



Published in final edited form as:

Nat Rev Gastroenterol Hepatol. 2018 April ; 15(4): 197–205. doi:10.1038/nrgastro.2017.173.

Role of priority effects in the early-life assembly of the gut microbiota

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Abstract

Understanding how microbial communities develop is essential for predicting and directing their future states. Ecological theory suggests that community development is often influenced by priority effects, in which the order and timing of species arrival determine how species affect one another. Priority effects can have long-lasting consequences, particularly if species arrival history varies during the early stage of community development, but their importance to the human gut microbiota and host health remains largely unknown. Here, we explore how priority effects might influence microbial communities in the gastrointestinal tract during early childhood and how the strength of priority effects can be estimated from the composition of the microbial species pool. We also discuss factors that alter microbial transmission, such as delivery mode, diet and parenting behaviours such as breastfeeding, which can influence the likelihood of priority effects. An improved knowledge of priority effects has the potential to inform microorganism-based therapies, such as prebiotics and probiotics, which are aimed at guiding the microbiota towards a healthy state.

It is now widely recognized that the human body is colonized by many species of microorganisms that can influence a range of metabolic, developmental and physiological processes affecting host health. These microorganisms, especially those of the gut, help liberate and make available to their host otherwise inaccessible components of the diet¹, stimulate development of the host immune system² and protect against pathogen invasion³, among other functions beneficial to the host. The gut microbiota has also been implicated in

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Author contributions

All authors researched data for the article and provided substantial contributions to discussion of the content. D.S. wrote the article. All authors contributed equally to reviewing and/or editing of the manuscript before submission.

Competing interests statement

The authors declare no competing interests.

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several chronic gastrointestinal inflammatory disorders, including Crohn's disease^{4,5}, ulcerative colitis^{6,7}, primary sclerosing cholangitis⁸, NAFLD⁹ and environmental enteropathy^{10,11} as well as other chronic disorders such as obesity^{12–14}, chronic periodontitis^{15,16} and cardiovascular disease¹⁷.

Clinical studies correlating specific taxonomic groups with disease states have yielded valuable insight but have often assumed that host–microorganism interactions occur independently of the rest of the microbial community. Under this assumption, multispecies interactions that modulate the effect of specific taxa on health of the host would be overlooked. In community ecology, the field that focuses on multispecies interactions¹⁸, one phenomenon that is receiving increasing interest is priority effects, or the effects that the history of species arrival has on how species affect one another in communities¹⁹. Through this lens, human health can be viewed as the net result of dynamic interactions that involve both the host and its microbiota²⁰. In this Review, we apply the concept of priority effects to the infant gut and explore how knowledge of the order and timing of microbial colonization of the infant gut might help predict the development of the early-life microbiota and guide it towards a healthy state. We focus on bacteria because more data are available for them than for other components of the microbiota, but the same concepts might apply to fungal, viral and other microbial components.

Gut microbiota assembly in early life

Community ecologists have proposed different concepts over the past century to explain observed patterns of species distribution and abundance. Mark Vellend synthesized these concepts by categorizing the processes that affect community assembly into four groups: dispersal, selection, drift and diversification^{21,22} (FIG. 1). Taxa are added to local sites through dispersal from the regional species pool and through *in situ* diversification, and the relative abundances of taxa are further shaped by selection and drift. In this section, we describe each process in reference to the infant gut to provide a context for discussing priority effects in the next section.

Dispersal.

The gastrointestinal tract of a newborn baby represents a large suite of physical and metabolic niches that microorganisms can colonize via dispersal^{23,24}. Stool samples collected within the first 8 days of life suggest that initial colonizers largely originate from the maternal microbiota²⁵. For example, the microbiota of vaginally delivered infants are dominated by taxa found in their mother's vagina (*Lactobacillus* spp., *Prevotella* spp., *Atopobium* spp. or *Sneathia* spp.), whereas those of infants delivered by caesarian section are enriched for taxa found on human skin (*Staphylococcus* spp., *Corynebacterium* spp. and *Propionibacterium* spp.)^{25,26}. The mother's gut can also be a source of the initial microbial inoculum^{27–30}, and the sharing of strains between mothers and newborn babies is commonly observed. Maternal strains of *Helicobacter pylori*^{31,32}, *Escherichia coli*^{33,34}, *Bacteroides vulgatus*³⁴ and *Parabacteroides distasonis*³⁴ have been found to colonize the gastrointestinal tract of infants, as have *Bifidobacterium longum* subsp. *longum* and other *Bifidobacterium* spp.^{34–36}. While species-level similarities between mothers and their children tend to

increase over the first several years of life, strain-level sharing decreases over time. For example, one study found that 91% of strains were shared between the stool of mothers and their newborn babies 4 days after birth, yet that figure dropped to 55% 1 year later³⁴. In addition, healthy, full-term infants can be influenced by their mother's microbiota even before the rupture of amniotic membranes³⁷. Although the existence of a persistent, metabolically active microbial community in the placenta remains controversial^{38,39}, microbial DNA has been reported in the placenta^{40,41}, amniotic fluid^{41,42} and meconium^{43–45}. Microorganisms or microbial components can arrive in the prenatal intrauterine environment by ascending from the vagina⁴⁶ or by spreading haematogenously from the oral cavity or gut⁴⁷. It has also been postulated that dendritic cells or lymphoid tissues can translocate bacteria or bacterial DNA to the placenta⁴⁸. However, we do not yet have enough information about the potential role of these events in healthy human pregnancies to assess how they might influence priority effects. Even if there were a microbial community in the placenta or amniotic sac, its contributions to the membership of the postnatal infant microbiota are likely overwhelmed by the vast numbers of microorganisms to which the infant is exposed at birth. Overall, specific taxa from the mother's microbiota are commonly transmitted to the infant's gut in early life. Variation in microbiota among mothers should therefore result in variation in dispersal among their infants. In addition to the mother, there are many other origins of microbial dispersal to the infant, which we will discuss later.

Selection.

Selection occurs when fitness and niche differences among taxa cause them to reproduce or die at different rates. In the infant gut, two primary sources of selection are the immune system and the diet. For instance, commensal *E. coli* strains colonizing the gastrointestinal tract of *Rag2*^{-/-} mice, which lack B cells and T cells, adapted more slowly than strains colonizing mice with an intact adaptive immune system⁴⁹. In gnotobiotic zebrafish, a statistical model that assumed that species are identical to one another in their birth and death rates predicted microbiota composition well in early life, but selection became more important as the adaptive immune system of the fish became active⁵⁰. Similarly, as an infant's immune system matures, it might exert increasing selection on the microbiota, causing largely homogeneous communities to become increasingly body-site-specific^{23,51}.

Drift.

After a microorganism colonizes the infant gut, its growth rate and abundance can be shaped not just through deterministic forces such as selection but also via stochastic processes such as ecological drift. Drift is the random changes in population size that occur regardless of species identity⁵². The effect of drift is stronger on low-abundance species because they are more likely to be stochastically pushed to local extinction. Some species are at low abundance in the gut because they arrive infrequently as a small population or because they experience large reductions in number by a major perturbation such as diarrhoea⁵³ or antibiotic treatment⁵⁴. These species can be affected by drift more strongly than by selection. However, the effect of drift on gut microbiota assembly has not been well characterized, in part because factors that cause drift often alter selection as well, making it difficult to tease apart the two processes.

Diversification.

Microorganisms, with their large population sizes, high growth rates and high mutation and recombination rates, are able to rapidly diversify and adapt when faced with the strong selective regimes found in the human body. One example is the diversification of *Pseudomonas aeruginosa* in the airways of patients with cystic fibrosis. Several adaptations were observed over a decade of mostly constant selective pressures inside the cystic fibrosis lung^{55,56}. By comparison, communities that assemble in the infant gut experience frequently shifting selective regimes related to immune system development, the addition of complementary foods, the cessation of breastfeeding and increasing competition resulting from increased taxonomic diversity. Because diversification often requires persistent selective pressure, the extent of diversification in the infant gut during assembly remains uncertain.

Some factors affect more than one of the four processes simultaneously. For example, breast milk affects both dispersal and selection because it is both a source of microorganisms dispersing to the gut and the primary nutrient source for the infant and their microbiota⁵⁷. Breast milk commonly harbours *Bifidobacterium* spp.⁵⁷⁻⁶⁰, *Lactobacillus* spp.^{57,59-61}, *Staphylococcus* spp.^{57,62} and *Streptococcus* spp.^{59,60,62} and is composed of a rich mix of proteins, fats and human milk oligosaccharides (HMOs), which are a diverse set of unconjugated glycans that cannot be digested by the host and can be digested by only a subset of the microbiota⁶³. The complex composition of breast milk selects for both HMO specialists and mucus-adapted species with a wide range of glycoside hydrolases capable of metabolizing diverse carbon sources that become abundant after complementary foods are introduced into the infant's diet⁶⁴. Breast milk also contains many antimicrobial factors such as lysozyme, lactoferrin and secretory immunoglobulin A (IgA)^{65,66}, which impose additional selection on the gut microbial community. Formula milk, by contrast, lacks many of these bioactive compounds as well as the microorganisms that are adapted to the milk environment, which might result in altered dispersal and selection compared with those related to breast milk, although the effects of these foods remain unclear.

What makes the four processes interesting and challenging to understand is that they do not always have simple additive effects but can instead exert complex interacting effects on community assembly⁶⁷. Priority effects are an example of such interactive effects in which dispersal history modulates how selection, drift and diversification influence community structure.

Priority effects in the infant gut

Each local microbial community can be viewed as a subsample of the regional pool of species that passed through a set of biotic and abiotic filters. From this perspective, it might seem that species composition at equilibrium is predictable from the local environmental conditions and the list of species that are available to colonize the local habitat. However, the order and timing of dispersal can have large effects on final species composition, even if environmental conditions and regional species pools are identical¹⁹. It is these effects of the order and timing of past species immigrations on interspecies interactions that are known as priority effects (FIG. 2).

Little is known about how priority effects shape microbial community assembly in early childhood because few studies report the timing and order of colonization, but indirect evidence suggests that priority effects are plausible. For example, in a 2016 study, Yassour *et al.*⁶⁸ classified infant gut microbiota into two groups based on the abundance of *Bacteroides* spp. present in the first 6 months of life. Of the 35 infants in their cohort, 11 were characterized as having low levels of *Bacteroides* spp. and were instead dominated by either Proteobacteria or Actinobacteria (especially *Bifidobacterium* spp.)⁶⁸. These ‘low-*Bacteroides*’ microbiota remained less diverse than the ‘high-*Bacteroides*’ group for at least the first 36 months of life, well after *Bacteroides* spp. membership expanded in relative abundance⁶⁸. In other work, facultative anaerobes such as Enterobacteriaceae (for example, *Escherichia* spp.) have been found in high abundance in meconium or early stools but gradually yield to strict anaerobes such as *Bifidobacterium* spp., *Bacteroides* spp. and *Clostridium* spp. over the first few months of life^{28,69}. Collectively, these findings suggest a degree of mutual exclusion between *Bacteroides* spp., *Escherichia* spp. and lactic acid producers such as *Bifidobacterium* spp. and *Lactobacillus* spp. that might be partially mediated by the infant’s exposure history and the patterns of dispersal from various sites in or on their mother.

Priority effects occur when microorganisms either pre-empt or modify a given ecological niche and thereby alter the ability of subsequent microbial immigrants to colonize. For example, *Bifidobacterium* spp. consume a wide range of HMOs found in breast milk^{60,70}. Their arrival soon after birth likely depletes the intestinal lumen of these carbon sources, thereby limiting the ability of later species to colonize^{60,64,70–72}. Niche pre-emption necessarily results in the inhibition of later immigrants, but taxa that modify niches can either inhibit or facilitate later immigrants. For example, the gut commensal *Bacteroides thetaiotaomicron* liberates mucus-derived sugars such as fucose and sialic acid, which provide efficient carbon sources for late-arriving pathogens such as *Clostridium difficile* and *Salmonella enterica* subsp. *enterica* serovar Typhimurium⁷³. Similarly, some early colonizers such as *E. coli* deplete oxygen in the infant gut, facilitating subsequent colonization by obligate anaerobes such as *Bacteroides* spp.⁶⁹ while making the environment less hospitable to facultative anaerobes.

Newly arriving microbial taxa vary in both the effect they have on the local environment and the resources that they must acquire from it for survival and reproduction. Strong priority effects can occur when early-arriving species have a large effect on the local environment or when late-arriving species have high environmental requirements¹⁹ (FIG. 3a,b). Furthermore, for an early-arriving species to pre-empt a niche from a late-arriving species, the two must have a high degree of niche overlap^{19,74} (FIG. 3c). This condition has been demonstrated in mouse colonization models in which isogenic strains with complete niche overlap exhibit strong priority effects over one another^{75,76}. Although the mechanisms of priority effects are usually unknown, Lee *et al.* identified a bacterial genetic locus, commensal colonization factor (*ccf*), that mediates priority effects in host-associated *Bacteroides* spp.⁷⁷. Consistent with the niche overlap expectation (FIG. 3c), gnotobiotic mice that are colonized with a single *Bacteroides* sp. are resistant to colonization by the same, but not different, species⁷⁷. The *ccf* locus enables *Bacteroides* spp. to associate with colonic crypts, thereby excluding later immigrants⁷⁷. In fact, non-toxin-producing

Bacteroides fragilis can limit the colonization of enterotoxigenic *B. fragilis* in specific pathogen-free (SPF) mice, demonstrating that priority effects through niche pre-emption could be a powerful tool in the design of probiotic-based prophylaxis⁷⁸.

Microorganisms can also modify niches found in the human body through interactions with the host immune system. For example, *Bacteroides* spp. colonization can affect innate immune signalling⁷⁹, endotoxin tolerance⁷⁹ and T helper 1 (T_H1) cell immune responses²⁷, and *Bifidobacterium* spp. can modulate vaccine response⁸⁰ and increase cytokine production *in vitro*⁸¹. These immune-mediated effects can occur even as the result of prenatal microbial exposure. Colonization of pregnant mice with the HA107 strain of *E. coli*, which was genetically engineered to be unable to persist in the intestine, demonstrated that microbial metabolites, independent of the microorganisms themselves, can increase both intestinal group 3 innate lymphoid cells and F4/80⁺ CD11c⁺ mononuclear cells in neonate pups while also decreasing bacterial translocation to the mesenteric lymph nodes⁸². The transient gestational colonization affecting both immune development and microbiota structure in offspring suggests that priority effects can occur before microorganisms even have the opportunity to colonize⁸².

Species pools in early life

The role that priority effects play during community assembly is determined by the characteristics of the microbial taxa contained in the pool of potential colonizers¹⁹. For example, a species pool that is taxonomically and functionally more diverse might be more likely to contain taxa that yield priority effects¹⁹. Therefore, to understand whether priority effects influence community assembly, it is helpful to characterize the set of microorganisms that have the potential to colonize the infant gut in early life, including those originating from host-associated, environmental and yet unknown sources (FIG. 4). However, defining a species pool is often challenging, and few investigations of early-life colonization have attempted to characterize all sources of microorganisms that are capable of colonizing an infant.

The microbiota of family members, medical personnel, birth attendants and other caretakers can all contribute to the species pool of an infant's gut (FIG. 4). The first site with which many infants come into contact is the maternal birth canal. Vaginal communities have been classified into five distinct community state types (CSTs), with four of the five exhibiting somewhat low diversity and domination by a distinct *Lactobacillus* spp.⁸³. If delivered via caesarian section, infants can instead first come into contact with the mother's skin²⁶, which harbours more diverse communities than the vagina and therefore might contain more species capable of causing priority effects. Although delivery mode is correlated with differences in early postnatal microbiota structure, mothers who deliver via caesarian section (both planned and emergency) are commonly prescribed antibiotics⁸⁴ and are often not able to breastfeed as early as those who deliver vaginally⁸⁵, confounding the effect of delivery mode on microbiome assembly. Nonetheless, some mothers intentionally wipe their caesarian-delivered infants with their vaginal secretions in an attempt to simulate the priority effects that occur following vaginal delivery, although the health benefits remain unproven⁸⁶.

The skin microbiota has ample opportunity to disperse while the infant is in contact with their mother during sleep or feeding^{23,87,88}. Kangaroo mother care, or immediate and continual skin-to-skin contact between mothers and newborn babies immediately following birth, is commonly recommended for pre-term infants because it decreases the risk of sepsis and increases breastfeeding rates⁸⁹, effects that could be partially mediated by increased transmission of commensal bacteria⁹⁰. As discussed earlier, breast milk contains bacteria, although its composition varies with lactational stage, delivery mode and the mother's health^{59,91}. Microbial diversity and abundance are several orders of magnitude higher in the gastrointestinal tract, and transmission of the mother's gut microbiota to the newborn baby has been observed in many studies^{28,35,36,68}. A mother's diet affects both the structure of her gut microbiota and the nutritional and microbial composition of her breastmilk^{92,93}. In addition to mothers, studies have reported an effect of fathers^{25,94}, older siblings^{95,96}, furry pets⁹⁷ and day care attendance⁹² on microbiota assembly.

In addition to microbiota found on the mother's body or other family members' bodies, a newborn infant is exposed to a myriad of other microorganisms in their environment, each with their own habitat-specific features (FIG. 4). Experiments with gnotobiotic mice demonstrate that microorganisms from many diverse environmental and host-associated habitats can colonize the mouse gut⁹⁸. Competitive invasion assays showed that a soil-derived *Ruminococcus* sp. was able to invade gut-adapted microbial communities⁹⁸. Furthermore, bacteria from the human gut colonize co-housed germ-free mice via coprophagy even faster than microorganisms from conventionally raised mice⁹⁸. This counterintuitive result can be explained in part by priority effects because well-adapted species are limited in their ability to diversify. Specifically, it is possible that well-adapted species can outcompete less-adapted mutants and dominate regardless of their colonization order, while nonadapted strains are able to diversify rapidly and exert priority effects, but this occurs only if they arrive early enough to pre-emptively exploit the resources in that niche¹⁹.

The role of microorganisms from the built environment might be underappreciated during host-associated assembly. Infants born at home are less frequently colonized by *E. coli* and *C. difficile* than those born in a hospital⁹⁵, although these environmentally acquired microorganisms can also vary between hospitals⁹⁹. This effect is especially apparent in premature infants that lack normal immune development and might therefore be more susceptible to priority effects owing to reduced host selection¹⁰⁰.

Infant-care-associated behaviours (ICABs) that affect microbial dispersal have evolved owing to changes in societal and family structures, diets, medical practices, travel, migration patterns, urbanization and housing environments. Parents can transmit oral microorganisms to their infants by kissing¹⁰¹, pre-masticating solid foods¹⁰², cleaning pacifiers with their mouths¹⁰³ or other ICABs that place newborn babies in contact with an adult's microbiota (FIG. 4). ICABs are variable across cultures. For example, anointing newborn babies with oil or other emollients¹⁰⁴ is a common practice across southeast Asia. In many parts of India, it is customary to not breastfeed for the first several days of an infant's life and instead administer pre-lacteal foods that include honey, ghee (clarified butter), water, tea, jaggery (brown sugar) and ghutti (a herbal paste)^{105–107}. Infants themselves instinctively explore

their local environment with their hands and put their hands and other nonfood items in their mouth, which when persistent is characterized as a psychological disorder known as pica¹⁰⁸. A large comparative study found that the gut microbiota of Guahibo Amerindian mothers living in Venezuela were more similar to those of their own child than to those of unrelated children, while mother–child dyads from Malawi were not more similar than unrelated pairs¹⁰⁹. Differences in the occurrence and timing of ICABs among cultures could explain some of the observed differences in microorganisms that are shared between mothers and their infants. If priority effects are a major driver of gut microbiota assembly, it might be possible to steer the trajectory of microbiome assembly towards a healthy adult-like state by modifying ICABs related to parturition and early life.

Consequences of priority effects

Priority effects could explain some puzzling observations of microbiota assembly and consequences for the host. For example, one study based on the use of an SPF porcine model of microbiota assembly discovered strong batch effects during efforts to replicate the findings¹¹⁰. Two groups of identical animals housed in the same SPF animal facility ended up with divergent communities. The investigators found that stochastic variation in Clostridia colonization in the first day of life caused sustained, broad colonization differences at day 35 (REF. 110). Priority effects driving the communities towards alternative states might have been responsible for this finding. Priority effects can also cause a community to enter an oscillating compositional cycle or cause more complex patterns, such as those arising from nontransitive or ‘rock-paper-scissors’ types of interactions¹¹¹. Examples of compositional cycles include predator–prey dynamics, such as those that have been observed during infant gut assembly between strains of *Staphylococcus epidermidis* and their bacteriophages¹¹². The population dynamics of these communities are historically contingent because their composition is dependent on the specific sequences of species arrival.

Broad-spectrum antibiotics are commonly used in early life in humans, often with little regard for potential long-term consequences of priority effects for microbiota assembly¹¹³. Broad-spectrum antibiotics cause a strong perturbation of the microbial communities in the infant gut, possibly altering its maturational trajectory^{68,69,95,114–117}. Antibiotic use by mothers can also alter the regional species pool of the infant¹¹⁸. These perturbations can have lasting effects on host metabolism, immune development and health, especially if they occur during critical immune developmental windows early in life^{117,119}. Realizing the benefits of probiotics in mitigating these adverse effects requires an understanding of possible priority effects and the consequences of alternative assembly patterns. Priority effects can be particularly important to consider when they involve catalytic species, which, given the right timing, invade a community, change its composition and then go locally extinct¹²⁰. These species create ‘Humpty-Dumpty’ communities; that is, communities that cannot be reassembled just from the set of species that they contain¹²⁰. Such circumstances underscore the need for detailed records of colonization history.

Future research needs

Perhaps the greatest challenge for investigating factors that influence gut microbiota assembly is the limited set of opportunities for experiments with humans. Experimental manipulation of bacterial colonization history, which is necessary to rigorously evaluate priority effects, might pose health risks to the developing infant and therefore should not be implemented without careful review. Nevertheless, some clinical situations might be amenable to interventional studies in which bacterial exposure is intentionally altered through the use of antibiotics, probiotics or techniques such as vaginal microbiota transfer⁸⁶. For example, when populations of comparable infants vary in the timing of probiotic supplementation relative to antibiotic use, this variation could be used to test for priority effects and clinical consequences for the host. In fact, the results of probiotic interventions might depend on the specific organism and the timing and dosage of its administration, which might be in part caused by priority effects in the microbiota. One study found that *Bifidobacterium breve* BBG-001 administered within the first 48 hours of life had no effect on necrotizing enterocolitis or late-onset sepsis¹²¹, while another found that use of *Lactobacillus plantarum* ATCC-202195 in conjunction with a prebiotic fructooligosaccharide in the first week of life reduced neonatal sepsis by 40%¹²². Broad conclusions, such as the suggestion in a 2014 Cochrane review that probiotics can help prevent necrotizing enterocolitis in preterm infants¹²³, seem premature at this stage. This meta-analysis pooled results from 24 randomized trials using a range of organisms, including *Saccharomyces boulardii*, *Lactobacillus* spp., *Bifidobacterium* spp. or a mixture of several bacteria and/or fungal taxa, administered at different time points and for different durations. The effects of specific strains and the timing of their administration on priority effects and subsequent microbiota beneficial services should be examined carefully before this practice is widely endorsed.

Other opportunities to observe and investigate priority effects with limited additional risk to the infant include cases in which there is natural variation in microbial colonization or in the species pools, such as during cross-cultural comparisons of ICABs, although confounding variables make inference complicated. Moreover, stool provides only a limited view of the microbial interactions that occur throughout the lumen of the gut and poorly reflects interactions among mucosa-associated microorganisms, especially those that take place in more proximal regions of the gastrointestinal tract^{4,124}. Endoscopic biopsies, mucosal brushings and other sampling approaches are likely necessary to observe these fine-scale interactions. In addition, studying how communities assemble at other body sites that are more amenable to experimental intervention, such as transplant experiments among skin or oral communities¹²⁵, might yield insight into the factors that shape community assembly in the gut. In concert with experimental and clinical data collection, statistical techniques for analysing the data should be improved, and methods developed in the ecological literature¹²⁶ should be helpful.

We have focused primarily on bacteria, but priority effects are also possible across domains of life (that is, between bacteria and archaea and/or eukaryotic microorganisms)^{127–130}. In particular, diverse fungal communities are present in infants¹³¹. Fungi are transmitted from mother to infant in early life, their dispersal history can be highly variable among infants,

and once immigrated, they can interact strongly with bacteria⁸⁷. Yet we have little understanding of how they affect microbial community assembly via priority effects. Studies on the infant gut should consider the broadly defined microbial community.

Conclusions

We have discussed the mechanisms, conditions and consequences of priority effects that might affect microorganisms in the gastrointestinal tract. Ecological theory and circumstantial evidence strongly suggest that priority effects are important to infant health, but definitive direct evidence is largely lacking. Given that we now have the foundational concepts from community ecology and many of the molecular and computational tools needed to study the microbiome, we believe the time is ripe for studying priority effects by use of clinically relevant data to improve microbiome management.

Acknowledgements

The authors' work is supported by the US National Science Foundation (NSF) Graduate Research Fellowship award number DGE-114747 (D.S.), the National Institute of General Medical Sciences of the NIH under award number T32GM007276 (D.S.), the Thomas C. and Joan M. Merigan Endowment at Stanford University (D.A.R.), The Leona and Harry B. Helmsley Foundation grant number 2014PG-IBD014 (D.A.R.), US NSF award numbers DEB-1555786 and DEB-1737758 (T.F.) and the Terman Fellowship of Stanford University (T.F.). Any opinion, findings and conclusions or recommendations expressed in this material are those of the authors and do not necessarily reflect the views of the US NSF or the NIH. The authors especially thank E. Costello for her helpful feedback.

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Community assembly

The construction and maintenance of local communities through sequential, repeated immigration of species from a regional species pool.

Regional species pool

The set of species that could potentially colonize and establish within a community.

Niche pre-emption

Occurs when the first species to arrive in a given habitat uses or otherwise sequesters resources and, as a consequence, inhibits the colonization of later species.

Community state types

(CSTs). Categories of stereotypical microbial communities that are typically defined by their dominant taxa and found at a given body site.

Key points

- Infant gut microbiota assembly is driven by four ecological processes — dispersal, diversification, drift and selection — and can be understood by resolving their relative contributions, mechanisms and interactive effects
- Priority effects, whereby the order and timing of dispersal alters how diversification, drift and selection affect infant gut microbiota assembly, could have long-lasting consequences for host health
- Priority effects in the infant gut are influenced by the regional species pool, which is made up of numerous local communities, some of which are host-associated, while others are not
- To understand the role of priority effects in the infant gut, future studies in model systems should intentionally vary dispersal order and timing
- In future studies, when intentional variation in dispersal order is not feasible, dispersal order should be carefully recorded along with relevant environmental variables
- An understanding of the processes that govern priority effects can be used to inform microorganism-based therapies and manage strategies aimed at guiding the microbiota towards a healthy state

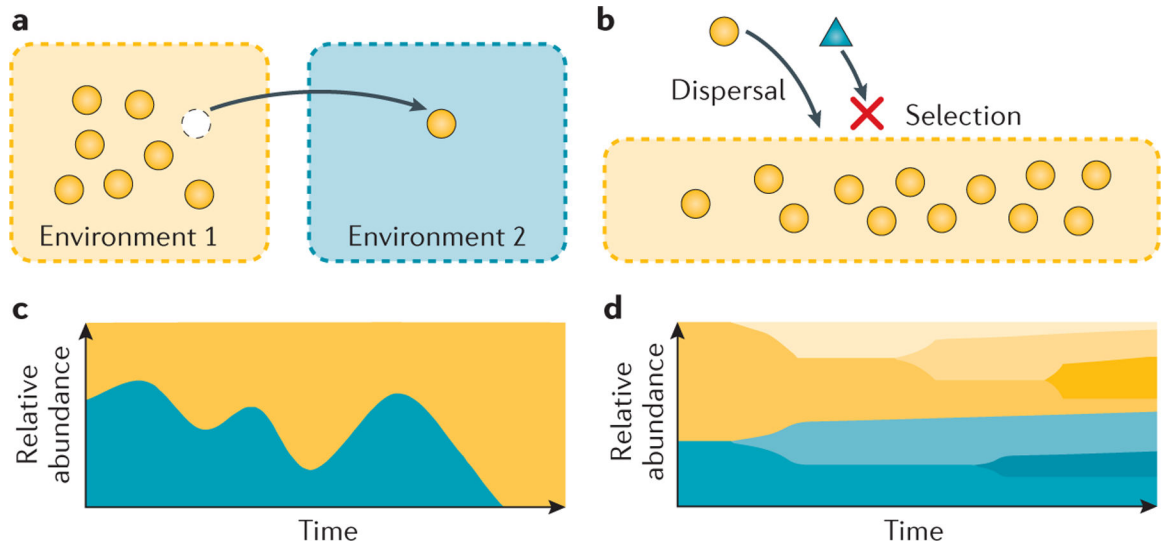


Figure 1 | Four processes that affect ecological communities.

a | The arrow represents dispersal of an organism (orange circle) from Environment 1 (orange shading) to Environment 2 (blue shading). **b** | Deterministic fitness differences between two species (orange circle, blue triangle) cause the orange environment to select for one (orange circle) and against the other (blue triangle). **c** | Stochastic changes in the relative abundances of two species (orange area and blue area) result in changes in community structure within one environment through time. As a result, one population (blue) has gone locally extinct by the end of the time period. **d** | Mutation and/or recombination within a population (blue and orange areas) results in new genetic variation through time, leading to new strains (as denoted by different shades).

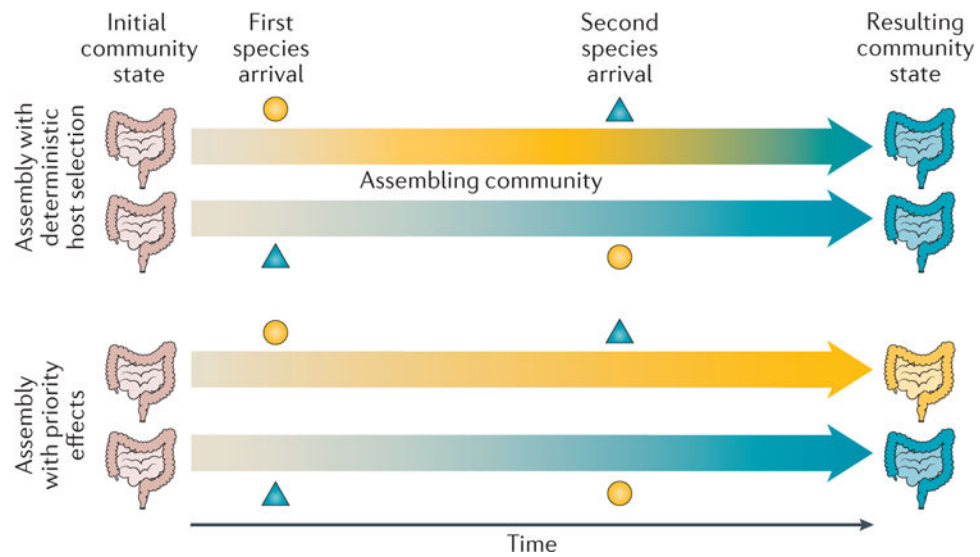


Figure 2 |. Contrasting hypothetical patterns of community assembly in the infant gut. An illustration of how infant microbial communities assemble with deterministic host selection (top) or priority effects (bottom). The shapes represent different taxa, while the colours represent the community state. Under deterministic host selection, the state of the assembling community is determined by host features that select for the blue microorganisms regardless of colonization order. With priority effects, colonization order can matter more than species identity.

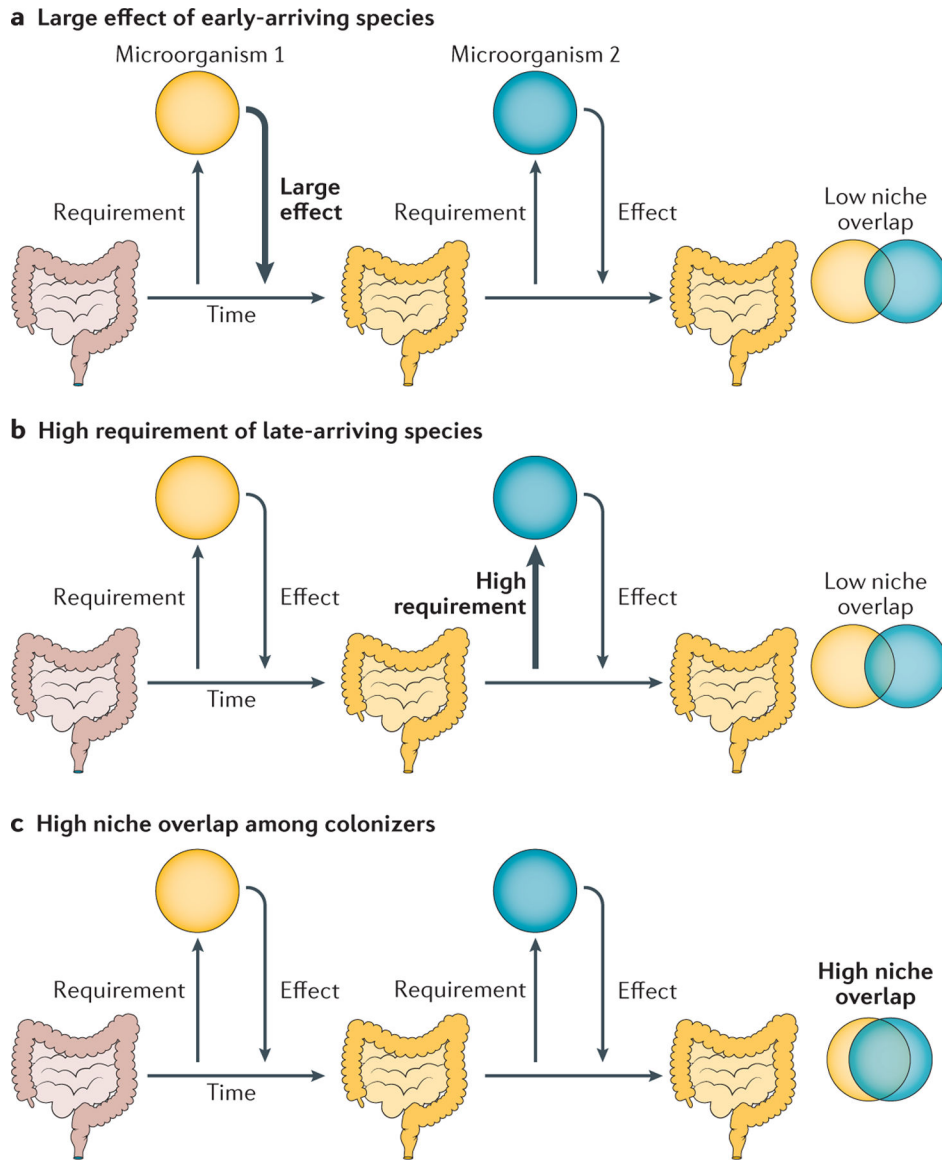


Figure 3 | Hypotheses on species features causing strong priority effects.

Both early-colonizing (Microorganism 1) and late-colonizing (Microorganism 2) microorganisms have their own set of requirements for colonizing a given environment as well as a distinct effect on that environment⁷⁴. The width of the arrow denotes the strength of each microorganism's effect niche and requirement niche. **a** | Microorganism 1 has a large effect on its environment, resulting in a modified niche that inhibits colonization by Microorganism 2. **b** | Microorganism 2 has a high niche requirement and is therefore more sensitive to smaller modifications to the niche that can inhibit its colonization. **c** | Microorganisms 1 and 2 have high niche overlap, meaning that Microorganism 1 is able to pre-empt the niche and inhibit colonization by Microorganism 2. Niche overlap is not necessary if the priority effects occur by way of the environment, as in parts **a** and **b**.

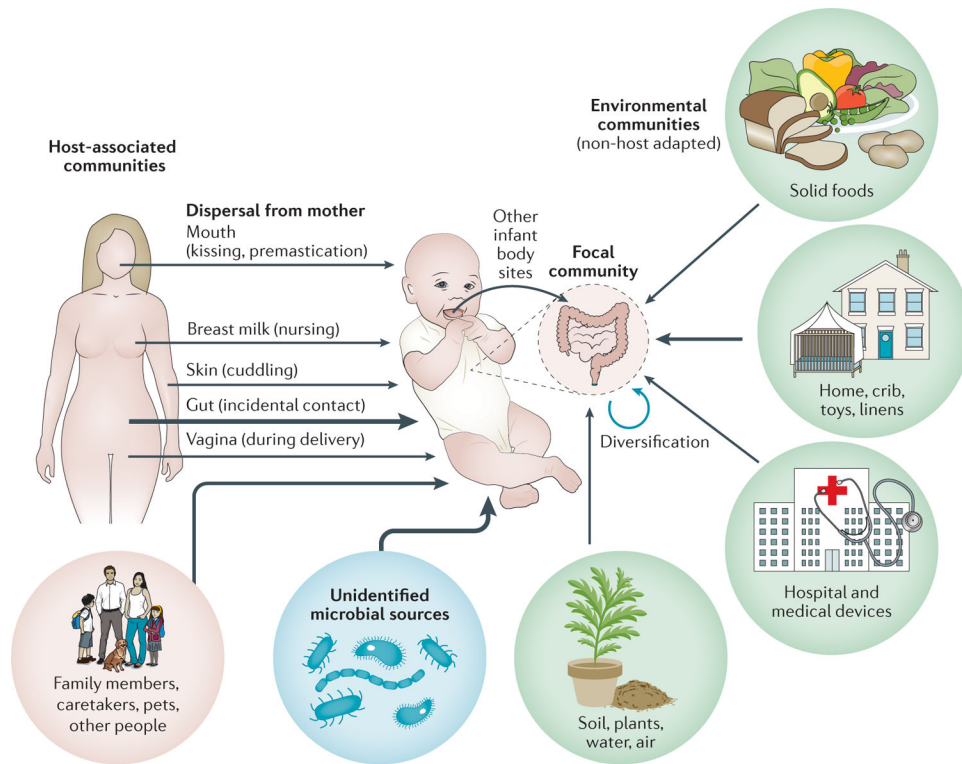


Figure 4 |. Local species pools that contribute to the regional pool of microorganisms available for colonization of the infant gut.

Infants are colonized by microorganisms from host-associated communities, environmental communities that are not host adapted, and unknown microbial sources. The thickness of the arrows denotes the hypothesized relative contributions of microorganisms from different sources that disperse to and stably colonize the local community (infant gastrointestinal tract).