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Parasites and the Microbiome: A Complex Relationship and Health Impacts in human and plant

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I. Abstract

Pathogens are foreign entities, such as bacteria, viruses, and parasites, and their main goal is to survive and pass. They contrast with microbiota, of commensal microbes in the human body, in that they may devise adaptive ways of avoiding biochemical and cellular defenses, there are millions of microbes in the gastrointestinal tract and their interaction with the host, parasite, and microbiota determines parasite success and disease outcome. The knowledge of this host-parasite-microbiota axis may result in new treatment modals of intestinal parasitic infections. Suppression of soil-borne pathogens and parasites, such as Nematodes that parasitise plants (PPN), are inhibited by disease suppressive soils, which may be of microbiological origin. They are resistant to conventional approaches to management and pose a great threat to agricultural produce. Synthetic microbial community development as a PPN biocontrol methodology could lead to the requirement of using fewer nematicides and fertilizers since the connection between plant-beneficial microbial communities and disease suppression mechanisms can be well comprehended. This examines the relationship between parasites, gut microbiota, host defense and immune response.

Keywords : Parasite, Microbiome, Infection, Defense.

II. Introduction

Pathogens are foreign invaders that mainly seek to proliferate and survive, and they include viruses, bacteria, and parasites. They are in need of their hosts and by exploiting them, can grow and breed at the other. Pathogens are different to microbiota because they may develop specific mechanisms to avoid the biochemical and cellular defenses.

Intestinal parasites cause infections in an estimated 3.5 billion people in the world, and their presence has a significant adverse effect on the health and economy of the people and the entire world [1,2]. Helminths and protozoa cause a proportion of parasitic diseases that can potentially afflict the human gastrointestinal system. These bowel infections constitute a severe health threat, especially to the developing children and often result in severe diarrhea, nausea, vomiting, and malnutrition. Enterobiasis, schistosomiasis, trichuriasis, strongyloidiasis and ascariasis are common intestinal helminth diseases [3]. The most common intestinally related protozoan infections include giardiasis, amebiasis and cystosporidiosis, cystoisosporiasis and balantidiasis [4]. host immune mechanisms have evolved more complicated detection and immune response mechanisms [5,6,7]. An environment of suitable vulnerability of the host is required in which the parasite can survive and thrive, and invaders must be capable of exploiting the host to make the process of parasitism successful [8,9,10]. In this connection, the situation of the intestinal environment and, ultimately, the disease outcome largely depends on the conditions of the parasite-host dynamic interaction [8,9,10,11,12,13,14]. As such host-parasite interactions are not in isolation, they are affected by the broader ecological environment, such as the commensal microbiota, of the gut. It is reported that the gut microbiota contributes greatly in regulating the relationship between the host and the parasite through its ability to regulate the host immune system in addition to its direct interaction with the parasitic host [15]. The environment of the host-parasite-microbe axis provides each microbial group in the gut with a different repertoire of potential interactions that may disrupt the finely tuned homeostatic balance in the intestine and influence the pathogenicity of parasites [16,17]. These host-parasite interactions are not in isolation and therefore are affected by the bigger ecological environment of the stomach, which consists of the commensal microbiota [10].

The effect of microbes in infection of parasites is proven by research on ger-free (GF) mice, which lack a microbiome. GF animals have been found to have a varied expression of helminth H. polygyrus gene as compared to worms that parasitize the use of a particular pathogen free mice. This implies that the gut microbiota could influence the host trends of parasite gene expression with or without the presence. The adhesive effect of the gut microbiota on infection was demonstrated by the association between these alterations in the gene expression patterns and reduced worm in mice [18]. Microbial burden can determine the progression of parasite infection. In vitro experiments involving mouse cecum explants showed that particular bacterial strains and the yeast Saccharomyces cerevisiae stimulate T. muris egg hatching and that the bacteria and egg need to be in direct contact. The authors propose that this process is mediated by bacterial adhesion through type 1 fimbriae which is species specific [19]. The presence or lack of microbiota is essential in the fitness and establishment of parasites yet it may influence infection because of the ability of the organisms to adjust the intestinal environment. Local microorganisms may influence the intestinal environment and the parasites by their production of microbial-produced compounds and absorption of essential nutrients. There are several microorganism-derived metabolites that can inhibit the Cryptosporidium parvum growth. Precisely, indoles seem to influence the growth and intracellular life stages of this protozoan by modulating host mitochondrial activity, inducing endoplasm reticulum stress, and damaging the activity of the parasitic mitosomes. Mice receiving indoles or microorganisms producing the same demonstrated better resistance to C. parvum infection which supports our in vivo results [20].

The study identifies the special impacts of the different parasites on the gastrointestinal microbiota. In the case of Trichuris muris (whipworm), it causes the production of mucus to change, changes in the composition of the microbiota, since the increase of mucus can cause the expansion of the beneficial microbes. An example of this is in the case of Heligmosomoides polygyrus (the intestinal worm) which alters the gut environment and boosts production of short chain fatty, which alleviates inflammation and improves the health of microbiota. The diversity of microbiota is influenced by Ascaris suum that results in alterations in the microbial composition of the gut and can cause dysbiosis. When it comes to protozoa, the amoeba (Entamoeba histolytica) may disrupt the balance of the microbiota by being able to compete with the microbiota and inducing intestinal inflammation, whereas the toxoplasma (Toxoplasma gondii) can have an impact on the production of the mucus, altering the interaction between the microbiota and the mucosal barrier and potentially favoring some of the pathogenic species. Giardia intestinalis (the giardia) leads to inflammation of the intestines and changes the microbiotic composition, which may enhance the number of harmful bacteria, as well as decrease the diversity. The species of cryptosporidium (cryptosporidium species) cause inflammation, as well as increase intestinal permeability, which adversely impact the microbiota balance. Lastly, the presence of Blastocystis species (blastocystis species) can result in alteration in microbial diversity and interaction with other forms of microbes in the gut, which is one of the ways these parasites directly or indirectly impact the microbiota and change host health [21].

The Effects of Gut Microbiota on Intestinal Parasites

The development of a healthy host immune system depends on the gut microbiota [22], which also aids in direct competition and defense against harmful organisms [23,24,25]. Therefore, the methods that parasites themselves use to infect microorganisms directly or indirectly through host manipulation contribute to the development of infection. In both clinical and animal models, parasite infection has been shown to modify the gut microbiota's makeup and role [26,27,28,29]. Mice infected with the parasite Trichuris muris exhibited altered microbial composition and diversity on days 14 and 28 [26]. Trichinella spiralis-infected mice also exhibit a different gut microbiome profile than controls, with a significant rise in Proteobacteria relative abundance and a decrease in Bacteroidetes and Clostridiales [30, 31]. Furthermore, [32] alterations in microbial diversity of the foregut and hindgut were observed in Giardia-infected mice. All of these results show that intestinal microbiota in mice can be changed by parasite infections caused by helminths and protozoa. There have also been reports of helminth and protozoan infections in humans causing changes in the microbial composition. The number and diversity of Paraprevotellaceae microbial species were higher in rural Malaysian populations invaded by helminth parasites [33]. In contrast to those who are not infected, nematode-infected individuals in a Sri Lankan community showed a considerable increase in beta diversity but no change in alpha diversity. When compared to uninfected controls, Verrucomicrobiaceae and Enterobacteriaceae were elevated in infected people [34]. Research conducted in Southwest Cameroon also showed a strong association between Entamoeba prevalence and alterations in microbial diversity and composition, independent of sex, age, body mass index, ancestry, or geography [35].

Parasitic Infection via Microbial Manipulation

Intestinal helminthes and protozoa cause millions of infections annually worldwide, especially in developing nations, malnutrition, development retardation, and dehydration are some of the outcomes of these diseases that have a significant detrimental impact on quality of life and present serious health risks [1,3,4]. Among the leading causes of the worldwide illness burden are intestinal parasites, both helminthes and protozoan, such as Ascaris, Entamoeba, Toxoplasma, Cyclospora, Giardia, and Cryptosporidium [4,36]. Therefore, public health greatly depends on the control and treatment of these illnesses.

Present-day public health initiatives focus on preventing parasite infections by promoting handwashing, hygienic food preparation methods, and ensuring access to clean water to halt transmission [37]. Chemotherapeutic approaches, such the well-known antihelminth medication praziquantel, have also been used to inhibit transmission and quickly reduce individual parasite burden [39,40]. In regions where helminth or protozoan infections are prevalent, mass medication administration (MDA) can be used; however, this approach is costly to implement, offers only a temporary fix, and sometimes lacks efficacy across parasitic species [37]. Additionally, there is a significant risk of drug resistance, post-treatment reinfection, and problems with longer-term control with these chemotherapeutic approaches [38,39]. Therefore, it is essential to find alternative tactics, and research into the host-parasite-microbiota interaction may lead to new therapeutic choices for those infected with parasites.

There have been reports of a marked decrease in parasitic survival, especially when these bacteria are utilized together; In vitro studies suggest that administering probiotics in coculture with Entamoeba can affect growth, proliferation, and survival rates [41]. L. casei and L. rhamnosus have also shown promise in clearing Giardia in animal models [42,43]. Clinical investigations indicate that combining the yeast Saccharomyces boulardii with metronidazole is more effective than using metronidazole alone for various protozoan illnesses [44,45,46]. Probiotics may also help boost the effectiveness of conventional medications. Apart from probiotics, the potential indirect effects of antibiotics on the intestinal environment through the promotion of microbial dysbiosis are also being considered for the management of helminth and protozoan infections [47]. Reintroducing heritage species with recognized immunoregulatory qualities or lost "old friends" [17,48], Supplementing with post-biotics or bacterially generated compounds, including SCFA, and nutritional therapies targeted at changing the microbiota could all offer fascinating new research directions.

Research on Microbiota in Nematode-Suppressive Soils That Depends on Culture

To combat the decline in nematode population density caused by antagonistic microbial species, it is essential to cultivate these organisms on growth media for effective large-scale multiplication and long-term nematode control. Research has shown various microbiomes associated with plant-parasitic nematodes in suppressive soils, which will be discussed further in the next section. Nevertheless, it has been suggested that just 1% of naturally occurring microbes can be grown [51]. The mass production of nematode antagonists is limited, particularly due to the requirement for a nematode host in the cultivation of obligatory parasites. Additionally, in vitro studies indicate that various microorganisms exhibit antagonistic effects on free-living nematodes, or they have arisen as a result of studies on the soil's capacity to prevent other plant parasites and illnesses [52].

Microbial Species Linked to the Repression of Sedentary Endoparasitic Nematode Migratory Stages

The bacterium Pasteuria is the most researched microorganism linked to PPN migration stages in suppressive soil. Pasteuria species are a promising option for PPN biocontrol due to their obligatory nature. It has been documented that a number of Pasteuria species parasitize worms. The parasite Pasteuria penetrans, along with Pasteuria nishizawae, parasitizes Meloidogyne spp. (root-knot nematodes), while Pasteuria thornei targets Globodera and Heterodera species, which are cyst-forming worms. Additionally, Pasteuria usgae interacts with Pratylenchus spp. (root-lesion nematodes) parasitize The stinging nematodes Belonolaimus spp. [53]. The initial step of parasitism is when endospores of Pasteuria spp. adhere to the worm's cuticle. The spores initially adhere to the infectious second-stage juveniles (J2) in the soil when P. penetrans parasitizes Meloidogyne. Bacteria form microcolonies inside the worm's pseudocelom once J2 has entered the roots. Ultimately, the development of females' eggs is disrupted [54]. The juvenile nematode generates more endospores due to other plant-parasitic nematodes (PPN) like Pasteuria on H. avenae, allowing the endospores to germinate through the cuticle and complete the bacterial life cycle. However, Pasteuria endospores in soil do not necessarily indicate nematode parasitism, and minimal attached spores may not lead to PPN infection [55]. There are instances where a highly strong nematode-bacterium selectivity results in a low parasitism rate. [56] examined the persistence of antagonism and the concentration of bacterial endospores in soil.

Microbial species like N. gynophila and P. chlamydosporia have been isolated for their parasitic effects on sedentary stages of plant-parasitic nematodes, significantly reducing populations of the cyst nematode H. avenae. P. chlamydosporia, a saprophytic fungus in soil, often interacts with nematode eggs and cysts [57]. Numerous studies have examined the suppression of H. schachtii in Californian soil, and nematode reproduction has significantly decreased when as little as 0.1% of this soil is transferred to a suitable soil [58]. High levels of the fungus Fusarium oxysporum and Dactylella oviparasitica in nematode cysts and eggs were associated with soil suppressiveness. However, since F. oxysporum did not result in a nematode decline in a number of later investigations, its role in worm suppression remains conjectural. Furthermore, viable eggs continued to be resistant to D. oviparasitica despite the fungus's great effectiveness in egg parasitism. In an isolated strain of Pseudomonas, Several potential genes causing egg toxicity have been identified, alongside studies isolating fungi from root-knot and cyst nematodes. Greenhouse tests indicate that some of these fungi exhibit antagonistic effects against nematodes, with various microbial strains from diseased nematode stages demonstrating effective methods to counter them[59]. These methods included parasitism, the creation of poisons and traps, and plant-mediated methods. Since the isolation of antagonists comes before their mass manufacturing, a culture-dependent method of studying nematode-suppressive microorganisms is crucial. However, microbial consortia linked to PPN suppression are more accurately represented by microbial identification using DNA-based techniques; investigations in this area are included in the sections that follow.

The majority of potential microbial antagonists could not antagonize PPN in a specific field environment, despite success in laboratory and greenhouse settings. This failure is attributed to their inability to survive within complex soil microbial communities or to effectively colonize plant roots across diverse environmental conditions [60].

The study investigates the composition and diversity of microbial communities associated with different life phases of plant-parasitic nematodes, emphasizing the relationship between nematode mobile stages and soil microorganisms. Dominant bacterial genera identified in nematode-suppressive soils include Sphingomonas, Micrococcus, Bacillus, Methylobacterium, Rhizobium, and Bosea, along with fungal species such as Davidiella and Rhizophydium. Additionally, certain fungi from Malassezia, Plectosphaerella, Gibellulopsis, and Lectera were found to enhance J2 of M. incognita in these suppressive soils, [61] also discovered that M. incognita J2 in soil was associated with the fungus Plectosphaerella cucumerina and the bacteria Bacillus thuringiensis. Proteinaceous protoxin crystals, also known as crystal protein or Cry protein, are produced by B. thuringiensis and cause intestinal lysis and nematode death [62]. The study analyzed microbial populations through ITS amplicon sequencing and bacterial 16S rRNA gene analysis in female G. pallida, uncovering diverse microbiota, Including bacterial genera such as Burkholderia, Bosea, Rhizobium, Devosia, Ralstonia, and Streptomyces, along with fungal taxa like Davidiella, Hirsutella, Malassezia, Microdochium, Monographella, and Penicillium, which are predominantly found in potato monoculture soil [63]. Prior research has linked certain bacterial species to lesion nematodes and root-knot infectious phases in suppressive soils, the microbial community analysis of G. pallida females showed that the potato monoculture soil was dominated by the fungal genera Davidiella, Hirsutella, Malassezia, Microdochium, Monographella, and Penicillium, as well as the diverse microbiota Burkholderia, Bosea, Rhizobium, Devosia, Ralstonia, and Streptomyces. Certain bacterial genera have been linked in the past to lesion nematodes and root-knot infectious stages in suppressive soils. The mature brown cysts that the adult female cyst nematodes develop into eventually end up in the surrounding soil after initially appearing on the roots. Numerous microorganisms colonize the eggs inside the cysts [64], and the cysts have been shown to be able to introduce suppressive microorganisms into a nematode-permissive soil [65]. OFRG was utilized to analyze the bacterial and fungal microbiota present in cysts from suppressive soil.

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