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Trends in Microbiology

Opinion

Swimming towards each other: the role of chemotaxis in bacterial interactions

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Chemotaxis allows microorganisms to direct movement in response to chemical stimuli. Bacteria use this behaviour to develop spatial associations with animals and plants, and even larger microbes. However, current theory suggests that constraints imposed by the limits of chemotactic sensory systems will prevent sensing of chemical gradients emanating from cells smaller than a few micrometres, precluding the utility of chemotaxis in interactions between individual bacteria. Yet, recent evidence has revealed surprising levels of bacterial chemotactic precision, as well as a role for chemotaxis in metabolite exchange between bacterial cells. If indeed widespread, chemotactic sensing between bacteria could represent an important, but largely overlooked, phenotype within interbacterial interactions, and play a significant role in shaping cooperative and competitive relationships.

Introduction

Bacteria experience chemical landscapes that are heterogeneous over spatial scales traversable by individual cells, whereby the ability to purposefully direct movement can enhance fitness [1]. Chemotaxis delivers this capacity by allowing cells to migrate up or down chemical gradients, towards beneficial chemicals or away from toxic substances, and is therefore an important phenotype that is common across diverse prokaryotic lineages [2]. This behaviour can influence the growth, diversity, pathogenesis, distribution, and symbiotic relationships of microbial communities [3,4], while also potentially shaping the productivity and biogeochemistry of ecosystems [5,6].

It has long been known that bacteria release metabolites into the surrounding environment, which can be used by other bacterial cells [7]. There is also evidence that chemotaxis towards microbial metabolites is involved in the establishment and maintenance of some intermicrobial relationships [8]. Yet, previous estimates based on the chemotaxis parameters of *Escherichia coli* have concluded that the smallest target cell that can be sensed by a chemotactic bacterium is 4 μm in diameter [9], thereby precluding chemosensing of all but relatively large bacterial species. However, by considering deviations from the classical model for bacterial chemotaxis and integrating recent evidence for a role of chemotaxis in metabolic interactions among small bacterial cells [10,11], we ask whether chemotactic sensing between individual bacterial cells might indeed be common, and what this would mean for interbacterial relationships.

The classical model for bacterial chemotaxis

The biophysical and biochemical processes involved in bacterial chemotaxis have been remarkably well characterised in a handful of model organisms, in particular the enteric bacterium *E. coli*. Within the classical *E. coli* model, motility is achieved through the rotation of multiple (four to eight) flagella, which propel cells through the environment in what has been described as 'run and tumble motility'. This motility pattern consists of a sequence of relatively straight 'runs' that are intermittently interrupted by random reorientations or 'tumbles' [12]. The stochastic switching between

Highlights

Bacteria release metabolites into the surrounding environment, which can potentially be utilised by other bacteria.

Current understanding of the limits of bacterial chemotaxis derived from the classic *Escherichia coli* model suggests that bacteria cannot use chemotaxis to detect targets smaller than a few micrometres in diameter, precluding the utility of chemotaxis in interactions between individual bacteria.

Many bacteria exhibit chemotactic capacity that deviates from the classic *E. coli* model for chemotaxis, with some species displaying substantially heightened levels of chemotactic precision, potentially permitting chemosensing of small bacterial targets.

There is recent evidence for a role for chemotaxis in metabolite exchange between small bacterial cells.

Chemotactic sensing between bacteria could play a significant role in shaping interbacterial interactions.

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runs and tumbles ultimately results in a random-walk exploration of the environment. The direction of this random walk can, however, be biased through chemotaxis, allowing cells to migrate up or down chemical gradients. This is achieved through the modulation of tumbling frequency according to temporal measurements of the external chemical environment made with membrane-bound chemoreceptors, whereby information from the chemoreceptors is transferred to the flagella motor via a sophisticated intracellular transduction pathway [13]. The precision of the chemotactic response is governed by a suite of parameters, including the sensitivity of chemoreceptors [14], signal processing times [15], and, in some bacteria, the cell's swimming speed [16].

The traditional view of chemotactic targets

Bacteria possess chemoreceptors for a wide diversity of chemicals [17] and use chemotaxis to migrate towards a variety of microenvironments, such as those associated with the internal and external surfaces of other organisms [4]. Indeed, chemotactic responses often represent a critical phenotype within pathogenic, mutualistic, and commensal interactions between bacteria and host organisms. Some notable examples include the establishment of animal–bacteria symbiosis following chemotactic colonisation of the light organ of the bobtail squid by *Aliivibrio fischeri* [18], and chemotaxis to root exudates by beneficial bacteria within the plant rhizosphere [19]. Furthermore, several significant pathogens use chemotaxis to colonise infection sites within the human body, including microenvironments associated with damaged or inflamed tissue [20].

A number of intermicrobial interactions, including mutualistic partnerships that bacteria develop with phytoplankton [21], amoebae [22], and protozoans [4], require bacterial chemotaxis towards metabolites released by the partner microorganism. There is also some evidence for the importance of chemotaxis in interbacterial relationships involving large filamentous bacteria [23,24], biofilms [25], or macroscopic colonies [26], and the clustering of bacteria into patches will potentially generate high concentration substrate plumes that are readily detectable by chemotaxis [27,28]. However, the role of chemotaxis in single cell-to-cell interactions among small bacteria has rarely been considered.

Not all bacteria swim like *E. coli*

The enteric bacterium *E. coli* is one of the most celebrated model systems for chemotaxis, and many conclusions about the implications of chemotactic navigation (e.g., for enhancing nutrient uptake and facilitating microbial interactions) are based upon this system. The sophisticated signalling pathway underpinning *E. coli*'s run-and-tumble motility [29] has been completely characterised, from structural and biochemical standpoints, making it one of the best studied pathways in biology [13]. Consequently, the full pathways can be simulated using mathematical models, making it an appealing model system for examining the role of chemotaxis. However, many bacteria have fundamentally different cell architecture and signalling pathways. For example, many species – including most marine bacteria – possess only one flagellum, and employ a run-reverse-flick mode of motility [30], which involves a simple back-and-forth movement, whereby reorientation of cells occurs as a consequence of a buckling instability of the flagellar hook [31]. This and other motility patterns that diverge from the *E. coli* model in fact appear to be relatively widespread across different bacterial species and, importantly, can result in heightened chemotactic performance [31–33].

Compared with *E. coli*, much less is known about the chemotaxis signalling pathways of other bacteria. Observed behavioural responses reveal major differences in the chemotactic capabilities, in both the speed of the response and the final tightness of bacterial accumulation around the source of the chemoattractants. Both of these parameters are important determinants of a bacterium's capacity to navigate towards a small source of chemoattractant, such as another bacterial

cell, with evidence that the minimum nutrient pulse or gradient that can be sensed by chemotactic bacteria can vary dramatically between species. For example, the marine bacterium *Pseudoalteromonas haloplanktis* responded ten times more rapidly than *E. coli* to microscale chemical pulses [32], while *Vibrio alginolyticus* accumulated threefold faster and sevenfold more tightly than *E. coli* towards the amino acid serine at a concentration of 500 μM [33], and chemotactic responses of *Vibrio ordalii* were observed at distances up to 0.5 mm from a 0.01 pmol pulse of glutamate [34]. It is hypothesised that the reason behind this exquisite sensitivity is that some bacteria (e.g., those inhabiting marine environments) have adapted mechanisms for navigating in nutrient-poor environments towards extremely small targets, which is in stark contrast to the nutrient-rich environments typically experienced by *E. coli* [35].

Could chemotaxis play a role in the interactions between bacterial cells?

Biophysical constraints

Motility and chemotaxis have the capacity to increase spatial interactions between bacteria, given that the importance of other physical processes, such as Brownian motion, are negligible compared with motility-induced encounters. Indeed, a bacterium of radius 1 μm, swimming at 30 μm/s would have a motility-induced diffusion coefficient approximately three orders of magnitude larger than the translational diffusion coefficient of a non-motile cell due to Brownian motion [29], indicating that Brownian motion does not play a significant role in bringing motile bacteria close together.

The ecological roles of bacterial chemotaxis are determined by the size and nature of chemical gradients that bacteria are capable of sensing. The mechanisms by which individual microorganisms produce chemical gradients vary, from constant exudation to cell lysis, and these qualitatively distinct chemical profiles and spatiotemporal dynamics can elicit different chemotactic responses by other cells. The size of a chemical gradient surrounding a bacterium can be influenced by the size of the emitting cell, the growth rate of the cell, the identity of the exuded chemical, its exudation rate, and its background concentration in the environment. To explore the potential for smaller cells (i.e., bacteria) to act as chemotactic targets, here we focus mainly on the effect of the size of the emitting cell. Varying the chemoattractant source size not only influences the quantitative features of chemotactic responses (e.g., level of nutrients acquired by the chemotactic bacterium), but can have qualitative effects, such as impacting the type of target cells that chemotactic bacteria can interact with. It is therefore important to determine the fundamental limits for chemotactic navigation.

The precision of bacterial chemotaxis refers to how well a cell can sense and navigate chemical gradients (Figure 1). A variety of quantitative methods can be used to characterise chemotactic precision. These can include macroscopic properties of bacterial behaviour, such as the chemotactic drift velocity of cells along a chemoattractant gradient, or the tightness of bacterial accumulation around a chemical source [16] (localisation precision). It is often instructive to compare the measured chemotaxis capabilities with fundamental limits set by physics. Many bacteria integrate a time-series of encounters with attractant molecules [12]. These molecular encounters are inherently discrete due to ligand binding/unbinding, and subject to significant noise for weak gradients, which can prevent gradient detection. The precision of bacterial chemotaxis is ultimately limited by the cell's estimate of the gradient, with other characteristics (e.g., signalling pathways, motility modes) placing additional limitations on the precision. Berg and Purcell's pioneering work modelled a cell as a sphere that absorbs all molecules reaching its surface [36], and therefore represents an optimal detector. Their study and the many that have built upon it [37–39] have assessed the performance of cells with respect to these fundamental limits and provided quantitative benchmarks for characterising chemotactic precision.

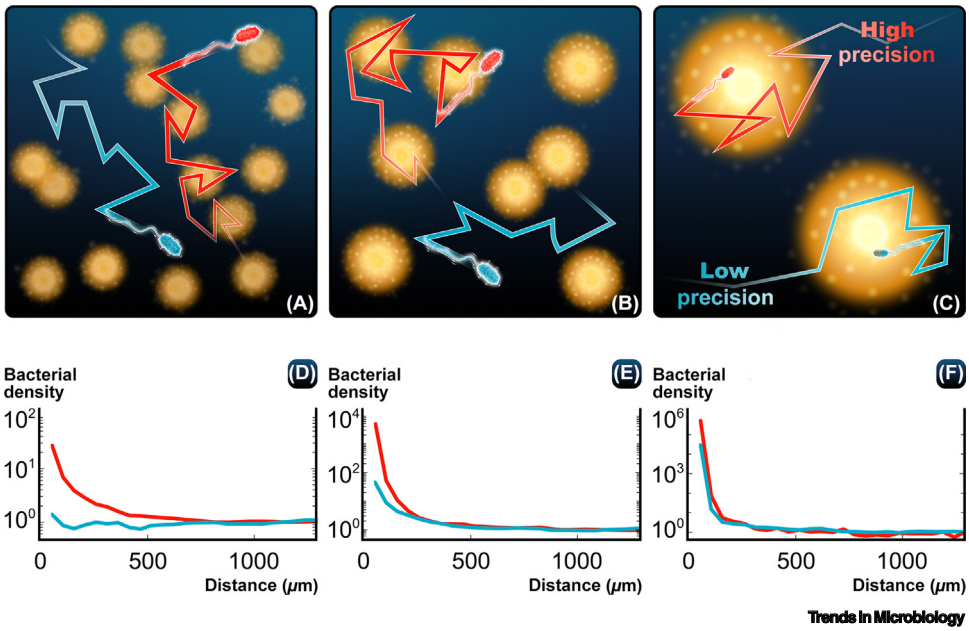

Figure 1. The capacity of chemotactic bacteria to use chemotaxis to home in on other bacteria depends on their chemotactic precision and the size of the target cells. Example trajectories are shown for cells having high (red) and low (blue) chemotactic precision navigating a suspension of (A) small, 1 μm; (B) medium, 5 μm; and (C) large, 50 μm, target cells (here only represented by the size of the chemical gradients they emit). High precision chemotaxis is required to locate small target cells, whereas large target cells can elicit a chemotactic response from a greater variety of bacteria. Simulations of large numbers of chemotactic bacteria using established models [10,34] yield the steady state density of bacteria around single target cells of different sizes (D, E, F corresponding to target sizes in A, B, C, respectively). The chemotactic precision most strongly influences the bacterial distribution around small targets (D, 1 μm), where gradients are weak and spatially localised, whereas its importance diminishes for larger targets (E, 5 μm; F, 50 μm), which produce strong gradients that bacteria can navigate well also with relatively low precision chemotaxis. These results reveal that the capacity to use chemotaxis to target individual bacteria of approximately 1 μm in size is highly sensitive to the chemotactic precision of bacteria. Artwork: Philippe Plateaux.

The features of bacterial motility strongly influence the precision of the chemotactic response. The temporal gradient perceived by a moving cell is proportional to its swimming speed, v, and in the limit of weak gradients, increasing v can enhance the cell's ability to sense the gradient [38]. Examples include *V. alginolyticus* and *V. ordalii*, which are known to swim several times faster than *E. coli* and exhibit higher chemotactic performance [29,33]. However, an increased swimming speed typically comes at the cost of an enhanced bacterial diffusivity, D, which grows as the square of the swimming speed, v^2 [40]. This higher diffusivity results in a reduced capacity for a bacterium to retain its position at the top of a chemoattractant gradient (i.e., near to the source) once the cell has located it. Some bacteria prevent this increase in diffusivity by turning more frequently when their speed increases [16], which reduces the tendency of cells to disperse, thereby improving their precision. High performance chemotaxis towards small targets indeed likely arises from trade-offs across a suite of motility and chemotaxis parameters (e.g., swimming speed, turning frequency, signal processing times, motility modes).

In addition to the movement strategies and sensing capabilities of cells, quantitative features of the chemical landscape also determine whether chemotactic bacteria can detect and migrate across chemical gradients. For any attractant profile, the landscape can be partitioned into zones where chemotaxis is possible and those where noise dominates. The nature of this partition depends on many factors, including the diffusivity of the chemoattractant (Box 1). Weaker gradients are typically associated with smaller chemoattractant sources [9] – the combined

Box 1. The importance of chemical diversity in interbacterial chemotaxis

The chemotactic capacity of bacteria is not the only factor dictating their ability to navigate towards other cells. The physicochemical characteristics of emitted molecules also play an important, albeit overlooked, role in this process. Cellular exudation and lysis of bacterial cells lead to the release of an enormous diversity of molecules into the surrounding environment [69], ranging from large polymers (e.g., proteins, polysaccharides), to low-molecular-weight compounds (e.g., lipids, amino acids, monosaccharides), and even gases (e.g., organic or inorganic volatiles). To what extent these molecules are used as chemotactic cues for other nearby bacteria will depend on how rapidly the exuded chemicals disperse from the emitting cell after their release [70]. This will be dictated by the size and polarity of the exuded metabolites. Upon release, large or non-polar molecules will remain close to the cell for longer periods than small and polar molecules, which will diffuse away more rapidly from the exuding cell. If we consider three types of molecules released by a bacterial cell in equal amounts, a polysaccharide (diffusivity: $D = 10^{-12}$ m^2 s^{-1}), a small amino acid ($D = 10^{-10}$ m^2 s^{-1}), and an organic volatile ($D = 10^{-9}$ m^{2}s^{-1}), their concentration profiles around the cell will differ markedly, creating different chemotactic signals for other bacteria (Figure I). This is important from the standpoint of neighbouring chemotactic bacteria because (i) these cells have the capacity to simultaneously detect gradients of multiple molecules; and (ii) the spatial distribution of the gradients will differ according to the molecule type (Figure I). Indeed, small molecules and volatiles will produce long-range but weaker gradients that attract diverse chemotactic cells from afar, while more complex and specific molecules will produce short-range gradients that will remain near the exuding cell and might be involved in more selective interbacterial interactions. Note: the production of large molecules may come at greater metabolic cost, perhaps influencing the amount exuded and therefore their ability to act as signalling chemicals.

Until now, experimental work and simulations have mostly explored the behaviour of chemotactic prokaryotes towards gradients composed of only one molecule. Although this body of work has been invaluable in identifying physical and biological constraints influencing prokaryotic behavioural responses, the chemical diversity of the gradients encountered by chemotactic prokaryotes and their effect on behaviour have been overlooked. Such complex chemical landscapes, composed of hundreds of overlapping gradients, can increase the spatial footprint of chemotaxis, potentially allowing for the recruitment of chemotactic prokaryotes from greater distances and towards smaller targets than previously estimated.

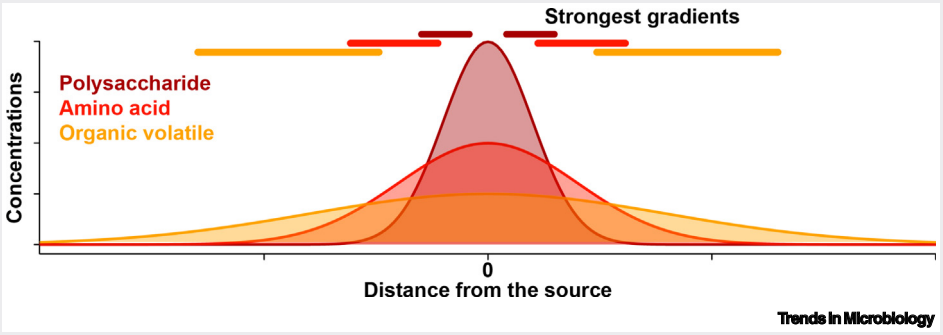

Figure I. Chemoattractant concentration profiles vary. Concentration profiles of three types of molecules with different diffusivities, released in equal amounts by a cell (the 'source'). Diffusivities in water were approximated to 10^{-12} m^2 s^{-1} for the polysaccharide, 10^{-10} m^2 s^{-1} for the small amino acid, and 10^{-9} m^2 s^{-1} for the organic volatile. Regions displaying the strongest gradient (i.e., the strongest chemotactic signal) are displayed above the graph for each molecule.

effects of gradients being smaller and weaker highlight the difficulty of finding a single bacterial target using chemotaxis. A key parameter which characterises the nature of chemotactic interactions is the typical size of the chemoattractant source, R_g, compared with the mean run length, L, of a chemotactic bacterium executing a random walk. For many chemical sources emanating from larger microbes such as phytoplankton, R_g/L exceeds 100, indicating that chemotaxis can facilitate navigation towards the target [41]. However, for small bacterial targets, R_g/L can be in the order of ~1 [10], whereby the random motion of chemotactic bacteria places significant limits on their capacity to locate the target. Targets of this size were previously considered too small to be detected by chemotactic bacteria [9], based on the chemotactic motility and in particular precision of *E. coli*. However, recent evidence points towards much greater precision in some bacteria [34], which could facilitate chemotaxis towards small targets.

Environmental evidence

Most prokaryotic symbioses described to date involve eukaryotic hosts, whereby chemotactic bacteria can colonise both external surfaces and internal organs of their hosts [4,42]. Similarly, direct cell–cell interactions between prokaryotes likely require either attachment or close spatial proximity. With the exception of interbacterial interactions involving large filamentous bacteria (e.g., *Anabaena* spp., *Thioploca* spp., Ca. *Electronema* spp.), which can be mediated by chemotaxis [23,24,43], close spatial associations between smaller prokaryotes have rarely been investigated.

Lake waters harbour some of the earliest reported examples of direct prokaryotic interactions, including the phototrophic consortia formed by episymbiotic green-sulfur bacteria that completely surround a central motile and chemotactic cell phylogenetically related to Burkholderiaceae [44,45]. At least ten phylogenetically distinct types of phototrophic consortia have been described to date, and they can represent up to two-thirds of the total bacterial biomass at the chemocline of stratified freshwater lakes [44,45]. Similar tight associations between green-sulfur bacteria and motile Desulfuromonadaceae have been reported in other aquatic environments [46]. While the onset of these symbiotic consortia is still a mystery, there remains the possibility that chemotaxis is involved.

In the marine environment, metabolites produced by the picocyanobacteria *Synechococcus* and *Prochlorococcus* (the most abundant photosynthetic organisms on the planet) can attract heterotrophic bacteria in both laboratory-based [47] and *in situ* [5] chemotaxis experiments. Furthermore, a recent study demonstrated that the heterotrophic marine bacterium *Marinobacter adhaerens* can use chemotaxis to interact with *Synechococcus* cells, and that this behaviour significantly enhances reciprocal exchanges of metabolites between the partners [10]. These interactions exhibit surprising spatiotemporal dynamics, whereby *Marinobacter* cells do not physically attach to *Synechococcus*, but reciprocal exchanges occur through short-lived encounters (lasting on the order of seconds) underpinned by chemotaxis [10]. Crucially, interbacterial associations mediated through chemotaxis at this scale are highly stochastic, and the encounter dynamics between bacteria are fundamentally different to prolonged interactions involving larger organisms [10]. Further evidence for bacterial chemotaxis towards picocyanobacteria was presented in a recent study which demonstrated that *V. alginolyticus* exhibits chemotaxis towards virus-infected *Synechococcus* cells [11].

In recent years, the number of known episymbiotic relationships among prokaryotes has expanded. Indeed, there is evidence that bacteria from the candidate phyla radiation (CPR) and DPANN archaea, which are two very large evolutionary radiations accounting for a substantial portion of prokaryotic diversity (~25%), are likely episymbionts of other prokaryotes [48]. Many of these ultra-small cells are predicted to be motile (either through flagella/archaella or pili) [49] and some harbour genes encoding proteins that resemble CheY [50], which controls the direction of flagellar rotation in chemotactic cells. In the few CPR bacteria isolated to date, type IV pili play key roles in enabling motility and adhesion to their hosts [51], suggesting that motile behaviour may be involved in episymbioses in these enormous prokaryotic radiations.

A potential expansion of the ecological significance of bacterial chemotaxis

If the use of chemotaxis to mediate interbacterial interactions is prevalent in the environment, it could have far-reaching ecological consequences. First, this behaviour could drastically enhance symbiotic interactions and metabolite exchanges among bacteria. Indeed, chemotaxis may be used by some bacteria to facilitate interactions with specific partners, rather than simple random encounters with their nearest neighbours, particularly within environments with high prokaryotic densities (e.g., gut, sediment, soil, where cells may be separated by less than ten body lengths)

[52]. Even in aquatic environments, where the distance between cells can often be greater than 100 body lengths, chemotaxis can promote short-lived yet repeated interactions between partners [10] and may underpin the clustering of cells previously observed in the water column [53,54]. By reducing distances through chemotaxis, interacting cells could more readily benefit from the diffusible molecules arising from their partners' activity, leading to an increase in the amount of metabolites they exchange, which would ultimately positively impact their fitness.

Chemotaxis could also enhance interactions between autotrophic and heterotrophic prokaryotes in aquatic ecosystems. Photosynthesis by bacterial and eukaryotic phytoplankton contributes to approximately half of the biosphere's net primary production [55]. Although the relationships between heterotrophic prokaryotes and eukaryotic phytoplankton reflect a key ecological interdependency that controls energy transfer to higher trophic levels [21,56,57], small photosynthetic bacteria are between 10 and 100 times more abundant than large phytoplankton [58–60] and dominate the photosynthetic biomass in the resource-poor open ocean [58,61] (Figure 2). This means that the capacity of prokaryotes to interact through chemotaxis could allow direct ecological and metabolic linkages between heterotrophs and the most numerous primary producers in the ocean [10,11].

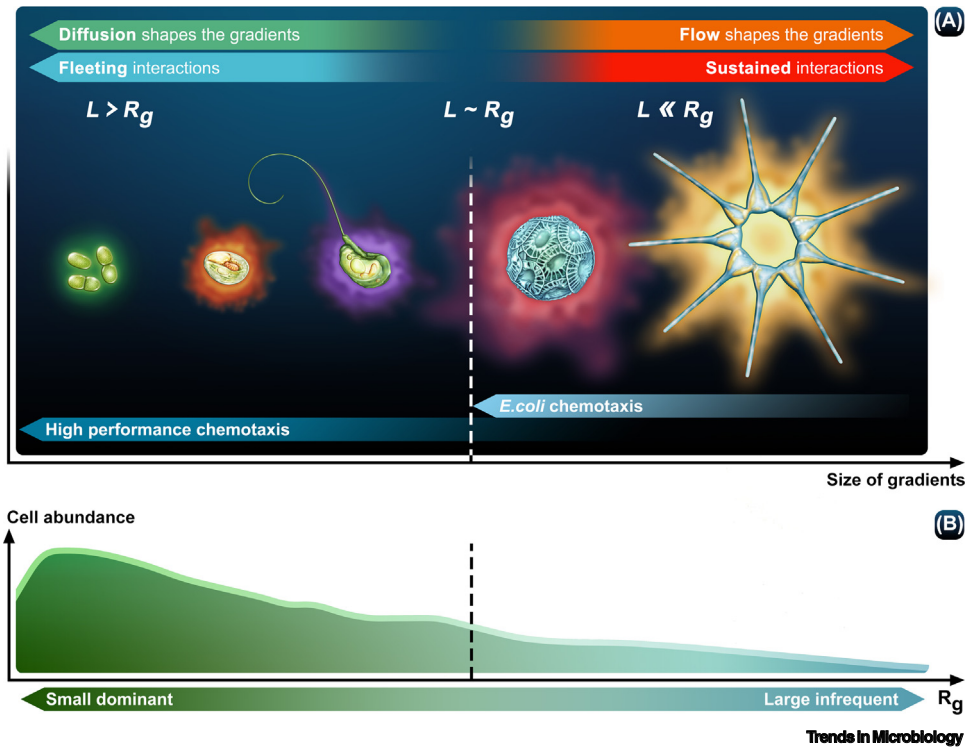

Figure 2. The widespread use of chemotaxis between prokaryotes may vastly expand the ecological importance of this behaviour. (A) The ability of bacteria to detect gradients of different sizes is dictated by biophysical constraints [71]. Larger gradients are shaped by fluid flow, allowing prolonged interactions with chemotactic bacteria [10]. Smaller gradients, such as the ones arising from bacterial cells, are shaped by diffusion. Interbacterial interactions may be possible for cells capable of high performance chemotaxis, but these encounters would be more stochastic and short-lived than for larger cells [10]. *L*, mean run length of a motile bacterium; R_g, radius of the gradient. (B) Typical cell size spectrum of surface oceanic water (i.e., the number of cells depending on their sizes) [72], which highlights that most cells are smaller than 4 µm and would not be detected chemotactically by *Escherichia coli*, but may be sensed by bacteria with higher chemotactic performance. The larger abundance of small cells is not specific to the marine environment and may vastly increase the number of 'targets' for chemotactic cells in most ecosystems. Artwork: Philippe Plateaux.

Of course, not all interbacterial interactions involve mutualistic relationships, and chemotactic sensing of other bacteria could facilitate uptake of bacterial-derived organic matter by scavenging bacteria that do not reciprocate the exchange of substrates. Chemotaxis could even permit predatory bacteria, such as *Bdellovibrio*, to home in on individual prey. The ability of predatory bacteria to respond to chemical gradients is well established [62,63], but the role of this behaviour in locating their bacterial prey is unclear. Predatory bacteria are usually fast swimmers, and the increase in prey encounter rate afforded by motility is believed to mediate their ability to attack biofilms and planktonic cells [63]. If chemotaxis further increases the ability of bacterial predators to encounter individual prey cells, it might constitute an overlooked mechanism regulating the structure of prokaryotic communities.

Chemotaxis may also increase the likelihood of horizontal gene transfer (HGT) between prokaryotes. HGT is the exchange of genetic material between a donor and a recipient cell and is an important process driving the evolution of bacteria and archaea [64]. One HGT mechanism, conjugation, requires cells to be in physical contact through a pilus [65], allowing rapid DNA transfer (~45 kb min^{-1}) [66]. As chemotaxis can drastically enhance the frequency of physical contact between cells, this behaviour may play an as-yet overlooked role in governing the rate of HGT in prokaryotes.

Chemotaxis between prokaryotic cells is further expected to increase the rate of biogeochemical transformations. Indeed, as cells come into close contact, they can experience concentrations of exuded metabolites that can be orders of magnitude higher than those in the background environment [56,67]. Most metabolic processes are concentration-dependent, meaning that substrate uptake, catabolism of nutrients, remineralization, or even predation rates occur much faster when cells are close to each other [67,68]. For example, if chemotaxis supports an increase in prokaryotic growth efficiency, by enhancing chemical exchanges between cells in resource-poor environments, it will potentially lead to greater fluxes of carbon into the foodweb.

Concluding remarks

While the importance of chemotaxis in the establishment and maintenance of ecological associations between bacteria and larger organisms is well documented, the potential for this behaviour to mediate interactions among individual bacterial cells has been largely overlooked. This has, in large part, been due to conclusions based on the chemotactic capacity of the model organism for bacterial chemotaxis – *E. coli* – that the chemical gradients associated with small prokaryotic cells will be too small to be sensed by a swimming bacterium [9]. However, recent experimental evidence has indicated that chemotaxis significantly enhances the capacity for small bacterial cells to engage in exchanges of metabolites, highlighting that chemotactic sensing between small cells is not only possible, but ecologically important [10,11]. Our goal has been to begin to reconcile this gap between theory guided by the *E. coli* chemotaxis model [9] and direct experimental observations. We conclude that divergences from the *E. coli* model (e.g., differences in swimming speeds, signal processing times, motility modes) likely afford other bacterial species with heightened capacity to sense chemical gradients emanating from small sources. This points to the possibility of significant roles of chemotaxis in the ecological interactions among bacteria, which we propose warrants further consideration in assessments of interbacterial relationships within all ecosystems (see Outstanding questions).

Outstanding questions

What is the size of the smallest target cell that can be sensed by a chemotactic bacterium?

To what extent do bacterial chemotaxis and motility strategies that deviate from the classic *E. coli* model permit chemotactic sensing of small microbial targets?

What bacterial chemotaxis parameters (e.g., swimming speed, signal-processing times, modes of motility) are most important for governing chemotactic precision?

How widespread is chemotactic sensing of small bacterial targets by other chemotactic bacteria?

How important is chemotaxis in the exchange of metabolites between bacterial cells, and to what extent does it govern interbacterial symbiosis and competition?

Acknowledgments

This research was funded by Australian Research Council grants DP200100919 and DP230100127 to J.R.S, J.-B.R., and R.S. J.-B.R. was supported by an Australian Research Council Fellowship FT210100100, and D.R.B. was supported by an Australian Research Council Fellowship DE180100911. R.S. acknowledges support from a grant by the Simons

Foundation (542395) as part of the Principles of Microbial Ecosystems Collaborative (PriME), a Gordon and Betty Moore Symbiosis in Aquatic Ecosystems Initiative Investigator Award (GBMF9197; https://doi.org/10.37807/GBMF9197) and a grant from the Swiss National Science Foundation (315230_176189). The artwork in Figures 1 and 2 was produced by Philippe Plateaux and is used with his permission.

Declaration of interests

No interests are declared.

References

1. Stocker, R. (2012) Marine microbes see a sea of gradients. *Science* 338, 628–633
2. Szurmant, H. and Ordal George, W. (2004) Diversity in chemotaxis mechanisms among the Bacteria and Archaea. *Microbiol. Mol. Biol. Rev.* 68, 301–319
3. Keegstra, J.M. *et al.* (2022) The ecological roles of bacterial chemotaxis. *Nat. Rev. Microbiol.* 20, 491–504
4. Raina, J.-B. *et al.* (2019) The role of microbial motility and chemotaxis in symbiosis. *Nat. Rev. Microbiol.* 17, 284–294
5. Raina, J.-B. *et al.* (2022) Chemotaxis shapes the microscale organization of the ocean's microbiome. *Nature* 605, 132–138
6. Seymour, J.R. *et al.* (2010) Chemoattraction to dimethylsulfoniopropionate throughout the marine microbial food web. *Science* 329, 342–345
7. McKinlay, J.B. (2023) Are bacteria leaky? Mechanisms of metabolite externalization in bacterial cross-feeding. *Annu. Rev. Microbiol.* 77, 277–297
8. Sonnenschein Eva, C. *et al.* (2012) Chemotaxis of *Marinobacter adhaerens* and its impact on attachment to the diatom *Thalassiosira weissflogii*. *Appl. Environ. Microbiol.* 78, 6900–6907
9. Jackson, G.A. (1987) Simulating chemosensory responses of marine microorganisms. *Limnol. Oceanogr.* 32, 1253–1266
10. Raina, J.-B. *et al.* (2023) Chemotaxis increases metabolic exchanges between marine picophytoplankton and heterotrophic bacteria. *Nat. Microbiol.* 8, 510–521
11. Henshaw, R.J. *et al.* (2023) Early viral infection of cyanobacteria drives bacterial chemotaxis in the oceans. *bioRxiv*, Published online October 24, 2023. https://doi.org/10.1101/2023.10.24.563588
12. Berg, H.C. (2004) *E. coli in Motion*, Springer
13. Wadhams, G.H. and Armitage, J.P. (2004) Making sense of it all: bacterial chemotaxis. *Nat. Rev. Mol. Cell Biol.* 5, 1024–1037
14. Sourjik, V. and Berg, H.C. (2002) Receptor sensitivity in bacterial chemotaxis. *Proc. Natl. Acad. Sci.* 99, 123–127
15. Segall, J.E. *et al.* (1982) Signal processing times in bacterial chemotaxis. *Nature* 296, 855–857
16. Son, K. *et al.* (2016) Speed-dependent chemotactic precision in marine bacteria. *Proc. Natl. Acad. Sci.* 113, 8624–8629
17. Miller, L.D. *et al.* (2009) Diversity in bacterial chemotactic responses and niche adaptation. *Adv. Appl. Microbiol.* 66, 53–75
18. Mandel, M.J. *et al.* (2012) Squid-derived chitin oligosaccharides are a chemotactic signal during colonization by *Vibrio fischeri*. *Appl. Environ. Microbiol.* 78, 4620–4626
19. Feng, H. *et al.* (2021) Chemotaxis of beneficial rhizobacteria to root exudates: the first step towards root–microbe rhizosphere interactions. *Int. J. Mol. Sci.* 22, 6655
20. Zhou, B. *et al.* (2023) Bacterial chemotaxis in human diseases. *Trends Microbiol.* 31, 453–467
21. Seymour, J.R. *et al.* (2017) Zooming in on the phycosphere: the ecological interface for phytoplankton–bacteria relationships. *Nat. Microbiol.* 2, 17065
22. Shu, L. *et al.* (2018) *Burkholderia* bacteria use chemotaxis to find social amoeba *Dictyostelium discoideum* hosts. *ISME J.* 12, 1977–1993
23. Fukui, M. *et al.* (1999) Physiology, phylogenetic relationships, and ecology of filamentous sulfate-reducing bacteria (genus *Desulfonema*). *Arch. Microbiol.* 172, 193–203
24. Paerl, H.W. and Gallucci, K.K. (1985) Role of chemotaxis in establishing a specific nitrogen-fixing Cyanobacterial–Bacterial association. *Science* 227, 647–649
25. Jani, S. *et al.* (2017) Chemotaxis to self-generated AI-2 promotes biofilm formation in *Escherichia coli*. *Microbiology* 163, 1778–1790
26. Ben-Jacob, E. *et al.* (1998) Cooperative organization of bacterial colonies: from genotype to morphotype. *Annu. Rev. Microbiol.* 52, 779–806
27. Seymour, J.R. *et al.* (2009) Resource patch formation and exploitation throughout the marine microbial food web. *Am. Nat.* 173, E15–E29
28. Seymour, J.R. *et al.* (2000) Heterogeneity in bacterioplankton abundance from 4.5 millimetre resolution sampling. *Aquat. Microb. Ecol.* 22, 143–153
29. Berg, H.C. (1993) *Random Walks in Biology*, Princeton University Press
30. Son, K. *et al.* (2013) Bacteria can exploit a flagellar buckling instability to change direction. *Nat. Phys.* 9, 494–498
31. Stocker, R. (2011) Reverse and flick: hybrid locomotion in bacteria. *Proc. Natl. Acad. Sci.* 108, 2635–2636
32. Stocker, R. *et al.* (2008) Rapid chemotactic response enables marine bacteria to exploit ephemeral microscale nutrient patches. *Proc. Natl. Acad. Sci.* 105, 4209–4214
33. Xie, L. *et al.* (2011) Bacterial flagellum as a propeller and as a rudder for efficient chemotaxis. *Proc. Natl. Acad. Sci.* 108, 2246–2251
34. Brumley, D.R. *et al.* (2019) Bacteria push the limits of chemotactic precision to navigate dynamic chemical gradients. *Proc. Natl. Acad. Sci.* 116, 10792–10797
35. Mitchell, J.G. *et al.* (1996) Clustering of marine bacteria in seawater enrichments. *Appl. Environ. Microbiol.* 62, 3716–3721
36. Berg, H.C. and Purcell, E.M. (1977) Physics of chemoreception. *Biophys. J.* 20, 193–219
37. Endres, R.G. and Wingreen, N.S. (2009) Accuracy of direct gradient sensing by cell-surface receptors. *Prog. Biophys. Mol. Biol.* 100, 33–39
38. Hein, A.M. *et al.* (2016) Natural search algorithms as a bridge between organisms, evolution, and ecology. *Proc. Natl. Acad. Sci.* 113, 9413–9420
39. Mora, T. and Wingreen, N.S. (2010) Limits of sensing temporal concentration changes by single cells. *Phys. Rev. Lett.* 104, 248101
40. Taktikos, J. *et al.* (2014) How the motility pattern of Bacteria affects their dispersal and chemotaxis. *PLoS ONE* 8, e81936
41. Blackburn, N. *et al.* (1998) Microscale nutrient patches in planktonic habitats shown by chemotactic bacteria. *Science* 282, 2254–2256
42. Bright, M. and Bulgheresi, S. (2010) A complex journey: transmission of microbial symbionts. *Nat. Rev. Microbiol.* 8, 218–230
43. Bjerg, J.J. *et al.* (2023) Cable bacteria with electric connection to oxygen attract flocks of diverse bacteria. *Nat. Commun.* 14, 1614
44. Müller, J. and Overmann, J. (2011) Close interspecies interactions between prokaryotes from sulfureous environments. *Front. Microbiol.* 2, 146
45. Overmann, J. and Schubert, K. (2002) Phototrophic consortia: model systems for symbiotic interrelations between prokaryotes. *Arch. Microbiol.* 177, 201–208
46. Kyndt, J.A. *et al.* (2020) Simultaneous genome sequencing of *Prosthecochloris ethylica* and *Desulfuromonas acetoxidans* within a syntrophic mixture reveals unique pili and protein interactions. *Microorganisms* 8, 1939
47. Seymour, J.R. *et al.* (2010) Chemotactic response of marine bacteria to the extracellular products of *Synechococcus* and *Prochlorococcus*. *Aquat. Microb. Ecol.* 59, 161–168
48. Castelle, C.J. and Banfield, J.F. (2018) Major new microbial groups expand diversity and alter our understanding of the tree of life. *Cell* 172, 1181–1197

49. Castelle, C.J. *et al.* (2018) Biosynthetic capacity, metabolic variety and unusual biology in the CPR and DPANN radiations. *Nat. Rev. Microbiol.* 16, 629–645
50. Gios, E. *et al.* (2023) Ultra-small bacteria and archaea exhibit genetic flexibility towards groundwater oxygen content, and adaptations for attached or planktonic lifestyles. *ISME Commun.* 3, 13
51. Xie, B. *et al.* (2022) Type IV pili trigger episymbiotic association of *Saccharibacteria* with its bacterial host. *Proc. Natl. Acad. Sci.* 119, e2215990119
52. Whitman, W.B. *et al.* (1998) Prokaryotes: the unseen majority. *Proc. Natl. Acad. Sci.* 95, 6578–6583
53. Krembs, C. *et al.* (1998) Nanoscale patchiness of bacteria in lake water studied with the spatial information preservation method. *Limnol. Oceanogr.* 43, 307–314
54. Malfatti, F. and Azam, F. (2009) Atomic force microscopy reveals microscale networks and possible symbioses among pelagic marine bacteria. *Aquat. Microb. Ecol.* 58, 1–14
55. Field, C.B. *et al.* (1998) Primary production of the biosphere: integrating terrestrial and oceanic components. *Science* 281, 237–240
56. Azam, F. and Malfatti, F. (2007) Microbial structuring of marine ecosystems. *Nat. Rev. Microbiol.* 5, 782–791
57. Cole, J.J. (1982) Interactions between bacteria and algae in aquatic ecosystems. *Annu. Rev. Ecol. Syst.* 13, 291–314
58. Flombaum, P. *et al.* (2013) Present and future global distributions of the marine Cyanobacteria *Prochlorococcus* and *Synechococcus*. *Proc. Natl. Acad. Sci.* 110, 9824–9829
59. Leblanc, K. *et al.* (2012) A global diatom database – abundance, biovolume and biomass in the world ocean. *Earth Syst. Sci. Data* 4, 149–165
60. Vogt, M. *et al.* (2012) Global marine plankton functional type biomass distributions: *Phaeocystis* spp. *Earth Syst. Sci. Data* 4, 107–120
61. Buitenhuis, E.T. *et al.* (2013) MAREDAT: towards a world atlas of MARine Ecosystem DATa. *Earth Syst. Sci. Data* 5, 227–239
62. Caulton, S.G. and Lovering, A.L. (2023) Moving toward a better understanding of the model bacterial predator *Bdellovibrio bacteriovorus*. *Microbiology* 169, 001380
63. Lai, T.F. *et al.* (2023) Advances in cellular and molecular predatory biology of *Bdellovibrio bacteriovorus* six decades after discovery. *Front. Microbiol.* 14, 1168709
64. Soucy, S.M. *et al.* (2015) Horizontal gene transfer: building the web of life. *Nat. Rev. Genet.* 16, 472–482
65. Arnold, B.J. *et al.* (2022) Horizontal gene transfer and adaptive evolution in bacteria. *Nat. Rev. Microbiol.* 20, 206–218
66. Arutyunov, D. and Frost, L.S. (2013) F conjugation: back to the beginning. *Plasmid* 70, 18–32
67. Blackburn, N. *et al.* (1997) Spatially explicit simulations of a microbial food web. *Limnol. Oceanogr.* 42, 613–622
68. Smriga, S. *et al.* (2016) Chemotaxis toward phytoplankton drives organic matter partitioning among marine bacteria. *Proc. Natl. Acad. Sci.* 113, 1576–1581
69. Aksenov, A.A. *et al.* (2017) Global chemical analysis of biology by mass spectrometry. *Nat. Rev. Chem.* 1, 0054
70. Crank, J. (1979) *The Mathematics of Diffusion*, Oxford University Press
71. Hein, A.M. *et al.* (2016) Physical limits on bacterial navigation in dynamic environments. *J. R. Soc. Interface* 13, 20150844
72. Ward, B.A. *et al.* (2012) A size-structured food-web model for the global ocean. *Limnol. Oceanogr.* 57, 1877–1891