



Pathogenicity of *Salmonella* During *Schistosoma-Salmonella* Co-infections and the Importance of the Gut Microbiota

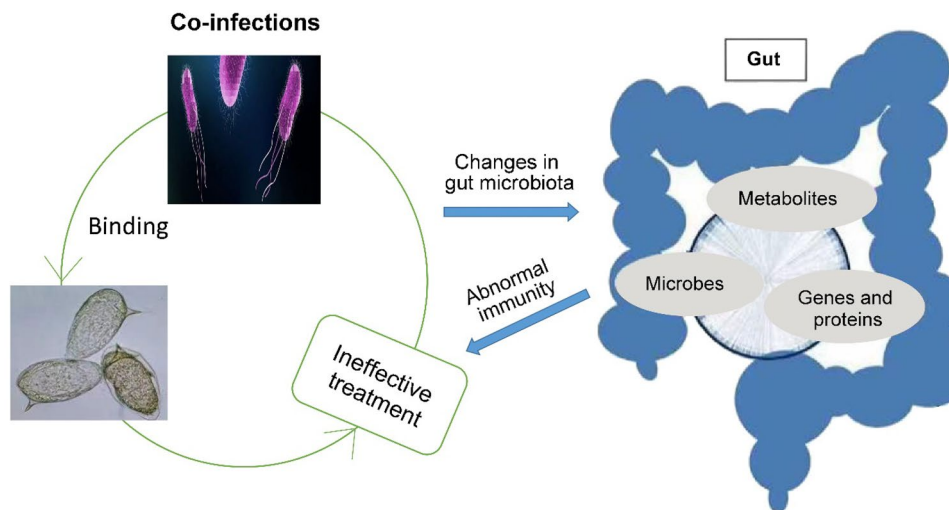
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Abstract

Antibiotic inefficacy in treating bacterial infections is largely studied in the context of developing resistance mechanisms. However, little attention has been paid to combined diseases mechanisms, interspecies pathogenesis and the resulting impact on antimicrobial treatment. This review will consider the co-infections of *Salmonella* and *Schistosoma mansoni*. It summarises the protective mechanisms that the pathophysiology of the two infections confer, which leads to an antibiotic protection phenomenon. This review will elucidate the functional characteristics of the gut microbiota in the context of these co-infections, the pathogenicity of these infections in infected mice, and the efficacy of the antibiotics used in treatment of these co-infections over time. *Salmonella-Schistosoma* interactions and the mechanism for antibiotic protection are not well established. However, antimicrobial drug inefficacy is an existing phenomenon in these co-infections. The treatment of schistosomiasis to ensure the efficacy of antibiotic therapy for bacterial infections should be considered in co-infected patients.

Graphical Abstract



Co-infections of *Salmonella* and *Schistosoma mansoni* confers the protective mechanisms that give ineffective treatment of salmonella. The functional characteristics of the gut microbiota in the context of these co-infections influence the pathogenicity of the both pathogens thereby decreasing immunity and brings changes in gut metabolism.

Introduction

The severity and treatment efficacy of schistosomiasis on bacterial, viral or other parasitic co-infections has a growing concern. Among the much studied are cases of *Salmonella* infection during schistosomiasis. Co-infections of

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Schistosoma and hepatitis B or C, malaria, leishmaniasis and HIV also are under study [1]. Moreover, *Schistosoma* as co-infection with other protozoa, with helminths and with bacteria other than *Salmonella* are also been studied [2]. Co-infections with *Schistosoma* and *Salmonella* confound the clinical picture of both diseases. Evidence emerging from in vitro [3, 4], animal model experiment [5] and clinical observations [6] regarding the symbiotic relationship existing between *Schistosoma* and *Salmonella* showed efficacy in the drug administered for treatment is only optimal when concurrent anti-Schistosomal therapy is administered. Although number of studies centred on the study of the concurrent *Schistosoma-Salmonella* infections, their complicated mechanisms where bacteria adhere to the adult Schistosomes present in the mesenteric vasculature require further research [3]. The pathogenicity of *S. mansoni*, alteration in host gut microbiota, and the evolution of drug resistance in concurrent *Schistosoma-Salmonella* infections in vitro and in vivo is yet to shed light on the pathogenicity of the two pathogens that might give rise to the evolution of antibacterial drug resistance [7]. To this end, the phenomena that give rise to persistent *Salmonella enterica* serovar Typhimurium bacteraemia or bacteriuria in the presences of *S. mansoni* will be explored in this review. The paper will investigate these synergistic effects of schistosomiasis and salmonellosis as a co-infectoin.

The most common bacterial genus causing foodborne infections is *Salmonella*. They infect wide range of hosts including human and bird species [8]. Worldwide, the various serovars of *Salmonella* spp. are known as a water and food borne gastrointestinal pathogens, and a systemic diseases pathogen. Typhoid fever alone is estimated at 10.9 million cases annually, most in low- and middle-income countries [9]. In each year, 129.5 million cases of non-typhoidal *Salmonella* (NTS) human cases give between 100,000 and 1 million deaths worldwide [9]. With more than 2600 serovars, *Salmonella enterica* subspecies *enterica* infections are a persistent public health burden, among animals and food industry [10]. The pathogen is transmitted through contamination of food, water and fomites. Some serovars are species-specific but the vast number are “host-adapted” (broad host spectrum) serovars [8].

It is estimated that, 230 million people from the 74 developing tropical and subtropical countries are infected by schistosomiasis yearly. 200,000 deaths are recorded per year [11]. Furthermore, there are number of asymptomatic cases and those with the appearance of symptoms. Asymptomatic infections represent approximately 16.7% of the 120 million affected persons [11].

In human, the clinical manifestations of schistosomiasis are in three phase and these are; acute, sub acute and chronic stages. Once the matured parasite settled in the targeted organs, for example, in the lower urinary tract with

Schistosoma haematobium and the other species in colon and rectum, it develop into secondary manifestations, which happens in liver, lungs, kidneys etc. The healing of granulomata by fibrosis and calcification in the renal glomeruli by deposition of schistosomal antigen-antibody complexes, the development of secondary amyloidosis or at the sites of oval entrapment are attributed to chronic morbidity [1]. Based on the immune response, the clinical manifestations of schistosomiasis full under acute, sub-acute and chronic stages. The acute stage (Katayama fever) is species-specific is seen during the early invasion and migration [12]. During the log phase of parasite growth curve, granulomata around the eggs are formed. Immunity is seen during the chronic stages of disease. During this stage, the pathogen will gain an upper hand against innate, TH1 and TH2 adaptive cells [1]. Complications are seen among some patients. Co-infections or associated pathogenic agents will persist and this condition avails salmonella diseases treatment inefficacy [2]. Inflammation, liver fibrosis, micro abscess formation, ulceration, polyposis and hyperplasia are abnormal physiological functions induce by *Schistosoma* ova [13]

Treatment Options

Salmonella enterica serotypes Typhi and Paratyphi and Typhimurium may persist in the gut, causing ineffective antibiotic treatment and subsequently antimicrobial resistance [14]. Eradication and treatment of salmonellosis is becoming complicated by the emergence of multi-drug resistance (MDR) *Salmonella* spp. [15]. Increasing antibiotic-resistance in strains of *Salmonella* are an increasing infection, public health and economic burden in SSA [16]. In addition to the resistant strains, antibiotics disrupt the gut microbiota and the persisting antibiotic-induced diarrhoea promotes the reduction of benign bacterial population that produce the protective short chain fatty acids (SCFAs). SCFAs are required for various energy supplies such as colon cell proliferation and differentiation by Butyrate [17]. To curb this situation, alternative treatments options are required. The supplementation of probiotic-organisms seems promising. However, the strain and organism type used as probiotic might encourage the growth of opportunistic pathogens. Furthermore, antibiotic susceptibility and antibiotic-resistant carriers are other phenomenal issues associated with probiotic complementary therapy. To this end, a holistic study on probiotic mechanisms and their efficacy is needed [18].

The current state in the treatment of salmonella infections does not look promising. Although the burden of infectious disease lies in the least developed countries, routine surveillance for antimicrobial resistance is not robust. For instance, NTS is now taken to be 50–70% MDR, including resistance to flouroquinolones and 3rd generation cephalosporins.

Furthermore, fluoroquinolones, which is the choice for MDR cases are not effective in treating *Salmonella* Typhi and *Salmonella* Paratyphi A [19]. Chloramphenicol, ampicillin and co-trimoxazole are also ineffective leaving quinolones as a choice to treat MDR *Salmonella* [20]. Kanamycin with an enhanced MDR *Salmonella* swarming properties on number of isolates is a promising treatment strategy [21]. Due to the poor economic status and inadequate resource in sub-Saharan Africa, the prudent use of effective antimicrobials looks unrealistic [19]. What this review will recommend is the typhoid vaccines and hope that there will be acceleration of trials for novel iNTS vaccines [19]. Again, a radical and aggressive approach is the only way to establish rational use of antibiotics during treating infections [20].

The preventive measures for schistosomiasis will not be effective without effective education and periodic mass treatment. The implementation of chemical mollusciciding-based control of *Bulinus* and *Biomphalaria* spp., snails is proven effective. With the elimination of these intermediate hosts, local transmission is drastically reduced, albeit incomplete. *S. mansoni* and *S. haematobium* transmission are minimized even in the in high risk areas [22]. Praziquantel as the drug of choice has 80% cure rate and can only be supplemented with effective vaccine for absolute eradication of schistosomiasis [2]. However, for fibrotic lesions, surgical treatment is the last resort. In effective reduction of infection intensity, Praziquantel 40 mg/kg is recommended among preschool- and school-aged children [23]. To elicit a mucosal response, attenuated *S. Typhimurium* strain (YS1646) is produce as multi-modality vaccine. This intervention is targeting Cathepsin B (CatB) is a promising intervention for complete protection against *S. mansoni* [24]. *Schistosoma* vaccine development is promised on oral delivery of the antigen by nirB-driven *S. Typhimurium* type III secretion system [25].

Schistosoma and Salmonella Co-infections

Dual *Schistosoma* and *Salmonella* infection is a public health challenge and other schistosomiasis endemics. The interactions of *Schistosoma* and *Salmonella* is favored by the immunosuppression of the host due parasitic infections [26]. As both are water-borne human pathogens common in areas with poor sanitation, the co-existence of *Schistosomes* and *Salmonella* infections is a common occurrence. The type of organisms involved, order and time of interval between the infections, the pedigrees of the parasites, infectious agents are all associating factors that appear to determine the synergistic pathogenicity of the co-infection [2]. Another confounding factor in the study of *Schistosoma* co-infection is the prior infection with *Schistosoma*, which has effects on the subsequent infection. With this prior infection, the severity of subsequent infection with *Fasciola hepatica*, *Plasmodium*, *Echinostoma* or *Helicobacter pylori* is decreased [2]. In contrast to *Toxoplasma gondii*,

Leishmania, *Staphylococcus aureus*, *Entamoeba histolytica* or *Salmonella*, the subsequent infection appear to present in a more severe form with a prior infection with *Schistosoma* [2]. Co-infection is projected to be increasingly associated with the prevalence uncomplicated *P. falciparum* infection in children. However, an interesting reduction of haemoglobin level in high density *P. falciparum* infection was observed [27].

Medical Importance of Co-infections

The incidence of high morbidity and mortality of helminth infections come with intracellular pathogens such as *Salmonella*. Prolonged fever and enlarged liver and spleen are some clinical manifestation associated with co-infections, in addition to chronic septicemic salmonellosis. These are seen with patients with *Salmonella*-*Schistosoma* co-infections [28]. Conversely, complicated persistent *Salmonella* urinary tract infection was found to be associated with urinary schistosomiasis [28]. *Schistosoma*-*Salmonella* co infections lead a chronic septicemic salmonellosis. In addition to higher bacterial load, this co-infection will first impair IFN- γ and IL-17 responses. This is facilitated via basophils recruitment by a glycoprotein secreted live schistosome eggs (IPSE/alpha-1). IPSE/alpha-1 will trigger IL-4 and IL-13 release from basophils and the overall immunoregulatory activities are studied to give a prolong fever and enlargement of liver and spleen [14].

Pathogenicity of Co-infection

The co-infection of *Schistosoma* with *S. Typhimurium* can ameliorate schistosomiasis in the metabolic alterations associated with infection since the host immune response is manipulated by the secondary bacterial infection [6]. *Salmonella* can evade the effects of antibiotics via adherence to *Schistosomes* (Table 1). *Salmonella* can attach to the outer cuticle of adult schistosomes. In this state, are resistant to antibiotics via a protective mechanism [29]. The protective mechanism and proven treatment inefficiency is hypothesized to be the overall immunoregulatory activities of *Schistosomes*. These activities include induction of Tregs, Bregs degrades antibodies and alternatively activated macrophages [14]. In vitro design of study to qualitatively assess some common antibiotics has gathered evidence regarding *Salmonella* adhering to schistosomes.

The Effects of Antibiotic Treatment on Co-infection

Antibiotic Protection

In a bid to treat patients infected with Schistosomiasis, anthelmintic praziquantel (PZQ) is a common therapeutic drug. However, dysbiosis seems an effect associate with this

Table 1 Various studies on the protection mechanisms of *Salmonella*-*Schistosomes* co-infections

Study design	Significant findings	Conclusion
Intraperitoneal application of live <i>S. mansoni</i> eggs prior to infection with <i>S. Typhimurium</i> [14]	An impairment of IFN- γ and IL-17 responses together with a higher bacterial load compared to <i>Salmonella</i> infection alone IPSE/alpha-1 is known to trigger IL-4 and IL-13 release from basophils, which in turn is known to suppress Th1/Th17 responses	<i>S. mansoni</i> infection impairs a protective immune response against <i>Salmonella</i> infection
Evaluation of <i>Schistosoma</i> -mediated protection of <i>S. Typhimurium</i> strain SL1344 from other antibiotics in flatworm [32]	A reduction in efficacy of antibiotics due to the association of <i>Schistosomes</i> and <i>Salmonella</i> Insignificant elevation in the antibiotic resistance when the non-invasive isostrain and hyperinvasivostrain were recalcitrant to the antibiotics	The protection mechanism is related to the glycolyx of <i>Schistosoma</i> integral milieu. Fimbrial protein (FimH) found in the surface of the bacterium is the feature conferring abilities for <i>Salmonella</i> to bind
Elucidating rheumatoid factors in <i>Salmonella</i> and <i>Schistosoma</i> infections [52]	Titres of rheumatoid factor decreased. 2-mercaptoethanol was consistently eliminated Similar complete elimination of <i>Salmonella</i> somatic antigen agglutinins was observed in sera of some patients with either chronic or acute <i>Salmonella</i> infection	Further study is deemed on the pathogenesis of IgM anti-globulin antibodies associated with infections
NMR-based metabonomics and immunological techniques for the systemic metabolic and immune responses using a mouse model of co-infection [45]	<i>S. Typhimurium</i> (ATCC14028) infection reduced the number of adult <i>S. japonicum</i> adults and eggs, relieved symptoms of schistosomiasis and also abated the mortality of mice infected by <i>S. japonicum</i> <i>S. Typhimurium</i> co-infection counteracted the metabolic disturbances associated with schistosomiasis, which was reflected by the reverted levels of metabolites in co-infected mice	<i>S. Typhimurium</i> infection can ameliorate <i>S. japonicum</i> -induced schistosomiasis in BALB/c mice. This is most likely due to inverse immune polarization
To elucidate the mechanism(s) of the parasite-parasite interaction of <i>S. Typhimurium</i> LT2 on the surface of <i>Schistosoma mansoni</i> , <i>S. haematobium</i> and <i>S. japonicum</i> [53]	Shift of the immune response to different pathogens is a result of indirect interactions between <i>S. japonicum</i> and <i>S. Typhimurium</i> within the host 100% association of the <i>gaE</i> and <i>fla</i> mutants with male schistosomes, but a reduced interaction with female worms Reduction in the rough A and pilimutants' ability to associate with both male and female <i>S. mansoni</i> Pili function in adhesion of <i>Salmonella</i> to the surface tegument of <i>S. mansoni</i> and <i>S. haematobium</i>	Persistence of <i>Salmonella</i> infection may due to the association with <i>Salmonella</i> spp.
<i>Salmonella Typhimurium</i> and Enteritidis intestinal carriage and <i>S. mansoni</i> infection using multi-locus variable-numbers tandem repeat analysis (MLVA) [6]	The proportion of <i>Salmonella</i> carriage is higher among <i>S. mansoni</i> infected participants and even higher in those showing fever	<i>Salmonella</i> intestinal carriage was associated with a heavy intensity of <i>S. mansoni</i> infection
Pilus-negative and a pilus-producing transductant strain of <i>S. Typhimurium</i> in an in vitro system [3]	The association of <i>S. Typhimurium</i> to the surface tegument of <i>Schistosoma</i> The <i>Schistosoma</i> helminths provide a multiplication focus for these bacteria in the portal mesenteric system, with a persisting bacteremia	Pili are the ligands for bacterial adherence to the schistosome surface tegument. Prolonged salmonellosis in <i>Schistosoma</i> -infected patients is due to an association of <i>Salmonella</i> spp. with the <i>Schistosoma</i> worms themselves

intervention. A shift in gut microbiota composition pre and post PZQ treatments was seen [30]. Although the gut bacterial population varies between people infected with schistosomiasis and those who do not, the abundance phyla were *Bacteroides*, then *Firmicutes* and *Proteobacteria* between the pre and post-treatment [31]. Furthermore, only limited variations in the relative abundance of taxa among bacterial classes and this variation is not affiliated to age or sex of the participants.

Antibiotic Concentration Against Bacteria

As a result of *Schistosoma*-associated *Salmonella*, the adherence of bacteria to the flatworm reduces the efficacy of antibiotic treatments targeting those *Salmonella*. The concentrations of the antibiotic used during the in vitro antibiotic assay assessment against *Salmonella-Schistosoma* co-infection were studied to effect killing bacteria at a relative rate. Using a novel antibiotic protection assay, an absolute (100%) efficacy of antibiotic (amoxicillin (32 µg/ml), cefepime (32 µg/ml), cefpodoxime (32 µg/ml), chloramphenicol (32 µg/ml), ciprofloxacin (4 µg/ml), streptomycin (32 µg/ml), sulfadimethoxine (512 µg/ml), or tetracycline (16 µg/ml) was seen with *Salmonella* strains incubated alone, while a decreased efficacy of less than 12% of the same strains when incubated with adult *Schistosoma mansoni* [32]. This protective mechanism is in contrast to the hypothesis that arises on the basis of the virulent nature of the strain type of *Salmonella*. Specific fimbrial protein (FimH) present on the surface on the bacterium confers binding to Schistosomes. When both invasive strains and non-invasive strains of *Salmonella typhimurium* were incubated with *Schistosoma mansoni* under the same amoxicillin concentration (32 µg/ml), the protective mechanism against the effects of amoxicillin enables the bacteria to live. Based on concentration on co-incubation with the control free-living flatworm *Girardia tigrina* and with Hep-2 mammalian tissue culture cells showed no replication of this protective mechanism. Unlike *Salmonella* spp., *Escherichia coli* did not benefit from the protective mechanism of attachment to schistosomes [32]. In order to achieve therapeutic levels or treatment efficiency of the antibiotic used in co-infections study, perturbing the binding mechanism to schistosomes is required to eliminate *Salmonella* [32].

Antimicrobial Treatment Failure Due to Co-infections

It is ascertained that any ineffective use of antibiotics may result in resistance gene acquisition and expression [32]. *Salmonella* factors facilitate the attachment to *Schistosoma* and they catalogued the antibiotics that are infective against the co-infection [32]. *Schistosoma-Salmonella* co-infections are as a result of the enteroinvasive *Salmonella* entering the

systemic circulation whereby the *Salmonella* attach to the tegument of adult *Schistosoma* in the mesenteric vasculature [4, 5, 33]. In a normal *Schistosoma* infected patient, the anthelmintic praziquantel is a key choice of therapy. However, in cases of *Schistosoma*-associated *Salmonella*, such therapy is observed to cause a massive release of *Schistosoma*-associated *Salmonella*, leading to acute septicaemia among children when *Salmonella* treatment options are not co-administered [34, 35].

Salmonella Interactions with the Microbiome

Salmonella infection in a mouse model has been seen to drastically alter the homeostasis of gut microbiota and thus the intestinal metabolome. The physiological functions and hormone metabolism were significantly altered [36]. *S. Typhimurium* is a prominent competitor with commensal gut microbiota. Once they dominate the gut microbiota population, their invasion signals the onset of infection. Both intestinal and urinary schistosomiasis will also alter the gut microbiome (Table 2).

Microbiome and Co-infection

Commensal microorganisms called gut microbiota are vast number of organism living gastrointestinal (GI) tract of vertebrates. Their functions range from maintenance of energy balance, nutrition and host immunity [37], and the production of antimicrobial products, bacteriophages deployment and enhancing gut barrier integrity [38]. A healthy gut microbiome is a critical defence against colonization of pathogenic or exogenous microorganisms. This effect is referred to as colonization resistance (CR) and helps to minimize exogenous pathogens, which many colonize the gut and ultimately cause infection [36]. An imbalance of these dysbiosis is associated with number of chronic and autoimmune disorders [39]. Besides environmental factors, macrobiota including parasitic helminths with their pathogenic effects including metabolic activity, immune system and lead to infection [36].

Of recent, the role of gut microbiome is shedding more lights to health of host and the functions not limited to are the biochemical, immunological and nutritional response of the gut microbiome are more a less biomarkers [40]. To add scholarly evidence to the existing and emerging theories, this review will create literature for a further study to investigate the role of the gut microbiome in parasitic infection, co-infections, and the antibiotic resistance due to the pathology. The acquired immunity among patients when exposed to helminths, aggravated with bacterial infections and the resulting immune response to the concurrent infections [41, 42]. In a bid to assess the impact of sequential infection of

Table 2 Various studies on *Schistosomes* and its influence on gut microbiota

Study methodology	Effects on gut microbiota	Study conclusion
NMR-based metabolomics and immunological techniques to detect systemic metabolic and immune responses of <i>S. japonicum</i> and <i>S. Typhimurium</i> (ATCC14028) coinfection in BALB/c mice [45]	<i>S. Typhimurium</i> infection reduces the number of adult schistosomal worms and eggs. Due to inverse immune polarization, <i>S. Typhimurium</i> infection can ameliorate <i>S. japonicum</i> -caused schistosomiasis and counteracts the metabolic disturbances associated with schistosomiasis	The study indicates the development of new tools for controlling <i>Schistosoma japonicum</i> -associated diseases
Shotgun metagenomic sequencing used to characterise the gut microbiome and resistome of Zimbabwean preschool-aged children (1–5 years) [53]	Bacteria phyla <i>Bacteroidetes</i> , <i>Firmicutes</i> , <i>Proteobacteria</i> , and fungi phyla <i>Ascomycota</i> , <i>Microsporidia</i> , <i>Zoopagomycota</i> dominate the microbiome. Specifically, infection is associated with increases in <i>Pseudomonas</i> , <i>Stenotrophomonas</i> , <i>Derrxia</i> , <i>Thalassospira</i> , <i>Aspergillus</i> , <i>Tricholoma</i> , and <i>Periglandula</i> , with a decrease in <i>Azospirillum</i>	A novel metagenomic dataset that indicates an association between urogenital <i>schistosome</i> infection and changes in the gut microbiome
Screening the gut microbiota of <i>S. mansoni</i> infected and uninfected children from Côte d'Ivoire using V3 and V4 regions of 16S rRNA genes	Over-abundance of <i>Fusobacterium</i> spp. in cured children. No significant effect on the microbial composition	Dysbacteriosis of the gut microbiota was not induced by <i>S. mansoni</i> and a specific microbiome profile could not influence praziquantel response
Follow-up on samples after administering 60 mg/kg praziquantel or placebo [54]		
Assessing the influence of gut microbiota in the 28 kDa glutathione <i>S</i> -transferase (P28GST; a schistosome derived enzyme)-mediated anti-inflammatory effects of mice faecal microbiota transplantation		
The experimental data were supplemented by the temporal fecal microbiota compositions of P28GST-treated Crohn's disease patients from a pilot clinical study [55]		
Liquid chromatography tandem mass spectrometry (LC-MS/MS) platform for comparison between the metabolic profiles of the male and female <i>S. japonicum</i> worms collected from SCID mice and BALB/c mice at 5 weeks post infection [40]	There is an association between the schistosome with retarded growth and development in SCID mice Their perturbed metabolites and metabolic pathways provided a new insight into the growth and development regulation of <i>S. japonicum</i> worms At metabolic level, this indicated great clues for discovery of drugs or vaccines against the parasites and disease with more researches	This study opens the door to helminth-derived molecules, as promising safe therapeutic use of immunomodulation This study gives great clues for discovery of drugs or vaccines against the parasites and disease

bacteria and helminths on the host, this review is vowed to consider the co-infection of *S. Typhimurium* and *S. mansoni*.

Metabolic Response to the Co-infection

Metabolomics has been a robust tool in studying metabolic response to series of stimuli and one such is a co-infection [43]. Chromatography coupled to mass spectrometry or ¹H nuclear magnetic resonance (NMR) spectroscopy, with the multivariate statistical analysis aid to determine metabolic changes in system response to stress or stimuli [44]. Alternative therapeutic such as personalized medicine based on microbiome might get its roots from the effects of *Salmonella* in the co-infection provided that, the salmonella serotype is non-invasive and non-pathogenic.

Using the NMR-based Metabolomics and immunological techniques to detect the systemic metabolic and immune responses, respectively, this study concluded *Salmonella enterica* serovar Typhimurium effects reduction in egg counts and the number of adult worms and relieves symptoms of schistosomiasis [45]. The metabolic disturbance of co-infected mice was compared with *S. japonicum*, reverted levels of metabolites result from the former infection. Due to inverse immune polarization, the bacteria have been seen to ameliorate *S. japonicum* induced schistosomiasis in BALB/c mice [45]. In order to explore on this pathogenicity, other forms of *Schistosoma* should be studied in co-infection with the same serotype of *Salmonella*.

Immune Response to the Co-infection

A shift in host immune response from Th1 to Th2 polarization is studied to be an effect of *Schistosoma* infection of a typical schistosomiasis [45]. The alteration is achieved due to the progress of the disease including cercariae intrusion, migration of larvae, pairing in adult and laying of eggs [46]. Unlike *Schistosoma*, infection caused by *S. Typhimurium* only induces Th1 polarization [47]. The clinical significance of the host immune impairment by the combined effects of the *S. Typhimurium* and *S. mansoni* could draw much attention to the interaction between these two species. One instance is the influence of gut microbiota on the generation of Th17 cells. The effector lineage of CD4 T cells with protective abilities against inflammatory and harmful autoimmune conditions are Th17 cells [48]. They mobilize host immunity against microbial pathogens such as *Salmonella* [49]. Expansion of segmented filamentous bacteria (SFB) is also inhibited with an increase in α -defensin expression of IL-17. Low number of IL-17-producing Th17 cells in the lamina propria signals loss of α -defensin and expansion of SFB [50]. While much attention is paid on bacterial benefits to the host immunity, benign worms and viral species are yet to be explored.

Future Research

Salmonella resistant to multiple antimicrobials worldwide is a threat to global health. The emerging of clones of resistant strains even in the under developed world requires a holistic approach on food chain and distribution system [51]. An improved understanding of the impact of genome variation of bacterial pathogens on pathogen-host and pathogen-environment interactions has the potential to improve quantitative risk assessment and reveal how new pathogens evolve [10]. The physical barrier theory of mammalian cell-docking site for FimH protein [32], begs for a further study despite it is ascertained that the resistance is transient and is observed only during adherence.

The efficacy of antibiotics will be determined by the weekly faecal culture for bacteria responsible for urinary tract infections and stomach disorders. Such study is hoped to ascertain the body's immune response to *S. mansoni* infection in co-infection. This will be based on the granulomatous reaction involving T cells, macrophages, and eosinophil of group of antibiotic and non-antibiotic interventions and on the *Schistosoma* weekly egg counts through time. With respect to in vitro study, novel antibiotic protection assay of antibiotic-sensitive, *Salmonella* strains are ought to be developed, incubated with a known concentration of effective therapeutic proven antibiotic. In sense, the lethal dose should be 100% effective to eliminate *Salmonella* strains in the void of concurrent *Salmonella* infections [3]. The study of co-infections involving *Schistosoma* and *Salmonella* should be based on model that will explain a wholesome range of parameters. Study of the mucosal cell gene expression, innate and adaptive mucosal immune responses, the virulence expressed by the pathogens involved, microbiota gene expression and the genetic profiling of the host will confer clear explanation to the homeostasis [37].

Conclusion

In a bid to curb with the emerging infectious diseases in sub-Saharan Africa, much paid attention should be equally paid to the treatment inefficacy arising as a result of co-infection. These combined disease mechanism has ways to escape antimicrobial treatment. We dwelled on co-infections of *Salmonella* and *S. mansoni* to ascertain the antibiotic protection phenomenon and functional characteristics of the gut microbiota. *Salmonella-Schistosoma* co-infections need more study to decipher on the exact phenomenon existing with regards to the pathogenicity. Establishing the protective mechanism conferred by schistosomes for *Salmonella* to survive antibiotic treatment are still not clear as per mechanism.

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Declarations

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