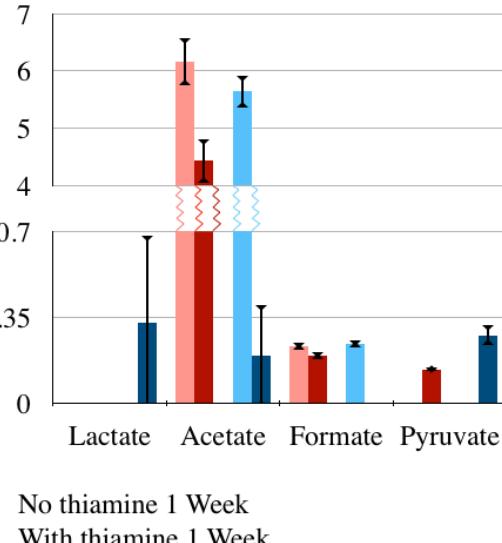
a

B. subtilis supernatant



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S. indica in *B. subtilis* supernatant



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Supplementary Figure 4. Concentrations of key organic acids in the supernatant of *B. subtilis* growth media in the presence of absence of *S. indica*. The left chart shows the supernatant after one week of *B. subtilis* cultivation in liquid medium containing glutamine as sole nitrogen source. The right chart shows the supernatant after one week of cultivation of *S. indica* in *B. subtilis* supernatant mixed with the same volume of fresh medium. T0 and T1 indicate the initial condition and after 1 week of growth respectively. Note that T0 concentrations in the right chart correspond to concentrations in the left chart diluted with fresh media.

704

705 **Supplementary Table 1.**

706 Comparison of the thiamine-related genes/proteins of *S. indica* with those of *S. cerevisiae*.

Gene name	Function	Source organism for sequence	Blastx result using <i>S.indica</i> genome Max score/Query covery/E value
THI6	Bifunctional hydroxyethylthiazole kinase/thiamine-phosphate diphosphorylase	<i>Saccharomyces cerevisiae</i> S288c	No
THI80	Thiamine diphosphokinase		104/84%/4e ⁻²⁶
Thi4	1. Thiamine thiazole synthase 2. Mitochondrial DNA damage tolerance		47.8/15%/2e ⁻⁰⁶
THI5	Pyrimidine precursor biosynthesis		No
THI11	Pyrimidine precursor biosynthesis		No
THI12	Pyrimidine precursor biosynthesis		No
THI13	Pyrimidine precursor biosynthesis		No
PHO3	Thiamin-repressible acid phosphatase		114/86%/3e ⁻²⁷
THI10 (THI7)	Thiamin transporter		176/92%/5e ⁻⁴⁸
PDC2	Pyruvate decarboxylase, transcriptional activator in response to thiamin starvation.		No
RPI1	Transcriptional regulator		No

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709 **Supplementary video 1.** *S. indica* monoculture on synthetic medium without thiamine.

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711 **Supplementary video 2.** *S. indica* monoculture on synthetic medium with thiamine.

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713 **Supplementary video 3.** *S. indica* and *B. subtilis* co-culture on synthetic medium without thiamine.

714

715 **Supplementary video 4.** *S. indica* and *B. subtilis* co-culture on synthetic medium with thiamine.

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