



PART 1

Read the text below and answer questions 1–13.

THE HUMAN MICROBIOME: OUR INTERNAL ECOSYSTEM

The human body is inhabited by vast communities of microorganisms—bacteria, viruses, fungi, and archaea—that live on the skin, in the mouth, and throughout the digestive tract. Collectively known as the microbiome, these organisms are not simply hitchhikers. Many exist in a symbiotic relationship with the host, competing with pathogens for space and nutrients and producing compounds that can affect human tissues. Researchers increasingly describe the body as an ecosystem in which health depends partly on balance and interaction, rather than on the unrealistic goal of eliminating microbes altogether. One important role of this internal ecosystem is its dialogue with immunity: microbial signals help train the immune system to distinguish between genuine threats and harmless stimuli, shaping inflammation and tolerance across the lifespan.

Most microbiome research has focused on the gut, partly because it contains the greatest microbial biomass and diversity and partly because it is tightly connected to nutrition. In the intestine, microbes help break down dietary fibre that humans cannot digest on their own. This fermentation produces short-chain fatty acids, which are widely studied because they can influence inflammation, gut barrier function, and energy metabolism. Microbes also contribute to the synthesis of certain vitamins and to the transformation of bile acids, linking the microbiome to metabolic pathways that extend beyond digestion. The gut community is responsive rather than fixed: changes in food intake—such as shifting from a fibre-rich diet to a highly processed one—can alter microbial composition within days. This rapid responsiveness suggests that adult lifestyles can still modify the ecosystem, even if early life sets important baseline patterns.

The microbiome begins forming at birth and changes quickly during infancy. Newborns acquire microbes from their mothers and their immediate surroundings, and early feeding practices can influence which species thrive. Breast milk contains compounds that nourish beneficial bacteria and shape colonisation patterns, while formula feeding can be associated with different microbial profiles. Antibiotics during infancy can disrupt colonisation by removing susceptible organisms and creating ecological space for opportunistic species to expand. Researchers debate the extent to which these early shifts persist, but many agree that early life represents a sensitive period in which microbial communities are especially malleable and may have long-term consequences for immune development and disease risk. The idea is not that one early event determines destiny, but that early ecosystems can influence how resilient the system becomes to later shocks.



Microbial diversity is often discussed as a marker of resilience because diverse communities may be better at resisting invasion by pathogens and at maintaining function when conditions change. However, “more diversity” is not automatically better in every context. What matters is which organisms are present, what they do, and how they interact with each other and with the host. Some communities are stable and protective; others may contain species that are harmless under normal conditions but become problematic when the host is stressed or when the ecosystem is disrupted. The term dysbiosis is used to describe an imbalance or disturbance that is associated with conditions such as inflammatory bowel disease, allergies, and metabolic disorders. Yet dysbiosis is not a single microbial signature shared by all patients. Because microbiomes vary widely between individuals, scientists are cautious about universal “ideal” profiles. Genetics influences the ecosystem, but geography, sanitation, medication, stress, and cultural diets also shape microbial communities. Even within one person, composition can differ across gut regions and can change over time, complicating research that relies on a single sample.

This variability has led researchers to explore interventions aimed at shifting the microbiome in targeted ways. Probiotics can introduce live organisms, but many strains do not colonise permanently and may have modest or temporary effects that depend on the existing community and the host environment. Prebiotics—specific fibres that feed certain microbes—attempt to alter the ecosystem indirectly by changing its food supply. A more dramatic intervention is faecal microbiota transplantation (FMT), which transfers processed stool from a healthy donor to a patient to restore community structure. FMT has shown strong effectiveness for recurrent *Clostridioides difficile* infection, where repeated antibiotic exposure can leave the gut vulnerable to relapse. For other conditions, however, results are mixed, and long-term safety questions remain, including how to screen donors and how stable the introduced ecosystem will be over time.

As the field has matured, tools have shifted attention from simply “who is there” to “what they are doing”. Metagenomics sequences genetic material in a sample, identifying organisms and the functional genes they carry, which can suggest potential capabilities such as fibre fermentation or toxin production. Metabolomics measures the chemical outputs of microbial activity, offering a closer link to biological mechanisms because it captures molecules that interact with host tissues. These approaches generate enormous datasets and allow researchers to connect microbial communities to metabolic pathways and immune signalling. However, interpretation remains challenging. A gene’s presence does not guarantee it is expressed, and a chemical signal may originate from the host, the microbes, or both. Establishing causation therefore requires careful study design,



repeated sampling, and, where possible, clinical trials that test whether changing the microbiome changes health outcomes.

The microbiome also raises public-health and ethical questions as interest spreads beyond laboratories. Commercial tests often promise personalised advice based on a single stool sample, but scientific consensus on individualised recommendations remains limited, particularly because microbiomes fluctuate and because associations do not automatically reveal mechanisms. Privacy concerns also arise, since microbial profiles can reflect diet, medication use, and potentially disease risk. Regulators must decide how microbiome-based products should be classified, how donor screening should be governed for FMT, and how to balance innovation with safety. Overall, the microbiome is best understood as a dynamic system shaped by feedback between microbes, diet, immunity, and environment. Future progress is likely to depend on integrating careful clinical trials with mechanistic work that identifies which microbial functions matter most—and for which people—rather than searching for a single one-size-fits-all microbial “recipe” for health.

Questions 1–4

Select the correct answer.

1 What is the main point made about microorganisms in the human body?

- A** Their main benefit is preventing pathogens from obtaining space and nutrients.
- B** They form an ecosystem whose interactions can influence human health.
- C** Their most important role is enabling humans to digest dietary fibre.
- D** Their effects on health are determined primarily during infancy.

2 What does the passage say about the gut microbiome’s response to diet?

- A** Dietary changes affect microbial activity without altering community composition.
- B** Only a shift toward highly processed food can modify the adult microbiome.
- C** Its composition can change rapidly, although early life establishes important baseline patterns.
- D** Adult dietary changes matter only after antibiotics have disrupted colonisation.

3 Which statement best summarises the passage’s view of microbial diversity?

- A** Diversity may indicate resilience, but the identities and functions of organisms are also important.
- B** High diversity provides a reliable definition of an ideal microbiome for every individual.
- C** Community stability is more important than whether particular organisms become harmful.



D Genetic differences largely determine diversity, while environmental influences are minor.

4 What is said about faecal microbiota transplantation (FMT)?

A It changes the ecosystem indirectly by supplying fibres to selected microbes.

B It produces similarly strong results for recurrent infection and other conditions.

C Its long-term safety is assured when healthy donors are carefully screened.

D It can restore community structure and is highly effective for recurrent *C. difficile* infection, although results elsewhere are mixed.

Questions 5–9

Choose **TRUE** if the statement agrees with the information given in the text, choose **FALSE** if the statement contradicts the information, or choose **NOT GIVEN** if there is no information on this.

5 The passage suggests that the microbiome can influence how the immune system distinguishes between harmful and harmless signals.

6 Antibiotics during infancy can disrupt microbial colonisation by removing susceptible organisms.

7 The passage suggests scientists have identified a single “ideal” microbiome profile that applies to everyone.

8 Probiotic strains generally establish permanent colonies in the gut after they are consumed.

9 Commercial microbiome tests are regulated in the same way as prescription medicines.

Questions 10–13

Complete the notes below. Choose **NO MORE THAN TWO WORDS** from the text for each answer.

Microbiome research and intervention

- Gut microbes help break down dietary fibre into short-chain **10** that can influence inflammation and energy metabolism.
- Early life is considered a **11** for microbial development, and antibiotics may disrupt colonisation.



- One intervention, faecal microbiota transplantation, has shown strong effectiveness for recurrent **12** infection, although results are mixed for other conditions.
- New methods such as metagenomics and **13** expand research by linking microbes to potential functions and chemical outputs.

Answer Key

1. B
2. C
3. A
4. D
5. TRUE
6. TRUE
7. FALSE
8. FALSE
9. NOT GIVEN
10. fatty acids
11. sensitive period
12. Clostridioides difficile
13. metabolomics