Is the gut microbiome better understood as an organ, system or ecosystem?

Word Count: 1433

Introduction

From 2000 to 2020, the number of research papers published about the gut microbiome has gone from 500 per annum to 9,500 [1]. This shows its increasing importance in the scientific world. The gut microbiome is the community of microorganisms, predominantly bacteria, residing in the gastrointestinal tract [2]. It is referred to by different terms such as organ, system and ecosystem in papers, articles and books. An organ is a group of tissues in a living organism that have been adapted to perform a specific function; in higher animals, organs are grouped into organ systems, e.g. the oesophagus, stomach and liver of the digestive system [3]. A system is a group of related parts that move or work together [4]:and an ecosystem, a sub-category of system, is the complex of living organisms, their physical environment, and all their interrelationships in a particular unit of space [5]. Using incorrect definitions leads to ambiguity in research papers which weakens the validity. So, whether the gut microbiome is, 'better understood as an organ, system or ecosystem,' must be defined for productive communication in the scientific community. This essay will evaluate the strengths and flaws in the compatibility of each of these term with-the 'gut microbiome'.

Why the gut microbiome is not an organ

The gut microbiome is not an organ, because it is not a collection of tissues. Tissues are an organisation of multicellular organisms of structurally and functionally similar cells and their intercellular material [6]. Unlike tissues, the gut microbiota is a collection of trillions of single celled organisms of which there are millions of species, these species are far from being similar and are multifarious in form, oxygen and energy usage. Some of the main categories include coccid, rod-shaped, spirillum; budding shapes, aerobic, anaerobic; microaerophilic respiration; and heterotrophic, phototrophic or lithotrophic energy production processes [7].

These inhabitants of the gastrointestinal tract, primarily the colon, (see fig.1), each perform many different functions including fermentation, educating the immune system, vitamin production, modulation of the hosts behaviour and more [8]. This is unlike any other organs, e.g. the heart whose function is to pump blood around the body. Microorganisms, despite being intrinsically connected with us at a neural, immune and metabolic level, are independent of us and unlike other organs in the body are not always cooperative. An example of this incompatibility is dysbiosis. Dysbiosis is a dysregulated interaction within a bacterial community or between a microbiome and host [9], which leads to bloating, diarrhoea, constipation, fatigue, inflammation and can influence the metabolism, potentially leading to chronic conditions [10]. It is often caused by unvaried diet, as the higher the variation of nutrients the higher the variation of microorganisms (see fig.2) [11], and a lack of

variation leads to unhealthy amounts of single species [12].

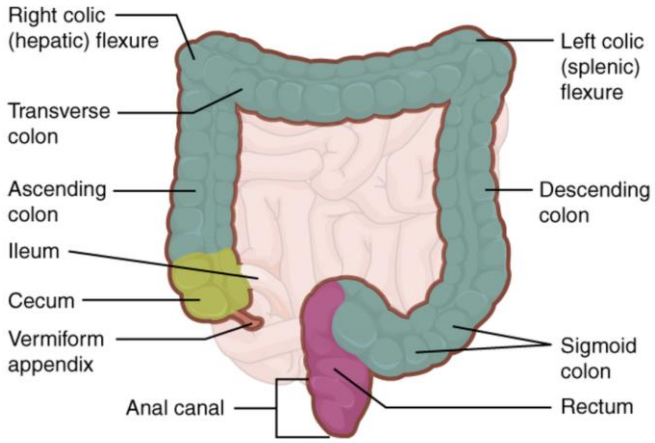


Figure 1: Annotated diagram of the colon, the colon is where the highest concentration of microorganisms in the gut microbiome is. Adapted from [24].

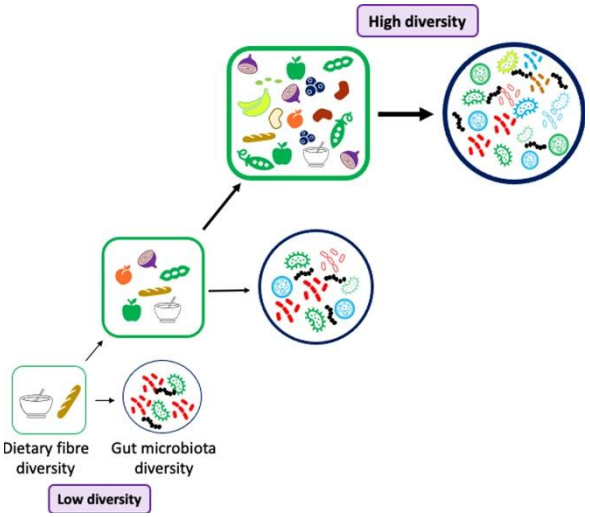


Figure 2: Representation of how fibre diversity leads to microorganism diversity. Adapted from [11].

The gut microbiome as an ecosystem

The gut microbiome is an ecosystem. An ecosystem is a complex system composed of many factors, the first of these being biotic constituents (living elements) and the second being abiotic constituents. Biotic constituents are categorised into autotrophs (self-sustaining organisms) and heterotrophs [5], and abiotic constituents are everything else: rocks, air, temperature etc. These factors are linked by two major forces: the flow of energy and the cycling of nutrients. The flow of energy starts at the fundamental source, which is different for photoautotrophs, chemoautotrophs and lithoautotrophs: the sun, inorganic compounds and carbon and inorganic compounds, respectively. [5] [13]. Nutrient cycling is the process by which nutrients – chemical substances required by the body to sustain basic functions of life [14] – are moved up the trophic levels and around the biogeochemical cycles. Heterotrophs, unlike autotrophs, cannot produce their own nutrients and rely on consuming other biotic constituents. Trophic levels (see fig.3) are the stages of nutrient cycling in an ecosystem between autotrophs and heterotrophs [5]. The first stage is the producer level, made up of

autotrophs. The second stage are the primary consumers who consume the producer level, following this are the secondary consumers, tertiary consumer etc., and the decomposers. Decomposers are mainly scavenging birds, bacteria, fungi and humans who return the consumed nutrients to the producer level through waste products e.g. via stool [5]. The gut microbiome aligns with all these criteria, the fundamental source is the food the host ingests, the heterotrophic bacteria and autotrophic archaea, the trophic levels and biotic constituents (the bacteria, the environment - the hosts gastrointestinal tract etc.) and the abiotic constituents (the temperature, air, pH etc.).

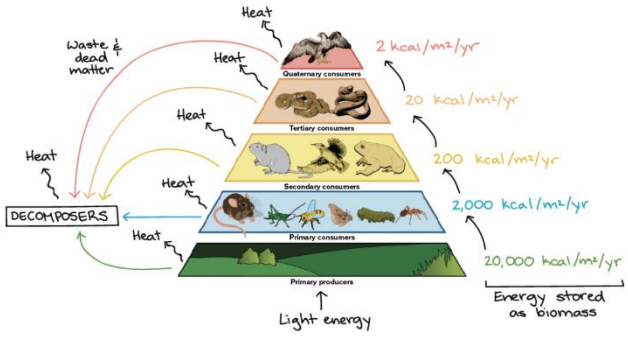


Figure 3: An example of trophic levels in an ecosystem. Adapted from [25]

Although they do fit under these categories, it is important to note how the gut microbiome is unique in comparison to other ecosystems. For example, the trophic levels within the gut microbiota do not follow the standard producer to consumer to decomposer stages. As the anaerobic conditions and lack of light prevent autotrophs from producing nutrients, this ecosystem relies entirely on another ecosystems' producer level [15] [16]. Like cave ecosystems, which have no producer level and rely on organic material e.g., dead leaves, wood, animal waste and dissolved organic carbon to be washed in by water flow or brought in by animals [17]. The cave system consists of mostly decomposers, similar to our gut, which means it is simply a case of interconnectivity at a more reliant level [18]. However, unlike caves, this does not mean that the gut microbiome has no autotrophs; it has chemoautotrophs [19]. Methanogenic and acetogenic archaea are chemoautotrophs that are responsible for hydrogen sink (the processing of hydrogen which prevents its build up) and efficient production of SCFAs (Short-Chain-Fatty-Acids). When hydrogen builds up, it can cause IBD (Inflammatory Bowel Disease). So, the trophic levels often start at primary degraders, for example, clostridium butyricum which produces hydrogen during fermentation, allowing the methanogenic archaea to process the hydrogen, preventing IBD, and releasing methane as a product [19]. In this sense the methanogenic archaea aren't the producer level but more a 'secondary producer level', which isn't present in any other ecosystems.

The ecosystem and relationship of microbiota in the gut is also unique to its host, as shown by the diversity of diet causing diversity in microbes (see fig.2) and how different fibres

cause different microbe cultures to flourish (see table.1) [11]On account of this, some animals, such as humans and ruminants (hoofed mammals including cattle, sheep and goats, that have a unique digestive system), have an obligatory mutualistic relationship between the host and microbiome. For example, ruminant animals cannot produce their own enzymes and rely entirely on the fermentation by the microbes of high roughage feedstuffs for 50% of their nutrients [20]. Humans also couldn't live without the gut microbiome, as it would weaken the immune system to a level where it would be impossible to live except in an almost entirely sterile environment. This is different from some animals who live and digest nutrients entirely without a gut microbiome [21].

Fibre	Dose (g daily)	Consumption	Design	Control	Duration (weeks)	Population (Human subjects)	*N*	Measures	Microbiome changes	Ref
Isolated fibres										
Arabinoxylan-oligosaccharides (AXOS)	10·4	Powder dissolved in water (2× daily) and in biscuits (4× daily)	R, X	None	4	Overweight and obese (BMI: 25–40 kg/m2) (36–52 years)	15	16s rRNA (shotgun sequencing (Illumina))	↑ *Actinobacteria* spp., *Bifidobacteriaceae* spp., *Bifidobacterium* spp. and *Prevotella* spp.	[73]
FOS (short-chain)	5	Powder dissolved in water (2× daily)	R, Pa, PI, DB	Maltodextrin (5 g)	4	IBS (18–60 years)	68	qPCR	↑ Bifidobacteria (+0·34 log_{10} copies of 16s rRNA gene/g faeces compared to control)	[74]
Inulin (oligofructose enriched)	8	Powder dissolved in water (1× daily)	R, DB, PI	Maltodextrin (3·3 g)	16	Obese (≥85th BMI percentile) (7–12 years)	38	16s rRNA (amplicon sequencing (Illumina))	↑ Actinobacteria and *Bifidobacterium* (+4·9 and 4 mean % bacterial abundance compared to initial respectively)	[75]
RS4	33	Crackers (100 g daily)	R, X, DB	Native wheat starch crackers (100 g)	3	Healthy (23–28 years)	10	16s rRNA (454 pyro-sequencing)	↑ Actinobacteria and Bacteroidetes (+7·3 and 5·9 % (proportion of bacterial taxa) compared to control), ↓ Firmicutes (−14 %)	[76]
β-Glucans (barley, HMW)	3	Breakfast foods (crepes, tortillas, porridge and chips)	R, X, SB, PI	Wheat and rice	5	Metabolic syndrome (TC: 5–8 mM) (27–78 years)	19	16s rRNA (amplicon sequencing (Illumina)	↑ Bacteroidetes (+9·23 % relative abundance in faeces compared to control), *Bacteroides* spp. (+6·3 %), ↓ Firmicutes (−11·78 %), *Streptococcus* spp. (−0·235 %)	[77]
Intact cereal fibres										
Barley (WGB), brown rice (BR) and combination of both (BR + WGB)	60 (or equal mix of both: 30 + 30)	Whole grain barley flakes or brown rice flakes	R, X	None	4	Healthy (mean age: 25·9 years)	28	16s rRNA (454 pyro-sequencing)	All ↑ relative abundance (% of total microbiota in faeces) of Firmicutes (BR: +7·76 %, WGB: +8·12 %, BR + WGB: +8·23 %) and ↓ Bacteroidetes (BR: −7·25 %, WGB: −7·67 %, BR + WGB: −8·14 %)	[78]
Whole grain oat (WGO) granola	45	Granola breakfast cereal	R, PI, DB, X	Non-whole grain (NWG) breakfast cereal (45 g)	6	Mild hyperglycaemia or mild hyper-cholesterolaemia (mean age: 42) (mean BMI: 26·4)	30	FISH	WGO ↑ *Bifidobacterium* spp. (+0·38), *Lactobacillus* spp. (+0·16) and total bacterial count (+0·11) (log_{10} cells/g faeces). NWG ↓ bifiddobacteria (−0·12) and total bacterial count	[79]
Wholegrain (WG) wheat breakfast cereal	48	Breakfast cereal	R, DB, X	Wheat bran (WB) breakfast cereal (48 g)	3	Healthy (mean age: 32 years)	31	FISH	↑ *Bifidobacterium* spp. (WG: +0·8 (log_{10} cells/g faeces)), Lactobacilli/ enterococci (WG: +0·6, WB: +0·4) (significantly greater ↑ with WG compared to WB)	[80]
Whole grain (WG) wheat (Shredded wheat)	70	WG: biscuits, RW: crackers and toast	R, PI, P	Refined wheat (RW) (70 g)	8	Overweight and obese (mean BMI: 30) (mean age: 38·5 years)	68	16s rRNA (amplicon sequencing (Illumina))	WG: ↑ relative abundance of Bacteroidetes (9·6–14·5 %) and Firmicutes (75·3–79·7 %) and ↓ Clostridium (3·1–1·6 %)	[81]

Table 1: A table showing how the different types of fibres affect the number of microorganisms of different species. This is related to dysbiosis. Adapted from [11]

The gut microbiome as a system

As already shown the gut microbiome can best be understood as an ecosystem, and therefore also as a system. Nonetheless, due to its complex nature it is only one system but is instead made up of many 'micro' systems. An example of a system in the microbiome is how the primary degraders (often Bacteroides, Bifidobacterium and ruminococcin) depolymerise polysaccharides forming smaller units that can be used by the primary degrader or secondary degrader. This is known as cross-feeding; the secondary degraders ferment the sugars into SCFAs which the colon can then also absorb [22]. This is a system lacking a unanimous function, much like a societal system, where each component in the system is working for its own benefit and in turn benefits other components. These 'micro'-systems between specific microbes and the hosts' colon are an example of the mutualistic relationship between them as they are both benefiting each other.

Conclusion

In conclusion, the gut microbiome is better understood as an ecosystem, not a system nor an organ. This is because of its independence of the host and alien-nature to the rest of the hosts'

body, as well as the lack of uniformity in the millions of different species of single celled organisms with different functions, beneficial or not to the host. The complexity of the microbiota means it is more than a system and the fact it has all the main attributes of an ecosystem (fundamental source, nutrient cycling, trophic levels, autotrophs, heterotrophs, biotic and abiotic constituents and a unique environment) mean it falls into this subcategory. This complexity, though, is what makes it so different from most other fields in medicine and is why so much confusion over the correct term exists in the scientific community. It can be difficult to research, as the more standard scientific 'reductionist approach' (see table.2) cannot explain it adequately [23], but knowing and understanding the definition of something before trying to learn more about it is one of the most vital rules of scientific inquiry. How we class the gut microbiome matters, because it changes the way we see and understand it.

Simple linear systems	**Complex nonlinear networks**
Deterministic systems are highly predictable	Deterministic systems may show chaotic behavior and extreme sensitivity to initial conditions
Stability reflects static equilibrium	Stability can reflect trapping within a complex dynamical attractor
Shared properties among different instances of the same type of system suggest shared external influences	Shared properties may reflect a system attractor
Differing properties among instances suggest different external influences	Differing properties may reflect system multistability

Table 2: A table showing the standard scientific approach towards simple linear and complex nonlinear networks. The gut microbiome is a complex nonlinear network which is why the standard reductionist approach isn't effective. Adapted from [23].

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