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2 **Close-Range Interactions Favor Growth in Random-Paired Extracted Soil Bacteria**

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30 **Abstract**

31 Species interactions at the cellular level are thought to govern the formation and functioning of  
32 microbial communities, but direct measurements of species interactions are difficult to perform  
33 between the hundreds of different species that constitute most microbial ecosystems. We  
34 developed a methodology to examine interactive growth of random cell pairs encapsulated inside  
35 40–70  $\mu\text{m}$  diameter agarose beads. We focused on a sandy soil as a test microbial ecosystem. By  
36 using gentle washing procedures, we detached microbial cells from sand and encapsulated them  
37 either in the absence or presence of pure culture inoculants. We then tested whether inoculants  
38 had on average positive or negative effects on the growth of resident community members  
39 depending on the growth substrate. Surprisingly, all the tested inoculants (including *Pseudomonas*  
40 *veronii* 1YdBTEX2, *Pseudomonas putida* F1, *Pseudomonas protegens* CHA0 and *Escherichia coli*  
41 MG1655) stimulated the growth of 40-80 percent of sand-derived cells when grown pair-wise in  
42 close proximity (i.e., within the same bead). This was true essentially irrespective of the growth  
43 substrate. Beneficial inoculant-sand cell partnerships resulted in up to 100-fold increase in  
44 productivity of the sand cell partner and up to 100-fold decrease in that of the inoculant. However,  
45 the maximum productivity attained by inoculant-sand cell partners within beads did not surpass  
46 that of inoculants alone. Further surprisingly, random pairs of sand cells encapsulated within the  
47 same bead also benefited growth in comparison to individual sand cells in a mutualistic manner  
48 (i.e., productivity when grown together was greater than the sum of individual productivities), but  
49 less than productivities observed in partnerships with the tested inoculants. This suggests that  
50 partnerships between inoculants and sand cells are not so much characterized by competition for  
51 substrate as by carbon loss through metabolite provision of the inoculant to sand cells (competitive  
52 exploitation).

53

54 **Introduction**

55 Natural ‘free-living’ microbial communities and those in association with animal or plant hosts are  
56 exemplified by complex and high-density species interactions, being composed of dozens (e.g.,  
57 certain insect hosts)<sup>1</sup> up to many thousands (e.g., soils<sup>2</sup>) of individual species that live within short  
58 distances from each other ( $\mu\text{m}$  to mm-scale). Understanding the general principles of the

59 formation, structure and functioning of microbial communities is one of the major questions in  
60 microbial ecology, and is still largely fragmentary<sup>3-6</sup>. Species compositions in communities vary,  
61 being subject to in- and outflow of species members<sup>7</sup>, to losses from selective predation<sup>8,9</sup> or as a  
62 consequence of phage infection and lysis<sup>10</sup>, and as a result of fluctuating nutrient and chemical  
63 conditions in their environment. It is generally assumed that species interactions shape the  
64 community's functioning within the physico-chemical boundary conditions of the system or the  
65 host<sup>11-13</sup>. However, given their complexity, species interactions within microbiota are challenging  
66 to dissect. Improved methodologies to infer interactions from community species  
67 characterization<sup>11</sup>, studies on simplified synthetic communities<sup>14,15</sup> and mathematical  
68 modeling<sup>11,16-18</sup> have helped to advance the understanding of community functioning<sup>6,19-22</sup>, but  
69 methods and studies that target complex and highly diverse systems are currently lacking<sup>21</sup>.

70

71 Frequent approaches to study microbial species interactions consist of coculturing two or three  
72 (labeled) species in spatially structured range-expansion experiments<sup>23,24</sup>, or inferring positive or  
73 negative interactions from species abundance fluctuations in defined well-mixed communities and  
74 conditions during prolonged culturing<sup>15,25</sup>. Our aim here was to develop a complementary approach  
75 that can assess species interactions from growth of randomly mixed cell pairs in small ( $\varnothing$ 40–70  
76  $\mu\text{m}$ ) beads, as it had been suggested that pair-wise interactions are a reasonable predictor for  
77 interactions in higher order communities<sup>15,26</sup>. In particular, we aimed to study and infer the  
78 behaviour of pure cultures that can be used as inoculants to, for example, rationally manage,  
79 restore or complement existing communities with damaged functionalities (e.g., gut microbiome of  
80 diseased individuals, contaminated soils)<sup>4,13,19,27</sup>. Inoculants are typically selected for particular  
81 functional characteristics that are decisive for the intended complementation (e.g., expression of a  
82 xenometabolic pathway, expression of secondary metabolites for plant growth protection)<sup>13</sup>. On  
83 the other hand, there is only a limited knowledge base that could be used to predict survival and  
84 success of exogenously added strains within the target community, which may depend on the  
85 many interactions that the inoculant displays *vis-à-vis* the resident species members or vice-versa.  
86 Recent experimental studies have tried to infer inoculant behaviour by capturing genome-wide  
87 gene expression in complex environments like soil, but the number of detected differentially

88 regulated functions has been too daunting to delineate simple complementation characteristics<sup>28</sup>  
89 <sup>30</sup>. Our initial assumptions were thus that favorable inoculants may be differentiated by the  
90 magnitude of positive interactions with resident bacteria, but only on the type of substrate or  
91 condition they are functionally intended for.

92

93 To test this idea experimentally, we designed a methodology to randomly pair-wise encapsulate  
94 microbial cells within agarose beads, which are incubated in the presence of different growth  
95 substrates (Fig. 1, Table 1). Pair-wise productivity is then quantified from microcolony size  
96 estimations over time using microscopy imaging. As a test resident microbiota, we extracted and  
97 dispersed microbial cells from a sandy soil (*sand community* or SC). We then sought to  
98 encapsulate pairs of individuals into beads in the absence or presence of different inoculants  
99 (Table 1), with encapsulated inoculants serving as separate controls. Four inoculants were  
100 examined depending on their capacity to complement a xenometabolic pathway or because of  
101 their assumed competitive character. Xenometabolism was tested with *Pseudomonas veronii*  
102 1YdBTEX2 (Pve)<sup>30-32</sup> and with *Pseudomonas putida* F1 (Ppu)<sup>33</sup>, both capable of growing on  
103 toluene. We further tested *Pseudomonas protegens* CHA0 (Ppr), a plant growth promoting soil  
104 bacterium but which does not degrade toluene<sup>34</sup>, and *Escherichia coli* MG1655 (Eco), a non-native  
105 soil bacterium. In line with theory of microbial social interactions<sup>35,36</sup>, we expected that interactions  
106 between the many genotypes of soil bacteria would be dominated by competition (here: negative  
107 growth). Further, we expected that the inoculants Pve and Ppu would promote the growth of soil  
108 bacteria, but only in the presence of toluene. Namely, because toluene can have growth-inhibiting  
109 effects<sup>37</sup>, the consumption of toluene by Pve and Ppu should alleviate inhibition to soil cells and  
110 stimulate their growth. We assumed that the inoculant Ppr, on the basis of its capacity to produce  
111 antimicrobial secondary metabolites<sup>38</sup>, would yield on average less positive interactions, whereas  
112 Eco would be largely outcompeted in pair-wise growth with SC–cells. Surprisingly, however, all  
113 inoculants increased the productivity of sand-extracted bacteria and on any substrate, but only in  
114 close proximity interactions (i.e., within beads). Also close-proximity (within bead) presence of two  
115 or three SC–cells was on average positive on growth of either partner. In contrast, very little  
116 evidence for additive effects on productivity from inoculant addition was observed. Although

117 demonstrated here for soil, our method is widely applicable for studying pair-wise growth  
118 interactions in any microbial community.

119

## 120 RESULTS

### 121 **Encapsulation and growth measurements of randomized pair-wise strain combinations.**

122 To develop a system to infer potential species interactions in a complex microbial community we  
123 studied randomized pair-wise growth of dispersed community-derived cells, without or with  
124 intermixed specific bacterial inoculants, and on a variety of externally added substrates (Fig. 1,  
125 Table 1). We chose agarose microbeads as containers to impose long-term close spatial proximity  
126 (<70  $\mu$ m) of the starting cells, assuming that if their interaction would be positive, the cells would  
127 divide and form detectable microcolonies, whereas if it would be negative, one or both of the starter  
128 cells would not or poorly divide. Long distance interactions (i.e., between beads) may also occur,  
129 as agarose beads are permissive for diffusion of small molecules (e.g, substrates, metabolic  
130 intermediates), but we expect their influence to be minor given the dilution in the experimental  
131 setup. Growth of cells over time was inferred from the changes in biovolume of the microcolonies  
132 within individual beads, estimated from the fluorescence area taken up by SYTO9-stained cells  
133 times their mean fluorescence intensity (to account for multiple cell layers). Inoculants were  
134 differentiated specifically from resident community species by genetic labeling with a constitutively-  
135 expressed mCherry fluorescence protein (Fig. 1). As the starting composition of cells in the beads  
136 was Poisson random (aiming at 1–2 cells per bead), the image-analyzed bead mixtures contained  
137 both single, double or higher numbers of microcolonies, of SC–cells alone or in combination with  
138 one of the inoculants (Fig. 1).

139

140 We tested four different inoculants (*P. veronii* [Pve], *P. protegens* [Ppr], *P. putida* [Ppu] and *E. coli*  
141 [Eco]) and four different carbon substrate regimes (succinate, toluene, a mixture of 16 C-  
142 substrates, and a ‘sand extract’; although not in all combinations, Table 1). When grown alone, all  
143 the inoculants were able to divide and form colonies inside agarose beads, given that cell  
144 microcolony sizes increased over time of the incubation in the different deployed growth media  
145 (Fig. 2, Fig. S1). The size of Pve and Eco cells at time of inoculation in the beads was slightly

146 larger than that of Ppr and Ppu and that of a (typical) SC-cell after extraction from soil (Fig. S1).  
147 To estimate the maximum number of cell divisions, we compared the maximum microcolony area  
148 range after 24–72 h of growth for the inoculant compared to that at time of inoculation (Fig. 2).  
149 Assuming a round microcolony with densely packed cells, the observed increase of 50–100-fold  
150 would correspond to maximum cell numbers of approximately 450–1000 from a single starting Pve  
151 or Ppr cell (~9–10 generations). Importantly, our method thus enabled us to isolate ecological  
152 processes (i.e., species interactions) from evolutionary processes that occur over longer time-  
153 scales, such as the appearance of genetic changes that could modulate growth properties.  
154 Microcolonies from encapsulated cells from the sand community also increased in size over time  
155 (Fig. 2, SC), confirming their growth, albeit to a smaller extent than for the inoculants. If we assume  
156 the decrease in the proportion of the smallest microcolony area compared to time=0 as being  
157 indicative for the proportion of SC-cells capable of dividing in the respective medium, we estimated  
158 some 20 % of SC-cells to divide within 6–24 h (Table S1, depending on the substrate). Microcolony  
159 size distributions in the coculture incubations (e.g., inoculant plus SC) were on first sight a  
160 combination of that of inoculant and SC incubated separately, with characteristic ‘peaks’ appearing  
161 during incubation, attributable to, e.g., Pve or Ppr (Fig. 2A, B), suggesting inoculant cells to grow  
162 in coculture with SC.

163

#### 164 **Aggregate productivity in the presence or absence of inoculant.**

165 In order to compare the total productivities across the various incubations as aggregate properties  
166 of all beads, but considering that the assays had varying amounts of beads, we normalized the  
167 observed biomass growth (as particle area times fluorescence intensity) on a per-bead basis for  
168 each experiment. As an example, Figure 3 summarizes per-bead productivities of incubations of  
169 SC-cells without or with the inoculant Pve on different carbon substrates. The normalized per-  
170 bead productivity of Pve (Fig. 3, magenta bars) surpassed that of SC-cells (Fig. 3, cyan bars) on  
171 all four carbon substrates ( $p<0.001$ , ANOVA followed by post-hoc Tukey test). The type of  
172 substrate affected the observed productivities, but since the total amount of C in the case of ‘sand  
173 extract’ and toluene may be different than for mixed-C or succinate (both at 0.1 mM C), we cannot  
174 test for this significance.

175 Although different in individual experiments and at singular time points (e.g., Fig. 3), the maximum  
176 normalized per-bead productivity at any time point of the coculture incubations (Pve+SC) on any  
177 of the substrates was statistically significantly smaller from that of Pve alone, across multiple  
178 independently repeated experiments (Fig. S2,  $p=0.04614$ , Wilcoxon rank sum test on medians).  
179 This suggests that growth of Pve–cells at system’s level (i.e., the incubation vial) is negatively  
180 influenced by the presence of SC–cells, resulting in a smaller yield of the inoculant. Across all  
181 incubations, the maximum per-bead productivity of the SC incubations was less than either Pve or  
182 Pve+SC (Fig. S2,  $p<0.001$ , ANOVA followed by post-hoc Tukey test). Importantly, the difference  
183 in mean per-bead productivity between Pve and Pve+SC was statistically the same as the  
184 productivity of SC alone ( $p=0.7244$ , Wilcoxon rank sum test). This suggests there were on average  
185 no additive effects and total productivity was determined by the total available carbon substrate.  
186 The per-bead productivity increased statistically significantly in two out of five Pve+SC cocultures  
187 compared to Pve alone, in case of the mixed-C substrates (Fig. 3A, Fig. S2,  $p=6.84\times10^{-5}$  and  
188  $p=0.0055$  in paired t-test). For those particular incubations, one might conclude that the growth  
189 interactions between partners at system’s level had been positive and additive (i.e., yielding higher  
190 biomass than either achieved in separation). The reason for this may be that the sand community  
191 was extracted freshly at each occasion and assay from samples taken at the natural location, and  
192 may have constituted a slightly different starting species composition.

193

#### 194 **Inoculant- and substrate-dependent system productivity**

195 The normalized per-bead productivity averaged across the assay as a whole did not illustrate  
196 specifically the types (e.g., positive or negative) or extent of interactions between inoculant and  
197 SC–cells occurring inside the same beads. The reason is that the encapsulation process is random  
198 and Poisson-distributed. Therefore, even though the inoculant (e.g., Pve) is mixed with SC–cells  
199 in the agarose, they do not necessarily end up within the same bead (as schematically illustrated  
200 in Fig. 1B). To get a better picture on the average interactions when inoculant and SC–cells grow  
201 inside the same bead, we discriminated in the coculture (e.g., Pve plus SC) for beads that carried  
202 (by chance) only Pve colonies, for only SC colonies, and for those that carried both Pve and SC  
203 colonies. Their mean productivity was subsequently compared to incubations on the same carbon

204 substrate(s) with Pve or SC–cells separately. On mixed-C substrates this indicated, for example,  
205 that Pve incubated separately without SC (Fig. 4A, mixed carbon, dark green bars) had a far  
206 greater productivity than either Pve alone in beads but combined with SC–cells in the same flask  
207 (Fig. 4A, green bars), or Pve within the same beads as SC–cells (orange bars, ANOVA with post-  
208 hoc Tukey test,  $p<0.0001$ ). However, the latter two did not have statistically significantly different  
209 productivity. In contrast, SC–cells in the same experiment had a far greater productivity when they  
210 found themselves within the same beads as Pve ( $p<0.005$ , ANOVA with post-hoc Tukey test, Fig.  
211 4B, mixed carbon). This explains the average loss of Pve productivity in the same beads, but it is  
212 curious that both beads with Pve or SC alone that occur in the mixed Pve+SC incubation did not  
213 profit from a significant increase in productivity. A similar situation occurred on sand extract as  
214 carbon regime (Fig. 4). Pve incubated separately on sand extract had a higher per-bead  
215 productivity than in combination with SC–cells ( $p<0.005$ , Fig. 4A), but in this case Pve–cells that  
216 happened to be co-encapsulated with SC–cells within the same beads on average fared better  
217 than Pve–cells that occurred alone in beads in the mixed incubation (Fig. 4A, SAND EXTRACT,  
218  $p<0.05$ ). SC–cells again showed the highest per-bead productivity when they found themselves  
219 with Pve inside the same bead ( $p<0.005$ ), but only slightly significantly lower when they occurred  
220 alone inside the combined incubation (Pve + SC,  $p<0.05$ , ANOVA followed by post-hoc Tukey test,  
221 Fig. 4B). This suggests that under those conditions, SC– and Pve–cells on average interacted  
222 positively within the close range of the same bead, which increased productivity. In the extreme  
223 case of toluene as substrate, which only Pve and Ppu can metabolize, the Pve per-bead  
224 productivity declined both in the mixture with SC and even more inside the same beads as SC  
225 (Fig. 4A, TOLUENE,  $p<0.001$ ), suggesting that part of the toluene metabolites produced by Pve  
226 were being lost and utilized by SC–cells. On the other hand, the mean SC productivity under those  
227 conditions was very small and not significantly different for SC–cells within the same beads as Pve  
228 (Fig. 4B, ANOVA followed by post-hoc Tukey test).

229

230 To place these observations with Pve as inoculant in perspective, we repeated experiments on  
231 mixed-C substrates with Ppr (as an assumed competitive soil bacterium) and with Eco (as atypical  
232 soil bacterium), and on toluene with Ppu (as another toluene degrading bacterium). In contrast to

233 Pve, Ppr displayed the same mean per-bead productivity whether incubated alone or finding itself  
234 alone inside agarose beads in the mixture with SC (Fig. 4A, Ppr, ANOVA followed by post-hoc  
235 Tukey test). Also the mean productivity of SC–cells was not statistically significantly different  
236 among beads with a direct Ppr partner, or alone in incubation (Fig. 4B, ANOVA). Eco productivity  
237 on mixed-C substrates was clearly lower than that of Ppr or Pve, and was lower in combination  
238 with SC–cells, irrespective of being inside the same beads or alone in beads in the mixture (Fig.  
239 4A, Eco,  $p<0.001$ ). In contrast to Pve, the mean productivity of SC–cells did not significantly  
240 increase in combinations with Eco (Fig. 4B, Eco). In comparison to Pve on toluene, Ppu took  
241 slightly longer to develop the same mean productivity and Ppu–cells incubated with SC were less  
242 productive (Fig. 4, TOLUENE,  $p<0.005$   $t=72$  h, ANOVA followed by post-hoc Tukey). In contrast,  
243 SC–cells in the same beads with Ppu hardly increased their productivity than in its absence (Fig.  
244 4B, TOLUENE,  $p<0.05$ ,  $t=24$  h, ANOVA). In terms of aggregate productivity these results  
245 suggested, therefore, that SC–cells develop better with Pve than with the other inoculants,  
246 irrespective of the growth substrate (Fig. 4B).

247

#### 248 **Pair-wise growth analysis suggests widespread positive effects of inoculants**

249 Even though, in some cases the mean per-bead productivity of SC–cells increased in presence of  
250 inoculant cells within the same bead (e.g., Fig. 4), the process of averaging masked the types and  
251 extent of individual pair-wise interactions. Next, therefore, we analysed solely those beads having  
252 at least one inoculant and at least one SC microcolony. We scored the individual microcolony sizes  
253 of both partners, as well as those observed in individual beads of either SC– or inoculant cells  
254 incubated separately (Fig. 5). As example, in the case of toluene as substrate, SC–cells alone on  
255 average developed very poorly (as displayed in Figs 3 and 4), but those SC–cells being within  
256 beads with Pve developed much more strongly. Now, whereas the mean per-bead normalized  
257 productivities were not statistically significantly different for SC growth in presence or absence of  
258 Pve (e.g., Fig. 4B, sand cells, TOLUENE), individual bead analysis indicated that 42.6% of all  
259 beads with Pve partners at any time point led to SC growth above the 95th percentile of SC alone  
260 (Fig. 5A, Table 2,  $p=1.80\times 10^{-5}$ ), which corresponds to a 100-fold increased productivity of SC (Fig.  
261 S3). In contrast, the productivity of those Pve–cells in beads together with SC–cells decreased by

262 100-fold, and in no single case Pve–cells profited from SC–cells in their productivity compared to  
263 the 95<sup>th</sup> percentile of its growth alone (Fig. 5A, Table 2,  $p=5.4\times10^{-5}$ ). The distribution of summed  
264 productivities of SC+Pve among those beads in which SC-cells largely profited (>95<sup>th</sup> percentile)  
265 was statistically significantly different from that of Pve cell productivities incubated on toluene  
266 separately (Fig. S4,  $p=0.005$  Fisher's exact test for productivity distributions). This suggests that  
267 the productivity of SC+Pve incubations on toluene did not surpass that of Pve alone.  
268 In the incubation with mixed-C substrates the general productivity by SC–cells was much higher  
269 than on toluene, but compared to the 95<sup>th</sup> percentile at 24 h a further significant increase was  
270 observed for 46.6% of the beads with Pve partnerships at any time point (Fig. 5B, Table 2,  
271  $p=1.21\times10^{-12}$ ). This indicated that despite containing a mixture of very general carbon substrates,  
272 half of the SC–cells at start still profited from being in the same bead with a Pve inoculant cell.  
273 Interestingly, on mixed–C substrates we also observed a small percentage of beads where both  
274 SC and Pve profited of being together (Fig. 5B). With sand extract as substrate, SC–cells on  
275 average had the highest productivity, but in coculture still 44.5% of beads profited from partnering  
276 with Pve (i.e., >95<sup>th</sup> percentile of SC–cells incubated separately, Table 2,  $p=9.9\times10^{-13}$ ), and with  
277 0.4% of beads where both partners profited (Fig. S5, Table 2). For this subclass of SC+Pve beads  
278 (with SC>95<sup>th</sup> percentile) the distribution of summed productivities was shifted to higher values  
279 than that of Pve alone (Fig. S4,  $p=0.0005$  in Fisher's exact test).  
280 In case of Ppr as inoculant and with mixed–C substrates, SC profited even more (80.1% of beads  
281 with increased growth, and 0.5% with increased growth of both SC and Ppr; Fig. S5, Table 2,  
282  $p=1.2\times10^{-12}$ ), but without significantly increased productivity of this subset of cocultured beads  
283 compared to Ppr growing on mixed-C alone (Fig. S4,  $p=0.0645$ ). Eco as inoculant with mixed–C  
284 substrates yielded similar proportional benefits to SC–cells as Pve, i.e., 48.4% (Fig. S5, Table 2,  
285  $p=4.3\times10^{-5}$ ). A further small 0.8% proportion of beads occurred in which both SC and Eco had  
286 profited (Table 2), and, interestingly, the distribution of summed productivities for SC+Eco  
287 partnering beads was significantly different from that of Eco alone, suggesting that the inoculant  
288 profited to some extent from being with SC–cells (Fig. S4,  $p=0.0005$  in Fisher's exact test). Ppu as  
289 inoculant was profitable to partner SC–cells on toluene in 27.2% of beads (Fig. S5, Table 2,  
290  $p=1.8\times10^{-5}$ ). The distribution of summed productivities for Ppu+SC pairs was statistically

291 significantly shifted to lower values than that of Pve+SC pairs (Fig. S4,  $p=0.0005$  Fisher's exact  
292 test), suggesting SC–cells profit less from Ppu than from Pve as inoculant on toluene.

293

294 In order to infer the magnitude of potential negative interactions, we estimated the loss in  
295 productivity of the inoculant in pairs with SC–starting cells, and the percentage of inoculant–SC  
296 pairs under the different conditions where one of the partners did not grow at all (Table 2). In  
297 comparison to the inoculant incubations alone, all inoculants significantly lost productivity when in  
298 the same bead with SC–cells (Table 2,  $p$ -values between  $10^{-5}$  and  $10^{-17}$  for the decrease of  
299 boosted average inoculant microcolony sizes). In comparison to either partner alone on the same  
300 substrate, in case of general substrates a lower percentage of SC–cells (2.3–8.2%) did not seem  
301 to grow at all in partnership (i.e., particle area  $\times$  intensity at 24, 48 or 72 h  $< 10^{\text{th}}$  percentile at  $T=0$ ,  
302 Table 2,  $p=0.0103$ – $0.0332$ ), and in less than 0.1% of all pair-wise combinations no growth of either  
303 partner occurred. Notable exceptions were for growth on toluene, where the percentage of non-  
304 growing SC–cells with Ppu increased to 22.7% and with Pve to 11.9% (Table 2,  $p=0.0904$ ,  
305  $p=0.0079$ , respectively). In contrast, in three cases the percentage of non-growing inoculant  
306 slightly increased in combination with SC–cells to between 4.3–11.9% (Table 2,  $p=0.0021$ –  
307  $0.0258$ ). This suggested that maximally some 10% of pair-wise interactions might be inhibitory on  
308 one of the partners.

309

### 310 **Interactions between sand cell partners are positive for productivity**

311 Finally, the bead interactomes also contained numerous cases of only SC–SC partnership beads  
312 that randomly contained two or more starting SC–cells (without any inoculant). When pooling all  
313 such beads of SC–SC partnerships from the experiments conducted either in mixed–C or sand-  
314 extract as growth substrates, and ordering the biggest partner on the x– and the smaller partner  
315 on the y–axis, we could see that around two-thirds of SC-SC partnerships are dominated by one  
316 big and one small microcolony (i.e., more than two-fold size difference). In about one-third of cases,  
317 both SC microcolonies inside single beads are less than two-fold different (Fig. 6A, B). No effect  
318 of the distance between both SC-microcolonies on their mutual size was discernable (Fig. 6C,  
319  $r^2=0.00032$ ), which might have been intuitively expected. In contrast, for SC–cells in pairs within

320 the same bead (without inoculant), and across both substrates, there was an overall strong  
321 overproportional increase (i.e., more than twice) of per-bead productivity compared to that of  
322 single SC-microcolonies (Fig. 6D,  $p<0.05$  for  $t=24$  h,  $p<0.005$  for  $t=48$  or 72 h). There was no  
323 further additive effect when beads contained, by chance, more than two SC-microcolonies (Fig.  
324 6D, yellow box-plot data,  $p=0.3229$ – $0.7611$ ). This suggests that, even though in the majority of  
325 cases, paired SC-cells grow to unbalanced microcolony sizes (i.e., more than twofold different),  
326 their interactions are on average positive for their collective productivity.

327

## 328 **DISCUSSION**

329 We developed a method to measure growth interactions from complex mixtures of microbial cells  
330 randomly encapsulated inside individual agarose beads. We tested our method on resident  
331 microbes washed from a sand-microbiota system, and incubated in absence or presence of  
332 specific inoculant bacteria, in order to compare whether inoculants may be positive for growth of  
333 the resident community. Our method permitted to follow pair-wise growth in hundreds of beads  
334 simultaneously that can be averaged to assess mean normalized bead productivity changes as a  
335 function of carbon substrate(s) (e.g., Fig. 3) or inoculant type (Fig. 4). The method further provides  
336 estimates of the proportions of positive and negative growth interactions within the resident  
337 community members itself, or in presence of inoculant (e.g., Fig. 5 and 6, Table 2).

338 Most strikingly, the sand community as a whole (Fig. 4B) and a substantial subset of SC-cells in  
339 particular (27–80%, depending on inoculant and substrate, Fig. 5, Fig. S5, Table 2), increased  
340 productivity in presence of the inoculant, but only in case of close proximity of growing within the  
341 same bead. In contrast, productivity of all inoculants under all conditions declined in pair-wise  
342 growth with SC-cells in close proximity (i.e., being within the same bead, Fig. 5, Table 2), but  
343 mostly also at larger distance (i.e., inoculant alone in a bead, but in the same mixture with  
344 encapsulated SC-cells, Fig. 4). On average, in some 10% of the inoculant–SC pairs one of the  
345 partners did not develop (Table 2), suggesting clear negative (inhibitory) interactions. Finally, these  
346 effects occurred almost irrespectively of the type of inoculant, although some inoculants (notably  
347 Ppr) yielded extremely positive effects on SC-cells (80% above the 95<sup>th</sup> percentile of SC growth  
348 alone). Mostly, the summed productivities of beads with partnering inoculant and SC-cells did not

349 surpass that of inoculants on the same substrate alone (Fig. S4). From these results we thus  
350 conclude that the used inoculants were in close proximity interactions beneficial for the productivity  
351 of dispersed resident cells from the sandy soil.

352  
353 Our results suggest that the majority of interactions between inoculants and SC–cells in close  
354 proximity are highly imbalanced, with SC–cells increasing their mean productivity by a factor of  
355 100 and inoculants losing productivity by a factor of 100 (Fig. 5, Fig. S3). These imbalanced  
356 interactions are neutral with respect to total productivity (i.e., distribution of summed SC+inoculant  
357 bead productivities does not surpass that of inoculant alone, Fig. S4), but the SC–cells are largely  
358 dependent on the inoculants, since without their presence the SC productivity is very low. This  
359 suggests that it is not so much competition for growth substrate per se that dominates these  
360 interactions, but either specific growth factors (e.g., amino acids) or metabolic intermediates (e.g.,  
361 acetate) produced by the inoculants that favor excessive growth of a large proportion of SC–cells.  
362 Instead of competition (both partners suffer), therefore, this type of interactions might be defined  
363 as competitive exploitation (rather than parasitism<sup>11</sup>). In a small proportion of cases (~0.5%, at  
364 >95<sup>th</sup> percentile of individual growth, Table 2), and pronounced on sand extract as substrate (Fig.  
365 S4), we found evidence for additive effects on productivity of both inoculant and SC–cells. If one  
366 would consider the additive case as being representative for cooperative behaviour, it would  
367 confirm the theory that only a minority of social interactions in communities is cooperative<sup>36</sup>.  
368 However, results from beads of co-occurring SC–SC pairs within the same experiment (Fig. 6)  
369 suggest that also among the sand community itself, it is largely profitable for productivity to be with  
370 partners (although this productivity increase does not rival the increase obtained from being paired  
371 with any of the inoculants). This result is therefore a strong indication that partnerships within close  
372 distance in complex communities are favorable for increased productivity, perhaps as a result of  
373 metabolite exchange in general or metabolites favoring growth of auxotrophs<sup>39,40</sup>. The inferred  
374 behaviour of SC–inoculant partnerships (i.e., competitive exploitation) may thus not be  
375 representative for the majority of interactions within complex carbon-limited communities as in soil  
376 that show higher-than-additive productivities (i.e., mutualistic interactions) in pair-wise random  
377 incubations in close proximity (Fig. 6D).

378

379 One of our initial assumptions was that inoculants would specifically favor SC productivity in the  
380 case of xenometabolic complementation (here: toluene) and less so for general available  
381 substrates. SC productivity was overall impaired on toluene in comparison to other substrates (Fig.  
382 4B). Although we did find a strong positive effect of the two toluene-degrading inoculants Pve and  
383 Ppu on SC growth in pair-wise analysis (Fig. 5A), this was not very well visible in the mean bead  
384 productivities (Fig. 4B), and the proportion of non-growing SC-cells even slightly increased (Table  
385 2), suggesting that the beneficial effects may be limited as a result of the nature of the specific  
386 metabolites which are leaking from toluene-metabolizing cells (e.g., catechols). To our surprise,  
387 however, the inoculants were also extremely beneficial for SC-productivity on the other types of  
388 carbon substrates (Fig. 5B, Fig. S5, Table 2). Even more surprising was that Ppr, considered to  
389 be a strong competitor<sup>34</sup>, actually provided the largest measured benefit on SC-cells, with 80% of  
390 observed pair-wise SC+Ppr interactions having SC productivities above the 95<sup>th</sup> percentile of SC  
391 growth alone (Table 2). The major benefit of all inoculants on the sand community could thus be  
392 their capacity to provide growth factors or direct central metabolites from the primary carbon  
393 substrates to community members, which is reminiscent of the types of carbon sharing reported  
394 in simplified communities<sup>41</sup>. When assuming that the proportion of beneficial pair-wise interactions  
395 on SC cells (>95<sup>th</sup> percentile of its own incubation) is an indication for the potential ‘hub’ of  
396 interactions in a community network<sup>5,42</sup>, one might consider that a species like Ppr is a strong  
397 potential keystone member for a soil community (in case it is sufficiently abundant).

398

399 Productivity measurements to assess strain-strain interactions have typically been based on cell  
400 density changes in suspended growth<sup>15,25</sup>, on species abundance fluctuations in natural-derived  
401 communities<sup>41</sup>, or on expansion-range experiments from droplet cocultures placed on agar  
402 plates<sup>23,24</sup>. Both of these cannot readily be parallelized for multiple strain-strain interactions. The  
403 agarose bead containers deployed in our experiments supported microcolony growth at the  
404 expense of diffusing carbon and nutrients from the medium, and allowed simultaneous growth  
405 monitoring of hundreds of pairs. Pair-wise growth interactions were shown to be reasonably good  
406 predictors for septet and octet artificial communities<sup>15</sup>, and thus, an upscaling of observable pair-

407 wise interactions as demonstrated here, may help to extrapolate functional behaviour in more  
408 complex communities. Our method is widely amenable to different starting communities, given the  
409 ease of bead encapsulation. The methodology can be adapted by limiting long-distance  
410 interactions as a result of nutrient- and metabolite exchange to the medium, through the use of  
411 bead-in-oil emulsions or other type of bead variations. The method may be further improved by  
412 combining bead growth analysis to either a global analysis of the (changes) in species  
413 compositions of the targeted community in the bead incubations, or to methods that would identify  
414 species pairs on a per-bead basis<sup>43,44</sup>. In conclusion, the randomized pair-wise bead encapsulation  
415 growth methodology is widely applicable to study the collective growth interactions (the  
416 *interactome*) of microbiomes.

417

418

## 419 **Methods**

### 420 **Bacterial strains and pre-culturing procedures**

421 Four strains were selected as inoculants for the soil interactome experiments: *P. veronii*  
422 1YdBTEX2, a toluene, benzene, *m*- and *p*-xylene degrading bacterium isolated from contaminated  
423 soil<sup>31</sup>; *P. putida* F1, a benzene-, ethylbenzene- and toluene-degrading bacterium from a polluted  
424 creek<sup>33</sup>; *P. protegens* CHA0, a bacterium with plant-promoting character as a result of secondary  
425 metabolite production<sup>34</sup>; and *E. coli* MG1655<sup>45</sup>, as a typical non-soil dwelling bacterium. Variants  
426 of the four strains were deployed that constitutively express mCherry fluorescent protein.

427

428 *P. veronii* 1YdBTEX2 was tagged with a single-copy chromosomally inserted mini-Tn7 transposon  
429 carrying a  $P_{\text{tac}}-m\text{Cherry}$  cassette (Pve, strain 3433) as described in Ref<sup>46</sup>. *P. putida* F1 was tagged  
430 with the same cassette but using mini-Tn5 chromosomal delivery (Ppu, strain 5791). *P. protegens*  
431 CHA0 mini-Tn7: $P_{\text{tac}}-m\text{Cherry}$  (Ppr, strain 6434) has been described previously<sup>47</sup> and was kindly  
432 provided by Christoph Keel. mCherry expression in *E. coli* MG1655 was achieved from the same  
433  $P_{\text{tac}}-m\text{Cherry}$  present on plasmid pME6012<sup>48</sup> (Eco, strain 4514). All strains were kept at -80°C for  
434 long term storage and plated freshly for each experiment on nutrient agar (Oxoid Ltd.) containing

435 the appropriate antibiotic for selection of the  $P_{tac}$ -*mCherry* construct, from where individual colonies  
436 were transferred to liquid cultures.

437

438 Pve and Ppu colonies from nutrient agar were restreaked on 21C minimal media (MM)<sup>49</sup> agar with  
439 toluene as sole carbon source provided through the vapour phase in a desiccator as described  
440 elsewhere<sup>30</sup>. A single colony of each after 48 h incubation at 30 °C was subsequently inoculated  
441 into 10 ml of liquid MM containing 5 mM sodium succinate as sole carbon source. Ppr and Eco  
442 colonies from selective nutrient agar plates were directly transferred to liquid MM with 5 mM  
443 succinate. Pve, Ppu and Ppr cultures were grown for 24 h at 30°C with rotary shaking at 180 rpm.  
444 Eco cultures were incubated at 37°C for 24 h with rotary shaking at 180 rpm. After 24 h, the cells  
445 were harvested and washed for bead encapsulation, as described below.

446

#### 447 **Soil resident microbes**

448 We chose sand as the source of the microbial community (which was hereafter named *soil*  
449 *community* or SC). The sand was collected fresh for each experiment from a beach of St. Sulpice  
450 near Lake Geneva (GPS coordinates: 46.508032 N, 6.544050 E) as described in Moreno et al<sup>29</sup>.  
451 Of note is that the sand was taken at different seasons and sampling times and may thus have  
452 carried slightly different starting communities and cell densities. The sand was sieved through 2  
453 mm<sup>2</sup> pores to remove large particles. The sieved sand was stored at room temperature and used  
454 within 7 days for extraction of resident microbial cells.

455

456 Microbial cells were extracted from four times 200 g of sand, each aliquot transferred in a 1 litre  
457 conical flask. Each 200 g of sand was submerged in 400 ml of 21C minimal media salts (MMS)  
458 (containing, per litre: 1 g NH<sub>4</sub>Cl, 3.49 g Na<sub>2</sub>HPO<sub>4</sub>·2H<sub>2</sub>O, 2.77 g KH<sub>2</sub>PO<sub>4</sub>, pH 6.8). Flasks were  
459 incubated at 25°C under rotary shaking at 120 rpm for one hour. The sand was allowed to settle  
460 and the supernatant was decanted into a set of 50 ml Falcon tubes, which were centrifuged at 800  
461 rpm in an A-4-81 rotor in a 5810R centrifuge (Eppendorf AG.) for 10 min to precipitate heavy soil  
462 particles. Supernatants were decanted into clean 50 ml Falcon tubes and centrifuged at 4000 rpm  
463 for 30 minutes to pellet cells. The supernatants were carefully discarded, and the cell pellets were

464 resuspended and pooled (i.e., from the initial 800 g of sand) in one tube using 5 ml of MMS. The  
465 pooled liquid suspension was further sieved through a 40- $\mu$ m Falcon cell strainer (Corning Inc.) in  
466 order to remove any particles and large eukaryotic cells that may obstruct flow cytometry analysis  
467 (see below). A small proportion of the sieved liquid suspension was used for quantification of the  
468 extracted cell numbers (see below); the remainder was used within 12 h for bead encapsulation  
469 (see below). With this gentle method we extracted approximately  $3 \times 10^5$  cells g of sand $^{-1}$ .

470

#### 471 **Flow cytometry cell counting**

472 Cell numbers in suspensions of inoculants and extracted soil communities were counted by flow  
473 cytometry. Liquid cultures of the inoculant (10 ml) were centrifuged at 5000 rpm in a F-34-6-38  
474 rotor in a 5804R centrifuge (Eppendorf AG) for 10 min at room temperature. The supernatant was  
475 discarded and the cell pellet was resuspended in 10 ml of MMS. The suspension was again  
476 centrifuged as before, supernatant was discarded and cells were resuspended in 10 ml of MMS.  
477 The inoculant suspension was then diluted 100 times in MMS and aspirated at 66  $\mu$ l min $^{-1}$  on a  
478 Novocyte flow cytometer (ACEA Biosciences, USA). Inoculant cells were identified on the basis of  
479 their PE-Texas Red-H signal (channel voltage set at 592 V) representative for the mCherry  
480 fluorescence. An aliquot of the pooled SC cell suspension was diluted 100 times in MMS, and cells  
481 were stained by addition of SYTO-9 (1  $\mu$ M final concentration), and incubation in the dark at room  
482 temperature for one hour. An aliquot of 30  $\mu$ l was aspirated on the flow cytometer and cells were  
483 counted above the FSC-H threshold of 500 and identified on the basis of their FITC-H signal  
484 (channel voltage at 441 V).

485

#### 486 **Agarose bead encapsulation**

487 Quantified inoculant and SC cells were mixed in 1:1 ratio in a 1 ml microcentrifuge tube, such that  
488 both contained approximately between  $2 \times 10^7$  and  $10^8$  cells ml $^{-1}$ . As controls, batches of the  
489 inoculant-only or SC-only suspensions were used, each again between  $2 \times 10^7$  to  $10^8$  cells ml $^{-1}$ .

490

491 To prepare beads in a size range of 40–70  $\mu$ m, we used a procedure of rapid mixing of agarose–  
492 cell solution with pluronic acid in dimethylpolysiloxane and subsequent cooling and sieving. The

493 whole procedure was carried out in a room maintained at 30°C and near a gas flame to maintain  
494 antiseptic conditions. 1% (w/v) low melting agarose (Eurobio ingen, France) was prepared in PBS  
495 solution (PBS contains per L H<sub>2</sub>O: 8 g NaCl, 0.2 g KCl, 1.44 g Na<sub>2</sub>HPO<sub>4</sub>, 0.24 g KH<sub>2</sub>PO<sub>4</sub>, pH 7.4)  
496 and dissolved by heating in a microwave. The molten agarose solution was cooled down, aliquoted  
497 to 1 ml batches in eppendorf vials and equilibrated in a 37°C water bath. Separately, 15 ml of  
498 dimethylpolysiloxane (Sigma-Aldrich) was poured in a 30 ml glass test tube. 1 ml of the 37°C–  
499 agarose solution was mixed with 30 µl of pluronic acid (Sigma-Aldrich) by vortexing at highest  
500 speed (Vortex-Genie 2, Scientific Industries, Inc.) for a minute. Into this mixture of agarose and  
501 pluronic acid, 200 µl of prepared cell suspension at 0.2–1.0 × 10<sup>8</sup> cells ml<sup>−1</sup> (inoculant only, SC  
502 only, or the mix of SC plus inoculant) was pipetted, and vortexed again at highest speed for another  
503 minute. 500 µl of this mixture was added drop-wise into the glass tube with dimethylpolysiloxane  
504 that was being vortexed at maximum speed. Vortexing was continued for two min. The tube was  
505 then immediately plunged into crushed ice and allowed to stand for a minimum of 10 min. After  
506 this, the total content of the tube was transferred into a 50 ml Falcon tube. The tube was centrifuged  
507 for 10 min at 2000 rpm using an A-4-81 swinging-bucket rotor (Eppendorf). The oil was carefully  
508 decanted, retaining the beads pellet. 15 ml of sterile PBS was added to the pellet, and the beads  
509 were resuspended by vortexing at a speed set to 5. The tubes were again centrifuged at 2000 rpm  
510 for 10 min, and any visible oil phase on the top was removed using a pipette. The process was  
511 repeated once more to remove any visible oil phase. Beads of diameter between 40–70 µm were  
512 then recovered by passing the PBS–resuspended bead content of the tube first over a 70–µm cell  
513 strainer (Corning Inc.). A further 5 ml of PBS was added to the cell strainer to flush remaining  
514 beads (<70–µm) into the filtrate. The collected bead filtrate was subsequently passed over a 40–  
515 µm cell strainer (Corning Inc.) to remove beads smaller than 40 µm. Recovered beads on the sieve  
516 were washed with an additional 5 ml of PBS, and any smaller beads in the filtrate that stuck to the  
517 bottom side of the cell strainer were gently removed by absorption with a Whatman 3M filter paper.  
518 After this, the sieve was inverted and placed on top of a clean 50 ml Falcon tube. 1.5 ml of  
519 incubation medium (MM with the respective carbon substrates, see below) was used to collect the  
520 beads from the sieve into the tube. Per interactome mixture, two tubes were prepared in parallel,  
521 which were pooled in the same final Falcon tube to yield a total volume of 3 ml that was split in

522 three aliquots of 1 ml, to have triplicate interactome incubations. The encapsulation procedure  
523 produced  $\sim 1.2 \times 10^6$  beads per ml, with an effective volume of 10% of the total volume of the liquid  
524 phase in the incubations.

525

526 **Bead incubations**

527 Four different carbon regimes were imposed as listed in Table 1. Toluene was used as example  
528 of an inoculant-selective substrate (Pve and Ppu), which we assumed would be poorly utilisable  
529 by the resident soil microbes and give selective benefit to the inoculant. Succinate, mixed carbon  
530 substrates ('Mixed-C'), and sand extract (see below), were used as generally utilisable substrates  
531 for both inoculants and soil microbes. The external substrate concentration was limited to 0.1 mM  
532 (mixed-C) to avoid overgrowth of microcolonies inside the beads, which would lead to cell escape  
533 and their subsequent proliferation outside the beads. Experimental tests at higher succinate  
534 concentrations confirmed that overgrowth, cell escape and outside growth frequently occurred  
535 above 0.5 mM succinate.

536 Toluene was provided by partitioning from an oil phase. We diluted pure toluene 1000 times in  
537 2,2',4,4',6,8,8'-heptamethylnonane (Sigma Aldrich) and added 0.2 ml of this solution to each vial  
538 with 1 ml bead suspension. A further 4 ml of MM was added to the vials.

539 Mixed-C solution was prepared by dissolving 16 individual compounds (Table S2) in milliQ-water  
540 (Siemens Labostar) in equimolar concentration such that the total carbon concentration of the  
541 solution reached 10 mM C. These compounds are also listed in EcoPlates<sup>TM</sup> (Biolog Hayward, CA,  
542 USA) and have been previously used as soil representative substrates<sup>25</sup>. In the bead incubations,  
543 the mixed-C was diluted to 0.1 mM C final concentration in MM (total volume per vial again 5 ml).  
544 Sand extract was prepared by extraction with pre-warmed (70°C) sterile milliQ-water. A quantity  
545 of 100 g sand was mixed with 200 ml milliQ-water in a 250 ml Erlenmeyer flask and swirled on a  
546 rotatory platform for 15 min, after which it was subjected to 10 min sonication in an ultrasonic bath  
547 (Telesonic AG, Switzerland). Sand particles were sedimented and the supernatant was decanted,  
548 and passed through a 0.22– $\mu$ m vacuum filter unit (Corning Inc.). This formed the 'sand extract', of  
549 which 4 ml was added directly to the 1 ml bead suspension in the vials.

550 For incubations with succinate, we added 4 ml of MM with 0.02 mM sodium succinate to each vial.

551 Vials were incubated at 25 °C under rotary shaking at 110 rpm (to prevent too much settling of the  
552 beads), and were sampled for bacterial growth at regular time intervals (start, 6 h, 24 h, 48 h and  
553 72 h).

554

### 555 **Bead sampling and microscopy**

556 For sampling, the vials were removed from the incubator and beads were spun down at 1200 rpm  
557 using a swinging-bucket A-4-81 rotor (Eppendorf). An aliquot of 10 µl of bead suspension was  
558 carefully sampled from the bottom of the vials, mixed with 0.6 µl of 50 µM SYTO-9 solution to stain  
559 all cells, and incubated for 20 min at room temperature in the dark. Vials were placed back into the  
560 incubator. 5 µl sterile milli-Q water was added to the stained beads, and the complete aliquot (15  
561 µl) was spread on a regular microscope glass slide to minimise aggregation of beads. A coverslip  
562 (24 x 50 mm) was placed gently avoiding air bubbles and excessive squeezing of the beads. Ten  
563 random positions on the slide were imaged with the 20× objective (NA 0.35) using an inverted  
564 AF6000 LX epifluorescence microscope system (Leica AG, Germany), equipped with a  
565 DFC350FXR2 camera. Every position was imaged in four sequential channels (phase contrast, 25  
566 ms; mCherry, Y3-cube, 750 ms; SYTO-9, GFP-cube, 50 and 340 ms). The 50 ms-SYTO-9  
567 channel exposure was used for analysis; the 340-ms exposure was used for verification of weak  
568 signals, if necessary. Images were recorded as 16-bit TIF-files and further processed using a  
569 custom MatLab routine (described below).

570

### 571 **Microscopy image analysis**

572 A custom Matlab image processing and analysis routine was developed to segment beads and  
573 microcolonies inside beads from the image-series (Fig. S1), to identify and differentiate inoculant  
574 cell colonies (visible in mCherry and SYTO9) and colonies originating from sand cells (only visible  
575 in SYTO9). The mean fluorescence intensity and area of each identified microcolony type was  
576 quantified, from which the number of microcolonies within beads and their geometric distances  
577 were calculated.

578 For each time-point and experimental replicate, the phase contrast, mCherry, and SYTO-9 images  
579 were read using the *imread* function built in MatLab (version 2016b, MathWorks inc., USA). To

580 identify the beads on each image, sharp changes in intensity were detected in the phase-contrast  
581 images using the *edge* function. Individual beads within a specific radius range were then identified  
582 using the *imfindcircles* function. In the next step, the microcolonies inside each bead were  
583 identified, by thresholding and segmenting the mCherry and SYTO-9 images, exclusively within  
584 the identified bead areas. mCherry and SYTO-9 images were further aligned to identify  
585 microcolonies in SYTO-9 having mCherry signal, which corresponds to the inoculant. Overlapping  
586 signals were considered to originate from an inoculant colony if the area overlap between two  
587 channels was greater than 30%. Else, the areas were considered to consist of both inoculant and  
588 SC cells. All microcolonies were thus differentiated as corresponding to inoculant (mCherry plus  
589 SYTO-9 signal) or SC (SYTO-9 only), after which their area, fluorescence intensity and inter-  
590 particle distance (within the bead) were calculated.

591 Results were summarized for each incubation and time point to comprise the following information:  
592 (i) total number of beads for each of the treatments (SC-cell only, inoculant only, or SC plus  
593 inoculant); (ii) the product of the particle pixel area times its SYTO-9 fluorescence intensity (we  
594 refer to this as productivity); (iii) the number of particles per bead and bead types (i.e., being only  
595 SC, only inoculant, or both); (iv) the summed averaged per-bead productivity of the different  
596 experimental treatments (i.e., type of inoculant, type of carbon substrate, time effect); and (v) the  
597 individual productivities of beads with pairs of SC-inoculant, or SC-SC.

598 The MatLab routines are provided as Supplementary Code.

599

## 600 **Statistical testing**

601 Aggregate productivities in incubations and per category (inoculant, SC or both) or substrate were  
602 compared in ANOVA, with significance testing inferred post hoc according to Tukey. Maximum  
603 aggregate productivities across multiple different substrates (yielding different biomass) were  
604 compared in a non-parametric rank sum Wilcoxon test. Given their non-normal nature, bead  
605 productivity distributions were globally compared non-parametrically with the Fisher test. Further  
606 parametric (t-test and ANOVA) testing on bead productivity distributions was conducted using  
607 boosted averages (>75<sup>th</sup> percentile) and >95<sup>th</sup> percentile sums.

608

609 **ACKNOWLEDGMENTS**

610  
611 This work was supported by SystemsX.ch, and evaluated by the Swiss National Science  
612 Foundation, within grant 2013/158 (Design and Systems Biology of Functional Microbial  
613 Landscapes 'MicroScapesX').

614

615 **REFERENCES**

616

- 617 1. Engel, P., Martinson, V. G. & Moran, N. A. Functional diversity within the simple gut  
618 microbiota of the honey bee. *Proc Natl Acad Sci U S A* **109**, 11002-11007 (2012).
- 619 2. Delgado-Baquerizo, M. *et al.* A global atlas of the dominant bacteria found in soil. *Science*  
620 **359**, 320-325 (2018).
- 621 3. Widder, S. *et al.* Challenges in microbial ecology: building predictive understanding of  
622 community function and dynamics. *ISME J* **10**, 2557-2568 (2016).
- 623 4. Dolinsek, J., Goldschmidt, F. & Johnson, D. R. Synthetic microbial ecology and the dynamic  
624 interplay between microbial genotypes. *FEMS Microbiol Rev* **40**, 961-979 (2016).
- 625 5. Faust, K. & Raes, J. Microbial interactions: from networks to models. *Nat Rev Microbiol* **10**,  
626 538-550 (2012).
- 627 6. Johns, N. I., Blazejewski, T., Gomes, A. L. & Wang, H. H. Principles for designing synthetic  
628 microbial communities. *Curr Opin Microbiol* **31**, 146-153 (2016).
- 629 7. Endt, K. *et al.* The microbiota mediates pathogen clearance from the gut lumen after non-  
630 typhoidal *Salmonella* diarrhea. *PLoS Pathog* **6**, e1001097 (2010).
- 631 8. Karakoc, C., Radchuk, V., Harms, H. & Chatzinotas, A. Interactions between predation and  
632 disturbances shape prey communities. *Sci Rep* **8**, 2968 (2018).
- 633 9. Karakoc, C., Singer, A., Johst, K., Harms, H. & Chatzinotas, A. Transient recovery dynamics  
634 of a predator-prey system under press and pulse disturbances. *BMC Ecol* **17**, 13 (2017).
- 635 10. Gomez, P. & Buckling, A. Bacteria-phage antagonistic coevolution in soil. *Science* **332**, 106-  
636 109 (2011).
- 637 11. Zuniga, C., Zaramela, L. & Zengler, K. Elucidation of complexity and prediction of interactions  
638 in microbial communities. *Microb Biotechnol* **10**, 1500-1522 (2017).
- 639 12. Tecon, R. & Or, D. Biophysical processes supporting the diversity of microbial life in soil.  
640 *FEMS Microbiol Rev* **41**, 599-623 (2017).
- 641 13. Zomorrodi, A. R. & Segre, D. Synthetic ecology of microbes: Mathematical models and  
642 applications. *J Mol Biol* **428**, 837-861 (2016).
- 643 14. Thompson, A. W. *et al.* Robustness of a model microbial community emerges from population  
644 structure among single cells of a clonal population. *Environ Microbiol* **19**, 3059-3069 (2017).
- 645 15. Friedman, J., Higgins, L. M. & Gore, J. Community structure follows simple assembly rules in  
646 microbial microcosms. *Nat Ecol Evol* **1**, 109 (2017).
- 647 16. Song, H. S., Cannon, W. R., Beliaev, A. S. & Konopka, A. Mathematical modeling of microbial  
648 community dynamics: A methodological review. *Processes* **2**, 711-752 (2014).
- 649 17. Magnusdottir, S. *et al.* Generation of genome-scale metabolic reconstructions for 773  
650 members of the human gut microbiota. *Nat Biotechnol* **35**, 81-89 (2017).
- 651 18. Borer, B., Tecon, R. & Or, D. Spatial organization of bacterial populations in response to  
652 oxygen and carbon counter-gradients in pore networks. *Nat Commun* **9**, 769 (2018).
- 653 19. Sheth, R. U., Cabral, V., Chen, S. P. & Wang, H. H. Manipulating bacterial communities by in  
654 situ microbiome engineering. *Trends Genet* **32**, 189-200 (2016).
- 655 20. Stenuit, B. & Agathos, S. N. Deciphering microbial community robustness through synthetic  
656 ecology and molecular systems synecology. *Curr Opin Biotechnol* **33**, 305-317 (2015).
- 657 21. Tecon, R. *et al.* Bridging the holistic-reductionist divide in microbial ecology. *mSystems* **4**  
658 (2019).
- 659 22. Koskella, B., Hall, L. J. & Metcalf, C. J. E. The microbiome beyond the horizon of ecological  
660 and evolutionary theory. *Nat Ecol Evol* **1**, 1606-1615 (2017).

661 23. Goldschmidt, F., Regoes, R. R. & Johnson, D. R. Successive range expansion promotes  
662 diversity and accelerates evolution in spatially structured microbial populations. *ISME J* **11**,  
663 2112-2123 (2017).

664 24. Goldschmidt, F., Regoes, R. R. & Johnson, D. R. Metabolite toxicity slows local diversity loss  
665 during expansion of a microbial cross-feeding community. *ISME J* **12**, 136-144 (2018).

666 25. Celiker, H. & Gore, J. Clustering in community structure across replicate ecosystems  
667 following a long-term bacterial evolution experiment. *Nat Commun* **5**, 4643 (2014).

668 26. Xiao, Y. *et al.* Mapping the ecological networks of microbial communities. *Nat Commun* **8**,  
669 2042 (2017).

670 27. Grosskopf, T. & Soyer, O. S. Synthetic microbial communities. *Curr Opin Microbiol* **18**, 72-77  
671 (2014).

672 28. Roggo, C. *et al.* Genome-wide transposon insertion scanning of environmental survival  
673 functions in the polycyclic aromatic hydrocarbon degrading bacterium *Sphingomonas wittichii*  
674 RW1. *Environ Microbiol* **15**, 2681-2695 (2013).

675 29. Moreno-Forero, S. K. & van der Meer, J. R. Genome-wide analysis of *Sphingomonas wittichii*  
676 RW1 behaviour during inoculation and growth in contaminated sand. *ISME J* **9**, 150-165  
677 (2015).

678 30. Morales, M. *et al.* The genome of the toluene-degrading *Pseudomonas veronii* strain  
679 1YdBTEX2 and its differential gene expression in contaminated sand. *PLoS One* **11**,  
680 e0165850 (2016).

681 31. Junca, H. & Pieper, D. H. Functional gene diversity analysis in BTEX contaminated soils by  
682 means of PCR-SSCP DNA fingerprinting: comparative diversity assessment against bacterial  
683 isolates and PCR-DNA clone libraries. *Environ Microbiol* **6**, 95-110 (2004).

684 32. de Lima-Morales, D. *et al.* Draft genome sequence of *Pseudomonas veronii* strain  
685 1YdBTEX2. *Genome Announc* **1** (2013).

686 33. Zylstra, G. J., McCombie, W. R., Gibson, D. T. & Finette, B. A. Toluene degradation by  
687 *Pseudomonas putida* F1: genetic organization of the  *tod* operon. *Appl Environ Microbiol* **54**,  
688 1498-1503 (1988).

689 34. Jousset, A. *et al.* Full-genome sequence of the plant growth-promoting bacterium  
690 *Pseudomonas protegens* CHA0. *Genome Announc* **2** (2014).

691 35. Mitri, S. & Foster, K. R. The genotypic view of social interactions in microbial communities.  
692 *Annu Rev Genet* **47**, 247-273 (2013).

693 36. Foster, K. R. & Bell, T. Competition, not cooperation, dominates interactions among  
694 culturable microbial species. *Curr Biol* **22**, 1845-1850 (2012).

695 37. Ramos, J. L. *et al.* Mechanisms of solvent tolerance in gram-negative bacteria. *Annu Rev*  
696 *Microbiol* **56**, 743-768 (2002).

697 38. Natsch, A., Keel, C., Hebecker, N., Laasik, E. & Defago, G. Influence of biocontrol strain  
698 *Pseudomonas fluorescens* CHA0 and its antibiotic overproducing derivative on the diversity of  
699 resident root colonizing pseudomonads. *FEMS Microbiol Ecol* **23**, 341-352 (1997).

700 39. D'Onofrio, A. *et al.* Siderophores from neighboring organisms promote the growth of  
701 uncultured bacteria. *Chem Biol* **17**, 254-264 (2010).

702 40. Zengler, K. & Zaramela, L. S. The social network of microorganisms - how auxotrophies  
703 shape complex communities. *Nat Rev Microbiol* **16**, 383-390 (2018).

704 41. Goldford, J. E. *et al.* Emergent simplicity in microbial community assembly. *Science* **361**, 469-  
705 474 (2018).

706 42. Rivett, D. W. & Bell, T. Abundance determines the functional role of bacterial phylotypes in  
707 complex communities. *Nat Microbiol* **3**, 767-772 (2018).

708 43. Walser, M. *et al.* Novel method for high-throughput colony PCR screening in nanoliter-  
709 reactors. *Nucleic Acids Res* **37**, e57 (2009).

710 44. Spencer, S. J. *et al.* Massively parallel sequencing of single cells by epicPCR links functional  
711 genes with phylogenetic markers. *ISME J* **10**, 427-436 (2016).

712 45. Adams, J. Microbial evolution in laboratory environments. *Res Microbiol* **155**, 311-318 (2004).

713 46. Tecon, R., Binggeli, O. & van der Meer, J. R. Double-tagged fluorescent bacterial bioreporter  
714 for the study of polycyclic aromatic hydrocarbon diffusion and bioavailability. *Environ*  
715 *Microbiol* **11**, 2271-2283 (2009).

716 47. Rochat, L., Pechy-Tarr, M., Baehler, E., Maurhofer, M. & Keel, C. Combination of fluorescent  
717 reporters for simultaneous monitoring of root colonization and antifungal gene expression by  
718 a biocontrol pseudomonad on cereals with flow cytometry. *Mol Plant Microbe Interact* **23**,  
719 949-961 (2010).

720 48. Roggo, C. et al. Quantitative chemical biosensing by bacterial chemotaxis in microfluidic  
721 chips. *Environ Microbiol* **20**, 241-258 (2018).  
722 49. Gerhardt, P. et al. Manual of methods for general bacteriology (American Society for  
723 Microbiology, Washington, D.C., 1981).  
724

## 725 **SUPPLEMENTARY MATERIAL**

726 **Supplementary Fig. S1 Microcolony development in beads.** A. Starting cells in agarose beads  
727 of Pve, Eco, Ppr, Ppu and sand community (SC), stained by SYTO-9. B. Microcolonies of Pve,  
728 Eco, Ppr and Ppu after 24-72 h (constitutive mcherry signal) and of SC (SYTO-9).  
729

730 **Supplementary Fig. S2 Maximum productivities by *P. veronii* and SC across multiple**  
731 **independent incubation series.** Squares represent maximum productivity at any of the (triplicate)  
732 incubations at time points (24, 48 and 72 h) of Pve (black) or SC (light blue) separately, or in  
733 combination (green). MIXC1–C5, five independent repetitions of incubations with mixed C  
734 substrates; SUCC1–2, two independent repetitions with 0.1 mM succinate; TOL1–4, four  
735 repetitions with toluene (supplied through the vapor phase). Note that SC–cells were extracted  
736 from freshly taken sand material at different occasions (seasons) and thus may have different  
737 starting cell compositions. See main text for statistical tests.  
738

739 **Supplementary Fig. S3 Productivity shifts in inoculant–SC pairs compared to either**  
740 **inoculant or SC alone.** Productivity is defined as the product of particle area and fluorescence  
741 intensity. Distributions per category plotted using the gaussian density kernel on log scale.  
742 Substrates and inoculants abbreviated as before.  
743

744 **Supplementary Fig. S4 Summed productivities among inoculant–SC pairs of which the SC**  
745 **productivity was above the 95<sup>th</sup> percentile of the SC productivity separately after 24 h on**  
746 **the same carbon regime.** Distributions show log-scale productivities of the exclusive inoculant  
747 (Ino)–SC pairs (in green), compared to all inoculant–SC pairs (magenta) or inoculant alone (light  
748 brown). Compare to Figure 5 and Fig. S5. mixC, mixed carbon substrates; TOL, toluene. Inoculant  
749 abbreviations as before. P-values in Fisher's exact test of comparing normalized histogram  
750 distributions.  
751

752 **Supplementary Fig. S5 Productivities of inoculant–SC pairs.** A. Pair-wise productivity on  
753 mixed carbon substrates of co-occurring *P. protegens* (Ppr) and sand community (SC) within the  
754 same bead (colored bubbles), compared to productivity of Ppr or SC in separate individual  
755 incubations. B. As A, but for *E. coli* (Eco). C. as A, but for *P. putida* (Ppu) and toluene. D. as A, but  
756 for *P. veronii* and sand extract. Productivities are displayed on log-axes. Green lines indicate the  
757 95<sup>th</sup> percentile productivity of the individual incubation at t=24 h. Bubble diameters represent the  
758 Euclidian distance from the origin and are a relative measure of the microcolony sizes.

759 Percentages indicate the proportion of beads of the total, falling above the respective 95<sup>th</sup>  
760 percentile threshold. Values reported in Table 2.

761

762 **Supplementary Code**

763 MatLab subroutines for microcolony in bead analysis.

764

765

766

767 Table 1. Inoculant – sand community interactome experiments

768

Carbon Substrate	Inoculant			
	Pve	Ppu	Ppr	EC
Mixed Carbon	+	–	+	+
Sand Extract	+	–	–	–
Toluene	+	+	–	–
Succinate	+	–	–	–

769 a) +, carried out ; –, not carried out.

770

771 Table 2. Productivity increase or loss in inoculant–sand community (SC) cell pairs compared to either inoculant or SC alone.  
 772

Carbon Substrate	Bead Combination	Productivity increase <sup>a</sup>				Percentage no growth <sup>b</sup>			
		Inoculant	SC	Inoculant & SC	p-value <sup>c</sup>	Inoculant	SC	Inoculant & SC	p-value
Mixed Carbon	Pve+SC	0	46.6	0.3		8.5	8.2	<0.1	
	Pve <sup>d</sup>	2.7			$4.03 \cdot 10^{-7}$	9.2			0.4345
	SC <sup>d</sup>		7.6		$1.21 \cdot 10^{-12}$		7.4		0.2832
Mixed Carbon	Eco+SC	0.4	48.4	0.8		11.9	2.3	0	
	Eco	8.1			$7.10 \cdot 10^{-5}$	15.1			0.4632
	SC		7.3		$4.30 \cdot 10^{-5}$		9.2		0.0138
Mixed Carbon	Ppr+SC	0.1	80.1	0.5		10	2.5	<0.1	
	Ppr	1.2			$4.10 \cdot 10^{-7}$	1.6			0.0021
	SC		4.8		$1.20 \cdot 10^{-12}$		7.3		0.0103
Sand extract	Pve+SC	0.2	44.5	0.4		4.5	5.8	0	
	Pve	2.4			$2.60 \cdot 10^{-6}$	1.8			0.0258
	SC		3.8		$9.90 \cdot 10^{-13}$		12.1		0.0332
Toluene	Ppu+SC	0.9	27.2	0.4		10	22.7	<0.1	
	Ppu	10.2			$5.40 \cdot 10^{-5}$	12.7			0.2085
	SC		5.6		$1.80 \cdot 10^{-5}$		11.1		0.0904
Toluene	Pve+SC	0	42.6	0		4.3	11.9	0	
	Pve	3.2			$7.90 \cdot 10^{-16}$	0.7			0.0144
	SC		5.6		$1.30 \cdot 10^{-7}$		5.7		0.0079

773 a) Productivity increase defined as the proportion of microcolonies with productivity (area  $\times$  fluorescence intensity) at t = 6, 24, 48 or 72 h above the  
 774 95<sup>th</sup> percentile of either the inoculant's or the SC productivity at t = 24 h. See Figure 5.

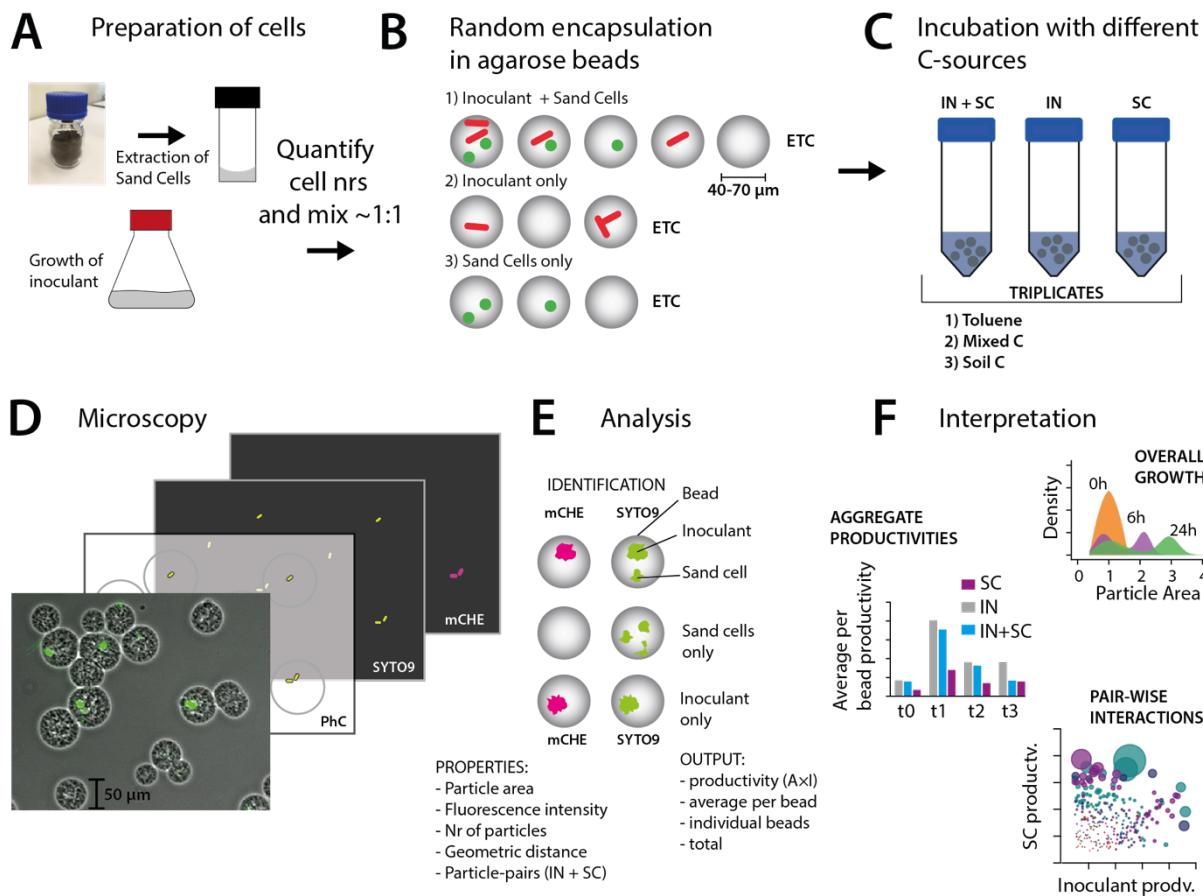
775 b) No growth defined as proportion of microcolonies with productivity (area  $\times$  fluorescence intensity) at t = 24, 48 or 72 h < 10<sup>th</sup> percentile of the  
 776 productivity at t = 0 h.

777 c) P-value from one-sided pair-wise t-test, unequal variance. Hypotheses: mean boosted average (>75<sup>th</sup> percentile) microcolony size for inoculant  
 778 alone > in bead with SC; mean boosted average (>75<sup>th</sup> percentile) microcolony size for SC alone < in bead with inoculant; mean percentage no growth  
 779 for inoculant alone < in bead with SC; mean percentage no growth for SC alone > or < in bead with inoculant.

780 d) Inoculant or SC incubations separately on the same substrate.

781

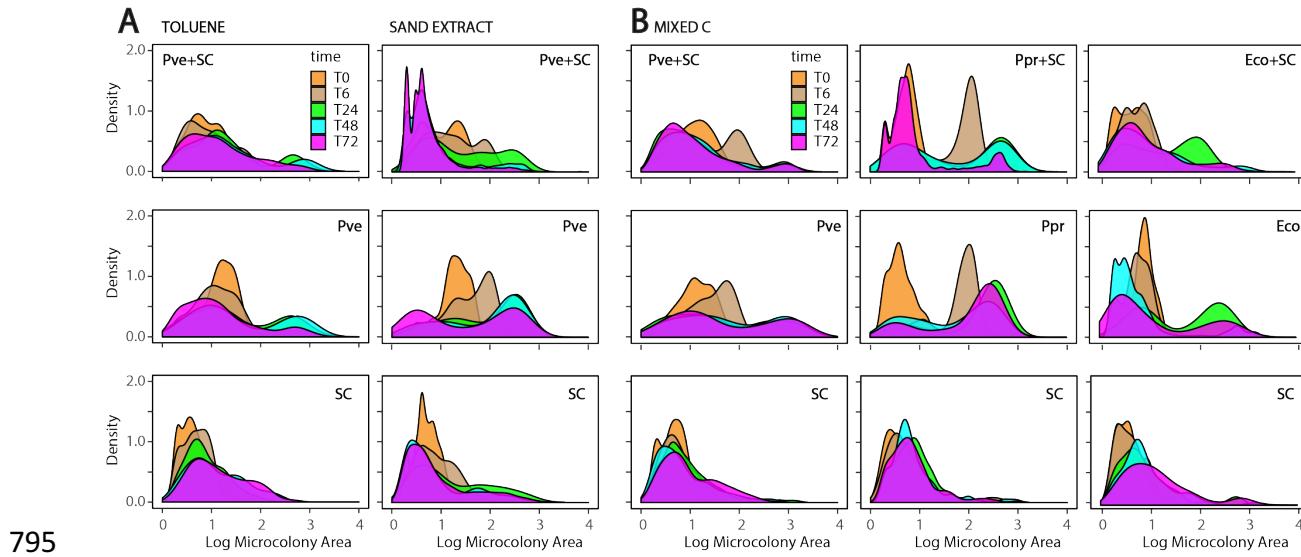
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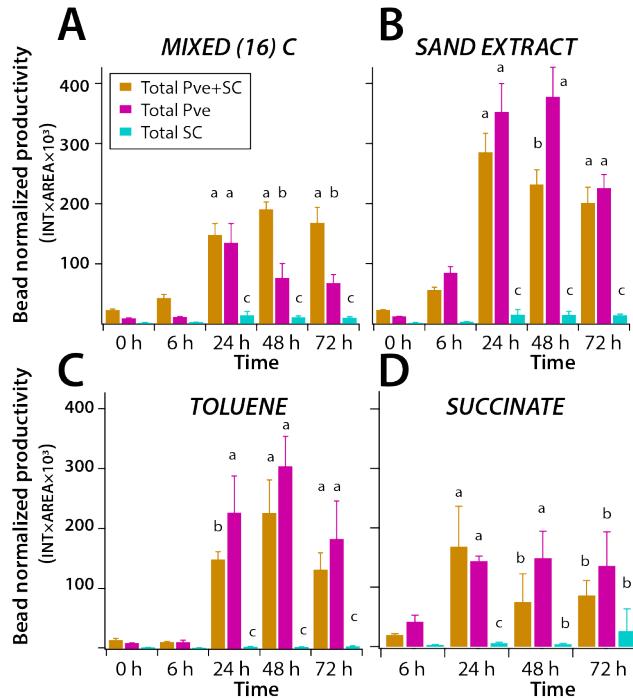


783

784 **Fig.1 Workflow overview of the interactome approach.** A. Sand community (SC) cells are  
785 extracted from fresh material and mixed with grown inoculant in equal ratio prior to encapsulation.  
786 B. Encapsulation generates random combinations of SC (green) and/or inoculant (red) in agarose  
787 beads having diameters between 40 to 70  $\mu$ m. C. Beads of the three setups (IN, inoculant only;  
788 SC, sand cells only; IN+SC, inoculant plus sand cells) are suspended and incubated in relevant  
789 growth media, and are sampled over time. D. Bead microscopy at five timepoints, and 10 random  
790 image positions, imaging in phase contrast (PhC), mCherry fluorescence (mCHE) and SYTO-9  
791 fluorescence. E. Data analysis pipeline identifies beads, and measures properties of microcolonies  
792 of inoculant (mCHE+SYTO-9) and sand cells. F. Output data types at system's or pair-wise  
793 interaction level.

794





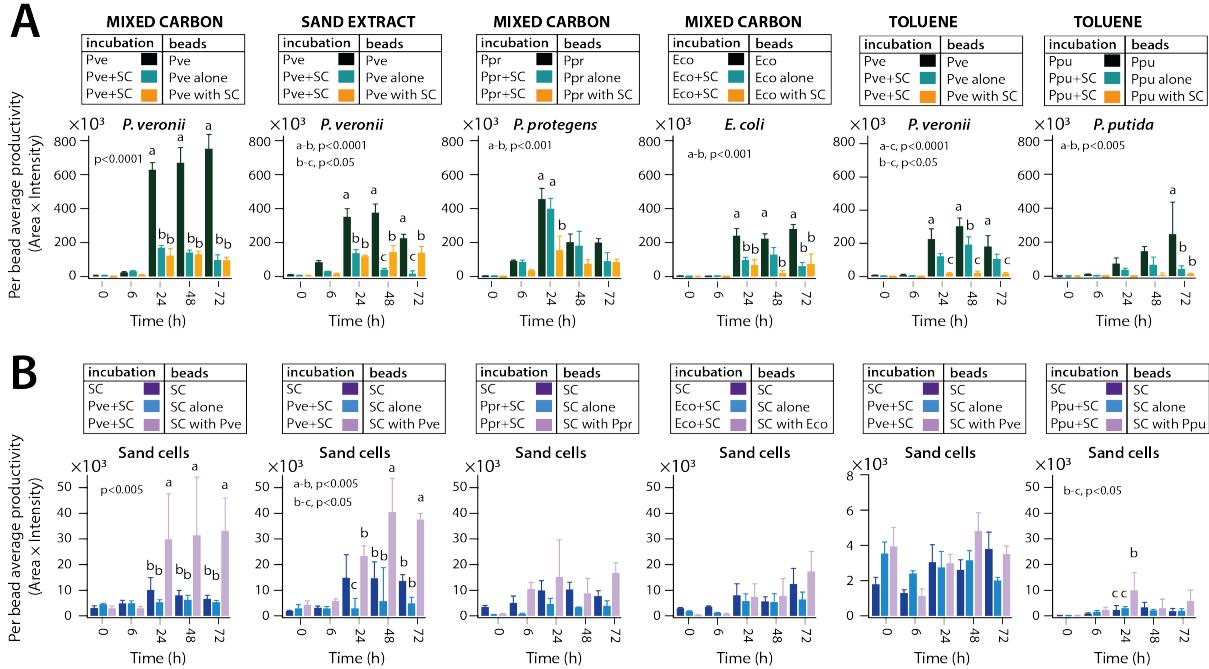
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806 **Fig. 3 Global productivity of sand community cells in presence or absence of *P. veronii* as**  
807 **a function of time and growth substrates.** A. Mixture of 16-carbon substrates (0.1 mM total). B.

808 Sand extract solution. C. Toluene (provided through the gas phase). D. Succinate (0.1 mM). Bars  
809 show mean productivity, defined as the product of particle area times particle fluorescence  
810 intensity, normalized across all observed beads per series time points. Error bars represent the  
811 standard deviation of the mean in triplicate incubations. Letters indicate significance groups in  
812 ANOVA followed by post-hoc Tukey testing (a-b, p<0.01; a-c, p<0.001).

813

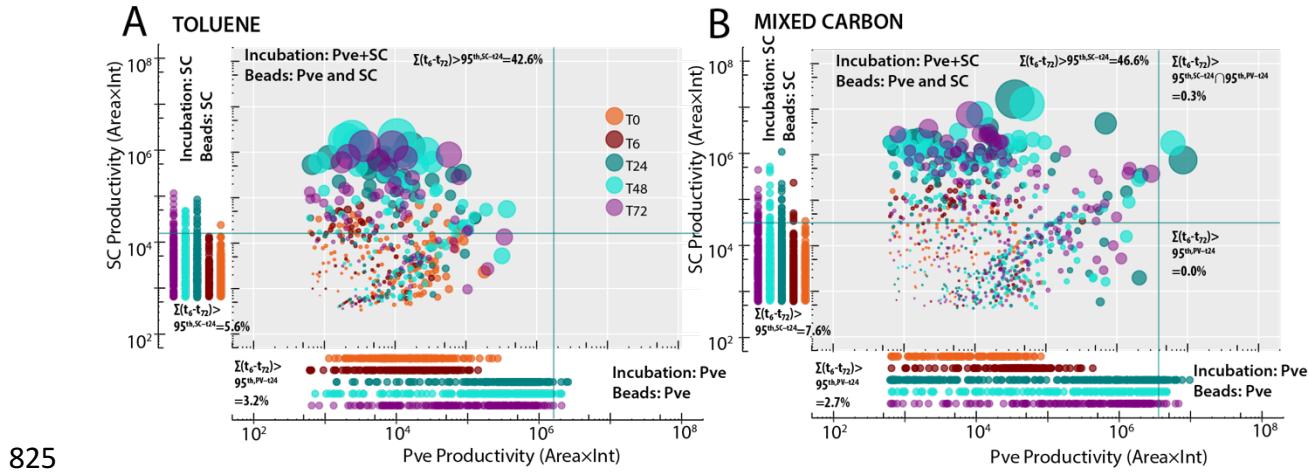
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815

816 **Fig. 4. Productivities of inoculant in presence or absence of sand cells within the same**  
 817 **bead.** A. Productivity for inoculant incubation alone (e.g., *incubation* Pve, *beads* Pve), or for  
 818 incubation in presence of sand community cells (Pve+SC), either for beads with Pve alone, or for  
 819 beads with Pve and SC co-occurring. B. As A, but for productivity of sand community cells. Bars  
 820 indicate the mean per-bead productivity across triplicate incubations. Error bars denote standard  
 821 deviations from the mean. Small letters indicate significance levels in ANOVA across time series  
 822 and categories followed by post hoc Tukey testing. Plots in A and B below each other correspond  
 823 to the same incubation and carbon substrate.

824

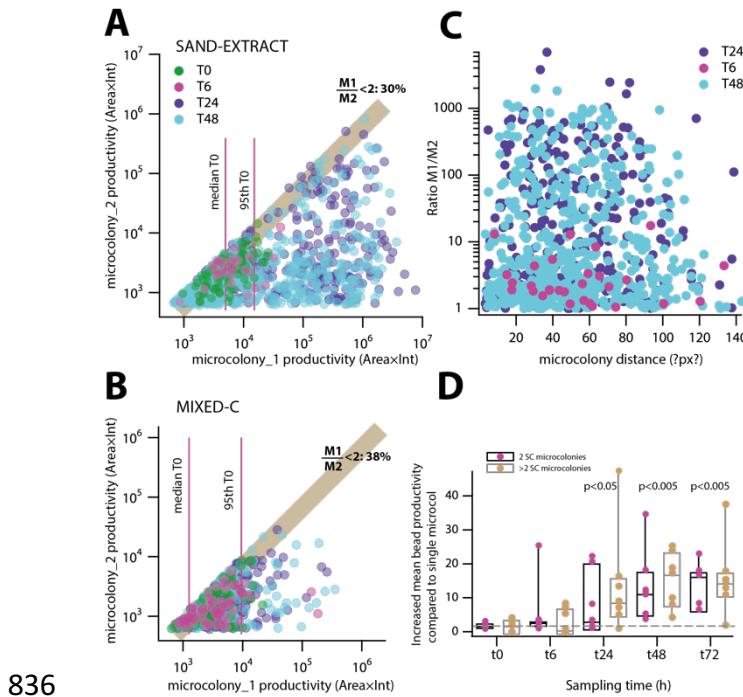


825

826 **Fig. 5. Pair-wise productivities within beads containing both inoculant and sand community**

827 **cells.** A. Individual pair-wise productivities on toluene of co-occurring *P. veronii* (Pve) and sand  
828 community (SC) within the same bead (colored bubbles), compared to productivity of Pve (bottom)  
829 or SC (left side) in separate individual incubations. B. As A, but for mixed-C substrates. Bead  
830 productivities are displayed on log-axes. Green lines indicate the 95<sup>th</sup> percentile productivity of the  
831 individual incubation at t=24 h. Bubble diameters represent the Euclidian distance from the origin  
832 and are a relative measure of the microcolony sizes. Percentages indicate the proportion of beads  
833 of the total, falling above the respective 95<sup>th</sup> percentile threshold (values summarized and tested  
834 for significance in Table 2).

835



836 **Fig. 6. Pair-wise interactions among sand community members.** A, B. Grouped beads with  
 837 exactly only two SC–microcolonies under sand-extract (A) or mixed carbon substrate (B) regime.  
 838 Pairs are ordered arbitrarily with the largest microcolony on the x– and the smaller microcolony on  
 839 the y–axis. Bead colors indicate sampling time points (in h). The light brown shading and  
 840 corresponding percentage indicate the proportion of pairs with a productivity difference of less than  
 841 2 (ratio M1/M2 <2). Cyan lines denote the median and the 95<sup>th</sup> percentile microcolony productivities  
 842 of all SC–pair beads at t=0. C. Paired microcolony ratio (M1/M2) as a function of geometric  
 843 distance of the microcolony centres. D. Mean bead productivity increase in SC–pairs or higher  
 844 SC–microcolony numbers compared to single SC occupancy across all incubations and substrates. Data points represent the means from the individual incubations and substrates, inside  
 845 box plots. The dotted line denotes the expected increase in productivity of an additive SC–pair  
 846 compared to single occupancy at t=0 (i.e., twofold). P-values are derived from pair-wise t-test  
 847 comparisons of the productivity measurements in all seven experimental conditions for beads with  
 848 two or more than two SC members, to that of single occupancy beads at the same sampling time  
 849 point.

852