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1 Title: A cross-species interaction with a symbiotic commensal enables cell-density-
2 dependent growth and in vivo virulence of an oral pathogen

3 Running title: Intra and interspecies cues enable pathogen growth

4

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33 succession, microbial communities, pathogen colonization and virulence

34 **Abstract**

35 Recent studies describe in detail the shifts in composition of human-associated
36 polymicrobial communities from health to disease. However, the specific processes that
37 drive the colonization and overgrowth of pathogens within these communities remain
38 incompletely understood. We used in vitro culture systems and a disease-relevant mouse
39 model to show that population size, which determines the availability of an endogenous
40 diffusible small molecule, limits the growth, colonization, and in vivo virulence of the
41 human oral pathogen *Porphyromonas gingivalis*. This bacterial pathogen overcomes the
42 requirement for an endogenous cue by utilizing a cell-density dependent, growth-
43 promoting, soluble molecule provided by the symbiotic early colonizer *Veillonella*
44 *parvula*, but not produced by other commensals tested. Our work shows that exchange of
45 cell-density-dependent diffusible cues between specific early and late colonizing species
46 in a polymicrobial community drives microbial successions, pathogen colonization and
47 disease development, representing a target process for manipulation of the microbiome
48 towards the healthy state.

49 **Introduction**

50

51 Diffusible signals allow bacteria to coordinate behaviors such as bioluminescence,
52 competence, biofilm formation, sporulation and virulence, according to the size of the
53 population (1-3). A less studied form of cell-to-cell communication is that which is
54 required for replication. In several bacterial species, the size of the inoculum is a critical
55 determinant of in vitro growth (4-8). Such an inability to grow at low cell-density is
56 relieved by addition of conditioned spent medium from the same species, highlighting the
57 endogenous nature of the required cue (4, 6, 7). A dependency on autoinducing molecules
58 to grow is likely to limit colonization of new habitats by bacterial populations at a low cell-
59 density. Bacteria could overcome this requirement by establishing in pre-existing
60 polymicrobial communities, where resident species provide the growth-initiating cues that
61 newcomers need.

62

63 The human oral cavity, in particular teeth and the gingival sulci, harbor diverse microbial
64 communities. These polymicrobial biofilms represent an accessible model in which to
65 study the role of inter-species interactions in community assembly and development
66 processes. The compositional shifts during oral community maturation have been
67 described in detail (9-11), with early colonizers creating niches conducive to the
68 establishment of later and often anaerobic colonizers (12). If oral hygiene fails to restrict
69 biomass accumulation and species successions continue, an inflammatory response in the
70 adjacent gingiva is triggered and is referred to as gingivitis (10, 13). In some individuals,
71 communities undergo further compositional shifts resulting in overgrowth of even more

72 pathogenic species, which trigger periodontitis, an inflammation-mediated destruction of
73 tooth-supporting tissues that leads to tooth loss and constitutes a risk factor for several
74 systemic diseases (9, 11, 14). Early and late oral biofilm colonizers have been shown to
75 cooperatively interact to degrade host macromolecules, to establish reduced (i.e. anaerobic)
76 environments and to exchange metabolic byproducts, thereby driving community
77 maturation and subverting host defenses (15-17). However, the role of population-
78 dependent inter-species communication on microbial successions and the emergence of
79 dysbiosis remains unclear. Whether late colonizers require growth-initiating factors that
80 otherwise limit their establishment during early biofilm development has not been
81 investigated.

82

83 *Porphyromonas gingivalis*, an anaerobic late-colonizer, becomes an abundant species in
84 dental communities of subjects affected by periodontitis (18, 19). *P. gingivalis* has been
85 associated with progression of human periodontitis, and shown to dysregulate immune
86 surveillance leading to bone loss, the hallmark of periodontitis, in animal models (20-23).
87 *P. gingivalis* has difficulty in becoming established in the oral cavity as shown by its
88 presence as a transient commensal in children and its low abundance, when present, in
89 early dental biofilms (10, 24, 25). While a reduced atmosphere created by early colonizers
90 and the availability of inflammation-derived proteinaceous nutritional substrates are
91 probably required for the establishment of *P. gingivalis* in the gingival crevices (26), an
92 inability to grow at low cell-density might also contribute to late colonization by this
93 species. Routine laboratory growth of *P. gingivalis*, especially in chemically-defined
94 medium, requires a large inoculum (27). Accordingly, we investigated whether *P.*

95 *gingivalis* requires a cell-density-dependent autoinducing factor to grow and whether this
96 cue could be provided by early biofilm colonizers. We present evidence that the growth of
97 *P. gingivalis* is controlled by a diffusible cell-density-dependent small molecule. Such a
98 dependency on an autoinducer is overcome by an inter-species interaction with the early
99 colonizing commensal *Veillonella parvula*, which allows low-cell-density *P. gingivalis* to
100 grow in vitro and also to colonize the mouse oral cavity, where it promotes periodontal
101 bone loss. Our work shows that although growth of the oral pathogen *P. gingivalis* depends
102 on an autoinducing diffusible small molecule, a cross-species interaction with an early
103 colonizing symbiotic commensal enables pathogen colonization and virulence.

104

105 **Methods**

106

107 **Strains and culture conditions**

108

109 *Porphyromonas gingivalis* strains 381, W83 and ATCC 33277 were maintained short-term
110 on agar containing brain heart infusion (BHI), 0.04% L-cysteine ·HCl, 5 µg mL⁻¹ hemin, 5
111 µg mL⁻¹ menadione and 5% defibrinated sheep's blood. Starter cultures were grown in
112 BHI, 0.04% L-cysteine ·HCl, 5 µg mL⁻¹ hemin and 5 µg mL⁻¹ menadione (BHI-H-M).
113 *Streptococcus sanguinis* SK36 and *Actinomyces oris* T14V were maintained on BHI agar
114 and grown in liquid BHI. *Fusobacterium nucleatum* subsp. *polymorphum* ATCC 10953
115 was maintained on agar containing BHI, 0.04% L-cysteine ·HCl and 5% defibrinated
116 sheep's blood and starter cultures were grown in BHI and 0.04% L-cysteine ·HCl.
117 *Veillonella parvula* strains PK1910, PK1941 and ATCC 10790 were maintained on agar

118 containing BHI, 0.04% L-cysteine ·HCl and 1.3% lactic acid and starter cultures were
119 grown in a similar liquid medium. Cultures of the previous microorganisms were incubated
120 in an anaerobic atmosphere consisting of 5% H₂, 5% CO₂, and 90% N₂. *Rothia*
121 *dentocariosa* ATCC 17931 was grown on BHI agar or in liquid BHI aerobically. The strain
122 *P. gingivalis* $\Delta luxS::ermF$ (28), kindly donated by Dr. Richard J. Lamont, University of
123 Louisville, was maintained in the presence of erythromycin at 15 $\mu\text{g mL}^{-1}$.

124

125 **Evaluation of growth from inocula of varying cell-densities**

126

127 To evaluate the ability of inocula of different size to grow, microorganisms were inoculated
128 into liquid cultures at cell densities ranging from 10³ to 10⁸ cells per mL followed by
129 anaerobic incubation at 37°C. Inocula of different biomass were obtained by diluting a
130 starter culture previously grown to mid logarithmic phase and normalized to an optical
131 density (600 nm) of 0.4, for which the number of cells was determined according to
132 microscopic counts on a Petroff Hausser chamber. Most experiments were conducted in
133 mucin-serum medium, which contained 2.5 mg mL⁻¹ hog gastric mucin (Sigma), 2.5 mg
134 mL⁻¹ KCl, 2.0 mg mL⁻¹ proteose peptone, 1.0 mg mL⁻¹ yeast extract, 1.0 mg mL⁻¹ trypticase
135 peptone, 1.0 $\mu\text{g mL}^{-1}$ cysteine ·HCl, 5 $\mu\text{g mL}^{-1}$ hemin and 10% (vol:vol) heat-inactivated
136 human AB serum (Sigma). Cultures were sampled daily, inside the anaerobic chamber.
137 Growth was monitored after serial dilutions and plating on appropriate media or evaluated
138 via qPCR.

139

140 **Evaluation of the effect of cell-free spent medium on growth of *P. gingivalis***

141

142 Spent medium was obtained from *P. gingivalis* cultures inoculated with 10^7 cells mL⁻¹ and
143 grown until late exponential phase (48 hours in BHI-H-M and 72 hours in mucin-serum),
144 followed by centrifugation for 15 min at $5,000 \times g$. Supernatants were filter-sterilized twice
145 through 0.22 μ m filter units. The filtered spent medium was checked for contamination by
146 plating a small volume on blood agar followed by aerobic and anaerobic incubation. Spent
147 medium was stored at 4°C for up to 48 h before using it to evaluate the growth of *P.*
148 *gingivalis*. The effect of spent media was tested by combining it in different proportions
149 (25 to 100%) with fresh medium, followed by inoculation of *P. gingivalis* at low-cell-
150 density (10^5 cells mL⁻¹). To evaluate the effect of spent media on solid growth on agar, *P.*
151 *gingivalis* was serially-diluted in either PBS or spent medium, and plated at different
152 densities onto BHI-H-M or BHI-H-M blood agar. Colonies were counted after anaerobic
153 growth for 8 days.

154

155 *V. parvula* spent medium was obtained at different time points of growth in mucin-serum
156 (with most experiments ultimately conducted with spent medium from 24-hour cultures).
157 Spent medium was processed in a similar manner to that described for *P. gingivalis*.

158

159 **Fractionation, heat inactivation and protease treatment of spent medium**

160

161 Spent medium was subjected to fractionation based on size of molecules by using spin
162 filter units with different molecular weight cut-offs (MWCO) (Amicon® Ultra or Microsep
163 TM Advance centrifugal devices). Samples were loaded and centrifuged at $5,000 \times g$ for 90

164 min and concentrates and filtrates were freeze-dried followed by reconstitution in dH₂O
165 giving 10X concentrated suspensions. These concentrated fractions were tested for their
166 ability to induce growth of a low-cell-density inoculum of *P. gingivalis* by adding them to
167 fresh mucin-serum (25% -75% vol:vol). Concentrated low molecular weight filtrates were
168 heat-inactivated by boiling for 10 min and then cooled before using them to evaluate
169 growth of *P. gingivalis*. Filtrate fractions were protease-treated by incubation, for 1 h, with
170 2 U mL⁻¹ of reconstituted proteinase K-agarose dry powder (Sigma). Protease-treated
171 fractions were then centrifuged to remove proteinase K-agarose and the supernatant
172 recovered and used to evaluate growth of *P. gingivalis*.

173

174 **Evaluation of the effect of quorum-sensing-related compounds on growth of *P.***
175 ***gingivalis***

176

177 A group of commercially available compounds potentially involved in cellular growth
178 induction, including D-pantothenic acid (D-PA), D-panthenol, β-alanine, tyrosol, 4-
179 aminobenzoate/para-amino benzoic acid (pABA), as well as the polyamines spermidine,
180 spermine, cadaverine and putrescine were tested for their ability to induce growth of a low
181 cell-density inoculum of *P. gingivalis* (10⁵ cells mL⁻¹). *P. gingivalis* was inoculated in
182 mucin-serum medium supplemented with each compound at the concentrations listed in
183 Supplementary Table 1, and growth was monitored for up to 10 days. A high-cell-density
184 inoculum (10⁸ cells mL⁻¹) of *P. gingivalis* and a co-culture of 10⁵ cells mL⁻¹ *P. gingivalis*
185 and 10⁵ cells mL⁻¹ *V. parvula*, placed in unsupplemented mucin-serum were included as
186 positive controls.

187

188 **Evaluation of the effect of cell-to-cell contact with *V. parvula* on growth of *P. gingivalis***

189

190 Mucin-serum aliquots inoculated with *P. gingivalis* and/or *V. parvula* at 10^5 cells mL⁻¹
191 were placed into 50 mL conical tubes separated by a 0.22 µm membrane (Steriflip-GP,
192 Millipore). Three conditions were tested: (i) *P. gingivalis* monoculture inoculated in one
193 chamber and *V. parvula* monoculture in the contiguous one, (ii) *P. gingivalis* + *V. parvula*
194 inoculated in both chambers, and (iii) *P. gingivalis* inoculated in both chambers. Cultures
195 were sampled and *P. gingivalis* growth was evaluated via qPCR.

196

197 **Evaluation of the effect of early colonizers on the growth of *P. gingivalis* in batch and**
198 **continuous culture**

199

200 *P. gingivalis* was inoculated in batch as a monoculture or in the presence of early colonizers
201 in mucin-serum. Inoculum size was 10^5 cells mL⁻¹ for all species. Cultures were sampled
202 daily inside the anaerobic chamber. Growth of all species was monitored after serial
203 dilution and plating on selective agar media or evaluated via qPCR.

204

205 Continuous culture experiments were performed in a Bioflow®/CelliGen® 115 Bioreactor
206 (New Brunswick) starting from standardized frozen inocula stored in medium specific for
207 each microorganism and 10% glycerol. At inoculation, cryovials containing standardized
208 stocks were rapidly allowed to thaw, followed by pooling of different strains and
209 inoculation into 500 mL of mucin-serum. Inoculation density was 10^8 cells mL⁻¹ for each

210 strain. After 24 hours of batch growth in the bioreactor vessel, the pump was turned on and
211 fresh medium allowed to flow for 48 hours at a dilution rate of $D=0.0462 \text{ h}^{-1}$ (doubling
212 time $t_d=15 \text{ h}$). The flow was then stopped and a new inoculation was performed, followed
213 by batch growth for 24 hours, after which continuous culture was resumed. This time point
214 was considered day 0. The gas phase was maintained anaerobically by sparging 5% CO_2
215 in N_2 ; temperature and pH were controlled automatically at 37°C and 7.15 ± 0.15 ,
216 respectively. Cultures were considered to have reached steady state after 15 mean
217 generation times (MGT), and evidence of sustained stability as evaluated via dry weights,
218 E_h and viable counts. Three different types of experiments were conducted to evaluate the
219 effect of *V. parvula* on the biomass of *P. gingivalis*. In one experiment, *A. oris*, *S. sanguinis*,
220 *F. nucleatum* and *R. dentocariosa* were inoculated together with *P. gingivalis*. In a second
221 set of experiments, *V. parvula* was included in the initial inoculum in addition to the strains
222 already mentioned. In a third set of experiments, *V. parvula* was initially excluded but
223 introduced later once the culture had achieved steady-state, after which the culture was
224 monitored until a second steady-state was reached.

225

226 **Cultivation and molecular methods for quantification of microorganisms from batch** 227 **and continuous cultures**

228

229 Growth of *S. sanguinis*, *A. oris*, *V. parvula* and *F. nucleatum* were quantified by plating on
230 appropriate selective media. Culture samples were vortexed, followed by a 10s sonication
231 at 15% amplitude in a Branson sonicator model 4C15, to disperse co-aggregated microbial
232 cells without affecting viability. After disaggregation, appropriate dilutions in sterile

233 phosphate buffered saline (PBS) were obtained and subsequently plated. BHI
234 supplemented with 5% defibrinated sheep's blood, 0.04% L-cysteine ·HCl and 0.0025 g L⁻¹
235 vancomycin hydrochloride was used to quantify *V. parvula* and *F. nucleatum*
236 (anaerobically), differentiating them by colony morphology. Actino-selective agar
237 consisting of trypticase soy agar supplemented with 0.5% glucose, 0.0013% cadmium
238 sulfate, 0.008% sodium fluoride, 0.00012% neutral acriflavine, and 0.000025% basic
239 fuchsin was used to quantify *A. oris* (anaerobically). Mitis-Salivarius agar was used to
240 quantify *S. sanguinis* (aerobically). *P. gingivalis*, and *R. dentocariosa*, were quantified by
241 qPCR. The reason for using a molecular technique to quantify *R. dentocariosa* is that no
242 suitable selective medium was found for its identification. qPCR was also more reliable to
243 quantify *P. gingivalis*, especially when the microorganism was present in low-abundance
244 as part of a multi-species community. For these assays, DNA extraction from cultures was
245 performed as previously described (9). *P. gingivalis* and *R. dentocariosa* were quantified
246 using primers targeting the 16S rRNA gene, and amplicons detected via SYBR green
247 chemistry or a Taqman probe, respectively (29, 30). Standard curves using the respective
248 genomic DNA were used to calculate number of 16S rRNA gene copies present in samples.
249

250 **Reanalysis of publicly available 16S rRNA gene amplicon libraries of subgingival**
251 **samples obtained from subjects with different periodontal conditions**

252

253 An evaluation of the prevalence and abundance of *P. gingivalis* and early colonizers in
254 subjects presenting with periodontal health, gingivitis and periodontitis was performed.
255 Integration and re-analysis of datasets from different published studies was required since

256 no simultaneous analysis of the microbiome of these three conditions, allowing direct
257 comparison and applying current clinical definitions, has been reported. Studies that used
258 16S rRNA gene amplicon sequencing of the V1-V3 hypervariable regions to characterize
259 the subgingival microbiome in health, gingivitis or periodontitis; and with downloadable
260 publicly available sequence datasets were included (9-11, 19, 31-36). Sample selection
261 from these studies was based on their compatibility with current definitions of periodontal
262 health, gingivitis and periodontitis. Studies included in the periodontal health group were
263 required to exclude subjects with >10% bleeding on probing and pocketing >3 mm. Studies
264 included in the gingivitis group enrolled subjects with naturally-occurring gingivitis defined
265 by >10% bleeding on probing but no pocket ≥ 5 mm, or periodontally-healthy subjects who
266 underwent an experimentally-induced gingivitis protocol. Subjects with periodontitis were
267 included based on the minimum case definition for the disease, which is interdental clinical
268 attachment loss (CAL) detectable at ≥ 2 non-adjacent teeth, or buccal CAL ≥ 3 mm with
269 pocketing >3 mm detectable at ≥ 2 teeth. Only those samples from subjects who were non-
270 smokers, non-diabetic and that did not have chronic kidney disease were included in the
271 analysis.

272

273 Downloaded sequences were processed in mothur, using standard pipelines (37).
274 Sequences were classified to species level by using the classify.seqs command and the
275 Human Oral Microbiome database (HOMD) V14.5 as reference. After processing,
276 sequence libraries were randomly subsampled at a threshold of 3,500 reads to contain the
277 same number of reads followed by generation of relative abundance tables.

278

279 **Effect of *V. parvula* on the in vivo colonization and virulence of *P. gingivalis***

280

281 All animal experiments were reviewed and approved by the Institutional Animal Care and
282 Use Committee (IACUC) of the University of Pennsylvania and were performed in
283 compliance with institutional, state, and federal policies. A previously described ligature-
284 induced periodontitis (LIP) mouse model was used (38), modified to include inoculation
285 of exogenous microorganisms. Briefly, ligatures were tied around molar teeth of 8 week-
286 old C57BL/6 mice and 50 μ L of a suspension, in phosphate buffered saline (PBS), of 10^5
287 cells mL^{-1} or 10^8 cells mL^{-1} of *P. gingivalis*, *V. parvula* or a combination of both was placed
288 directly on the ligatures. Only one inoculation, at the time of ligature placement, was
289 performed. Ligatures were removed 5 days post-placement and alveolar bone levels were
290 evaluated as previously described (38).

291

292 DNA was extracted from ligatures using a previously described protocol (9). Total bacterial
293 load was determined by qPCR using universal primers and a TaqMan probe (9). *P.*
294 *gingivalis*, and *V. parvula* load was determined using specific primers targeting the 16S
295 rRNA gene and detected via SYBR green chemistry or a TaqMan probe, respectively (30,
296 39). Standard curves were used to calculate number of 16S rRNA gene copies in each
297 condition. Data were expressed as 16S rRNA copy number normalized by ligature length.

298

299 Microbiome communities in ligatures were characterized by sequencing of the 16S rRNA
300 V1-V2 region using primers 8F 5'- AGAGTTTGATCMTGGCTCAG-3' and 361R 5'-
301 CYIACTGCTGCCTCCCGTAG-3' which included the adapter for MiSeq sequencing

302 (Illumina) and single end barcodes (10). Amplicon libraries were pooled and sequenced
303 using the MiSeq Reagent kit v3 (Illumina). 16S rRNA gene sequences were processed in
304 mothur using standard pipelines. Reads were clustered at 97% similarity into Operational
305 Taxonomic Units (OTUs). Individual reads were classified by comparison to the RDP
306 version 16 database, as implemented in mothur, with a cutoff=80. OTUs were classified
307 up to genus level when possible, according to the consensus taxonomy using the default
308 cutoff (51%). To enhance the taxonomical resolution of each OTU, the representative
309 sequence was compared using BLAST to the NCBI 16S rRNA gene sequence database and
310 the best match (with at least 97% similarity and coverage) is indicated in parenthesis.
311 Relative abundance graphs were generated using the packages ‘ggplot2’ and
312 ‘RColorBrewer’ within R (<http://www.r-project.org>) and RStudio
313 (<https://www.rstudio.com>). Differences in relative abundance between *V. parvula* alone
314 and *V. parvula* + *P. gingivalis* groups were tested using LEfSe (40) considering 0.01 as the
315 α value for statistical testing. These analyses included OTUs that were present in at least
316 20% of the samples.

317

318 **Results**

319

320 **Growth of *P. gingivalis* is dependent on a soluble factor produced at high cell-density**

321

322 The growth of *P. gingivalis* in a nutrient-restricted medium supplemented with an iron
323 source and host macromolecules (mucin-serum) was found to be dependent on the initial
324 cell-density as batch cultures inoculated with less than 10^7 cells mL⁻¹ were unable to grow

325 (Figure 1a). Identical inoculum size thresholds were seen for three different strains of *P.*
326 *gingivalis* (Figure 1a and Supplemental Figures 1a and 1b). However, growth from a low-
327 cell-density inoculum (10^5 cells mL⁻¹) was possible in the presence of cell-free spent
328 medium from a *P. gingivalis* early stationary phase culture, suggesting that growth
329 initiation was dependent on an endogenous soluble factor that had accumulated in the
330 medium (Figure 1b and Supplemental Figure 1c). Remarkably, even 100%
331 unsupplemented spent medium was able to support growth, with these cultures reaching
332 comparable maximum densities to those grown in the presence of fresh medium.

333

334 A 10^5 cells mL⁻¹ inoculum also failed to grow in a different medium (BHI-H-M), but again
335 spent medium from a stationary-phase culture restored growth (Figure 1c). In BHI-H-M,
336 however, growth in the presence of spent media was less consistent across replicates (n=6)
337 and higher proportions of fresh medium supported higher maximum densities. The effect
338 of spent medium was also tested on solid BHI-H-M, where resuspension of the inoculum
339 in spent medium from stationary-phase liquid cultures, grown either in mucin-serum or
340 BHI-H-M, significantly increased the number of colony forming units (CFUs) recovered
341 (Figure 1d). The addition of blood, which is commonly incorporated into solid media to
342 grow *P. gingivalis*, allowed the number of observed CFUs to approximate the expected
343 level (based on microscopic counts). In the presence of blood, spent media did not further
344 augment the number of recovered CFUs (Figure 1d).

345

346 To characterize the nature of the soluble factor(s) that facilitated growth of a low cell-
347 density inoculum of *P. gingivalis*, the spent medium of a stationary phase culture grown in

348 mucin-serum was fragmented with a 3kDa-MWCO filter, and both the concentrate and
349 filtrate (fraction <3kDa) were tested for activity. Only the filtrate supported growth of *P.*
350 *gingivalis* (Figure 1e). Filtrates of a 1kDa-MWCO membrane also enabled growth
351 (Supplemental Figure 1d). Furthermore, the growth-promoting activity of filtrates was
352 heat-stable and protease-resistant (Figure 1e).

353

354 Altogether, these data show that growth of *P. gingivalis* requires a threshold concentration
355 of a soluble endogenous heat-stable and protease-resistant small molecule. Growth can
356 only occur when cells are transferred to fresh medium at a density that allows accumulation
357 of the molecule to occur or in the presence of spent media containing the growth-promoting
358 factor.

359

360 **Known quorum-sensing mediators do not support growth of low cell-density *P.***
361 ***gingivalis***

362

363 A set of compounds previously found to mediate inter-cellular communication were tested
364 for their ability to stimulate growth of a low-cell-density inoculum of *P. gingivalis*
365 (Supplementary Table 1). Supplementation of mucin-serum medium with D-pantothenic
366 acid (D-PA), which regulates growth of low-cell-density *Cryptococcus neoformans* (41),
367 or with the metabolically-related molecules panthenol and β -alanine, had no effect.
368 Tyrosol, a quorum-sensing molecule that supports growth of low-cell-density cultures of
369 *Candida albicans* (42), also failed to stimulate *P. gingivalis*. A set of polyamines, including
370 spermidine, spermine, cadaverine and putrescine, which stimulate eukaryotic and

371 prokaryotic cell growth (43) had no effect. The addition of 4-aminobenzoate/para-amino
372 benzoic acid (pABA), which is needed for maximal biofilm accumulation of *P. gingivalis*
373 (15), also failed to stimulate growth. The LuxS system was not involved, since a *P.*
374 *gingivalis* $\Delta luxS::ermF$ mutant (28) showed similar behavior to the wild-type strain, only
375 growing in mucin-serum when inoculated at high cell-density; and spent medium from the
376 $\Delta luxS$ strain supported growth of a low-cell-density inoculum of wild-type *P. gingivalis*
377 (Supplemental Figure 1e).

378

379 **Early colonizers do not exhibit cell-density-dependent growth and enable growth of**
380 **low-cell-density *P. gingivalis***

381

382 In a cross-sectional evaluation of publicly available 16S rRNA gene datasets from human
383 subjects with periodontal health, gingivitis and periodontitis, it is clear that *P. gingivalis*
384 exhibits a progressively higher frequency of detection and abundance in subgingival
385 biofilms as periodontal health deteriorates (Figures 2a and 2b). We next evaluated if
386 species present during early stages of biofilm dysbiosis could support the growth of low-
387 cell-density cultures of *P. gingivalis*. We tested five species with high prevalence and
388 abundance in gingivitis (Figures 2c and 2d). Some of these species were also present in
389 high proportions in health, but we reasoned that since the total microbial load increases by
390 at least 3-log from health to gingivitis (10), these prevalent species and the diffusible
391 molecules they produce would accumulate during the gingivitis state to a threshold that
392 may allow the establishment and growth of *P. gingivalis*. As seen in Figure 2e, co-
393 inoculation of *P. gingivalis* in mucin-serum with the five early colonizing microorganisms

394 facilitated its growth from even a low-cell-density inoculum. The early colonizers all grew
395 within this community reaching their maximum yield in 2 days, while *P. gingivalis* reached
396 a biomass after 6 days that was comparable to that achieved when inoculated alone at high
397 cell-density (as shown in Figure 1a).

398

399 We next tested whether the early colonizers had a cell-density growth requirement when
400 inoculated as monocultures. All strains successfully grew in mucin-serum even when
401 inoculated at a cell-density as low as 10^3 cells mL^{-1} (Figure 2f), which suggests these
402 species are able to grow from small populations without requiring an autoinducing factor.

403

404 ***Veillonella parvula* is the key species that supports growth of low-cell-density *P.***
405 ***gingivalis***

406

407 Evaluation of the individual ability of each of the five early colonizing species to support
408 growth of a low-cell-density inoculum of *P. gingivalis*, showed that only *V. parvula*
409 enabled the latter to grow (Figure 3a). Furthermore, when all microorganisms were
410 inoculated as a community, elimination of *V. parvula* from the inoculum abrogated growth
411 of *P. gingivalis* (Figure 3b), confirming *V. parvula* as the key species.

412

413 The positive effect of *V. parvula* on *P. gingivalis* was strain-independent as three different
414 *P. gingivalis* strains (W83, 381 and ATCC 33277) grew when co-inoculated with any of
415 three different strains of *V. parvula* (PK1910, PK1941 and ATCC 10790) but failed to
416 grow as monocultures (Supplemental Figure 2).

417

418 ***V. parvula* supports growth of a low-cell-density inoculum of *P. gingivalis* through a**
419 **soluble cue**

420

421 Spent medium from *V. parvula*, collected after different lengths of time in culture, was
422 evaluated for its ability to stimulate growth of a low-cell-density inoculum of *P. gingivalis*.

423 As shown in Figure 3c, spent medium from early *V. parvula* cultures (8 hours) did not
424 support growth of *P. gingivalis* but that obtained from *V. parvula* cultures older than 16 h
425 supported growth, although the growth rate in spent medium was slower than when *V.*
426 *parvula* was present. The effect of spent medium from *V. parvula* was dependent on a
427 threshold concentration since addition of 25% spent medium to fresh medium did not allow
428 growth of *P. gingivalis*, while 50% or higher concentrations supported growth (Figure 3d).

429 Cell-to-cell contact was not essential for the interaction since separation of *V. parvula* and
430 *P. gingivalis* by a 0.22 µm filter still allowed the latter species to grow (Supplemental
431 Figure 3a). We also noticed that if only spent media from *V. parvula*, but not cells, were
432 allowed to interact with *P. gingivalis* (as in Figures 3c, 3d and Supplemental Figure 3a),
433 biphasic growth tended to occur with a slight decrease in growth rate as *P. gingivalis*
434 approached the threshold concentration needed to sustain its own growth. This biphasic
435 growth was not observed with a larger inoculum (Supplemental Figure 3b, left panel).

436 Spent medium of *V. parvula* was also seen to have no effect on inocula capable of
437 independent growth (Supplemental Figure 3b, right panel).

438

439 The spent medium of *V. parvula* showed similar characteristics to the auto-stimulatory
440 spent medium of *P. gingivalis*. That is, only the <1kDa filtrate fraction enabled growth of
441 *P. gingivalis* (Supplemental Figure 3c), and the activity of the filtrate was heat-stable and
442 protease resistant (Figure 3e).

443

444 In summary, these results suggest *V. parvula* produces a diffusible small molecule that
445 needs to accumulate to a threshold concentration to stimulate growth of low-cell-density
446 *P. gingivalis*. Although cell-free spent medium supported growth, the presence of *V.*
447 *parvula*, but not necessarily cell-to-cell contact, was beneficial to the interaction as it
448 allowed faster growth of low cell-density *P. gingivalis* than spent media.

449

450 ***V. parvula* allows *P. gingivalis* to maintain a high biomass in an open flow chemostat**
451 **system**

452

453 To evaluate if the interaction between *V. parvula* and *P. gingivalis* was relevant in an open
454 flow setting, which more closely resembles the conditions in natural oral communities, we
455 used a continuous culture system. For these experiments, early colonizers and *P. gingivalis*
456 were inoculated into a chemostat, allowing microorganisms to briefly grow in batch before
457 turning on the flow of growth medium. Since our objective was to evaluate whether *V.*
458 *parvula* helped *P. gingivalis* maintain its biomass under open flow, we used a high-density
459 inoculum during the culture establishment. *P. gingivalis* was able to grow in continuous
460 culture in the absence of *V. parvula* (Figure 4a), but its steady-state biomass was
461 significantly higher when *V. parvula* was part of the initial inoculum (Figure 4b) or

462 introduced after steady-state (Figure 4c). *V. parvula* not only allowed *P. gingivalis* to reach
463 higher cell numbers in this open-flow system, but it also reduced daily biomass fluctuations
464 of *P. gingivalis* (Figure 4d). These results suggest that *V. parvula* is also beneficial to high-
465 cell-density *P. gingivalis* enabling it to maintain a higher biomass under open-flow
466 conditions.

467

468 **Low-cell-density *P. gingivalis* is unable to colonize the oral cavity of mice unless aided**
469 **by *V. parvula***

470

471 The ligature-induced periodontitis (LIP) mouse model was used to evaluate whether the
472 requirement for a high-cell-density inoculum was relevant in an in vivo oral environment
473 and to explore if under these conditions *V. parvula* had a positive effect on colonization by
474 low cell-density *P. gingivalis*. In this model, ligatures that promote accumulation of
475 bacteria are tied around molar teeth leading to bacterial dysbiosis and an inflammatory
476 process that induces bone loss within 5 days. A small volume (50 μL) of a *P. gingivalis*
477 suspension was inoculated on the ligatures, at the time of placement, at a low (10^5 cells
478 mL^{-1}) or high (10^8 cells mL^{-1}) cell-density. Five days post-inoculation, *P. gingivalis* was
479 only detected when inoculated at high cell-density (Figure 5a). However, the inability of
480 low-cell-density *P. gingivalis* to colonize was reversed when *V. parvula* was co-introduced
481 in the inoculum, enabling low-cell-density *P. gingivalis* to reach similar colonization levels
482 to those achieved by *P. gingivalis* when introduced alone at high cell-density (Figure 5a).
483 Furthermore, *V. parvula* significantly enhanced the ability of high cell-density *P. gingivalis*

484 to colonize, in comparison to high-cell-density *P. gingivalis* when introduced alone (Figure
485 5a).

486

487 Figure 5b shows the levels of *V. parvula* in the different groups. *V. parvula* was a very
488 efficient colonizer reaching similarly high numbers when introduced alone or with *P.*
489 *gingivalis*. It was also observed that in the groups in which *V. parvula* was not exogenously
490 introduced, there was a low number of indigenous *V. parvula* present. This is an expected
491 finding as *V. parvula* has been shown to be a minor component of the oral microbiome of
492 certain strains of mice (44). These basal low levels of indigenous *V. parvula*, however,
493 were insufficient to facilitate colonization of *P. gingivalis*, in agreement with our in vitro
494 batch culture results, which indicated that growth of low cell-density *P. gingivalis* required
495 a minimum threshold biomass of *V. parvula*, beyond which the growth-promoting cue was
496 able to accumulate to a sufficient concentration in the culture spent media.

497

498 **Colonization of *P. gingivalis* promotes periodontal pathology (bone loss)**

499

500 We next assessed the consequences of *V. parvula* and *P. gingivalis* oral colonization by
501 measuring periodontal bone loss in the mice subjected to LIP and locally inoculated, or
502 not, with these bacteria separately or in combination. The colonization of *V. parvula* alone
503 did not increase bone loss in comparison to the PBS negative control group (Figure 5c),
504 confirming that *V. parvula* is normally a symbiotic commensal. In contrast, in mice in
505 which colonization of *P. gingivalis* occurred, either because it was introduced at high-cell-
506 density or at low-cell-density aided by *V. parvula*, there was significantly greater bone loss

507 compared to the PBS control group, in which bone loss is driven solely by dysbiotic
508 indigenous bacteria. Introduction of *P. gingivalis* in the oral cavity of healthy mice (not
509 subjected to LIP) has been shown to cause microbiome dysbiosis and an increase in the
510 total bacterial load (23). To examine if *P. gingivalis* induced greater dysbiosis than that
511 already occurring due to ligature placement, the microbiome composition was determined
512 (Figure 5d). In agreement with the qPCR observations, the 16S rRNA gene data confirmed
513 *P. gingivalis* to be as a minor component of the community, while *V. parvula* occupied
514 about a third of the total biomass when exogenously introduced (Figure 5d). The overall
515 community composition, however, was not dramatically modified by the introduction of
516 *P. gingivalis* but some changes in low-abundance species occurred. When comparing
517 species differentially enriched in mice inoculated with *V. parvula* and *P. gingivalis* versus
518 those inoculated with *V. parvula* alone, it can be seen that in the presence of *P. gingivalis*,
519 a few low-abundance species, including other members of the *Bacteroidetes* phylum,
520 became enriched, while certain *Enterococcus* spp. were depleted (Figure 5e). In contrast to
521 these compositional changes, *P. gingivalis* colonization was not associated with a higher
522 bacterial load (Figure 5f).

523

524 In summary, the symbiotic commensal *V. parvula* enabled a pathogenic species, *P.*
525 *gingivalis*, to colonize the mouse oral cavity and augment bone loss. In this model,
526 colonization of *P. gingivalis* increased the abundance of some minor microbiome
527 constituents, such as other *Bacteroidetes*, although it did not affect the total bacterial load
528 or dramatically altered the microbiome community composition.

529

530 **Discussion**

531

532 In this study, we show that the growth of a pathogen that is implicated in the etiology of
533 the oral disease periodontitis depends on cell-density, which determines the concentration
534 of an endogenous soluble small molecule that is essential for growth. Such an inability to
535 grow from a low cell-density population in vitro was also observed in vivo, as *P. gingivalis*
536 was unable to colonize the oral cavity of mice when introduced at low cell-density. The
537 requirement for this autoinducing soluble factor may restrict the colonization of *P.*
538 *gingivalis* in the human oral cavity. This is consistent with the low detection of *P. gingivalis*
539 in periodontal health, as shown by this study, and its unstable colonization in young
540 individuals (24). Periodontitis, however, is a prevalent condition with severe disease
541 affecting about 10% of the global population (45). As shown in our re-analysis of publicly
542 available subgingival microbiome datasets, about 70% of subjects with periodontitis had
543 detectable *P. gingivalis*. Among those individuals, about 60% had *P. gingivalis* at greater
544 than 1% relative abundance. This sets a scenario in which transmission of this pathogen
545 from humans with severe periodontitis to other unaffected hosts is likely to occur
546 frequently, but colonization of recipients is limited by the inability of *P. gingivalis* to grow
547 from low cell-density inocula.

548

549 Under specific circumstances, however, such as in the presence of undisrupted dental
550 biofilm accumulation, a specific cross-species interaction with a ubiquitous early-
551 colonizing species, *V. parvula*, may allow establishment of *P. gingivalis* in the human oral
552 cavity. *V. parvula* is one of the earliest colonizers of tooth surfaces and becomes a dominant

553 community component as dental biofilms mature (10, 25). *V. parvula* is also a core
554 subgingival species, that is, a species that is present at equal relative abundance in both
555 health-associated and dysbiotic microbiome communities (9). However, since the total
556 community biomass is higher in disease, the total load of *V. parvula* increases in the
557 dysbiotic state. Such increase in biomass of this commensal species during plaque
558 maturation seems to be a key component of the interaction with *P. gingivalis*, since both in
559 vitro and mouse experiments showed that the mere presence of *V. parvula* was insufficient
560 to enable growth of low-cell-density *P. gingivalis*, but instead, high cell numbers of *V.*
561 *parvula* were needed. Therefore, the accumulation of *V. parvula* in dental biofilms, such
562 as those associated with the gingivitis state, may allow establishment of *P. gingivalis* since
563 the soluble factor provided by *V. parvula* would only then reach a threshold concentration
564 for growth of the pathogen. Gingivitis also leads to sporadic bleeding upon tissue
565 stimulation (eg. during tooth brushing) and, as we show here, blood enables growth of *P.*
566 *gingivalis* from even small inocula. The inflammatory exudate present during gingivitis
567 also creates the necessary nutritional environment propitious for the growth of the peptide-
568 dependent and proteinase-rich *P. gingivalis* (26). Accordingly, here we observed a change
569 in detection of *P. gingivalis* from about 1% of subjects in health to about 25% in gingivitis
570 (Fig. 2a). Moreover, as community maturation progresses towards the periodontitis state,
571 *V. parvula* would still be beneficial to *P. gingivalis* helping it maintain a high biomass as
572 indicated by our chemostat and LIP experiments. A model depicting the interaction
573 between *V. parvula* and *P. gingivalis*, as mediated by the accumulation of soluble small
574 diffusible molecules during dental biofilm maturation is shown in Figure 6.
575

576 Although *P. gingivalis* and *V. parvula* are able to coaggregate together, physical contact
577 was not needed for growth stimulation to occur in a closed culture system. The presence
578 of *V. parvula* in co-cultures, however, was beneficial and allowed for faster growth of *P.*
579 *gingivalis*, compared to growth in spent media of the former species. These results suggest
580 that decay of the growth-promoting cue occurs in spent media. Therefore, although direct
581 inter-species cell-to-cell contact is not an absolute requirement for the interaction between
582 *V. parvula* and *P. gingivalis*, it is possible that close inter-species cell-to-cell distance in
583 the open-flow setting of a natural oral community, may facilitate the interaction by
584 delivering the growth-promoting cue to *P. gingivalis* before it decays. Close cell-to-cell
585 distance may also allow an adequate concentration of the cue around *P. gingivalis* cells.

586

587 Characterization of spent media from *P. gingivalis* and *V. parvula* showed that the growth-
588 inducing activity originates from a non-proteinaceous, heat-stable, small molecule, and is,
589 therefore, similar in nature to other quorum-sensing mediators (2). It is not clear, however,
590 whether the growth-promoting cues produced by *P. gingivalis* and *V. parvula* are
591 chemically identical. It is also not known if the growth-promoting factor is a signal that
592 conveys information on cell-density or whether it is a metabolic mediator or nutrient
593 required by *P. gingivalis* to “kick-start” replication. Although much more work is required
594 to identify the molecule(s) responsible for inducing growth, our data suggest that the nature
595 of the interaction between *P. gingivalis* and *V. parvula* is unidirectional (commensalism)
596 as no obvious benefit was seen for the latter species. In accordance with this, the molecule
597 mediating the interaction could be considered in an evolutionary context as a ‘cue’, and not
598 a ‘signal’ (2), as *V. parvula* does not seem to directly benefit from interacting with *P.*

599 *gingivalis*. In contrast, *P. gingivalis* exploits several aspects of the metabolism of *V.*
600 *parvula*. Apart from providing a growth-initiating factor, *V. parvula* has been shown to
601 produce heme which is the preferred iron source for *P. gingivalis* (46). *Veillonella* is also
602 able to detoxify hydrogen peroxide produced by other early colonizing species via its
603 catalase activity, facilitating growth of less oxygen-tolerant anaerobes (16). Therefore,
604 *Veillonella* interacts with *P. gingivalis* via distinct mechanisms that collectively support
605 the establishment of the latter in the gingival crevice. In this context, therefore, *V. parvula*
606 behaves as an ‘accessory pathogen’, *i.e.*, an organism that, while commensal in a particular
607 microenvironment, can also support or augment the colonization and/or virulence of
608 pathogenic microorganisms (47).

609

610 Different types of inter-species interactions occur in polymicrobial communities. While
611 two-species interactions are the simplest type, in natural environments interactions can
612 occur among several species, generating indirect and emergent effects. Despite this
613 potential complexity, here we demonstrate that the dual species interaction between *V.*
614 *parvula* and *P. gingivalis* was relevant within the context of a community; and although
615 we do not exclude the possibility that higher order interactions also took place, the pairwise
616 interaction remained valid in a polymicrobial environment. In one of the community
617 models tested *in vitro* (the 6-species community), it was shown that member species other
618 than *V. parvula* did not directly interact with *P. gingivalis*, and therefore, *V. parvula* was
619 the only relevant partner. However, in the mouse oral cavity, the interactions of local
620 commensals and *P. gingivalis* were uncertain and yet, low-cell-density *P. gingivalis* was
621 unable to grow when inoculated alone, whereas *V. parvula* was able to support its

622 colonization. These findings highlight the importance of the specific interaction discovered
623 and show that it is possible to identify key pairwise inter-interactions within complex
624 communities. It would be relevant to investigate if other human dental plaque species,
625 different to the early colonizers tested here, are able to support growth of *P. gingivalis*,
626 since our work suggests that limiting the biomass of potential accessory pathogens, such
627 as *Veillonella*, may preclude *P. gingivalis* from colonizing the oral cavity. Excluding *P.*
628 *gingivalis* could in turn block the growth of other species within pathogenic communities
629 whose growth depends on the immune dysregulation induced by *P. gingivalis* (23).

630

631 Experiments using the mouse LIP model show that *P. gingivalis* colonization of an already
632 dysbiotic microbiome augmented bone loss, confirming its pathogenic capacity, in contrast
633 to *V. parvula*, which did not have any effect in that regard. In another mouse model of *P.*
634 *gingivalis*-induced bone loss, the microorganism is inoculated via swabs into orally healthy
635 mice (48). In that oral inoculation model, repeated introduction of *P. gingivalis* leads to its
636 establishment as a low-abundance member of the microbiome that induces bone loss by
637 manipulating the host inflammatory response and undermining the effectiveness of
638 immune bacterial clearance (22, 23). Thus, in the oral inoculation model, *P. gingivalis* acts
639 as a keystone pathogen leading to an increase in the whole commensal community biomass
640 and to qualitative changes in community composition, which is thought as the cause of
641 bone loss (23). There are some similarities between that oral inoculation model (48) and
642 our current work. In the LIP model used in our study, *P. gingivalis* also became a minor
643 constituent (about 0.1%) of the total community biomass, augmenting bone loss beyond
644 that already produced by ligature placement alone. However, in contrast to the oral

645 inoculation model, here *P. gingivalis* did not cause an increase in bacterial load or dramatic
646 compositional changes to the microbiome beyond those already present. In other words,
647 whereas *P. gingivalis* induces *de novo* alterations to the community structure in the oral
648 inoculation model (23), it does not appear to profoundly enhance LIP-induced dysbiosis.
649 However, *P. gingivalis* colonization caused an enrichment of some minor microbiome
650 components, including other *Bacteroidetes* species, the significance of which in any
651 pathogenic process is currently uncertain. The two models therefore agree in that *P.*
652 *gingivalis* can promote bone loss even as a low-abundance community member, but the
653 mechanisms by which *P. gingivalis* augments bone loss in the two models may be different.
654

655 Although the tooth-associated subgingival biofilm is the predominant habitat of *P.*
656 *gingivalis*, this pathogen and virulence factors thereof have been localized in remote tissues
657 in association with comorbid conditions (14). For instance, in Alzheimer's disease, *P.*
658 *gingivalis* was shown to ectopically infect the brain of humans and mice and to correlate
659 with or cause neuronal pathology, in humans and mice, respectively (49). As shown here,
660 low cell-density *P. gingivalis* is able to grow in the presence of blood. Although the
661 mechanism by which blood promotes growth is still unclear, this finding has important
662 implications, suggesting that *P. gingivalis* can replicate, irrespective of its cell-density, in
663 the circulation. Therefore, approaches to control the growth of *P. gingivalis* in its
664 predominant habitat (which serves as a reservoir for its systemic dissemination) may help
665 reduce the risk of periodontal comorbidities in which *P. gingivalis* is implicated. Our work
666 provides a novel target to control the growth of *P. gingivalis* (and hence its dissemination);
667 although an indirect method, successful targeting of the accessory pathogen *V. parvula*

668 should prevent the ability of *P. gingivalis* to expand within the oral microbial community
669 to levels at which it can become pathogenic.

670

671 Altogether, our work demonstrates that a requirement for a cell-density dependent soluble
672 cue limits growth and colonization of the human oral pathogen *P. gingivalis*. This inability
673 to establish from a small inoculum is overcome by forming a specific partnership with a
674 ubiquitous commensal species of human dental biofilms, which, after increasing in
675 biomass, is able to provide the growth-initiating factor at the concentration required by *P.*
676 *gingivalis*. These results shed light into some of the mechanisms behind dental biofilm
677 microbial successions and highlight the role of cell-density-mediated interactions between
678 early- and late-colonizers ultimately leading to pathogen colonization and virulence.

679

680

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687

688 **Author Contributions**

689 PID, NMM, PDM and GH contributed to study design and supervised research. AH, HW
690 and AM performed experiments. PID, AH, LA and BYH analyzed data. PID and AH
691 drafted the manuscript. All authors read, critically revised and approved the manuscript.

692

693 **Competing Interests Statement**

694 All authors declare no conflict of interest with the research reported in this manuscript.

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831

832 **Figure Legends**

833

834 **Figure 1. Growth of *P. gingivalis* (Pg) is dependent on a soluble factor accumulated**

835 **at high cell-density. a.** Growth of Pg strain 381 in mucin-serum liquid medium is

836 dependent on the size (cells mL⁻¹) of the inoculum. Cultures inoculated at various cell

837 densities were incubated and sampled anaerobically, followed by determination of growth

838 via qPCR. **b.** Mucin-serum spent-medium (SM) from a Pg 381 stationary phase culture

839 restored the growth of a low-cell-density inoculum (10⁵ cells mL⁻¹) of Pg 381. Pg was

840 inoculated in fresh mucin-serum containing the indicated proportion (vol/vol) of SM. **c.**

841 SM from a Pg 381 stationary phase culture grown in brain heart infusion (BHI)

842 supplemented with cysteine, hemin (H) and menadione (M) restored the growth of a low-

843 cell-density inoculum (10⁵ cells mL⁻¹) of Pg 381. Pg was inoculated in fresh BHI-H-M

844 containing the indicated proportion (vol/vol) of SM and growth was monitored via optical

845 density (OD). * represents a p value <0.05, as determined by t tests, when comparing at

846 each time point the test conditions to the no SM control. Growth was considered

847 significantly different if a p <0.05 was achieved at days 3, 4 and 5. At least 6 replicates

848 were included per condition. **d.** SM from Pg 381 augmented the number of colony forming

849 units (CFUs) recovered on BHI-H-M agar. Pg was diluted in PBS or SM and plated at

850 different densities. The number of CFUs obtained was compared to the number expected

851 according to microscopic counts. * represents a p value <0.05 as determined by t tests. **e.**

852 Pg soluble factor capable of supporting its growth from a low-cell-density inoculum is

853 smaller than 3 kDa, is heat-stable and is protease resistant. SM from Pg 381 grown in

854 mucin-serum was filtered through 3 kDa membranes and either heat-inactivated (HI) or

855 treated with proteases, followed by lyophilization and reconstitution (10x) in dH₂O.
856 Reconstituted fractions (Conc = > 3kDa and Filtr = < 3 kDa) were added to fresh mucin-
857 serum medium (1:3, vol:vol) to evaluate growth of low-cell-density (10⁵ cells mL⁻¹) Pg.
858 Data in all panels represent replicates (mean and standard deviation) from at least three
859 independent experiments.

860

861 **Figure 2. Growth of low-cell-density *P. gingivalis* (Pg) is supported by a community**

862 **of species that are abundant in early subgingival biofilms.** Detection (a) and relative

863 abundance (b) of Pg in subgingival plaque in states of periodontal health (H), gingivitis

864 (G) and periodontitis (P). Detection (c) and relative abundance (d) of *Veillonella parvula*

865 (*Vp*), *Actinomyces oris* (*Ao*), *Streptococcus sanguinis* (*Ss*), *Fusobacterium nucleatum*

866 subsp. *polymorphum* (*Fn pol*) and *Rothia dentocariosa* (*Rd*) in subgingival plaque at

867 different disease stages. Lines in relative abundance graphs represent median and

868 interquartile range. Data in panels A-D were obtained from 10 publicly available studies

869 as raw sequences (9-11, 19, 31-36), then processed and analyzed as described in Methods.

870 e. Co-inoculation of Pg with *Vp*, *Ao*, *Ss*, *Fn* and *Rd* in mucin-serum results in growth of

871 all species and enables growth of a low-cell-density inoculum of Pg. All species were

872 inoculated together, each at a density of 10⁵ cells mL⁻¹ and cultures incubated and sampled

873 under anaerobic conditions. Cell numbers of *Vp*, *Ao*, *Ss* and *Fn* were determined by plating

874 on selective media. Biomass of Pg and *Rd* was determined via qPCR. f. Individual growth

875 of species in the supporting community is not cell-density-dependent as shown by the

876 ability of all species to grow in monoculture in mucin-serum when inoculated at a density

877 as low as 10³ cells mL⁻¹.

878

879 **Figure 3. *V. parvula* (Vp) is the key species that through a diffusible factor supports**
880 **growth of low-cell-density *P. gingivalis* (Pg).** **a.** Growth of Pg when co-inoculated (at 10^5
881 cells mL^{-1}) in mucin-serum with either Vp, *Actinomyces oris* (Ao), *Streptococcus sanguinis*
882 (Ss), *Fusobacterium nucleatum* (Fn) or *Rothia dentocariosa* (Rd). Graph shows Pg growth
883 as determined via qPCR. **b.** Presence of Vp is essential for the growth of a low cell-density
884 inoculum of Pg. Graph shows Pg growth, as determined via qPCR, when inoculated
885 together with all initial colonizers, in the absence of Vp, or as a monoculture. **c.** Evaluation
886 of the effect of Vp spent medium (SM), collected at different times during Vp growth, on
887 growth of low cell-density Pg. SM was collected from a Vp batch culture grown in mucin-
888 serum. Green curve in left panel indicates Vp cell concentrations during growth and arrows
889 show times at which Vp SM was collected. Right panel shows growth of low cell-density
890 Pg (10^5 cells mL^{-1}) in Vp SM collected at different time points of the Vp growth curve. **d.**
891 Evaluation of the effect of different concentrations of Vp SM (collected at 24 h) on growth
892 of a low-cell-density Pg inoculum showing dose-dependent stimulation of growth by Vp
893 SM. **e.** Soluble factor in Vp SM capable of supporting growth of low-cell-density Pg is
894 smaller than 3 kDa, is heat-stable and is protease resistant. SM from Vp grown for 24 hours
895 in mucin-serum was filtered through 3 kDa membranes and either heat-inactivated (HI) or
896 treated with proteases, followed by lyophilization and reconstitution (10x) in dH_2O .
897 Reconstituted fractions (Conc = $> 3\text{kDa}$ and Filtr = $<3\text{kDa}$) were added to fresh mucin-
898 serum medium (1:3, vol:vol) to evaluate growth of low-cell-density Pg (10^5 cells mL^{-1}).
899

900 **Figure 4. *V. parvula* (Vp) helps *P. gingivalis* (Pg) maintain a high biomass when**
901 **growing as part of a polymicrobial community under open-flow continuous-culture**
902 **conditions. a.** Pg was co-inoculated in a chemostat in mucin-serum with *Actinomyces oris*
903 (*Ao*), *Streptococcus sanguinis* (*Ss*), *Fusobacterium nucleatum* (*Fn*) and *Rothia*
904 *dentocariosa* (*Rd*). **b.** Vp was added to the initial inoculum together with Pg, Ao, Ss, Fn
905 and Rd. **c.** Pg was initially co-inoculated with Ao, Ss, Fn and Rd (in the absence of Vp)
906 and the culture was allowed to achieve steady-state, after which Vp was added. **d.** Direct
907 comparison of Pg biomass at steady-state (including 3 time points after 15 mean generation
908 times, MGT) in the absence and presence of Vp. In all experiments, a high density (10^8
909 CFU/mL) inoculum was employed for all species. Cell numbers of Vp, Ao, Ss and Fn were
910 determined by plating on selective media. Biomass of Pg and Rd was determined via qPCR.
911 **** represents $P < 0.0001$ after t-tests.

912

913 **Figure 5. *V. parvula* (Vp) allows a low-cell-density inoculum of *P. gingivalis* (Pg) to**
914 **colonize and augment bone loss in a ligature-induced periodontitis murine model. a .**
915 Pg levels measured via qPCR on ligatures retrieved 5 days post-inoculation. Horizontal
916 line shows limit of detection of the assay. **b.** Vp levels of retrieved 5-day ligatures as
917 evaluated via qPCR. Horizontal line shows limit of detection of the assay. **c.** Alveolar bone
918 levels after 5 days of ligature placement and inoculation. **d.** Microbiome composition of
919 retrieved 5-day ligatures as evaluated via 16S rRNA gene sequencing. **e.** LEfSe evaluation
920 of operational taxonomic units (OTUs) with different relative abundance when Vp was
921 inoculated alone in contrast to Vp co-inoculated with Pg. **f.** Total bacterial load of retrieved
922 5-day ligatures as evaluated via qPCR and universal primers. *** indicates a p value

923 <0.001, ** indicates a $p < 0.01$ and * a $p < 0.05$ (Mann-Whitney Rank tests). NS= not
924 statistically significant.

925

926 **Figure 6. Model depicting *V. parvula* (Vp)-*P. gingivalis* (Pg) interaction during dental**
927 **biofilm community development. a.** During early stages of biofilm formation on tooth
928 surfaces, Pg is not able to establish since it cannot grow from a low-cell-density population.
929 Vp does not depend on cell-density so it can grow and become established during early
930 stages of biofilm maturation. **b.** If dental communities are left undisturbed, as is the case
931 in gingivitis, Vp increases in biomass, producing a low-mass soluble factor that
932 accumulates to a threshold concentration capable of supporting growth of Pg. **c.** Once Pg
933 becomes established at high-cell-density, such as in a dysbiotic biofilm associated with
934 periodontitis, its growth is supported by its own soluble low-mass growth factor. Vp, which
935 is also an abundant species in mature plaque (core species) contributes to stabilizing Pg
936 biomass in the dysbiotic periodontitis-associated community.