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MARINE MICROBIOLOGY

An interkingdom partnership

> these molecules induce transcriptomic changes that facilitate a mutually beneficial exchange of metabolites

Bacterial inhabitants of the rhizosphere exchange nutrients and signals with plant cells, which often benefits the growth of both partners. Whereas plants are the primary producers of carbon in terrestrial ecosystems, photosynthetic microorganisms, such as the diatom *Pseudo-nitzschia multiseries* PC9, fulfil this function in the ocean and secrete chemicals into a rhizosphere analogue known as the phycosphere. However, whether diatoms and bacteria form tightly associated communities within the phycosphere has been challenging to establish, especially owing to the turbulent environment of the ocean and the free movement of diatoms. Now, Amin *et al.* report a highly specific partnership between *P. multiseries* PC9 and the bacterium *Sulfitobacter* SA11, which is the result of a mutually beneficial exchange of nutrients and signalling molecules.

To investigate interactions between diatoms and marine bacteria, the authors isolated 49 bacterial strains that co-occur with *P. multiseries* in the ocean, which were subsequently identified by 16S rDNA sequencing. Co-culture experiments with *P. multiseries* PC9 showed that only four of these isolates, all of which belonged to the *Sulfitobacter* genus, enhanced the growth rate of the diatom, whereas isolates from other genera did not. Notably, the growth advantage was mutually beneficial for the diatom and the bacterium, as co-culture with *P. multiseries* PC9 also sustained the growth of *Sulfitobacter* SA11. Furthermore, this partnership was highly specific: *Sulfitobacter* isolates stimulated the growth of only a subset of *P. multiseries* strains, whereas other *P. multiseries* strains and another diatom species were unaffected; and the growth of *Sulfitobacter* SA11 was sustained only by the subset of *P. multiseries* strains that responded to the bacterium.

To identify the mechanisms by which *P. multiseries* PC9 and *Sulfitobacter* SA11 provide a growth advantage to one another, the authors used transcriptomics to establish which metabolic pathways were differentially regulated in co-cultures compared with axenic cultures. These data revealed complementary changes in genes that function in the metabolism of carbon sources such as taurine, with upregulation of taurine biosynthesis in *P. multiseries* PC9 and upregulation of taurine uptake and catabolism in *Sulfitobacter* SA11, which suggested that diatom-produced carbon sources sustain the growth of *Sulfitobacter* SA11. In return, the bacterium seems to provide *P. multiseries* PC9 with ammonium, which is energetically costly; although *P. multiseries* PC9 can produce ammonium, the genes involved were downregulated in co-cultures, whereas the corresponding genes in *Sulfitobacter* SA11 were upregulated.

Changes in the biosynthetic pathways of two signalling molecules, tryptophan and its derivative indole-3-acetic acid (IAA), were also detected, which suggested that, in co-cultures, *P. multiseries* PC9 increases the production and secretion of tryptophan, which is taken up by *Sulfitobacter* SA11. The bacterium uses tryptophan as a substrate for the production and secretion of IAA, which is then taken up by *P. multiseries* PC9.

The authors conclude that tryptophan secreted by *P. multiseries* PC9 is naturally concentrated in the phycosphere, which enables *Sulfitobacter* SA11 to detect it; in response, *Sulfitobacter* SA11 signals its presence by secreting IAA. Together with additional signalling by unknown molecules, these molecules induce transcriptomic changes that facilitate a mutually beneficial exchange of metabolites, including carbon and nitrogen sources, in the phycosphere. The authors propose that the choice of signalling molecules might underlie the specificity of the partnership.

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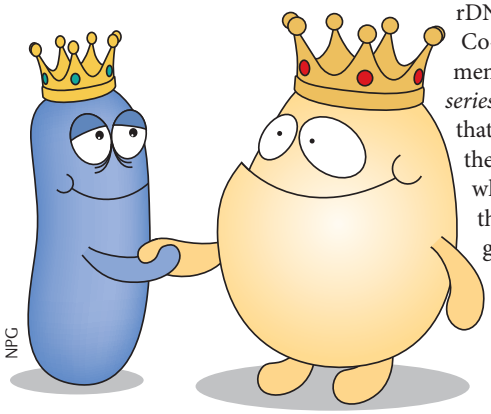

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ORIGINAL RESEARCH PAPER Amin, S. A. *et al.* Interaction and signalling between a cosmopolitan phytoplankton and associated bacteria. *Nature* **522**, 98–101 (2015)