Trends in Microbiology

Special Series: Microbial Communities

Review

The Ecology and Evolution of Microbial Competition

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Microbes are typically surrounded by different strains and species with whom they compete for scarce nutrients and limited space. Given such challenging living conditions, microbes have evolved many phenotypes with which they can outcompete and displace their neighbours: secretions to harvest resources, loss of costly genes whose products can be obtained from others, stabbing and poisoning neighbouring cells, or colonising spaces while preventing others from doing so. These competitive phenotypes appear to be common, although evidence suggests that, over time, competition dies down locally, often leading to stable coexistence of genetically distinct lineages. Nevertheless, the selective forces acting on competition and the resulting evolutionary fates of the different players depend on ecological conditions in a way that is not yet well understood. Here, we highlight open questions and theoretical predictions of the long-term dynamics of competition that remain to be tested. Establishing a clearer understanding of microbial competition will allow us to better predict the behaviour of microbes, and to control and manipulate microbial communities for industrial, environmental, and medical purposes.

Trends

Microbes express many competitive phenotypes in the presence of others; exploitative phenotypes include metabolic changes that increase growth rates or molecule secretion to harvest nutrients, while interference competition occurs through antimicrobial secretions or contact-dependent killing.

Microbial competition is common, although evidence suggests that, in many environments, interspecies interactions are weak.

Competition is expected on first encounter, but can be reduced over time through competitive exclusion, or niche partitioning via resource or spatial separation, leading to communities with a reduced local diversity of strains and species that can nevertheless coexist stably.

Many complementary methods exist for studying microbial communities. Combining them to analyse a simple community would reveal a more complete picture.

The Nature of Microbial Competition

Microbes dominate the tree of life in species number and **diversity** (see Glossary), and they inhabit the largest range of environments on earth. Like macroorganisms, microorganisms too live in a miniature entangled bank, where some species are tightly associated and rely heavily on each other to survive, such as the microbial guilds that convert nitrogen in the atmosphere to its various forms in the soil, or the symbiotic microbes that provide health benefits to their hosts. However, given the density in which microbes are found and the scarcity of resources in most environments, one cell's survival may mean starvation for another, leading to fierce **competition** for finite resources, be they sunlight, nutrients, or space.

We consider phenotypes in a focal strain to be competitive if they cause a **fitness** decrease in a competitor strain, and if they are more likely to have evolved as a consequence of biotic competition rather than environmental pressures. Competitors must overlap in resource use, which excludes behaviours such as predation and parasitism that also reduce the fitness of one of the players. The competing strains that we refer to throughout the article can differ by a single mutation or can be distantly related species.

The two main resources necessary for microbial survival are nutrients and space. Nutrients essential for microbial growth and metabolic functions include: carbon, nitrogen, phosphorus, sulfur, hydrogen, calcium, iron, and other metals [1–4]. Resource concentrations will vary between environments, such that microbes will be in competition for the limited components. As they grow and produce more biomass, microbial groups expand in space and compete with

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others to colonise areas in which nutrients are more abundant. A third and less commonly considered resource is genetic material. DNA is used as a nutrient source, but it may also provide its host with beneficial traits, enhancing its ability to survive and adapt [5]. The advantage of DNA uptake is particularly salient in the acquisition of antibiotic-resistance genes [6,7], but since there is also the possibility of taking up harmful genes, the net consequences of DNA uptake on microbial fitness remain unclear.

Competitive Phenotypes

There are two ways in which microbes compete for the resources listed above: (i) indirectly through exploitative competition, which occurs through resource consumption (passive competition) and (ii) directly through interference competition, where individual cells damage one another (active, chemical warfare).

Exploitative competition involves the consumption of a limiting resource by one strain restricting its supply to the competitor. This occurs either through increased nutrient uptake or through the extracellular secretion of molecules that harvest nutrients. As an example of the former, both *Saccharomyces cerevisiae* and *Escherichia coli* can metabolically shift from fermentation to respiration when oxygen is present, generating high growth rates but low yield, allowing them to absorb nutrients faster than their competitors [8–10]. Examples of the latter competitive strategy include the production of digestive enzymes to degrade complex nutrient molecules, or siderophores, which are iron-scavenging molecules that access insoluble iron. However, these molecules are often costly to produce, and because they are secreted outside of the producing cell, they are also ‘public goods’ that benefit neighbouring cells. Therefore, another competitive approach is to exploit the products secreted by others, and lose or reduce a strain's own secretions, a strategy often referred to as ‘cheating’. Of the best-studied systems involving the interplay between these two competitive mechanisms – cooperation that allows more access to nutrients, and cheating that saves the cost but relies on the presence of cooperators – is the production of iron-chelating siderophores [11–15] and of quorum sensing (QS) molecules that coordinate the expression and production of exofactors [16,17].

Strains also compete to position themselves in prime locations within a niche while preventing others from accessing it [18]. This can be achieved either by rapidly colonising uninhabited spaces or by killing or pushing out already established competitors [19]. A variety of molecules are involved in these strategies: rhamnolipids allow cells to swim to new areas or push competitors away [20,21]; adhesins bind to surfaces and prevent displacement by invaders [22]; extracellular polysaccharides (EPS) can smother and starve competitors, while also pushing clone-mates into nutrient-rich environments [18,23,24] (Figure 1A). Some microbes, such as *Myxococcus xanthus* and *Dictyostelium discoideum* produce fruiting bodies to glide toward food sources, and limit the diffusion of extracellular digestive enzymes outside of the fruiting body. In doing so, they achieve both enhanced motility to access new niches and adhesion to closely related cells to gain biomass and keep competitors away [24,25].

Similarly to these fruiting bodies, many microbes form cell aggregates – commonly known as biofilms – that protect cells from antimicrobials, predators, and other environmental hazards. Inhibiting the formation of these biofilms in others is another competitive strategy [26]. For example, on entry into biofilm, *E. coli* cells produce surfactants and EPS that inhibit biofilm formation in *Staphylococcus aureus* and *Pseudomonas aeruginosa* [27,28]. Similarly, *P. aeruginosa* cells swarm over a surface and occupy it to form a biofilm, a behaviour termed ‘surface blanketing’, which prevents *Agrobacterium tumefaciens* from forming its own biofilm [20]. Although the overall cell number of the ‘losing’ strain is not necessarily reduced on biofilm

Glossary

Competition: consider two strains A and B that differ on one or more loci. Strain A is a competitor of B if (a) B has a lower fitness in A's presence relative to its absence; (b) the phenotype in A resulting in a fitness change in B occurs in the long- or short-term presence of B; and (c) A and B require similar nutrients and space. Note that this definition is context-dependent. Furthermore, even if a phenotype did not evolve due to biotic competition, it may nevertheless result in a competitive advantage.

Diversity: the number of strains or species in a community (however they may be distinguished, e.g., Operational Taxonomic Units (OTUs) at 97%, or differentially labelled strains; a community also needs to be spatially delimited, e.g., a microbial colony, or strains living in the human oral tract).

Ecological stability: the probability that a community will return to its previous state following a small perturbation. We use this definition broadly to include measures such as resilience (the speed at which a community returns to its previous state) and permanence (all original species are maintained in the community) [62].

Evolutionary stability: evolutionary stability refers to evolutionary stable strategies (ESS), a game-theoretic concept whereby a population maintaining that strategy cannot be invaded by any alternative strategy that is initially rare [136].

Fitness: here we use fitness as a proxy for the rate of division and survival relative to the interacting competitors' division and survival.

Habitat filtering: a principle which predicts that phylogenetically similar species will tend to co-occur because the environment selects for species that are adapted to it.

Lotka-Volterra network: a system of differential equations that describes the population dynamics of two or more interacting groups (typically species).

Resource Ratio Theory: this theory states that a species in a community that is able to survive on the lowest abundance of a given nutrient will dominate the community if it is limiting. In the presence of two expulsion, it may nevertheless suffer significant losses under certain conditions, for example, in the presence of antibiotics [29,30]. Analogously, QS inhibition molecules, which are widespread among bacteria, may mediate competition [29,31–33]. For example, *Bacillus subtilis* produces enzymes that degrade QS molecules in *Vibrio cholerae*, which is subsequently unable to form biofilms [29,31].

limiting nutrients, it predicts that two species may coexist, provided that each is limited by one of the nutrients.

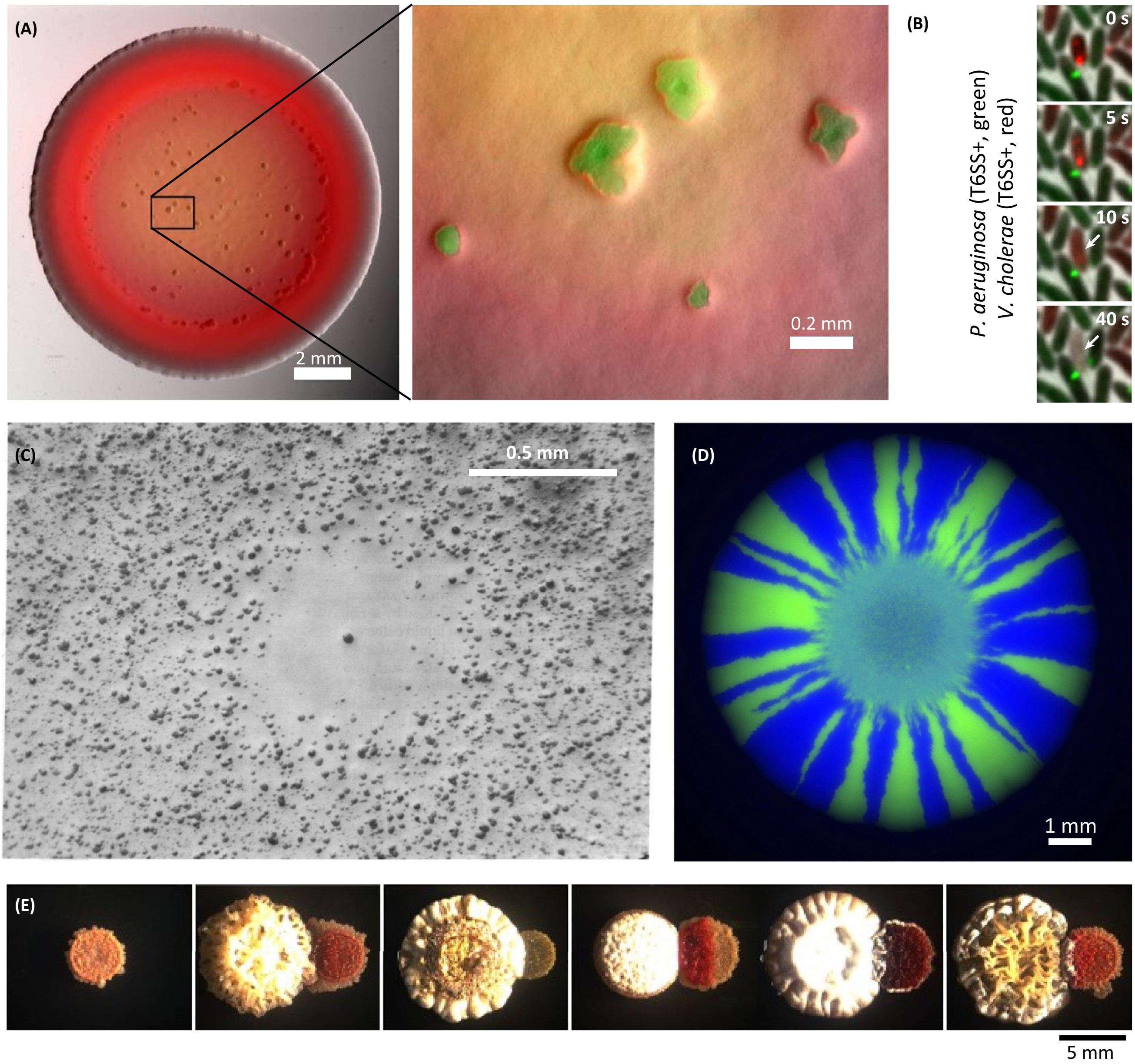

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Figure 1. Competitive Phenotypes. (A) Secretions by a *Pseudomonas fluorescens* mutant (green), allowing it to break through and colonise the top of the colony of the wild-type strain (red) and eventually outgrow it [18]. Left: whole colony, right: zoomed-in view of box in the left panel. (B) Type VI secretion systems (T6SSs) in *Vibrio cholerae* (red) and *Pseudomonas aeruginosa* (green) on cell contact leads to the lysis of *V. cholerae* cell (arrow) by 40s; 4.5 x 4.5 μm images are shown [40]. (C) Soft-agar plate with one central colony of colicin-producing *Escherichia coli*, surrounded by an inhibition zone and colonies of sensitive bacteria [34]. (D) Competitive exclusion in space. A drop with a 1:1 mixture of green and blue *P. aeruginosa* cells is left to grow into a colony. Over time, lineages from the centre die off, while only a few clonal patches grow toward the colony edge [79]. (E) *Streptomyces coelicolor* responds to the presence of other actinomycetes. Left panel: *S. coelicolor* alone, other panels show *S. coelicolor* on the right and a second species on the left. *S. coelicolor* colonies exhibit different phenotypes depending on the partner's identity [92].

The classical example of interference competition is the production of antimicrobials, which range in their killing spectrum from strain-specific bacteriocins to more broad-spectrum peptides and antibiotics [34,35] (Figure 1C). Although it has been proposed that, at subinhibitory concentrations, antibiotics may be used for cooperative purposes, such as signaling [36,37], recent data show otherwise, maintaining the classical understanding of antibiotics as weapons [38,39]. Other mechanisms of contact-dependent interference competition include type VI secretion systems (T6SS), whereby cells inject syringe-like protrusions containing toxins and other molecules into neighbouring cells that then lyse [5,40,41,42] (Figure 1B). The victim's DNA may also be transferred back into the attacker's cell [5]. The utility of taking up and integrating foreign DNA remains unclear, but some genes, such as those providing toxin immunity and antimicrobial resistance, can allow a strain to quickly dominate a population [7,43,44].

Many of these competitive phenotypes can be differentially expressed within clonal populations. This variability can enhance a genotype's competitive success [45]. For example, clonal cells within a population can perform different physiological roles, and thereby contribute to a collective functionality [46,47], such as enhanced growth in nutrient-fluctuating environments [48]. In cyanobacteria, a fraction of the population of clonal cells fixes nitrogen into a usable form, while the rest undergo photosynthesis, together increasing group productivity [45,49]. Similarly, in the intestinal pathogen *Salmonella enterica* serovar Typhimurium, some cells remain in the host gut lumen and divide, while others invade the tissue and induce an inflammatory response in the host that kills off other bacteria [50]. It is essential to better understand the extent to which such phenotypic heterogeneity occurs, the various roles that different cells can play, and how this can shape competitive interactions (Box 1).

Competition between Microbes Is Widespread

Given that so many competitive phenotypes have evolved (Table 1), competition must be an important part of microbial life. But how common is it? Are microbes largely living cooperatively with minimal conflict, or is it a constant battlefield of attack and counterattack? When is competition expected?

Data from different ecosystems suggest that competition is prevalent. Genomic analyses show that 25% of gram-negative bacteria have genes coding for a T6SS [51], while virtually all actinomycetes dedicate 5–10% of their genomes to secondary metabolites [52], which include antibiotics and other potentially damaging molecules. However, we still need to discover the functions of these metabolites – what percentage of them is in fact aggressive – and perform similar analyses in other microbial groups. A powerful approach to assessing the extent of exploitative competition is by using sequence data to build and simulate metabolic models [53,54]. In one of the first studies using this approach, Freilich *et al.* predicted abundant competition between a collection of widely sampled bacterial species, and few instances of unidirectional positive interactions [53].

Coculture studies have found similar patterns. Bacterial isolates from tree-holes, which are aquatic ecosystems found around the roots of beech trees, tend to compete with one another in coculture [55–57]. Soil isolates also grow less well in the presence of other species or even in their filtered growth media [58–60]. Another example comes from the mouse gut. By fitting a generalised **Lotka-Volterra network** model to a dataset quantifying different bacterial sequences over time, Stein *et al.* [61] found that competitive interactions – albeit weak ones – dominate the community [61,62]. Weak competitive interactions were also found in another microbiome study, this time in humans [63]. Empirical data from this and other microbiome studies indicate that, in agreement with the **‘habitat filtering’** principle, species with similar resource requirements tend to live in similar areas of the body [63–65], which may explain local competition. Finally, experiments using mixtures of model bacterial species for studying synergistic

Box 1. Approaches and Limitations to Studying Microbial Competition

Studying microbial competition involves different levels of abstraction. The daunting complexity of a microbial community can be approached from the bottom up, by focusing on a small aspect or a subpopulation that is dissectable and understandable. In contrast, top-down approaches allow a bird's-eye view of a community and the interactions within it; this lacks in-depth analysis but covers as many components as possible.

A powerful top-down approach to studying community interactions is using genomic, transcriptomic, and metabolomic data. A first analysis often involves constructing co-occurrence networks by calculating correlations in the abundance of species pairs [115,116]. These networks capture how diversity and species composition change over different community samples but are not necessarily suited to interpreting interspecies interactions. This is because it is impossible to tell whether a negative correlation between a species pair is due to competitive exclusion or habitat filtering (different species in different habitats) [63]. Interactions can instead be predicted by building metabolic models for different species, and simulating their growth under different resource compositions. This method has been widely applied, and standardised tools are becoming available [53,54,63,76,117]. However, only rarely are other social phenotypes taken into account, such as secondary metabolites (see Table 1; [118]). Furthermore, the models are based on the presence or absence of genes, regardless of whether they are expressed in reality. Even genes that share the same promoter, which were previously thought to be equally expressed - such as bacteriocin production and immunity genes - can vary largely in their expression patterns [119]. These issues can be resolved by studying gene expression profiles (transcriptomics). Finally, metabolomics can make more stringent links between gene expression and observed phenotypes by correlating them with cellular and secreted metabolites [120].

Bottom-up approaches include coculturing different strain combinations in the laboratory, which is an intuitive and powerful technique where the effects of careful manipulations can be monitored over time. However, a number of issues are relevant for interpreting the results. First, only a minority of environmental isolates will manage to grow in the laboratory, biasing toward lower metabolic diversity and higher competition (see Figure 2 in main text). In particular, strains that rely on the presence of others to grow – where one would detect a positive interaction – will be excluded [121]. Second, species may meet in the laboratory that would never meet in reality, possibly triggering an aggressive response. This may be the case in experiments involving interactions between ‘model’ bacterial species, such as *Escherichia coli* or *Pseudomonas aeruginosa*. Finally, growth in the laboratory often occurs over short timescales [95] in liquid cultures lacking spatial structure, and containing relatively high concentrations of nutrients whose composition is somewhat arbitrary and will certainly affect interactions [53,63]. Assuming that these problems can be weeded out, however, cocultures generate high-resolution data, which can be used to seed models of co-growth, such as generalised Lotka-Volterra models [61,122].

Another general problem is that studies typically consider whole populations and ignore phenotypic variation between individual cells. As the technology of single-cell microbiology advances, methods for taking this diversity into account are becoming more readily available. Furthermore, the spatial organisation of strains in the original environment is often destroyed through sampling. Two co-isolated strains that are found to compete in the laboratory may actually live in separate clonal patches that are millimeters away - potentially a large distance for a microbe. Accordingly, sampling is likely to exaggerate both diversity and competition between strains. There is then a need for sampling methods that conserve spatial structure, such as fluorescent *in situ* microscopy, where one can follow the identity and gene expression of individual cells over different areas and over time. These approaches have advanced significantly in recent years [123].

Finally, theoretical approaches have been, and can be, extremely valuable in capturing and predicting the ecology and evolution of competitive interactions, particularly over large data-sets and large (evolutionary) timescales, which are difficult to follow experimentally. These include the genomic models discussed above, which have so far focused on metabolomics, spatially explicit computer simulations, which can predict the role of space on competition between genotypes [23,80,83,84,100,124,125], and more abstract models, such as network models wherein diversity and stability can be calculated analytically [62,94] or social evolution models that can make predictions on the frequencies of different traits and how mutation and selection will shape them over time [108,126].

interactions must rely on evolving or engineering metabolic codependence between them as a means to get them to coexist in the laboratory, indicating that, in their natural state, these species may simply outcompete each other [66–69].

Even though the evidence for the high prevalence of competition is growing, some caveats need to be considered. First, the measured interactions may not be representative of those in the species’ natural environments. For example, because coculture experiments select for a subset of strains that are able to grow in the laboratory, they may be more likely to have similar

Table 1. Competitive Phenotypes in Microbes

Competitive Phenotype	Example of Molecule Type	Competitive Effect	Refs
Digestive enzyme secretion	Proteases	Enhanced access to nutrients	[16,29]
Siderophore secretion	Pyoverdin	Enhanced access to nutrients	[127,128]
Altering metabolic regulation	–	Enhanced access to nutrients	[8–10,45,131]
Reduced expression of costly genes	Reduced or no secretion of molecules that act as public goods, e.g., digestive enzymes and siderophores	Exploitation of cost-bearing cells	[13,16,101,104,128]
Production of structural and motility molecules	Surfactants, rhamnolipids, EPS, proteins, DNA, adhesion and anti-adhesion molecules	Enhanced access `to space	[18,20,22,24,129,130]
Antibiotic production (non-contact-dependent)	Bacteriocins, toxins, peptides	Eliminate competitor	[34,35,98]
Type VI secretion systems (T6SS) (contact-dependent)	Stabbing structures that release lethal effector molecules and enzymes	Eliminate competitor	[5,40,41,42]
Production of nonbiocidal molecules	Surfactin, anti-adhesion molecules, nucleases, proteases	Disrupt other's competitive phenotype	[27,28,132,133]
Inhibit quorum sensing	Quorum sensing inhibitors or quenchers	Disrupt other's competitive phenotype	[32,33,134]

metabolisms and compete with each other on first encounter. Second, genomic analyses suffer from another weakness: to what extent are the genes found in sequence data expressed? The difficulties of antibiotic discovery and biosynthesis indicate that expression levels may indeed be quite low [70,71]. We discuss the consequences of such experimental and analysis choices in more detail in Box 1.

Assuming that the pattern is real, however, when does competition occur? Why are some strains more aggressive than others? In Figure 2, we summarise our current understanding of the selective forces behind competition. Competition is predicted to be favoured under three conditions: (i) when coexisting strains have overlapping metabolic niches and require similar resources (Figure 2, top row), (ii) when cells of these different strains are spatially mixed on a scale where nutrients and secretions are shared (Figure 2, middle row), and (iii) when cell density is high relative to the available resources, such that they become limiting (Figure 2, bottom row) [72,73].

There are many environmental factors determining whether these conditions are met (Figure 2, central column). For example, environments with a high nutrient complexity, containing multiple resources or niches, can reduce selection for competition [58], particularly if each species is limited by a different resource **(Resource Ratio Theory)** [74,75]. Similarly, the more phylogenetically similar species within a community are, the more likely they will occupy overlapping metabolic niches and compete for the same resources [76]. Accordingly, distantly related species will tend to consume different resources and coexist with minimal – or even positive – effects on one another [77,78]. Even in the absence of phylogenetic similarity through common descent, metabolic overlap may occur through lateral transfer of metabolic genes [7,43]. It can also result from a lack of environmental disturbances, such that few new strains arrive in the environment bringing in organisms with different metabolic needs [7].

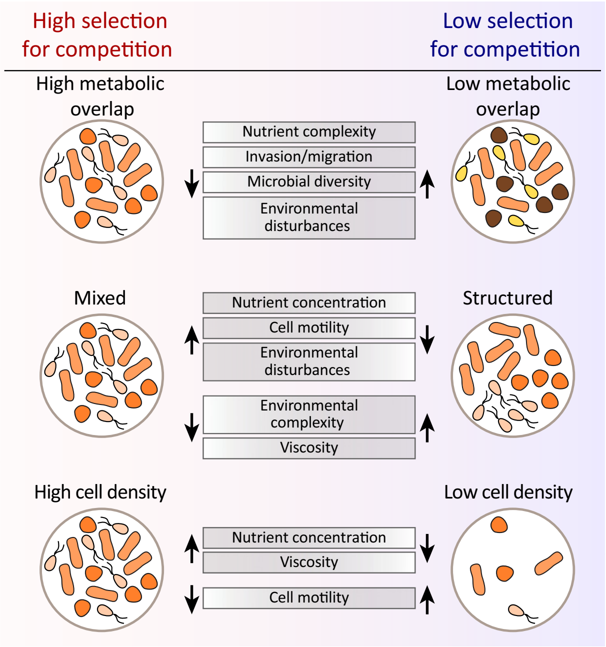

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Figure 2. When to Expect Competition. Ecological conditions leading to high selection for the acquisition or expression of competitive phenotypes include (i) high niche overlap between strains, (ii) if they are well-mixed over a spatial scale that is relevant for interactions, and (iii) if cells are at a high density relative to available resources. Whether these conditions are met depends on environmental factors listed in the centre (high or low: darker or lighter shading, arrow pointing up or down, respectively) such as nutrient abundance, its complexity, the rate at which other strains are entering the group from the outside [135], the diversity within the community, whether cells are motile or not, whether their environment is viscous and how often it is disturbed in a way that disperses cells to new locations, reducing phylogenetic and spatial structure. Note that the same factor may have opposing effects in promoting the conditions for or against competition (e.g., viscosity allows cells to form clonal patches to avoid competitors, but also leads to high cell density since it is harder for cells to migrate, which selects for increased competition).

Spatial mixing depends on multiple factors, including nutrient abundance [79,80], and various mechanical aspects of the environment, such as its viscosity and the diffusivity of different molecules, and the frequency at which it is disturbed [81]. Cardinale [82] showed that a mixture of algal species could coexist and take on complementary roles in removing nitrate from stream water only if the flow environment was heterogeneous (different flow velocities). A uniform environment instead led to competitive exclusion [82]. Apart from ecological conditions, different strains can remain mixed in space if they depend on each other for growth and survival [83–86]. Despite these heuristics, however, the effects of environmental manipulations on competition are not straightforward to predict. Indeed, the same manipulation – for example, increased viscosity or the frequency of environmental disturbances – may simultaneously drive selection for competition in opposite directions (Figure 2).

A recently proposed ‘competition sensing’ hypothesis suggests that cells may be able to detect and respond to competition [87,88], whereby physiological stress responses, induced by the presence of competitors, are used to regulate competitive phenotypes. Some cells can then recognise and tune their responses depending on whether they sense competition through a lack of nutrients, or cellular damage [87,88]. Consistent with this, *P. aeruginosa* cells can detect antibiotics, and induce the formation of biofilms [89]. They can also detect when neighbouring *P. aeruginosa* cells are killed, and trigger a counterattack using their T6SS [90]. *B. subtilis* cells in biofilms are able to detect nearby *Bacillus simplex* biofilms and secrete lethal toxins that kill them [91]. The presence of neighbouring colonies also alters the competitive behaviour of many species of soil bacteria [92,38,58] (Figure 1E). Depending on the identity of a neighbouring colony, a species pair can either upregulate or suppress its antibiotic production [38,93].

Consequences of Competition Over Time

Most microbial communities studied in the laboratory are snapshots in time resulting from a history of interactions between individual cells and genotypes. But what are the consequences of competition over ecological and evolutionary timescales? Two key measures are of interest when predicting the dynamics of a community: its diversity, and its stability.

Overall, competition is predicted to lead to a local reduction in diversity – where 'local' refers to the scale at which cells have fitness effects on each other – and an increase in **ecological stability** [62,94]. However, this may occur in a number of different ways (Figure 3, Key Figure). Three ecologically stable outcomes of competition are well accepted (Figure 3A–C): (i) the less competitive strains go extinct while others dominate the community [77,95], (ii) strains continue to coexist by occupying different metabolic niches, where each specialises on a different resource type, or (iii) strains separate into different spatial niches or patches.

A nice set of examples of niche differentiation in resources (Figure 3B) comes from experimental evolution in the tree-hole communities mentioned above [55–57], where initially competing species diverged in their use of resources as they coevolved. The species even evolved to use each other's waste products and increase overall productivity, suggesting that even when new niches are absent, species in the community can create and exploit alternative resources within the niche. Following niche differentiation then, competition can become neutralised through a reduction in interaction strength, potentially leading to symbiotic relationships and productive communities [56]. Coexistence of competitors through spatial separation (Figure 3C) is possible in solid or semi-solid structures such as mucus, soil, the surface of a leaf, or an agar surface, which consist of many spatial niches. This has been studied extensively in microbial colonies that begin from well-mixed populations containing millions of competing cells that expand outwards onto an agar surface and form clonal patches [79,96,97]. Although this process begins with the competitive exclusion of much of the original population, coexistence of multiple strains is possible in separate spatial areas, and has been shown in many different organisms and systems [69,73,98,99] (Figure 1D).

We outline three other possible scenarios following competition whose dynamics are currently less well established: First, strains may stably coexist in the same niche in an exploitative relationship (Figure 3D). The recent Black Queen Hypothesis suggests that, in a group of species in which a public good is required, if all but one species lose the ability to produce it, the producing species must continue to produce to avoid its own extinction, even if it benefits its competitors [11–13,100]. Similar equilibria have been described for cooperators and cheats of the same species [101–104], and for rock-paper-scissor dynamics, where cyclic dynamics occur between antibiotic producers, resistant cells (immune but do not kill) and sensitive cells [105,106]. These ideas are supported by experimental evidence, for example in siderophore production in marine bacteria [13]. While such communities may be ecologically stable and remain diverse, their **evolutionary stability** is questionable, since producers may evolve to produce more private or less costly secretions [102], to eliminate their competitors through interference competition, or exploiters may evolve to produce something in return, leading to a cooperative exchange with the producer [100,107].

Second (Figure 3E), if strains are unable to escape or avoid their competitors, they may maintain their aggressive phenotypes, increasingly ramp them up or diversify them in an arms race [81]. An arms race is an evolutionary process rather than an outcome of competition, and may eventually lead to one of the other outcomes (e.g., competitive exclusion). Otherwise, theory and experiments have shown that aggressive phenotypes and resistance to them can be maintained in a stable equilibrium in spatially structured populations [19,34,106,108]. The dynamics of stability and diversity, then, strongly depend on environmental conditions, and the nature of the competitive phenotypes. Phenotypes that incur a higher cost, for example, may be less readily maintained [34,109]. A study in soil bacteria found that there is a trade-off between two strategies: investing into efficient growth or into aggressive phenotypes such as antibiotics

Key Figure

Predicted Long-Term Consequences of Competition

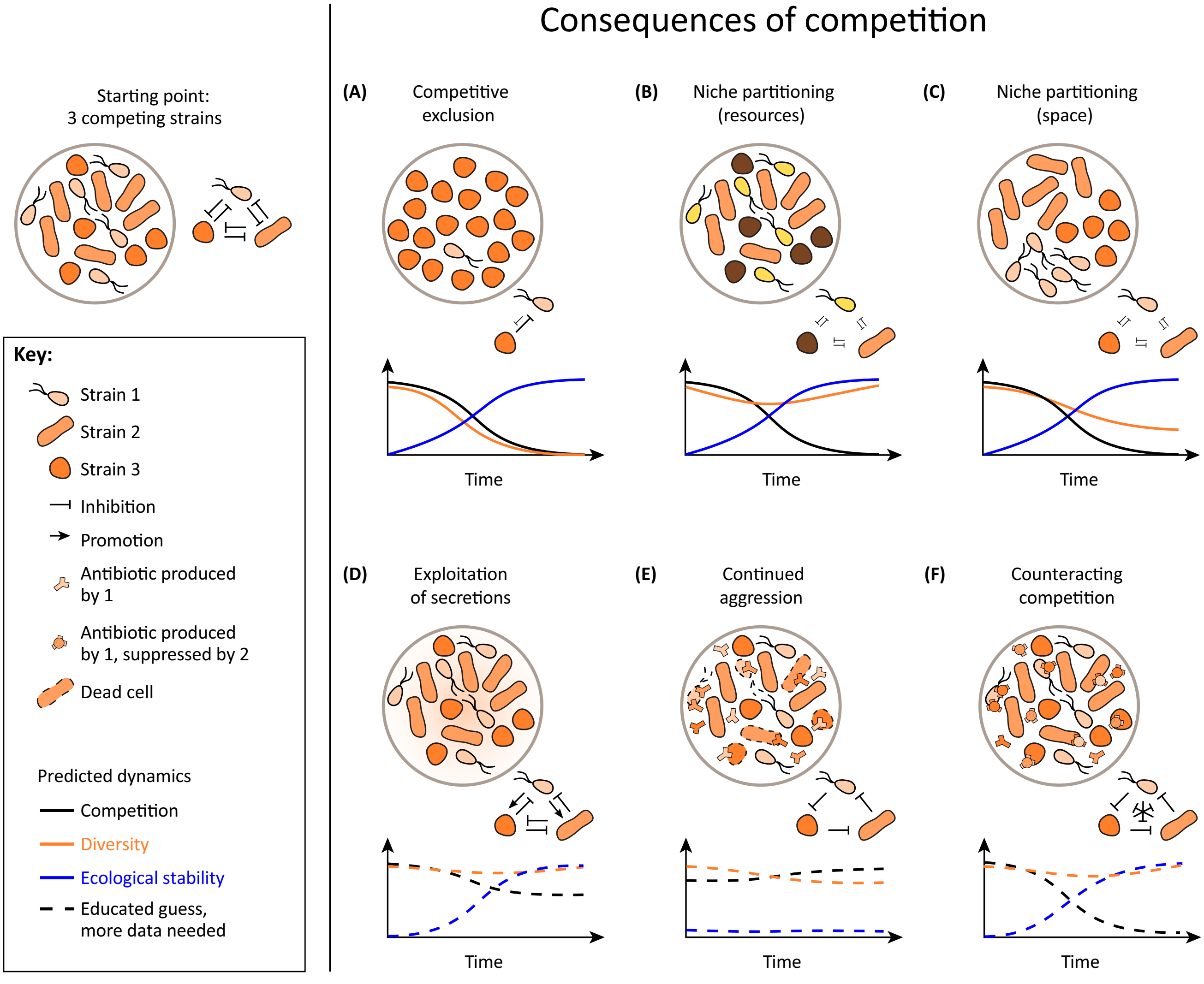

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Figure 3. We show three strains of microbe that compete with one another initially (high competition, high diversity and low stability, see top left) and the possible outcomes of this competition as proposed in the literature. Under the top three scenarios (A–C), we plot the predicted dynamics in competition, community diversity, and ecological stability over time, beginning from high competition and diversity, and low stability. The dynamics of competition, diversity and stability in the bottom three scenarios (D–F) are less well understood. Broken lines represent theoretical predictions that have not yet been extensively tested experimentally.

[110], a choice that may depend on environmental conditions (Figure 2) such as population density [111]. Soil *Streptomyces* indeed produce an exceptional range of antibiotics targeting many different species, which may be due to liquid flow in the soil, leading to more spatial mixing [80], or an increased probability of invasion. Another possibility is that, as weaker strains are outcompeted in the soil, diversity is reduced. And because high diversity isolates competitors from each other through buffer zones [84,112], novel warfare may be enhanced between the remaining strains as the buffer zones disappear.

A final scenario (Figure 3F), that has recently been proposed, is that warfare between two strains can be neutralised by other community members, as has been found in studies on antibiotic antagonism [38,93]. Kelsic *et al.* [93] have shown using a theoretical model, that this can lead to ecologically stable equilibria wherein different species neutralise all produced antibiotics, and diversity is maintained. On an evolutionary timescale, however, one might expect these protective mechanisms to break down.

In sum, competition generally reduces diversity and increases ecological stability on a local scale, although some exceptions exist. Which of the long-term dynamics are expected as a consequence of competition on a larger scale likely depends on the selection pressures of a given environment as listed above and in Figure 2. In fact, in different areas of the same environment, selection may result in an arms race in one area, competitive exclusion in a second and a synergistic division of labour in a third [113]. Exactly how these factors would influence diversity, stability, and the prevalence of competition and cooperation needs to be addressed by future research.

Concluding Remarks

Microbes grow in challenging environments where scarce resources must be shared with many other strains and species. Under these conditions, microbes have evolved many competitive strategies, including rapid growth to take up resources, direct aggression to eliminate or displace others, or alternative metabolisms that benefit from and exploit the presence of competitors. While this may sound like a highly aggressive microbial world, evidence suggests that competition often drops over time, leading to stable equilibria involving weak interactions between strains that have either eliminated their competitors or partitioned the available niches and space.

Decades of research are responsible for the details of this picture. Nevertheless, it remains preliminary. More effort will be needed to understand how these findings generalise. In particular, apart from the classical outcomes of competition, other evolutionary outcomes are less well understood and merit further focus (see Outstanding Questions). Microbial systems are excellent models to test such ecological and evolutionary predictions with scope for developing methods to compare microbial communities and disentangle interactions within them. Progress toward this goal can be accelerated through increased exchange between microbial ecologists and evolutionary biologists, as well as between researchers studying model systems and environmental samples (Box 1). Such collaboration would lead to more accurate and informed predictions on the nature of interactions in microbial communities. The ability to make such predictions can have many important implications in the management and design of microbial communities, whether to increase competition in soil communities to prevent the invasion of pathogens [81], or to decrease competition and thereby increase productivity in biofuel-producing communities [114]. A good understanding of microbial competition can result in expert microbial bioengineering.

Outstanding Questions

What is the effect of DNA uptake on fitness?

How does the environment dictate the prevalence of competition?

What determines the ability of a community to resist invasion?

Is competition always a temporary state or do constant battlefields exist? How stable are different outcomes (Figure 3D–F)?

Is it possible to manipulate competition by altering environmental conditions?

How often do secondary metabolites commonly found in genomic data result in aggressive phenotypes?

How variable is the expression of competitive phenotypes within a population of clonal cells, and how does this heterogeneity affect the success of genotypes?

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