



Review Article

Copyright © Rodney R Dietert

# The Embodied Microbiome

Rodney R Dietert<sup>1\*</sup> and Janice M Dietert<sup>2</sup>

<sup>1</sup>Department of Microbiology and Immunology, Cornell University, Ithaca, USA

<sup>2</sup>Performance Plus Consulting, Hereford, AZ 85615

\*Corresponding author: Rodney R Dietert, Department of Microbiology and Immunology, Cornell University, Ithaca, NY USA.

To Cite This Article: Rodney R Dietert\* and Janice M Dietert. *The Embodied Microbiome. Am J Biomed Sci & Res.* 2023 20(3) AJBSR.MS.ID.002708,

DOI: [10.34297/AJBSR.2023.20.002708](https://doi.org/10.34297/AJBSR.2023.20.002708)

Received: 📅 October 12, 2023; Published: 📅 October 20, 2023

## Abstract

Microbes are the most prevalent and widely distributed life form on planet Earth. They are also cognitive organisms with memory and superior problem-solving skills that use quantum phase transitions during their remarkably effective gathering and dissemination of information. This narrative review explores the biological ramifications of human holobionts physically embodying the human microbiome and connecting to the Internet of Microbes (IOM) beyond our body. Within the narrative review, we consider:

- 1) the ways in which our microbial co-partners exerted control over our ancestors and continue to influence our current human generation.
- 2) how they mold virtually every key aspect of our life and even remain with our body in death
- 3) how inward-looking contemplative tools such as meditation and embodied cognition provide an ideal opportunity to connect to the vast microbial network and tap the full range of human holobiont capabilities.

**Keywords:** Microbiome; Cognitive Bacteria; Embodied Cognition; Behavior; Holobiont; Meditation; Internet of Microbes (IOM); Developmental Programming; Quantum States; Hologenome

**Abbreviations:** IOM: Internet of Microbes; HC: Heart Centered; FMT: Fecal Microbiota Transplantation

## Introduction

“for men and germs are not widely different from each other.”

Mark Twain, from *Which Was the Dream “Three Thousand Years Among the Microbes.”* p. 437 [1].

A decade-plus ago we published a paper in the MDPI journal *Entropy* Dietert and Dietert [2] answering a semiotics question with what became known as: “The Completed Self Hypothesis.” The paper argued that the newborn baby had to fully self-complete with mom’s microbiota to be ready to face the world, and that this was the single best, predictive measure one could make as per health across that baby’s life course. Of course, now we know that self-completion via natural childbirth (followed by breastfeeding) results in the baby becoming the majority microbial as a human superorganism.

Now in this narrative review we explore the importance of The Embodied Microbiome. Of course, the human superorganism remains the majority microbial, but what does that really mean? Are our microbial collaborators silent partners or possibly puppet masters? Since the Completed Self paper, there has been progress in four major research areas, and those findings provide likely explanations for what our ninety-nine-plus percent microbial genes have been doing as part of to our body.

The first push on the microbiome research front demonstrated that the human microbiome exerts a massive influence over human systems biology. The status and function of virtually all tissues and organs are affected by the status of the human microbiome. A second push in the microbial arena showed that bacteria are sentient beings who use cognition and exquisite sensing technologies of

their surroundings to gain an adaptive advantage. They do these things by holding quantum vibrational states and using quantum entanglement. With this in mind, later we will explore the question of who's really in charge when it comes to our body. A third research area extended the concepts of whole body (embodied) cognition as well as the importance of teaching embodied cognition to science and other students in higher education. Embodied cognition is a subject we have previously researched, written about [3,4], and taught to Cornell University students (via Biomedical Sciences (BIOMS) course 4400 and The Cornell PREPARE Program). Finally, recent research into both organ and microbiota transplantation in humans and animal models has shown that personality and behavior can be transferred and driven by the donor transplanted organ or microbiota rather than by the recipient's brain.

In the following sections we discuss:

- a) Why our merged mammalian and microbial genetics, the hologenome, is important.
- b) How our microbes prepare the next generation and how they manage that generation throughout the lifespan.
- c) Why the microbial cognitive mind operating via quantum states and entanglements is critical to our relationship with and potentially derived from our microbes.
- d) Why embodied cognition can be a useful, contemplative problem-solving tool and not simply a point of scholarly debate.
- e) Why it is more important than ever to put microbiome approaches first for our self-empowerment. The impact can extend well beyond health.

## The Ancestral Hologenome

As described in the Cognitive Information Processing model of William B. Miller Jr. and colleagues [5], self-referential, observing cells may use environmental cues and stressors to form partnerships. In essence, this is the way in which holobionts are thought to have come into being resulting in a hologenome. But once formed, individual and collective information processing and cellular responses continue across evolution. The host microbiota is interested in flourishing both as a microbial consortium and as partners with the host. The immune cells are responding to environmental cues and stressors and have prime directives in self-integrity and self-defense. For this reason, critical body sites in holobionts are often where co-partner microbes meet the immune system (e.g., across the gut barrier). We have termed these systems biology units, the microimmunosome [6]. In the case of humans, gut microbiota is separated from the majority of human immune cells by only a single cell-thick columnar layer of epithelial cells. One of the hallmark features of the immune system is memory. The immune system remembers when it has seen a pathogen before and responds differently the second time. Recently, microbes (forming another part of the microimmunosome) were shown to exhibit memory as well [7,8]. When a significant incompatibility occurs between the microbiome and immune system in a new generation,

this immune-microbe incompatibility can cause immune-inflicted inflammatory damage within the holobiont.

Not all chimeric combinations of microbiome and immune system exist in harmony. One of the more surprising research findings during the past decade is what has been termed phylosymbiosis where relationships among the microbial community recapitulate host phylogeny [9]. In fact, significant compatibility between the microbiome and the host immune system is required for survival and/or reproduction [9-11]. Significant incompatibility within the microimmunosome results in microbe-assisted, immune facilitated lethality of hybrids effectively resulting in speciation [9]. Interactions within the microimmunosome have ramifications for therapeutic microbial engraftment. Long [12] discusses the home field advantage of the host where Fecal Microbiota Transplantation (FMT) and even probiotic administration may have to pass a host specificity test to engraft. This may explain why not all FMTs are equally successful. At least part of this issue may involve host immune acceptability.

Lesser forms of incompatibilities within the microimmunosome are a probable cause for many chronic diseases as we have previously discussed [13]. The take home lesson from this corresponds with what has been reported in microbiome research. Dysbiosis occurring in a formerly balanced microbiome increases the risk of both chronic diseases and infectious disease (via loss of colonization resistance) [13].

While this holobiont hallmark explains the importance of reproductively successful ancestry, it is also a sobering reminder that the human superorganism is only as resilient as its various body site-specific microbiomes. Conditions that are unsafe for the human microbiome are likely to be unsafe for the human superorganism. The beneficial side of this equation is that environmental cues and stressors that are beneficial for addressing microbiome consortia weaknesses are likely to be health-promoting for the host. As we will discuss in a later section of this paper, this is a probable basis for the benefits of many alternative health modalities but also the danger from many "unsuspecting" microbial hazards.

## Crafting and Managing the Next Generation

One of the more intriguing questions to emerge from recent microbiome research concerns the extent to which microbes may craft their future human as a copartner and/ or vessel for their future generations of microbes. Research areas of developmental programming and epigenetics only elevate the possibility of microbes as potential designers of future humans. Recent observations concerning the microbiome is that it is not only concerned with the present human co-partner, but it also plays a significant role in preparing the next generation of humans in their role of majority-microbial holobionts. This transgenerational preparation process occurs via the maternal microbes and results in microbes guiding human fetal development and also imprinting/programming on the offspring.

Studies of these microbial actions fall within the larger field of study called developmental basis of Adult Health and Disease (DoHAD). DoHAD emerged following the work of Dr. David Barker, M.D. concerning the fetal determination of cardiovascular disease [14,15]. This expanded to an examination of critical windows of development [16] and eventually Neo-Lamarckian, epigenetic-based, transgenerational programming and inheritance beginning in the womb [17,18].

The maternal microbiome has multiple roles affecting the offspring through its metabolome such as signaling and metabolic actions. Microbes are known to produce epigenetically active metabolites [19]. The maternal gut microbiome and its epigenetically active metabolites can produce epigenetic alterations (sometimes termed epigenetic marks) in the offspring [20]. Most of the studies have focused on problematic programming from dysbiotic microbiomes programming for offspring disease rather than balanced maternal microbiomes with favorable environmental exposure facilitating a next generation of healthy children and adults.

Banerjee, et al.[21] recently reviewed the significance of the maternal microbiome in the disposition and resulting fetal programming following exposure to a variety of environmental factors. Cadmium and polycyclic aromatic hydrocarbons were used as examples for biotransformations that had implications for both the pregnancy and the offspring. Driesbach, et al. [22] using retrospective, cross-sectional metagenomic analysis found that maternal microbiome composition in the late second trimester was an effective predictor of birth weight. Maternal microbiome composition at 36 weeks of pregnancy was also shown to be a good predictor of immune cell composition in the newborn at birth. Some of the associations were still present in the infant at 12 months of age [23]. Several additional studies focused on the maternal microbiome and the offspring's immune system with a focus on allergic and/or autoimmune diseases [24,25].

Another focus of maternal microbiome research and programmed offspring systems biology has been the neurological system. Gesu et al. [26] reviewed the spectrum of pregnancy metabolites produced from a dysbiotic gut microbiome that result in neurodevelopmental problems and elevated risk of offspring mental health challenges. Meckel and Kiraly [27] examined microbiota metabolites that affect fetal brain wiring during the pregnancy. Young [28] also reviewed microbiota effects on neurodevelopment both prenatally and postnatally. Relative to epigenetic alterations, Nohesara et al. [19] recently reviewed the spectrum of specific epigenetic marks (epigenetic modifications) attributable to dysbiotic microbiome metabolites that are also connected with psychiatric diseases.

Finally Hsu et al. [29] identified maternal fructose intake and resulting gut microbiome dysbiosis as an important pathway leading to problematic offspring programming of adult disease. While these studies focus on the adverse programming resulting from aberrant microbiota compositions, the findings support the role of the maternal microbiome in both initiating systems biology develop-

ment in the offspring as well as programming transgenerationally via microbiome-induced, epigenetic modification. The take home message is that balanced microbiota through healthy living of the human holobiont is reflected across subsequent generations providing ideal human descendants (healthy, reproducing, and long-lived) to copartner with subsequent generations of microbes. In many ways, this could be viewed as strategic planning by our microbes.

## Microbes as Puppet Masters?

Humans are known as naturally social animals. But the fact that humans in microbial dysbiosis are often anti-social suggests that it is the hologenome that can direct the extent to which human interactions come naturally. In past years, the idea that our microbes were significant players in human superorganism action, function, and capabilities may have been thought a stretch. But one thing is shifting. The prior predominate view of microbes as inconsequential "sidekicks" within the human holobiont is shifting toward a view where microbes are dominant, senior partners in the collaboration. The growing field of psychobiotics is a major reason for this shift. Dinan and colleagues [30] first coined the term psychobiotics a decade ago in referring to living organisms (such as probiotic bacteria) that alter human neurobehavior. Because the flood of neuroactive chemicals either directly produced by gut microbes or regulated by the same can overwhelm brain chemistry, gut microbes have been termed the brain's "puppeteers" [31]. Not everyone embraces the puppet master idea. Some researchers have argued against a puppet master model suggesting that the appearance of mind control by microbes is more likely to be a happenstance connected to microbe-positive local effects [32]. However, it is important to keep in mind that our gut microbiome controls fear extinction and a healthy gut microbiome is a critical factor in helping us to maintain appropriate balance during times of excessive fear [33].

In this exploration of our microbiota and control of human-human interactions, we are focusing on the balance of two factors: oxytocin-oxytocin receptor signaling contrasted production of Trimethylamine N-Oxide (TMAO). Oxytocin is a pleiotropic, hypothalamus-produced neuropeptide/hormone that supports a variety of pro-social functions including reward and motivation feedback for things like pair-bonding, social interactions, meals, and sexual contact [reviewed in 34,35]. Critical for human reproduction, oxytocin drives parturition and parental attachment including establishment and maintenance of mother-child bonding in response to social cues [34-36]. It also plays a role in sensory network plasticity [37]. Oxytocin signals through G-protein-coupled receptors as the mechanism for enhancing connectivity of the social brain across vertebrate species. Deficits in oxytocin-receptor driven signaling can produce isolation-promoting social deficits [38-41]. In effect, oxytocin appears to be a pivotal factor for humans being drawn to pro-social behavior.

The gut microbiome has the capacity to regulate oxytocin-sig-

naled pro-social behavior [42]. This puppeteer-like control of human sociability includes the capacity of certain gut microbiota to directly produce oxytocin [43]. Hence, we function as social animals primarily in the context of being a holobiont with specific microbiota urging us on to meet-greet, pair romantically, reproduce, and produce and nurture our babies. In fact, the case could be made that Earth's microbes have a vested interest in seeing humans survive and thrive.

This information concerning microbiome function is pertinent to two questions. These are:

- a) What is our true fundamental nature?
- b) Is there an instruction manual? One could argue that ancestral microbial partners in prior generations helped to prepare the way for our own appearance. If there is an instruction manual, it probably starts in our gut (rather than our brain) and is focused on our fully conscious, microbial co-partners. We are only beginning to fully appreciate the insights of Hippocrates [44].

For example, specific gut bacteria are able to influence the levels of oxytocin [45]. With oxytocin being critical for childbirth and infant nurturing, pair bonding, certain aspects of reproduction, and human social connectivity, then is the absence of oxytocin signaling the only thing driving anti-social behavior? The answer appears to be no. A good candidate for an anti-social molecule is Trimethylamine N-Oxide (TMAO), a metabolic product of the gut microbiome [46,47]. While many other bioactive compounds contribute to behavior, oxytocin and TMAO drive starkly opposite behaviors and interactions. One of the apparent actions of higher levels of TMAO is rapid aging of mid-brain regions connected to TMAO-stimulated inflammatory cytokine production [48].

Several other microbiota-regulated neurological factors affect behavior beyond oxytocin and TMAO. For example, serotonin and dopamine levels and/or signaling are controlled by specific gut bacteria [49-51]. In addition, the important role of a balanced gut microbiome in fear extinction helps to protect against anxiety, depression, and mental illness [33] Table 1 illustrates the areas where our body's microbiota intercedes to affect our life and even our body's immediate afterlife [22,29,33,42,52-80] (Table 1).

**Table 1:** Microbes Have Key Roles Across the Entire Lifespan.

Critical Aspects of Human Life [Reference(s)]	Processes/Functions Under Microbiome Regulation
Control of offspring maladies [52-54]	The specific hologenome, particularly at the level of the microimmunosome, can determine offspring fitness and inflammation-driven risk to the offspring
Preparation of the next generation in utero [22,29]	The maternal microbiome affects not only the course of the pregnancy but also the fetal and eventually postnatal development of the offspring
Infant maturation [55,56]	The newborn-infant microbiome determines whether systems like the immune and neurological systems can fully mature (for normal function).
Food preferences/choices [57,58]	Oral and gut microbiome composition can drive food choices and cravings.
Emotional balance [59,60]	Specific gut microbiota including psychobiotic bacteria make neuroactive chemicals that can help to alleviate anxiety and depression.
Fear regulation [33,61,62]	The microbiome regulates fear extinction, which is necessary for healthy, balanced fear responses.
Sociability [42,63-65]	Gut microbiota are involved in the regulation of oxytocin- signaling, and microbiome composition can affect social behavior.
Health risks [66-68]	Microbiome composition is known to affect the risk of both chronic and infectious diseases.
Sexual selection and reproductive success [69-72]	Sexual performance issues, infertility, conception problems and problems carrying to term have all been linked with dysbiotic reproductive microbiomes.
Aging [73-76]	Microbiome status affects disease burden, sleep quality, inflammation and oxidative damage level, telomere length, and circadian clock regulation
Postmortum [77-80]	Microbes are the ultimate recyclers of physical life on Earth

## Conscious, Problem-Solving, Quatum-Operating Bacteria

This section illustrates a progression of observations, experi-

ments, and thinking concerning the nature of microbes in general and of microbes that form holobionts including the human super-organism. While thoughts about microbes or at least their actions date back centuries, we focus on the early 20<sup>th</sup> century and ideas

about probiotic foods and the origins of chloroplasts to robust, vetted concepts of 2023 concerning microbes as fully cognitive beings that are supreme information gatherers making full use of quantum-based tools as they navigate the extremes of Earth and as well as our own body.

Several decades ago Lynn Margulis presented evidence supporting an endosymbiotic theory that virtually every cell in the human body was powered in large part by remnants of ancient archaea (protomitochondria) [81]. If ancient prokaryotes were the source for fundamental components of human and other eukaryotic cells, then the question is what else did they source to us and continue to provide directly via the human microbiome? Is our fundamental nature completely intertwined with the history of Earth's microbes?

The keys to rethinking our fundamental nature as well as that of microbes means inverting a dogmatic life-control pyramid. In

the past, genomes were purported to drive everything that follows within an organism. But in the microbiome era, genomes can be as fluid as your next meal of fermented foods. Now sentient cells use consciousness and cognition to sense information fields, perform creative problem solving and use the genome primarily as a toolbox and genes as cellular tools for this task [82-83]. If the ideas of Lynn Margulis were central to the idea of single cell cognition among bacteria and scaling to eukaryotic cell chimeras, then it was the 2016 seminal concept paper of William B. Miller Jr. [82] that provided the roadmap of how microbial-human holobionts operate via information fields and entanglement.

Table 2 illustrates a timeline of evolving concepts regarding microbes as a standard bearer that brings cognition, consciousness, intelligence, memory, associative learning, creative problem solving, energy-to-information phase transitions, and quantum entanglements to the holobiont and its external environment [81,84-109].

**Table 2:** Examples of significant contributions revealing the fundamental nature of the human holobiont and its quantum-operating microbes.

Category of Contribution (Date)	Researcher(s)	Contribution [Reference(s)]
Probiotics/Fermented Foods (1903 and 1907 papers)	Elie Metchnikoff	The Nobel Laureate developed the concept of orthobiosis in advocating for the consumption of friendly flora laden fermented milk to aid longevity (1903 and 1907 papers. [see 84]
Endosymbiosis (1905 and 1910 papers)	Konstantin Sergejewitch Mereschkowsky	Published an early model including endosymbiosis of chloroplasts in 1905 including a larger paper in 1910. [see 85,86]
A form of Endosymbiosis (written contributions during the 1940s)	Adolf Meyer-Abich	Developed Holism/Holobiosis concepts [87-89].
Endosymbiosis (1967 paper)	Lynn Margulis as Sagan	Endosymbiosis (ancient bacteria as the origins of mitochondria) [81]
Fractal nature of microbes (1990 paper)	Martin Obert and colleagues	Experimental evidence that microbial growth patterns follow fractal geometry [90]
Conscious microbes (2001 paper)	Lynn Margulis	Published her article "The Conscious Cell" in the New York Academy of Sciences [91]
Conscious life including microbes (2007 paper)	Shapiro	Supported the conclusions that life required cognition at all levels. [92]
Informational sensing systems among bacteria (2010 paper)	Reindert Nijland and J. Grant Burgess	Demonstrated that as part of an exquisite sensing system, bacteria detect and analyze volatile organic compounds (VOC) using a form of olfaction. [93]
Pharma-based degradation of the human microbiome (2014 book)	Martin Blaser	Illustrated the extensive degradation of the human microbiome through overuse of antibiotics and other factors [94]
Bacteria as fully functioning cognitive organisms. (2015 paper)	Pamela Lyon	Lyon presented evidence that bacteria, as cognitive cells, feature intelligence, sensing and perception, behavioral adaptation, memory, learning, anticipation, future prediction, complex decision making, and inter-kingdom communication all in the name of survival and reproduction. [95]
A keystone paper linking the quantum properties, states entanglement and operation of fully cognitive bacteria (2016 paper)	William B. Miller, Jr.	Miller demonstrated that the holobiont and its collection of complex collaborators are cognitively entangled in a Pervasive Informational Field (PIF) operating within a quantum framework. He argues that microbes can hold multiple ambiguity states until they take action to purposely resolve it. They can also exist in a duality of function operating within a larger community (such as a biofilm) while simultaneously demonstrating specialized individual behaviors. Miller argues that the PIF is robust including noise and that bacteria must use discernment for valued decision making. [82]

Extending bacteria cognition to a model of the Microbial Mind (2016 paper)	Daniela Pinto and Thorsten Mascher	Introduced the concept of bacterial nanobrain [96]
Specialized properties of bacteria (2016 paper)	Sima Baghbanzadeh and Ivan Kassal	This is an early demonstration of the novel properties of light harvesting by purple bacteria [97]
Clear evidence of quantum entanglement among bacteria (2018 paper)	Chiana Marletto and colleagues	The researchers used light-based stimulation in one of the early uses of green sulfur bacteria to demonstrate clear quantum entanglement [98]
Further development of bacteria as inherently quantum. (2018 paper)	John S. Torday and William B. Miller Jr.	The researchers argued that resolution of ambiguity (e.g., informational problem solving in microbes) is the basis of life and is inherently quantum in nature [99].
A reformulation of evolution based cognition (2020 paper)	William B. Miller, Frantisek Baluška and John S. Torday	The researchers described a model of cognition-based evolution [100]
A quantum explanation of microbes operating at a distance. (2020 and 2021 papers)	William B. Miller, Arthur S. Reber, Frantisek Baluška and John S. Torday	The researchers introduced the concept that prokaryotic bioelectric fields and senomic fields can interact together to form supracellular N-space fields that can couple cells in coherence at a distance. They also argue for prolonged memory in bacteria. [101,102]
Consideration of the holobiont mind and its implications (2021 paper)	Ismael Palacios-Garcia and Francisco J Parada	The researchers discussed the concept of “the holobiont mind,” which pertains to the current paper’s consideration of embodied cognition [103]
Important discovery of how bacteria use vibrational coupling as part of their quantum processing (2021 paper)	Jacob S. Higgins and colleagues	The researchers showed that green sulfur bacteria (via their protein complexes) can mix electronic and vibrational states (vibronic coupling) via quantum mechanics allowing them to steer excess photosynthetic energy excitation toward a quenching site. [104]
Coherence map creation (2022 paper)	Reshmi Dani and colleagues	The researchers studied the light harvesting antennae of purple bacteria to construct quantum coherence maps [105].
An important perspective of changing scientific dogma regarding quantum-based bacteria operating across a matrix of consciousness. (2023 paper)	Stephan A. Schwartz	The researcher argued that science is embracing a new view of reality where all beings of Earth are conscious and are living in a matrix of consciousness in which all beings are both interconnected and independent [106].
This is a clear proof-of-concept of the quantum nature of bacteria. (2023 paper)	Francisco Delgado and Marco Enríquez	Both quantum entanglement and state transference are clearly demonstrated using information-gathering Fenna–Matthews–Olson protein complexes derived green sulfur bacteria. [107].
Evidence of quantum processing in purple bacteria (2023 paper)	Lorenzo Cupellini and colleagues	Research on the light harvesting antennae of purple bacteria produced clear evidence of quantum chemical processing [108].
The concentric nanorings of bacteria quantum emitters (2023 paper)	Verena Scheil and colleagues	This study on the light-harvesting antennae of purple bacteria enabled a comparison of multiple stacked nanoring geometry vs. single rings in terms of quantum properties. [109]

The evolution of research on microbes and the development of new dogmas surrounding their quantum-based capacities and operating modes should prompt us to rethink our own human super-organism capacities as well. In the following sections, we consider how new views of the human microbiome and environmental microbes can influence our understanding concerning embodied cognition as well as recent observations regarding organ and microbial transplantation.

## Embodied Cognition and Meditation in the Holobiont

As previously mentioned, embodied cognition in its various forms has been a major component of our prior research, writing, higher education instruction, and scientific workshops [3,4]. Embodied cognition can be described as whole body cognition [110], which in our holobiont understanding of whole body would include

the microbiome. Embodied cognition encompasses any manner in which information can be accessed by utilizing any part of the body as the source and/or conduit. It also facilitates different perceptual vantage points (e.g., viewing something from the heart space vs. the brain). There are many different tools that can be used to access embodied information and several of these will be described. Meditation itself has been considered as one form of embodied cognition [111], because most meditation is directed inward into the body (as at least an initial step) rather than outward. For this reason, it will be included here. Importantly, embodied cognition has grown in recognition as a useful skill set in science education [4,112,113].

In the Cornell course BioMS 4400 a Heart Centered (HC) meditation served as the observational platform for much of the embodiment instruction. In its most basic form a 30-second, eyes-open HC meditation was used to compare first noticed observations of a complex Salvador Dali painting (Cygnus). The differences in view-

ing the painting from a normal perceptive state vs. a HC state was stunning and a core part of course instruction over the years. With this exercise, students would essentially double the total information that they gleaned from the painting as if looking at the painting using two completely different sets of eyes. In this course, the HC meditation was also paired with physical body work (The Lego/ Building Blocks Exercise) or movement-connectivity (The Wall of Information Exercise). Additional embodied cognition instruction involved a movement exercise (The Walk-Around Exercise), a body orientation/navigation exercise related to size and time embodiment, and The Body as a Weathervane Exercise related to sensory information and embodied emotions. The curriculum included two Role Playing Exercises and use of language (metaphors and mixed metaphors) as a reset when stuck on a problem [3,4].

Music and dance are also whole body contemplative tools used to increase understanding. One example was a recent holistic learning Dance Our Microbiome Event held at the Buffalo Museum of Science as described by *Buono and Burindge* [114]. Music also has special role in embodied cognition [115]. Meditation is not just a powerful contemplative tool. It is also a way to establish a bidirectional connection with our microbiome. The next section will examine routes through which the microbiome may inform us via meditation. But the communication link appears to be bidirectional. Table 3 [116-120] illustrates research into the ability of meditation not only to improve well-being but also to alter microbiome composition. At a minimum, this suggests that some health benefits accrued from meditation may be linked with meditation-driven host microbiome modification (Table 3).

**Table 3:** Examples of Reported Effects of Meditation Upon the Human Microbiome.

<p style="text-align: center;"><b>Type of Meditation</b></p> <p style="text-align: center;"><b>Protocol</b></p> <p style="text-align: center;"><b>[Reference]</b></p>	<p style="text-align: center;"><b>Results</b></p>
<p style="text-align: center;"><b>Mindfulness</b></p> <p>Experimental group of 21 young adults with high anxiety trait scores and 29 young adult controls.</p> <p>Protocol of 8 weeks of once a week (2-2.5 hours) group meditation session with daily personal (45 minute) meditation sessions. A 4-week post-intervention follow-up was used. A mindfulness attention awareness scale and a depression scale were used for the evaluation as well as fecal microbiota analysis. Pre and post treatment analyses were performed. [116]</p>	<p>Pre-intervention, fecal B diversity significantly differed between test and control groups. The higher anxiety group had lower diversity vs. health controls and an overgrowth of bacteria such as <i>Streptococcus</i>, <i>Blautia</i>, and <i>Romboutsia</i>. The high anxiety group had a decrease in genera such as <i>Faecalibacterium</i>, <i>Coprococcus_3</i>, and <i>Lachnospirillum</i> vs. controls. Mindfulness intervention significantly reduced trait anxiety and depression scores and increased resiliency in the test group. Relative abundance of 18 bacteria significantly changed during the intervention with the profile of the test group becoming more similar to that of the healthy controls. prevalence of Subdoligranulum was negatively correlated with mindfulness responsiveness and tryptophan metabolism. Tryptophan metabolic genes were enriched among high responders to the intervention.</p>
<p style="text-align: center;"><b>Mindfulness</b></p> <p style="text-align: center;"><b>(including yoga)</b></p> <p>A total of twelve patients undergoing treatment for interstitial cystitis (IC), or bladder pain syndrome (BPS) underwent an 8 week mindfulness meditation course. Urinary samples were collected for microbiome analysis both pre and post meditation therapy. [117]</p>	<p>All 12 patients showed a marked improvement in symptom scores post meditation sessions. Additionally, the urinary tract microbiome diversity increased significantly with major changes in some taxa.</p>
<p style="text-align: center;"><b>Mindfulness</b></p> <p>Beginning with 160 total participants, (two randomized groups of 80 pregnant women each), maternal mindfulness intervention was applied to prenatal care of 80 pregnant women with symptoms of depression or anxiety while another 80 pregnant women with the same symptoms received the usual prenatal care. For infant merconium microbiome analysis a total of 130 infant samples were able to be collected. Fecal samples from 66 of the intervention newborns and 64 of the controls were analyzed and the results compared. [118]</p>	<p>No change in alpha diversity was noted but there was a significant group change in beta diversity. Bifidobacterium and Blautia were abundant in the intervention group while <i>Staphylococcus</i> was abundant in the control group.</p>
<p style="text-align: center;"><b>Mindfulness</b></p> <p>The participants were among an elderly population residing in a community facility in China. They had been separated by the criteria of those diagnosed with Mild Cognitive Impairment (MCI) and those aging normally. A mindfulness awareness program was instituted for nine months among 28 MCI subjects and 40 normally functioning participants. Neuropsychological evaluation was performed at each evaluation interval. Blood and stool samples were collected and analyzed at 0, 3, and 9 months. The stool samples were analyzed for cytokine and microbiota profiles. [119]</p>	<p>Six taxa of bacteria were associated with improved cognitive function among the MCI -MAP group. <i>Ruminococcus</i> emerged as the bacteria positively associated with improvement in multiple cognitive test parameters.</p>

**Deep Tibetan Meditation**

Fecal microbiota samples were collected, analyzed, and compared among a group of Tibetan Chinese Buddhist monks from Qiongke, Jiaqu and Ezhi Temples who practiced long term deep meditation vs. a group of neighboring residents. A total of 37 samples from the monks and 18 from local residents were of a quality to permit microbiota analysis. All participants lived at high elevation. [120]

Compared to the control group, the meditation group had an increased prevalence of *Bacteroidales*, *Sutterellaceae*, *Burkholderiales* and *Betaproteobacteria*. After cut-off analysis, two bacterial genera (*Megamonas* and *Faecalibacterium*) were enriched in the meditation group. Based on the literature, the first of two bacteria genera are associated with a higher quality of life and the second genera is often reduced among anxiety disorder patients.

A final BIOMS 4400 course exercise for discussion (The Wall of Information Exercise) is a combination of meditation and embodied cognition. The exercise is discussed in the peer-reviewed Journal of Biomedical Education [4]. The students move to a wall of their choice, survey the wall with their hand to notice a distinction connected to a self-identified spot on the wall, enter the heart-centered meditative state, and ask an open-ended question "What if there were information here for me?" Students often received imagery, language or other cues. The instructors always shared what they received and that encouraged students to share their impressions. What is particularly interesting about the exercise is that the impressions received are often precognitive. An example of this from the 2014 fall class session (RRD) is illustrated in Figure 1. The class instructions are in the left panel and the impression received in the right. Because we have a background of extensive


published scholarly research on antique silver and goldsmiths in the UK (Scotland), the imagery of a table harp (the silver quality hallmark for Dublin, Ireland for centuries) from the Wall was unmistakable to RRD. The problem was that as RRD explained to the students at the completion of the Wall of Information Exercise, he had no real direct connection to Dublin, Ireland and no prior professional or leisure activity in Ireland. In the moment, the table harp imagery and representation (to RRD) of Dublin was a mystery. But that would change later that week (between the weekly meetings of the class). An invitation to lecture on the microbiome at an OB/GYN continuing education course in Dublin, Ireland was about to happen. Figure placement (Figure 1). Figure 1 Legend This instructional exercise became a core tool across several years of the Cornell course.

**Wall of Information Exercise**


**4 Step Instructions:**

1. Find Your Spot on the Wall (by making a distinction:
2. Do a Heart-Based Meditation (change your perceptual state)
3. Ask the Question – What if there were information here for me? (ask an open – ended question)
4. Write down anything you notice.

2014 Class Exercise - The Wall (Oct 8<sup>th</sup>)



Dr. Dietert got a harp Silver quality mark for ....Dublin assay office



**SPEAKER INVITATION - Oct. 13th**  
 Genomics & the Microbiome: What clinicians need to know  
**Lecture title: Healthcare in the Age of the Microbiome**  
 Obstetric & Neonatal Dilemmas Conference  
 Dublin 11 December 2014

**Figure 1:** Illustrates the student instructions for the exercise in October 2014 and the result (RRD) obtained, publically announced, and personally interpreted for the class at the end of that in-class exercise.

## Connecting to the IOM via Meditation, Embodied Cognition and Other Contemplative Practices

The human body has a massive consortium of microbiota that has two remarkable features. It shares microbes that are found in the harshest places in, on, and above planet Earth. In many cases, these microbiota are not only ancient but bring to the human body highly specialized functions (e.g., specialized magnetic sensing properties). But it is a mistake to view the human microbiome as rigid and separated from the environment. Instead, it is fluid and

exchanges microbiota with all surrounding environmental sources and other holobionts. Walking your dog in a park is much more than just a walk. Under some circumstances it can become a microbiome makeover both for you and your dog.

One of the intriguing aspects of inward-looking meditation is that we automatically connect to our body's various microbiomes (e.g., gut, skin, airways, mouth, urogenital tract) and also gain access to their sources of information. Our microbiome is open to the external environment and, beyond the soft-boundary confines of our body, to Earth's environmental microbes. As was shown in prior



sections, these microbes are not only Earth’s predominant life form and are distributed across the planet, they are premier information gatherers and disseminators. Microbes are using quantum-based antennae and other structural features to collect and phase shift energy to information and communicate over a distance. They are, also, using their cognitive abilities throughout the network. This interactive, informational network has been termed the “Internet of Microbes” by Slijepcevic and Wickramasinghe [121] and was recently discussed by us [122]. Here, we consider the familiar relations of microbes that exist within our own microbiome but also in all corners of Earth.

Table 4 [123-142] illustrates two fundamental principles about

our connection to microbes: 1) We are intimately connected to Earth’s microbes, 2) Even if much of our microbiome has some stability, we are constantly exchanging microbes, microbial genes, physiologically-modifying chemicals, and gathering information from and sharing information with the microbes beyond our body. The human body is open to the environment. Being an open system means we are informationally tapped into the IOM and that matrix of consciousness that physically continues beyond our skin. It is quite plausible that meditation, embodied cognition and other contemplative tools may be informed and supported by the IOM. Given the established connections that are already known, the IOM might be the grandest search engine on Earth (Table 4).

**Table 4:** Examples of Human-Related Microbiota Found in Extreme and Other Environments.

Microbes in Humans [Reference(s)]	Phyla/Genus Location in Environment	Feature(s)
Archaea <i>Methanomassiliicoccus luminyensis</i> gut) [123-125]	Geothermal hot spring (Indian ocean island), Mud volcano (Barents sea), Peat land soil (France), Deep sea hypersaline anoxic (Kyros) basin	Methanogenesis is the hallmark of these archaea.
Archaea <i>Halobacteriota</i> (skin) [126-128]	Alpine Permian-era bore core of a salt deposit, hypersaline-deep lake Antarctica, Solar salterns, Survives space launches, space conditions above the ozone layer as well as Mars-like conditions	Polyextremophilic with tolerance of saturating salinity, anaerobic conditions, high levels of ultraviolet and ionizing radiation, subzero temperatures, desiccation, and toxic ions.
Analysis of skin microbiota samples showed that computer key archaeological deposits from humans were primarily <i>Nitrososphaeria Nitrososphaeria</i> (54.3% of archaeal reads) and <i>Nanoarchaeota</i> . [126,129-131]	Nitrososphaeria are a prominent archaea in acid mine drainage sediments. While Nanoarchaeota are obligate ectobionts that are mainly found in deep-sea hydrothermal vents and geothermal springs (e.g., Yellowstone National Park) across the globe.	Both types of archaea seem to metabolize best under harsh conditions and are relatively resistant to metal toxicity.
Magnetotactic bacteria can be detected in several human tissues. Seven species were recently identified from the human gut ( <i>Magnetococcus marinus</i> , <i>Magnetospira sp. QH-2</i> , <i>Magnetospirillum magneticum</i> , <i>Magnetospirillum sp. ME-1</i> , <i>Magnetospirillum sp. XM-1</i> , <i>Magnetospirillum gryphiswaldense</i> , and <i>Desulfovibrio magneticus</i> ). [132-135]	They have wide global distribution including in extreme niches and are important in the global distribution of iron. Magnetotactic bacteria are potential symbiotes for deep-sea marine bivalves, detected in bats, whales, birds, and humans.	Important in both biomineralization, magnetite crystal formation, and navigation. These bacteria also have a high level of horizontal gene transfer for magnetite production capabilities.
Acidophilic and aciduric lactic acid bacteria are mild-moderate extremophiles in that they are acid resistant. They are also extremely important in fermented foods as well as in the human mouth, gut and female genital tract microbiomes and in initial colonization of the newborn’s colon. [136-140]	Beyond humans these bacteria are widespread in fermented foods, silage, and plant and animal species. The first isolate of what eventually became known as <i>Lactococcus lactis</i> was first used by Joseph Lister [140]	Lactic acid bacteria producing acidic niches (lactic acid) as a result of carbohydrate fermentation and also produce bacteriocins. These functions play a protective role in humans particularly in the vaginal microbiome.
Microbiome rewilding studies indicate that visiting green spaces can lead to increased acquisition of environmental microbes(e.g., skin and respiratory microbiota). Persistent gardening results in shared, prolonged skin acquisition of soil microbiota. [141,142].	Soil microbes ( <i>Sphingomonas</i> , <i>Blastococcus</i> (skin and nose), <i>Solirubrobacter</i> (skin), and <i>Massilia</i> (nasal) were consistently detected after green space visits. For gardeners, the most frequently transferred taxa were: <i>Sphingomonadaceae</i> , <i>Nocardiodiaceae</i> , <i>Xanthobacteraceae</i> , <i>Burkholderiaceae</i> , and <i>Pseudomonadaceae</i> .	We are constantly exchanging microbes with our surroundings. We can choose where and how we spend our time with this in mind.

An examination of ancient archaea and extremeophile bacteria reflected in Table 4 shows that we embody not only our ancestral history but also that of life on Earth. In the Table's first example, an archaean representative of *Methanomassiliicoccales* (designated as strain U3.2.1) was isolated via an enrichment culture from a Northern Germany peat soil and was shown to have a sequence identity with the 16S rRNA gene of human gut-isolated *Methanomassiliicoccus luminyensis* 10B of 88.6% [123]. Methanogenesis is an important process of life on Earth and can be significant in specialized ecological niches within our body.

Umbach et al. [126] recently reported salt-loving *Haliobacteriota* on human skin. Related Halobacterium have been isolated from a bore core of a Permian-era alpine salt deposit [143]. As the table shows, this is only one of many extreme and distant locations where these bacteria can be found on Earth. These bacteria are remarkably resistant to conditions that would easily kill most other life and are good candidates for life on other planets (e.g., Mars) [144]. Other examples in the Table show that our specific microbial relations extend to deep-sea vents, mining areas and even Yellowstone National Park.

Magnetotactic Bacteria (MTB) are globally distributed. They are found in a diverse ecological setting including as symbiotes for deep sea marine bivalves and also detected in bats, whales, and birds [132]. In a recent survey of 53,775 metagenomic samples, analyses showed that 55.3% were positive for MTB. This included positive detection of MTB in samples from the human gut, oral cavity, skin, and vagina. A study by Simon et al. [135] found an association between gut MTBs and volume of magnetite-rich brain regions involving navigation and orientation.

One of the important considerations of extremophiles is their massive spectrum of bioenergetic functions. Many of these archaea and bacteria have brought these capacities to our human gut. Using freely available data sets, researchers found a sequence of gut bacteria in children and adults that produce their energy from methanogenesis, iron oxidation, iron reduction, sulfate and arsenate reduction, and even anoxygenic photosynthesis [145]. This observation warrants further investigation.

Extremophiles in the microbiome are not just niche novelties. Krawczyk et al. [128] showed that the halophilic archaea *Halorhabdus rudnickae* and *Natrinema salaciae* (which are related to those found in our own microbiome) are able to work through dendritic cells to provide immunoregulation of T cell responses producing a balanced cytokine profile. These findings suggest that similar halophilic archaea may provide a useful function in the human gut. Another example in Table 4 is a well-known group of bacteria that are mild-moderate extremophiles in the acid loving category. Lactic

Acid Bacteria (LAB) are critical to our food and our body's ecological maintenance.

The final entry in Table 4 addresses "wilding" studies and provides evidence for our extensive microbial sharing. Such findings provide a take-home message that we can choose our surroundings for better conscious awareness and health.

## Embodied Personality and Behavior

Transplant biology and medicine has a long history of effort with successful kidney [146] and heart [147] transplantation dating back more than a half century. One of the surprising and largely unanticipated findings over the decades of successful organ transplantation is that the transfer of heart and possibly other organs from donor to recipient can also transfer donor personality and behavioral characteristics in some cases [148-150]. Case histories suggest that donor memories may also be transferred in some instances [150-152].

These findings over several decades by several clinical research groups are supportive of the significance of the embodied mind and embodied cognition. There are several different hypotheses for how fundamental donor characteristics are embedded in the donor heart and possibly other organs, but it is clear that the storage and transfer of donor information is not reliant on the donor brain.

Many of the personality and behavioral transplantation studies were conducted prior to or apart from consideration of the human microbiome. But as was discussed earlier in this paper, the microbiome and in particular the gut microbiome is a major driver of human neurochemical and endocrine balance, personality features, behavior, and even food choices. If the human microbiome can epigenetically influence human behavior, then does the donor microbiome play a role in donor organ coding? That question will likely require future research. However, it is already clear that Fecal Microbiota Transplantation (FMT) between human-human, human-rodent, and rodent-rodent all indicate that the microbiota can transfer personality and behavior characteristics.

Table 5 illustrates examples where Fecal Microbiota Transplantation (FMT) has been shown to change behavior [153-170]. Most of the examples in the literature pertain to neurological disorders, neurochemical and/or hormonal mood imbalances, aggressive behavior, and addictive behavior (Table 5).

The examples in Table 5 illustrate the major control that gut microbes are capable of exerting over human and animal behavior. Another frontier to explore regarding commensal microbes is the extent to which microbes experiencing events within the holobiont can carry the memories of those events to other locations/hosts.

**Table 5:** Examples of Microbe-Shifted Behavior Following FMT.

Condition or Disorder [Reference(s)]	Nature of FMT or Microbiota Transfer Therapy	Effect
Autism Spectrum Disorder (ASD) [153]	Human-Human Microbiota Transfer Therapy	Microbiota Transfer Therapy resulted in improvement of both behavioral and gastrointestinal symptoms among the autistic children for at least eight weeks after treatment (the duration of this study).
Autism Spectrum Disorder [154]	Human-Human Microbiota Transfer Therapy	A two-year follow-up for participants in the Kang et. al., 2017 study showed that composition changes in gut microbiota persisted and the behavioral improvements continued to increase even years after the initial study.
Autism Spectrum Disorder [155]	Human-Human	A systematic review of FMT as a treatment for pediatric ASD concluded that it is a promising intervention for reversing both behavioral as well as gastrointestinal symptoms.
Autism Spectrum Disorder [156]	Human-Human	FMT treatment of autistic children with standardized human gut microbiota resulted in improvement of both behavioral and gastrointestinal symptoms.
Autism Spectrum Disorder [157]	Human-Mouse	FMT transfer of microbiota from autistic children to mice produced autistic related behavioral changes in the mice (e.g., sociability, social cage test, novel object test, novel cage test) along with increased pro-inflammatory factors in the gut and brain.
Alzheimer's Disease Systematic Review [158]	Human-Human, Human-Mouse in review	Overall FMT transferring healthy microbiota improved the symptoms of Alzheimer's Disease
Alzheimer's Disease [Park, et al., 2021 159]	Human-Human	FMT treatment for <i>Clostridioides difficile</i> infection in an Alzheimer's Disease (AD) patient noticeably improved the symptoms of AD.
Dementia [160]	Human-Human	Five cases are described of dementia patients treated for <i>Clostridioides difficile</i> infection with FMT. They experienced improved cognition following the treatment.
Parkinson's Disease [161]	Human-Human	In a case series of Parkinson's Disease (PD) patients using FMT, there was improvement of both PD motor and non-motor symptoms.
Parkinson's Disease [162]	Mouse-Mouse	Using a rotenone-induced model of PD in mice, FMT with normal gut microbiota suppressed PD symptoms via suppression of inflammation-mediated cell signaling.
Autoimmune Encephalomyelitis [163]	Human-Mouse	Behavioral characteristics associated with the human condition were transferred to the mice with the microbiota transfer.
Depression [164]	Human-Human	A case study series is reported where irritable bowel plus depression patients received transplantation of healthy donor fecal microbiota, symptoms of depression improved in all three cases examined.
Depression [165]	Human-Human	Two case studies showed beneficial outcome after a four-week interval with significant continuing benefits in one patient after eight weeks.
Depression [166]	Human-Rat	FMT transfer of normal human microbiota reduced depressive symptoms in unpredictably mildly-stressed rats and also suppressed activation of glial cells and NLRP3 inflammasomes in the rat brain.
Depression [167]	Human-Mouse	FMT from human rheumatoid arthritis patients into antibiotic treated mice produced immune-inflammatory-based depression behavior in the mice.
Schizophrenia [168]	Human-Mouse	FMT transfer from drug-free schizophrenia patients produced metabolic alterations and schizophrenia-like behaviors (e.g., impaired spatial learning and memory) in the recipient mice.
Alcohol Use Disorder [169]	Human-Human	Phase 1 clinical trial found that in the short-term there were favorable gut microbiome changes as well as reduced cravings and misuse of alcohol among transplant recipients vs. placebo controls.

## Conclusions

Commensal microbes helped craft us in the womb, drive much of our systems biology development, protect us against pathogens via colonization resistance, and can keep chronic diseases at bay

and inflammation under control when given proper food and attention. They should be a first priority when it comes to medicine, safety, and public health [13,171].

This narrative review examined the potential for embodied mi-

crobes to facilitate human superorganism capabilities. Our commensal microbes along with the environmental microbes are cognitive, conscious beings with a long ancestry on Earth, memory, exquisite sensory mechanisms and a full range of quantum-based capabilities. They are connected to their own IOM and can exchange information gathered with us as well as with other microbes. They can also affect not just our physiology but also our behavior.

Finally, in this review we examined the use of contemplative tools to draw upon information within and beyond our physical bodies. Meditation and embodied cognition represent two illustrated examples. While there is much remaining to be learned about our microbial co-partners, there is much to be gained by looking inward within the holobiont to explore the full range of our capabilities.

## Author Contributions

Research and notes for Sections 1 and 4 were contributed by J.M.D. who also edited the manuscript. Additional research for other sections and the first draft was prepared by R.R.D. Both authors have read and agreed to the published version of the manuscript.

## Funding

This research received no external funding.

## Acknowledgments

The authors express appreciation to Dr. Richard Bartlett for the many helpful discussions.

## Conflicts of Interest

The authors declare no conflict of interest.

## References

- Twain M (1967) Three Thousand Years Among the Microbes. In *Which Was the Dream? And Other Symbolic Writings of the Later Years*, Tuckey, J.S. Ed. University of California Press, Berkeley and Los Angeles, CA USA: 433-553.
- Dietert R, Dietert J (2012) The completed self: an immunological view of the human-microbiome superorganism and risk of chronic diseases. *Entropy* 14(11): 2036-2065.
- Dietert RR, Dietert J (2013) *Science Sifting: Tools for Innovation in Science and Technology*. World Scientific: Singapore: 271.
- Dietert RR (2014) Integrating contemplative tools into biomedical science education and research training programs. *J Biomed Educ* 2014: 239348.
- Miller WB, Baluška F, Reber AS (2023) A revised central dogma for the 21<sup>st</sup> century: all biology is cognitive information processing. *Prog Biophys Mol Biol* 182: 34-48.
- Dietert RR (2017) The microbiome-immune-host defense barrier complex (microimmunosome) and developmental programming of noncommunicable diseases. *Reprod Toxicol* 68: 49-58.
- Lee CK, De Anda J, Baker AE, Bennett RR, Luo Y, et al. (2018) Multigenerational memory and adaptive adhesion in early bacterial biofilm communities. *Proc Nat Acad Sci* 115(17): 4471-4476.
- Wong AC, Levy M (2021) Microbial memories. *Immunity* 54(2): 201-204.
- Cross KL, Leigh BA, Hatmaker EA, Mikaelyan A, Miller AK, et al. (2021) Genomes of gut bacteria from *Nasonia* wasps shed light on phyllosymbiosis and microbe-assisted hybrid breakdown. *mSystems* 6(2): e01342-20.
- Brucker RM, Bordenstein SR (2013) The hologenomic basis of speciation: gut bacteria cause hybrid lethality in the genus *Nasonia*. *Science* 341(6146): 667-669.
- Bell K, Bordenstein SR (2022) A margulian view of symbiosis and speciation: the *Nasonia* wasp system. *Symbiosis* 87(4): 3-10.
- Long TJ (2023) Home-Field Advantage: Why Host-Specificity is Important for Therapeutic Microbial Engraftment. *Microbiol Biotechnol Lett* 51(1): 124-127.
- Dietert RR (2021) Microbiome First Medicine in Health and Safety. *Biomedicine* 9(9): 1099.
- Barker DJ (1990) The fetal and infant origins of adult disease. *BMJ* 301(6761): 1111.
- Gluckman, P.D, Hanson, M.A. (2006) The developmental origins of health and disease. In: *Early life origins of health and disease*. Adv Exp Med Biol 573, Wintour GM, Owens JA Eds. Springer Science+Business Media Landes Bioscience / Eurekah.com, Georgetown: 1-7.
- Dietert RR, Etzel RA, Chen D, Halonen M, Holladay SD, et al. (2000) Workshop to identify critical windows of exposure for children's health: immune and respiratory systems work group summary. *Environ Health Perspect* 108(Suppl 3): 483-490.
- Nilsson EE, Maamar MB, Skinner MK (2020) Environmentally Induced Epigenetic Transgenerational Inheritance and the Weismann Barrier: The Dawn of Neo-Lamarckian Theory. *J Dev Biol* 8(4): 28.
- Nilsson EE, Ben Maamar M, Skinner MK (2022) Role of epigenetic transgenerational inheritance in generational toxicology. *Environ Epigenet* 8(1): dvac001.
- Nohesara S, Abdolmaleky HM, Thiagalingam S (2023) Epigenetic Aberrations in Major Psychiatric Diseases Related to Diet and Gut Microbiome Alterations. *Genes* 14(7): 1506.
- Marín Tello C, Jintaridith P, Sanchez F, González C, Zelada Castillo L, et al. (2022) Epigenetic regulation by metabolites from the gut microbiome. *Benef Microbes* 13(6): 437-443.
- Banerjee S, Suter MA, Aagaard KM (2020) Interactions between environmental exposures and the microbiome: Implications for fetal programming. *Curr Opin Endocr Metab Res* 13: 39-48.
- Dreisbach C, Prescott S, Siega Riz AM, McCulloch J, Habermeyer L, et al. (2023) Composition of the maternal gastrointestinal microbiome as a predictor of neonatal birth weight. *Pediatr Res* 94(3): 1158-1165.
- Gao Y, Ohely M, Quinn TP, Ponsonby AL, Harrison LC, et al. (2022) Maternal gut microbiota during pregnancy and the composition of immune cells in infancy. *Front Immunol* 13: 986340.
- Nyangahu DD, Jaspan HB (2019) Influence of maternal microbiota during pregnancy on infant immunity. *Clin Exp Immunol* 198(1): 47-56.
- Tarrant I, Finlay BB (2022) Like mother, like child: The maternal microbiome impacts offspring asthma. *Cell Rep Med* 3(8): 100722.
- Di Gesù CM, Matz LM, Buffington SA (2021) Diet-induced dysbiosis of the maternal gut microbiome in early life programming of neurodevelopmental disorders. *Neurosci Res* 168: 3-19.
- Meckel KR, Kiraly DD (2020) Maternal microbes support fetal brain wiring. *Nature* 586(7828): 203-205.
- Vuong HE (2022) Intersections of the microbiome and early neurodevelopment. *Int Rev of Neurobiol* 167: 1-23.
- Hsu CN, Yu HR, Chan JYH, Wu KLH, Lee WC, et al. (2022) The Impact of Gut Microbiome on Maternal Fructose Intake-Induced Developmental

- Programming of Adult Disease. *Nutrients* 14(5): 1031.
30. Dinan TG, Stanton C, Cryan JF (2013) Psychobiotics: a novel class of psychotropic. *Biol Psychiatry* 74(10): 720-726.
31. Stilling RM, Dinan TG, Cryan JF (2016) The brain's Geppetto-microbes as puppeteers of neural function and behaviour? *J Neurovirol* 22(1): 14-21.
32. Johnson KVA, Foster KR (2018) Why does the microbiome affect behaviour? *Nat Rev Microbiol* 16(10): 647-655.
33. Dietert RR, Dietert JM (2023) The Human Superorganism: Using Microbes for Freedom vs. Fear. *Appl Microbiol* 3(3): 883-905.
34. Wang P, Wang SC, Liu X, Jia S, Wang X, et al. (2022) Neural functions of hypothalamic oxytocin and its regulation. *ASN Neuro* 14: 17590914221100706.
35. Tolomeo S, Chiao B, Lei Z, Chew SH, Ebstein RP (2020) A novel role of CD38 and oxytocin as tandem molecular moderators of human social behavior. *Neurosci Biobehav Rev* 115: 251-272.
36. Walter MH, Abele H, Plappert CF (2021) The role of oxytocin and the effect of stress during childbirth: neurobiological basics and implications for mother and child. *Front Endocrinol* 12: 742236.
37. Pekarek BT, Hunt PJ, Arenkiel BR (2020) Oxytocin and sensory network plasticity. *Front Neurosci* 14: 30.
38. Lee HJ, Macbeth AH, Pagani JH, Young 3rd WS (2009) Oxytocin: the great facilitator of life. *Prog Neurobiol* 88(2): 127-151.
39. Carter CS, Kenkel WM, MacLean EL, Wilson SR, Perkeybile AM, et al. (2020) Is oxytocin "nature's medicine"? *Pharmacol.Rev.* 72(4): 829-861.
40. Nunes AR, Gliksberg M, Varela SA, Teles M, Wircer E, et al. (2021) Developmental effects of oxytocin neurons on social affiliation and processing of social information. *J Neurosci* 41(42): 8742-8760.
41. Froemke RC, Young LJ (2021) Oxytocin, neural plasticity, and social behavior. *Annu Rev Neurosci* 44: 359-381.
42. Nagpal J, Cryan JF (2021) Host genetics, the microbiome & behaviour-A 'Holobiont' perspective. *Cell Res* 31(8): 832-833.
43. Natchin YV, Orlova OG, Rybalchenko OV, Shakhmatova EI (2022) Vasopressin and Oxytocin Secretion by Microorganisms. *Microbiology* 91(1): 104-106.
44. Lyon L (2018) 'All disease begins in the gut': was Hippocrates right? *Brain* 141(3): e20.
45. Varian BJ, Poutahidis T, DiBenedictis BT, Levkovich T, Ibrahim Y, et al. (2017) Microbial lysate upregulates host oxytocin. *Brain Behav Immune* 61: 36-49.
46. Lakshmi GBVS, Yadav AK, Mehawat N, Jalandra R, Solanki PR, et al. (2021) Gut microbiota derived trimethylamine N-oxide (TMAO) detection through molecularly imprinted polymer-based sensor. *Sci Rep* 11(1): 1338.
47. Luo Y, Zhao P, Dou M, Mao J, Zhang G, et al. (2021) Exogenous microbiota-derived metabolite trimethylamine N-oxide treatment alters social behaviors: Involvement of hippocampal metabolic adaptation. *Neuropharmacology* 191: 108563.
48. Lee Y, Kang JS, Ham OJ, Son MY, Lee MO (2022) Gut metabolite trimethylamine N-oxide induces aging-associated phenotype of midbrain organoids for the induced pluripotent stem cell-based modeling of late-onset disease. *Front Aging Neurosci* 14: 925227.
49. Legan TB, Lavoie B, Mawe GM (2022) Direct and indirect mechanisms by which the gut microbiota influence host serotonin systems. *Neurogastroenterol Motil* 34(10): e14346.
50. Margolis KG, Cryan JF, Mayer EA (2021) The microbiota-gut-brain axis: from motility to mood. *Gastroenterology* 160(5): 1486-1501.
51. Hamamah S, Aghazarian A, Nazaryan A, Hajnal A, Covasa M (2022) Role of Microbiota-Gut-Brain Axis in Regulating Dopaminergic Signaling. *Biomedicines* 10(2): 436.
52. Miller AK, Westlake CS, Cross KL, Leigh BA, Bordenstein SR (2021) The microbiome impacts host hybridization and speciation. *PLoS Biol* 19(10): e3001417.
53. Alberdi A, Andersen SB, Limborg MT, Dunn RR, Gilbert MTP (2022) Disentangling host-microbiota complexity through hologenomics. *Nature Rev Genet* 23(5): 281-297.
54. Rosenberg E, Zilber Rosenberg I (2019) The hologenome concept of evolution: Medical implications. *Rambam Maimonides Med J* 10(1): e0005.
55. Lin C, Lin Y, Zhang H, Wang G, Zhao J, et al. (2022) Intestinal 'Infant-Type' Bifidobacteria Mediate Immune System Development in the First 1000 Days of Life. *Nutrients* 14(7): 1498.
56. Hunter S, Flaten E, Petersen C, Gervain J, Werker JF, et al. (2023) Babies, bugs and brains: How the early microbiome associates with infant brain and behavior development. *PLoS One* 18(8): e0288689.
57. Schamarek I, Anders L, Chakaroun RM, Kovacs P, Rohde Zimmermann K (2023) The role of the oral microbiome in obesity and metabolic disease: potential systemic implications and effects on taste perception. *Nutr J* 22(1): 28.
58. De Wouters d'Oplinter A, Verce M, Huwart SJ, Lessard Lord J, Depommier C, et al. (2023) Obese-associated gut microbes and derived phenolic metabolite as mediators of excessive motivation for food reward. *Microbiome* 11(1): 94.
59. Butler MI, Cryan JF, Dinan TG (2019) Man and the microbiome: a new theory of everything? *Annu Rev of Clin Psychol* 15: 371-398.
60. Zhu R, Fang Y, Li H, Liu Y, Wei J, Zhang S, et al. (2023) Psychobiotic *Lactobacillus plantarum* JYLP-326 relieves anxiety, depression, and insomnia symptoms in test anxious college via modulating the gut microbiota and its metabolism. *Front Immunol* 14: 1158137.
61. Chu C, Murdock MH, Jing D, Won TH, Chung H, et al. (2019) The microbiota regulates neuronal function and fear extinction learning. *Nature* 574(7779): 543-548.
62. Maeng LY, Beumer A (2023) Never fear, the gut bacteria are here: Estrogen and gut microbiome-brain axis interactions in fear extinction. *Int J Psychophysiol* 189: 66-75.
63. Sherwin E, Bordenstein SR, Quinn JL, Dinan TG, Cryan JF (2019) Microbiota and the social brain. *Science* 366(6465): eaar2016.
64. Butler MI, Bastiaanssen TF, Long Smith C, Morck S, Berding K, et al. (2023) The gut microbiome in social anxiety disorder: evidence of altered composition and function. *Transl Psychiatry* 13(1): 95.
65. Cuesta Marti C, Uhlig F, Mugerza B, Hyland N, Clarke G, et al. (2023) Microbes, oxytocin and stress: Converging players regulating eating behavior. *J Neuroendocrinol* 35(9): e13243.
66. Vijay A, Valdes AM (2022) Role of the gut microbiome in chronic diseases: a narrative review. *Eur J Clin Nutr* 76(4): 489-501.
67. Davies M, Galazzo G, van Hattem JM, Arcilla MS, Melles DC, et al. (2022) Enterobacteriaceae and Bacteroidaceae provide resistance to travel-associated intestinal colonization by multi-drug resistant *Escherichia coli*. *Gut Microbes* 14(1): 2060676.
68. Duar RM, Kyle D, Casaburi G (2020) Colonization resistance in the infant gut: the role of *B. infantis* in reducing pH and preventing pathogen growth. *High Throughput* 9(2): 7.
69. Rowe M, Veerus L, Trosvik P, Buckling A, Pizzari T (2020) The reproductive microbiome: an emerging driver of sexual selection, sexual conflict, mating systems, and reproductive isolation. *Trends Ecol Evol*

- 35(3): 220-234.
70. Toson B, Simon C, Moreno I (2022) The endometrial microbiome and its impact on human conception. *Int J Mol Sci* 23(1): 485.
  71. Wang H, Xu A, Gong L, Chen Z, Zhang B, et al. (2022) The microbiome, an important factor that is easily overlooked in male infertility. *Front Microbiol* 13: 831272.
  72. Günther V, Allahqoli L, Watrowski R, Maass N, Ackermann J, et al. (2022) Vaginal microbiome in reproductive medicine. *Diagnostics* 12(8): 1948.
  73. Assis V, De Sousa Neto, Ribeiro FM, De Cassia Marqueti R, Franco OL, et al. (2022) The Emerging Role of the Aging Process and Exercise Training on the Crosstalk between Gut Microbiota and Telomere Length. *Int J Environ Res Public Health* 19(13): 7810.
  74. Boopathi S, Kumar RS, Priya PS, Haridevamuthu B, Nayak SRR, et al. (2023) Gut Enterobacteriaceae and uroaemic toxins-Perpetrators for ageing. *Exp Gerontol* 173: 112088.
  75. Ragonnaud E, Biragyn A (2021) Gut microbiota as the key controllers of "healthy" aging of elderly people. *Immun Ageing* 18: 1-11.
  76. Dietert RR, Dietert JM (2022) Using Microbiome-Based Approaches to Deprogram Chronic Disorders and Extend the Healthspan following Adverse Childhood Experiences. *Microorganisms* 10(2): 229.
  77. Zhang J, Wang M, Qi X, Shi L, Zhang J, et al. (2021) Predicting the postmortem interval of burial cadavers based on microbial community succession. *Forensic Science Int Genetics* 52: 102488.
  78. Zapico SC, Adserias Garriga J (2022) Postmortem Interval Estimation: New Approaches by the Analysis of Human Tissues and Microbial Communities' Changes. *Forensic Sci* 2(1): 163-174.
  79. Buckeridge KM, Mason KE, McNamara NP, Ostle N, Puissant J, et al. (2020) Environmental and microbial controls on microbial necromass recycling, an important precursor for soil carbon stabilization. *Commun Earth Environ* 1: 1-9.
  80. Wang B, An S, Liang C, Liu Y, Kuzyakov Y (2021) Microbial necromass as the source of soil organic carbon in global ecosystems. *Soil Biology and Biochemistry* 162: 108422.
  81. Sagan L (1967) On the origin of mitosing cells. *J Theor Biol* 14(3): 225-274.
  82. Miller WB (2016) Cognition, Information Fields and Hologenomic Entanglement: Evolution in Light and Shadow. *Biology* 5(2): 21.
  83. Miller WB, Enguita FJ, Leitão AL (2021) Non-Random Genome Editing and Natural Cellular Engineering in Cognition-Based Evolution. *Cells* 10(5): 1125.
  84. Podolsky SH (2012) Metchnikoff and the microbiome. *Lancet* 380(9856): 1810-1811.
  85. Sato N (2020) Mereschkowsky, Founder of Endosymbiotic Hypothesis. In: *Endosymbiotic Theories of Organelles Revisited*. Springer, Singapore: 23-31.
  86. Kowallik KV, Martin WF (2021) The origin of symbiogenesis: An annotated English translation of Mereschkowsky's 1910 paper on the theory of two plasma lineages. *Biosystems* 199: 104281.
  87. Meyer Abich A (1940) Hauptgedanken des holismus. *Acta Biotheor* 5(2): 85-116.
  88. Meyer Abich A (1955) Hauptgedanken des holismus. *Acta Biotheor* 11: 85-106.
  89. Amidon KS (2008) Adolf Meyer-Abich, holism, and the negotiation of theoretical biology. *Biol Theory* 3(4): 357-370.
  90. Obert M, Pfeifer P, Sernetz M (1990) Microbial growth patterns described by fractal geometry. *J Bacteriol* 172(3): 1180-1185.
  91. Margulis L (2001) The conscious cell. *Ann N Y Acad Sci* 929: 55-70.
  92. Shapiro JA (2007) Bacteria are small but not stupid: cognition, natural genetic engineering and socio-bacteriology. *Stud Hist Phil Biol Biomed Sci* 38(4): 807-819.
  93. Nijland R, Burgess JG (2010) Bacterial olfaction. *Biotech J* 5(9): 974-977.
  94. Blaser MJ (2014) Missing microbes: how the overuse of antibiotics is fueling our modern plagues. *Emerg Infect Dis* 20(11): 1961.
  95. Lyon P (2015) The cognitive cell: bacterial behavior reconsidered. *Front Microbiol* 6: 264.
  96. Pinto D, Mascher T (2016) (Actino) Bacterial "intelligence": using comparative genomics to unravel the information processing capacities of microbes. *Curr Genet* 62(3): 487-498.
  97. Baghbanzadeh S, Kassal I (2016) Geometry, supertransfer, and optimality in the light harvesting of purple bacteria. *J Phys Chem Lett* 7(19): 3804-3811.
  98. Marletto C, Coles DM, Farrow T, Vedral V (2018) Entanglement between living bacteria and quantized light witnessed by Rabi splitting. *J Physics Comm* 2(10): 101001.
  99. Torday JS, Miller WB (2018) The Cosmologic continuum from physics to consciousness. *Prog Biophys Mol Biol* 140: 41-48.
  100. Miller WB, Baluška F, Torday JS (2020) Cellular senomic measurements in cognition-based evolution. *Prog Biophys Mol Biol*. 156: 20-33.
  101. Miller WB, Torday JS, Baluška F (2020) The N-space Epigenome unifies cellular information space-time within cognition-based evolution. *Prog Biophys Mol Biol* 150: 112-139.
  102. Reber AS, Baluška F (2021) Cognition in some surprising places. *Biochem Biophys Res Commun* 564: 150-157.
  103. Palacios García I, Parada FJ (2021) The holobiont mind: A bridge between 4E cognition and the microbiome. *Adapt Behav* 31(8): 10597123211053071.
  104. Higgins JS, Lloyd LT, Sohail SH, Allodi MA, Otto JP, et al. (2021) Photosynthesis tunes quantum-mechanical mixing of electronic and vibrational states to steer exciton energy transfer. *Proc Natl Acad Sci U S A* 118(11): e2018240118.
  105. Dani R, Kundu S, Makri N (2023) Coherence Maps and Flow of Excitation Energy in the Bacterial Light Harvesting Complex 2. *J Phys Chem Lett* 14(16): 3835-3843.
  106. Schwartz SA (2023) Science slowly accepts the matrix of consciousness. *Explore (NY)* 19(1): 3-5.
  107. Delgado F, Enríquez M (2023) Quantum Entanglement and State-Transference in Fenna-Matthews-Olson Complexes: A Post-Experimental Simulation Analysis in the Computational Biology Domain. *Int J Mol Sci* 24(13): 10862.
  108. Cupellini L, Qian P, Nguyen Phan TC, Gardiner AT, Cogdell RJ (2023) Quantum chemical elucidation of a sevenfold symmetric bacterial antenna complex. *Photosynth Res* 156(1): 75-87.
  109. Scheil V, Holzinger R, Moreno Cardoner M, Ritsch H (2023) Optical Properties of Concentric Nanorings of Quantum Emitters. *Nanomaterials* 13(5): 851.
  110. Varela FJ, Thompson E, Rosch E (1992) *The Embodied Mind: Cognitive Science and Human Experience*. 1st ed. The MIT Press: 308.
  111. Matko K, Sedlmeier P (2019) What is meditation? Proposing an empirically derived classification system. *Front Psychol* 10: 2276.
  112. Euler E, Rådahl E, Gregorcic B (2019) Embodiment in physics learning: A social-semiotic look. *Physical Rev Physics Educ Res* 15: 010134.

113. Kersting M, Haglund J, Steier R (2021) A growing body of knowledge: On four different senses of embodiment in science education. *Sci & Educ* 30: 1183-1210.
114. Buono A, Burnidge A (2022) Dancing Our Microbiome at the Science Museum: A Dance/STEAM Collaboration. *J Dance Educ* 22(2): 98-107.
115. Perlovsky L (2015) Origin of music and embodied cognition. *Front Psychol* 6: 538.
116. Wang Z, Liu S, Xu X, Xiao Y, Yang M, et al. (2022) Gut microbiota associated with effectiveness and responsiveness to mindfulness-based cognitive therapy in improving trait anxiety. *Front Cell Infect Microbiol* 12: 719829.
117. Shatkin Margolis A, White J, Jedlicka AE, Tam T, Hill A, et al. (2022) The effect of mindfulness-based stress reduction on the urinary microbiome in interstitial cystitis. *Int. Urogynecology Journal* 33(3): 665-671.
118. Zhang X, Mao F, Li Y, Wang J, Wu L, et al. (2022) Effects of a maternal mindfulness intervention targeting prenatal psychological distress on infants' meconium microbiota: A randomized controlled trial. *Psychoneuroendocrinology* 145: 105913.
119. Khine WWT, Voong ML, Ng TKS, Feng L, Rane GA, et al. (2020) Mental awareness improved mild cognitive impairment and modulated gut microbiome. *Aging (Albany NY)* 12(23): 24371-24393.
120. Sun Y, Ju P, Xue T, Ali U, Cui D, et al. (2023) Alteration of faecal microbiota balance related to long-term deep meditation. *Gen Psychiatr* 36(1): e100893.
121. Slijepcevic P, Wickramasinghe NC (2020) An internet of microbes straddling the cosmos. *Adv Genet* 106: 109-117.
122. Dietert RR, Dietert JM (2023) Using the Internet of Microbes to Survive the Assault on the Human Microbiome. *Amer J Biomed Sci Res* 19(1): 71-76.
123. Weil M, Hoff KJ, Meißner W, Schäfer F, Söllinger A, et al. (2021) Full genome sequence of a methanomassiliococcales representative enriched from peat soil. *Microb Resour Announc* 10(48): e0044321.
124. Mafra D, Ribeiro M, Fonseca L, Regis B, Cardozo LF, et al. (2022) Archaea from the gut microbiota of humans: Could be linked to chronic diseases? *Anaerobe* 77: 102629.
125. Cozannet M, Borrel G, Roussel E, Moalic Y, Allieux M, et al. (2020) New insights into the ecology and physiology of Methanomassiliococcales from terrestrial and aquatic environments. *Microorganisms* 9(1): 30.
126. Umbach AK, Stegelmeier AA, Neufeld JD (2021) Archaea are rare and uncommon members of the mammalian skin microbiome. *Msystems* 6(4): e0064221.
127. DasSarma S, DasSarma P, Laye VJ, Schwieterman EW (2020) Extremophilic models for astrobiology: haloarchaeal survival strategies and pigments for remote sensing. *Extremophiles* 24(1): 31-41.
128. Krawczyk KT, Loch C, Kowalewicz Kulbat M (2022) Halophilic archaea *Halorhabdus rudnickae* and *Natrinema salaciae* activate human dendritic cells and orient T helper cell responses. *Front Immunol* 13: 833635.
129. Gupta A, Saha A, Sar P (2021) Thermoplasmata and Nitrososphaeria as dominant archaeal members in acid mine drainage sediment of Malanjkhanda Copper Project, India. *Arch Microbiol* 203(4): 1833-1841.
130. St John E, Flores GE, Meneghin J, Reysenbach AL (2019) Deep-sea hydrothermal vent metagenome-assembled genomes provide insight into the phylum Nanoarchaeota. *Environ Microbiol Rep* 11(2): 262-270.
131. Munson McGee JH, Rooney C, Young MJ (2020) An uncultivated virus infecting a nanoarchaeal parasite in the hot springs of Yellowstone National Park. *J Virol* 94(3): e01213-01219.
132. Natan E, Fitak RR, Werber Y, Vortman Y (2020) Symbiotic magnetic sensing: raising evidence and beyond. *Philos Trans R Soc Lond B Biol Sci* 375(1808): 20190595
133. Lin W, Wu LF (2021) Magnetotactic bacteria and magnetoreception. *J Oceanol Limnol* 39(6): 2001-2004.
134. Li J, Liu P, Menguy N, Zhang X, Wang J, et al. (2022) Intracellular silicification by early-branching magnetotactic bacteria. *Sci Adv* 8(19): eabn6045.
135. Simon RA, Ranasinghe PD, Barazanji N, Jungeström MB, Xu J, et al. (2021) Magnetotactic bacteria from the human gut microbiome associated with orientation and navigation regions of the brain. *J Oceanol Limnol* 39: 2044-2052.
136. Icer MA, Özbay S, Ağagündüz D, Kelle B, Bartkiene E, et al. (2023) The Impacts of Acidophilic Lactic Acid Bacteria on Food and Human Health: A Review of the Current Knowledge. *Foods* 12(15): 2965.
137. Saha UB, Saroj SD (2022) Lactic acid bacteria: Prominent player in the fight against human pathogens. *Expert Rev Anti Infect Ther* 20(11): 1435-1453.
138. Al Balawi M, Morsy FM (2020) *Enterococcus faecalis* is a better competitor than other lactic acid bacteria in the initial colonization of colon of healthy newborn babies at first week of their life. *Front Microbiol* 11: 2017.
139. Zhang D, Zhang J, Kalimuthu S, Liu J, Song ZM, et al. (2023) A systematically biosynthetic investigation of lactic acid bacteria reveals diverse antagonistic bacteriocins that potentially shape the human microbiome. *Microbiome* 11(1): 91.
140. Santer M (2010) Joseph Lister: first use of a bacterium as a 'model organism' to illustrate the cause of infectious disease of humans. *Notes Rec R Soc Lond* 64(1): 59-65.
141. Selway CA, Mills JG, Weinstein P, Skelly C, Yadav S, et al. (2020) Transfer of environmental microbes to the skin and respiratory tract of humans after urban green space exposure. *Environ Int* 145: 106084.
142. Mhuireach GÁ, Van Den Wymelenberg KG, Langellotto GA (2023) Garden soil bacteria transiently colonize gardeners' skin after direct soil contact. *Urban Agric Region Food Syst* 8: 1-22.
143. Gruber C, Legat A, Pfaffenhüemer M, Radax C, Weidler G, et al. (2004) *Halobacterium noricense* sp. nov., an archaeal isolate from a bore core of an alpine Permian salt deposit, classification of *Halobacterium* sp. NRC-1 as a strain of *H. salinarum* and emended description of *H. salinarum*. *Extremophiles* 8(6): 431-439.
144. Wu JH, McGenity TJ, Rettberg P, Simões MF, Li WJ, et al. (2022) The archaeal class Halobacteria and astrobiology: Knowledge gaps and research opportunities. *Front Microbiol* 13: 1023625.
145. Agioutantis P, Koumandou VL (2018) Bioenergetic diversity of the human gut microbiome. *Meta Gene* 16: 10-14.
146. Barker CF, Markmann JF (2013) Historical overview of transplantation. *Cold Spring Harb. Perspect Med* 3(4): a014977.
147. Stolf NA (2017) History of heart transplantation: A hard and glorious journey. *Braz J Cardiovasc Surg* 32(5): 423-427.
148. Bunzel B, Schmidl Mohl B, Grundböck A, Wollenek G (1992) Does changing the heart mean changing personality? A retrospective inquiry on 47 heart transplant patients. *Qual Life Res* 1(4): 251-256.
149. Pearsall P, Schwartz GE, Russek LG (2000) Changes in heart transplant recipients that parallel the personalities of their donors. *Integr Med* 2(2): 65-72.

150. Liester MB (2020) Personality changes following heart transplantation: The role of cellular memory. *Med. Hypotheses* 135: 109468.
151. Joshi S (2011) Memory transference in organ transplant recipients. *J. New Approaches Med Health* 19(1)
152. Lakota J, Jagla F, Pecháňová O (2021) Heart memory or can transplanted heart manipulate recipients brain control over mind body interactions? *Act Nerv Super Rediviva* 63(1): 49-51.
153. Kang DW, Adams JB, Gregory AC, Borody T, Chittick L, et al. (2017) Microbiota transfer therapy alters gut ecosystem and improves gastrointestinal and autism symptoms: an open-label study. *Microbiome* 5(1): 10.
154. Kang DW, Adams JB, Coleman DM, Pollard EL, Maldonado J, et al. (2019) Long-term benefit of Microbiota Transfer Therapy on autism symptoms and gut microbiota. *Sci Rep* 9(1): 5821.
155. Dossaji Z, Khattak A, Tun KM, Hsu M, Batra K, et al. (2023) Efficacy of Fecal Microbiota Transplant on Behavioral and Gastrointestinal Symptoms in Pediatric Autism: A Systematic Review. *Microorganisms* 11(3): 806.
156. Li N, Chen H, Cheng Y, Xu F, Ruan G, et al. (2021) Fecal microbiota transplantation relieves gastrointestinal and autism symptoms by improving the gut microbiota in an open-label study. *Front Cellular Infect Microbiol* 11: 759435.
157. Avolio E, Olivito I, Rosina E, Romano L, Angelone T, et al. (2022) Modifications of Behavior and Inflammation in Mice Following Transplant with Fecal Microbiota from Children with Autism. *Neuroscience* 498: 174-189.
158. Nassar ST, Tasha T, Desai A, Bajgain A, Ali A, et al. (2022) Fecal Microbiota Transplantation Role in the Treatment of Alzheimer's Disease: A Systematic Review. *Cureus* 14(10): e29968.
159. Park SH, Lee JH, Shin J, Kim JS, Cha B, et al. (2021) Cognitive function improvement after fecal microbiota transplantation in Alzheimer's dementia patient: A case report. *Curr Med Res Opin* 37(10): 1739-1744.
160. Park SH, Lee JH, Kim JS, Kim TJ, Shin J, et al. (2022) Fecal microbiota transplantation can improve cognition in patients with cognitive decline and *Clostridioides difficile* infection. *Aging (Albany NY)* 14(16): 6449.
161. Segal A, Zlotnik Y, Moyal Atias K, Abuhasira R, Ifergane G (2021) Fecal microbiota transplant as a potential treatment for Parkinson's disease—A case series. *Clin Neurol Neurosurg* 207: 106791.
162. Zhao Z, Ning J, Bao XQ, Shang M, Ma J, et al. (2021) Fecal microbiota transplantation protects rotenone-induced Parkinson's disease mice via suppressing inflammation mediated by the lipopolysaccharide-TLR4 signaling pathway through the microbiota-gut-brain axis. *Microbiome* 9(1): 1-27.
163. Chen H, Chen Z, Shen L, Wu X, Ma X, et al. (2020) Fecal microbiota transplantation from patients with autoimmune encephalitis modulates Th17 response and relevant behaviors in mice. *Cell Death Discov* 6: 75.
164. Collyer R, Clancy A, Borody T (2020) Faecal microbiota transplantation alleviates symptoms of depression in individuals with irritable bowel syndrome: a case series. *Med Microecol* 6(2): 100029.
165. Doll JP, Vázquez Castellanos JF, Schaub AC, Schweinfurth N, Kettelhack C, et al. (2022) Fecal microbiota transplantation (FMT) as an adjunctive therapy for depression—case report. *Front. Psychiatry* 13: 815422.
166. Rao J, Qiao Y, Xie R, Lin L, Jiang J, et al. (2021) Fecal microbiota transplantation ameliorates stress-induced depression-like behaviors associated with the inhibition of glial and NLRP3 inflammasome in rat brain. *J Psychiatr Res* 137: 147-157.
167. Pu Y, Zhang Q, Tang Z, Lu C, Wu L, et al. (2022) Fecal microbiota transplantation from patients with rheumatoid arthritis causes depression-like behaviors in mice through abnormal T cells activation. *Transl Psychiatry* 12(1): 223.
168. Zhu F, Guo R, Wang W, Ju Y, Wang Q, et al. (2020) Transplantation of microbiota from drug-free patients with schizophrenia causes schizophrenia-like abnormal behaviors and dysregulated kynurenine metabolism in mice. *Mol Psychiatry* 25(11): 2905-2918.
169. Bajaj JS, Gavis EA, Fagan A, Wade JB, Thacker LR, et al. (2021) A randomized clinical trial of fecal microbiota transplant for alcohol use disorder. *Hepatology* 73(5): 1688-1700.
170. D'Amato A, Di Cesare Mannelli L, Lucarini E, Man AL, et al. (2020) Faecal microbiota transplant from aged donor mice affects spatial learning and memory via modulating hippocampal synaptic plasticity-and neurotransmission-related proteins in young recipients. *Microbiome* 8: 1-19.
171. Dietert RR (2021) Microbiome First Approaches to Rescue Public Health and Reduce Human Suffering. *Biomedicines* 9(11): 1581.