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REVIEW AND SYNTHESIS

Scoping review on soil microbiome and gut health—Are soil microorganisms missing from the planetary health plate?

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Abstract

1. Evidence suggests that soil microorganisms, to which humans have been exposed throughout our evolutionary history, were essential for the evolution of the human gut microbiome and immunological resilience. In recent decades, gut microbial diversity has decreased along with urbanization and global loss of biodiversity. At the same time, the prevalence of chronic, non-communicable inflammatory diseases has been increasing in urbanized societies.
2. Here, we investigate whether the existing literature supports the hypothesis that ingesting soil microbiota provides immunological resilience. We focus on identifying research gaps and challenges that must be overcome to understand the effects of eating soil on immunological resilience. A scoping review of the peer-reviewed empirical literature was carried out. The search focused on studies that exposed mammals to direct soil contact and measured the gut microbiota and host response; 12 articles, including four human, six mouse and two other mammal studies, were identified for inclusion in the review. In addition, seven articles related to human health risks associated with soil consumption were included in the review.
3. Studies indicate that ingesting soil-bound microorganisms supports immunological resilience. There is a lack of intervention studies that include human study subjects that test orally the effect of soil microorganisms on the gut microbiota and immunological resilience.
4. Challenges, particularly soil heterogeneity and risks related to soil biological and chemical properties, have prevented progress to fully understand the effect of oral intake of soil-bound microorganisms on human gut microbiota and health.
5. The results encourage the development of technologies that allow daily exposure to soil microbiota. Future research should be aimed to precisely test the importance of oral intake of soil-bound microorganisms in gut microbial homeostasis and immunological resilience.

KEYWORDS
biodiversity, geophagy, gut microbiota, health, immune system, soil microbiota

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1 | INTRODUCTION

Soil is essential in the evolution of the human gut microbiome and provides beneficial gut microorganisms (Blum et al., 2019). In particular, there are functional similarities between soil bacteria and human gut bacteria (Blum et al., 2019). In recent decades, global comparisons have revealed a decrease in gut microbial diversity attributed to missing natural soil contacts, Western diets, high hygiene level, biodiversity loss and lifestyle and health-care practices such as caesarean section, antibiotic use and formula-feeding (Ege et al., 2011; Graham-Rowe, 2011; Haahtela et al., 2021; Hanski et al., 2012; Moeller, 2017; Shreiner et al., 2008; Tasnim et al., 2017).

A Western diet that includes a low amount of microbiota accessible carbohydrates found in dietary fibre has resulted in a progressive loss of diversity in the gut (Sonnenburg et al., 2016). This loss of diversity is not recoverable by only reintroducing carbohydrates into the diet. Recovery of the lost gut bacterial diversity would require the administration of missing taxa in combination with microbiota accessible carbohydrates consumption (Sonnenburg et al., 2016). It is also possible that the urban dweller gut microbial community, while compatible with the environment, is incompatible with the slowly adapting human genome (Sonnenburg & Sonnenburg, 2019). Our human genome has adapted to a wide variety of molecular signals provided by a diverse gut microbial community over the course of evolution, and the loss of these microbial signals could disrupt important pathways in the human body, such as the immune system, endocrine signalling pathways and neuroimmune interactions (Sonnenburg & Sonnenburg, 2019). In fact, while gut microbial diversity is decreasing along with urbanization and biodiversity loss, the prevalence of chronic inflammatory diseases such as inflammatory bowel disease, type 1 diabetes, allergies and asthma is on the rise in Westernized societies (Baothman et al., 2016; Haahtela et al., 2021; Tasnim et al., 2017; Zuo et al., 2018). Since the microbiota influences immunological resilience, microbial exposure may be a key factor in recovering gut microbial diversity and determining many of these susceptibility patterns to disease.

Indigenous people have routinely eaten soil for at least centuries, probably thousands of years. The phenomenon is known as geophagy. The most common occasion to eat soil in many societies is pregnancy (Bonglaisin et al., 2022; Callahan, 2003; Geissler et al., 1999; Kambunga et al., 2019; Kawai et al., 2009). In a review that focuses on geophagy during pregnancy, Callahan (2003) proposed that gut immunization by geophagy can produce high levels of immunoglobulin A (IgA) against endemic pathogens and other microbial antigens. He further concluded that regular consumption of soil could therefore boost the secretory immune system of mothers and that soil could act as a prophylactic therapy against many endemic pathogens (Callahan, 2003). Intentional eating of soil seems relatively unfamiliar and unpleasant to the vast majority of people; particularly members of a developed urban society may find it more difficult to accept that humans can deliberately eat soil (Abrahams, 2013). However, it was normal across the vast majority of cultures for people to regularly but incidentally consume non-negligible amounts of soil, for example, clinging to tubers and roots of vegetables (Bacigalupo & Hale, 2012; Wilson et al., 2013). Therefore, incidental consumption of soil may be an important conduit for the ingestion of soil microorganisms. However, in recent decades the consumption of processed food products has increased globally, decreasing the involuntary ingestion of soil and soil-bound microorganisms (Monteiro et al., 2019; Wicaksono, Buko, Kusstatscher, Cernava, et al., 2022; Wicaksono, Buko, Kusstatscher, Sinkkonen, et al., 2022).

Historically, emphasis in studies surveying soil eating has been paid on the negative impacts that soil has on human health, including exposures to toxins, pathogenic microorganisms and parasites (Brevik et al., 2020; Kawai et al., 2009). Only in recent decades has it been discovered that environmental and particularly soil-bound microorganisms may be important for gut microbiota homeostasis, immune regulation and mental health (Blum et al., 2019; Brame et al., 2021; Haahtela et al., 2021; Liddicoat et al., 2020; Nurminen et al., 2018; Rook & Brunet, 2002; Roslund et al., 2020, 2022). Soil microorganisms with which we have co-evolved are also called as our 'old friends' (Rook, 2005). These old friends were more representative among hunter-gatherers and populations in traditional farming environments, compared to urban dwellers today in developed societies. Old friends include soil-derived saprophytic *Mycobacterium* with anti-inflammatory and immunoregulatory properties (Smith, 2020; Smith et al., 2019) and *Streptomyces* producing antiproliferative immunosuppressants within gut (Bolourian & Mojtahedi, 2018). Studies indicate that living in biodiverse environments that provide rich microbial exposure, such as farms or forests, shapes the composition of the gut microbiota (Brame et al., 2021; Parajuli et al., 2020; Vari et al., 2021). Living in or near such environments is negatively associated with the risk of several immune-mediated diseases, for example, type 1 diabetes (Nurminen et al., 2021), asthma (Ege et al., 2011; Kirjavainen et al., 2019; Stein et al., 2016) and allergies (Hanski et al., 2012; Ruokolainen et al., 2015). A study with wild baboon species indicates that incidentally consuming soil microbes in daily food intake explains a large part of gut microbial composition, instead of taxonomic or geographic distance between baboon populations (Grieneisen et al., 2019). Comparison between the gut microbiota of wild and captive ring-tailed lemurs (*Lemur catta*) showed that soil-associated microbes were more prevalent in lemurs that had greater exposure to natural environments; however, gut microbial diversity was not consistently greater in wild than in captive lemurs (Bornbusch et al., 2022). Furthermore, a study with *Panthera* species indicates that the living environment has more influence on the gut microbiota of mammals than genetic relationships (Chen et al., 2022). For some reason, soil eating has hardly been studied in the context of the gut microbiota and immune regulation.

To address existing knowledge gaps and identify existing literature related to soil eating, gut microbiota composition and immunological resilience, we conducted a scoping review to describe the associations between these three. We emphasize the potential effects of soil microorganisms on the composition of the gut microbiota and host immune regulation. In addition, we discuss some of the challenges that have hindered progress towards a comprehensive understanding of the role of soil microbiota as a modifier of the human gut microbiota and immunological resilience. Finally, we identify research gaps that need to be addressed to prepare a

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preventive strategy against immune-mediated diseases in the context of the soil microbiota.

2 | MATERIALS AND METHODS

2.1 | Literature search

To identify relevant studies, a scoping review of empirical papers published up to 5 August 2022 was conducted. Methods and reporting were guided by the Preferred Reporting Items for Systematic Reviews and Meta-Analyses—Extension for Scoping Reviews (PRISMA-ScR) (Tricco et al., 2018). Academic Search Complete (EBSCO), Web of Science, PubMed, Ovid MEDLINE and SCOPUS (Elsevier) were searched using search terms based on those used in the existing literature. The search terms were [soil micro*] and [gut micro*] and [health*]. The reference sections of the articles found using the search terms were searched to find more publications and an Internet search was performed using Google Scholar with the same search terms. We included only English language original research articles. The initial search was conducted on 25 July 2022, with subsequent updates on 5 August 2022 and 14 December 2022 (for papers published until 5 August 2022). The identified titles and their abstracts were then examined for inclusion.

2.2 | Study selection

After removing duplicates, MIR performed title and abstract screening according to inclusion criteria, and OHL checked a 20% sample of exclusion decisions. MIR and AS performed a full-text screening and identified and categorized the reasons for exclusion. Disagreements were resolved after discussions among the three authors. Data extracted included information on the study design, outcome characteristics, follow-up time and the main effects of the study on the gut microbiota and immunological resilience.

The studies were classified into human and animal studies, and studies related to human health risks associated with soil consumption.

2.2.1 | Inclusion and exclusion criteria

Exclusion criteria:

A study did not analyse the soil microbiota.
A study did not analyse the gut microbiota.
A study did not include mammals.
A study only analysed the effect of probiotics.

Inclusion criteria:

A study included soil and gut microbiota.
A study included mammal study subjects.
A study focused on mechanisms or associations related to the effect of soil on the gut microbiota and indicators of immunological resilience.

In addition, studies of potential human health risks associated with soil eating were included.

3 | RESULTS

In total, the literature search retrieved 1430 citations and the review of references from relevant publications yielded 42 additional citations (Figure 1).

Most studies focused on the human health risks associated with exposure to soils. After removing 339 duplicates, 1043 publications that did not meet inclusion criteria based on titles/abstracts and 71 that did not meet inclusion/exclusion criteria based on full-text reviews, 19 publications were included in this review. The 19 studies we found fell into the following categories: in total, seven papers concentrated on the human health risks (Forsberg et al., 2012; Gao et al., 2017; George et al., 2015; Lu et al., 2019; Rosa et al., 2018; Roslund et al., 2019; Wei et al., 2016), six papers were mouse intervention studies (Foxx et al., 2021; González-Rodríguez et al., 2022; Liddicoat et al., 2020; Ottman et al., 2019; Reber et al., 2016; Zhou et al., 2016), three were human intervention studies (Nurminen et al., 2018; Roslund et al., 2020, 2022), one was comparative study with human study subjects (Brown et al., 2022), one was study with piglets (Vo et al., 2017) and one was study with lemurs (Borruso et al., 2021). Most of the included studies focused on bacteria (90%) (Forsberg et al., 2012; Foxx et al., 2021; Gao et al., 2017; George et al., 2015; González-Rodríguez et al., 2022; Liddicoat et al., 2020; Lu et al., 2019; Nurminen et al., 2018; Ottman et al., 2019; Reber et al., 2016; Rosa et al., 2018; Roslund et al., 2019, 2020, 2022; Vo et al., 2017; Zhou et al., 2016) and a single study on fungi (5%) (Borruso et al., 2021). In 15 studies, the gut microbiota was identified by metabarcoding using 16S rRNA for bacteria (Brown et al., 2022; Foxx et al., 2021; Gao et al., 2017; González-Rodríguez et al., 2022; Liddicoat et al., 2020; Nurminen et al., 2018; Ottman et al., 2019; Reber et al., 2016; Rosa et al., 2018; Roslund et al., 2019, 2020, 2022; Vo et al., 2017; Zhou et al., 2016) or ITS region for fungi (Borruso et al., 2021). One study used whole genome metagenomics sequencing in addition to 16S rRNA metabarcoding (Gao et al., 2017). Most articles have been published within the last 7 years (2016–2022).

3.1 | Human studies

Our literature search identified three human intervention trials that indicate that soil microorganisms drive anti-inflammatory and immunoregulatory mechanisms that inhibit inappropriate immune responses (Nurminen et al., 2018; Roslund et al., 2020, 2022) and one cohort study indicating that soil bacteria are transferred to the gut of gardening families (Brown et al., 2022; Table 1). Our

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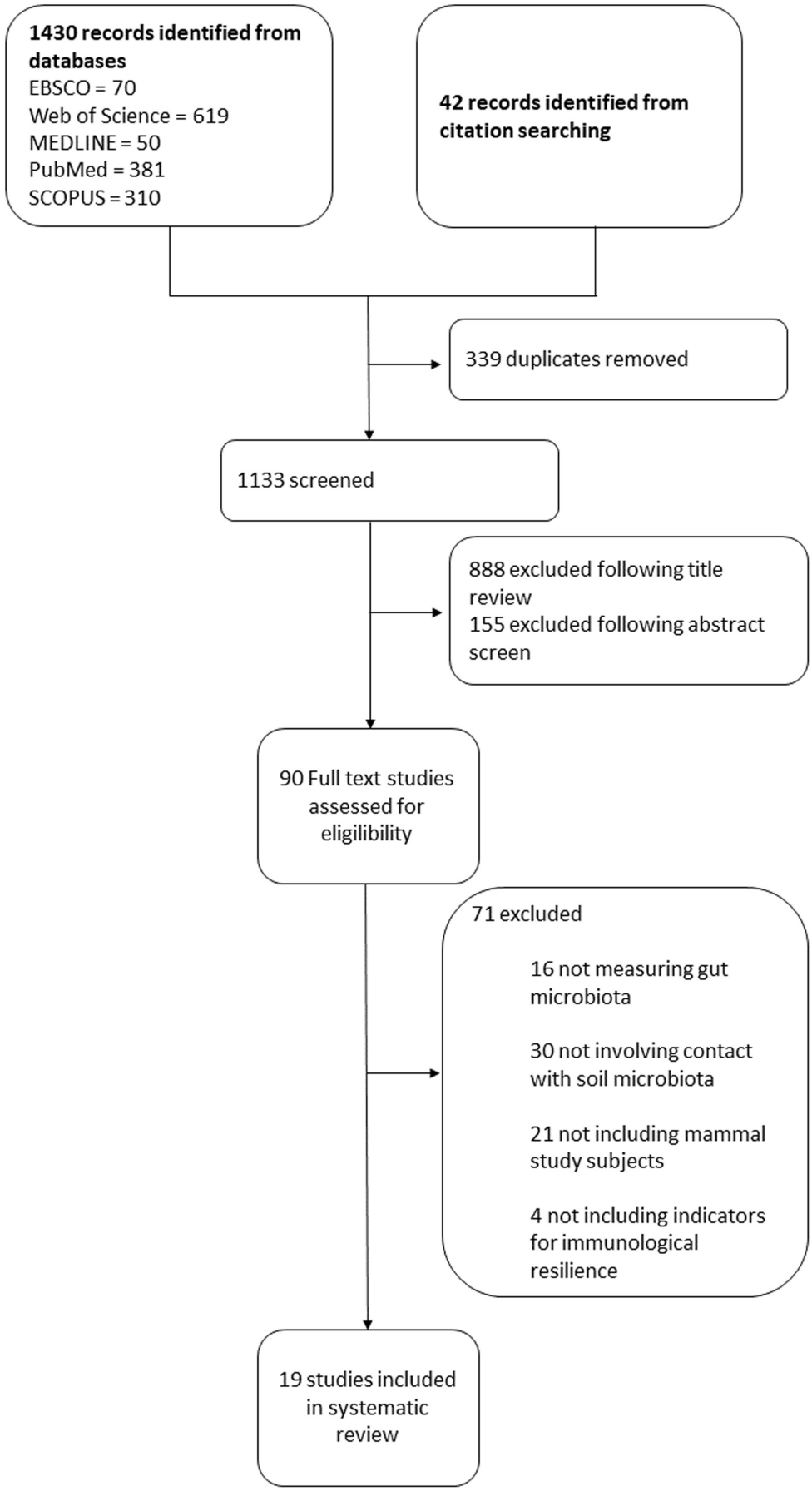

FIGURE 1 Flow chart showing the literature search and selection process.

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review identified only one human intervention study with adults in which a standardized and microbially rich soil-bound cocktail of live soil microbes was most likely transferred to the gastrointestinal system of the study subjects (Nurminen et al., 2018). This intervention study with controls included 14 study participants, seven per treatment group. The volunteers in the intervention arm rubbed their hands three times a day in microbially highly diverse soil: just before breakfast, dinner and before going to bed. Participants were instructed to rub the material for 20 s. They did not wash their hands with soap but rinsed their hands with tap water for 5 s and enjoyed a meal or went to sleep. According to Nurminen et al. (2018), soil exposure was associated with an increase in gut microbial diversity, which in turn was associated with an increase in transforming growth factor-β1 (TGF-β1) in peripheral blood mononuclear cells at the end of the exposure period (Nurminen et al., 2018).

Another recent cohort study revealed differences in the gut microbiota of gardening and non-gardening families (Brown et al., 2022). The study included 10 gardening families (30 study subjects) and nine non-gardening families (27 study subjects) that served as a control group. Each participating family included two adults and one child (5–18 years old). Although each family had one primary gardener, soil-derived bacteria were also observed in the gut microbiota of other members of the gardening family. In the gardening season, the gardening families had higher gut microbial diversity and richness, higher fibre intake and greater abundance of fibre fermenting bacteria compared to the control group (Brown et al., 2022).

An intervention trial among children showed that exposure to biodiverse soil microorganisms in daycare yards was associated with the Ruminococcaceae community and *Faecalibacterium* in the gut was associated with higher levels of anti-inflammatory interleukin (IL)-10 in plasma (Roslund et al., 2020). The study included 75 children in three different groups of daycare centres: biodiversity intervention ($n = 36$ children), standard urban ($n = 16$) and nature-oriented daycares ($n = 23$). In the biodiversity intervention daycares, the yards were modified with forest soil, transferable lawns and planters filled with commercial gardening soil. Roslund et al. (2020) also observed that the introduction of biodiversity at daycare yards was associated with a higher ratio of IL-10 to pro-inflammatory IL-17A and TGF-β level in plasma and higher frequencies of regulatory *T* (T_{reg}) $CD4^+$ cells.

In support of Roslund et al. (2020), a recent placebo-controlled double-blind intervention trial among daycare children observed a similar change in IL-10 levels and the ratio of IL-10 to IL-17A. The change was positive in the biodiversity intervention arm compared to the placebo arm (Roslund et al., 2022). In this placebo-controlled trial, daycare children received sandbox sand enriched with organic soil rich in microbes or visually similar sand enriched with peat with low microbial richness (13 study participants per treatment group). The study revealed several associations between gut bacteria and immune markers during a 14-day intervention period (Table 1). The study started with a 2-week supervision during which 3- to 5-year-old children received guidance to interact with the sandbox sand. The supervised period was followed by a non-guided period of 2 weeks and there were no significant differences in the gut microbiota after the 28-day intervention (Roslund et al., 2022). At the end of the supervised period (day 14), gut proteobacterial diversity was lower among children in the intervention arm compared to the placebo arm, but no longer on day 28 (Roslund et al., 2022). In parallel with changes in cytokines, T_{reg} cell frequencies were associated with soil exposure in the two daycare intervention trials by Roslund et al. (2020, 2022).

3.2 | Animal studies

Six studies have been conducted using murine models to investigate the effect of soil microorganisms on gut microbiome and host health (Table 2). Most studies focus on bacteria, while one study revealed that soil eating is also associated with gut fungal community (Borruso et al., 2021). Two murine model studies focused on soil-derived *Mycobacterium vaccae* strain (Foxx et al., 2021; Reber et al., 2016). Three experiments searched for the effect of the entire soil microbiome on mouse gut microbiome and immune modulation (González-Rodríguez et al., 2022; Ottman et al., 2019; Zhou et al., 2016) and one to anxiety-like behaviour (Liddicoat et al., 2020). One of the studies collected topsoil from the environment (Zhou et al., 2016) and another study used soil dust (Liddicoat et al., 2020). Two mouse experiments used commercially available fertilized peat-based soil products (González-Rodríguez et al., 2022; Ottman et al., 2019). In one of them, the soil product had been inoculated with cultured Bacillus strains, but the actual existence of the strains was not monitored (Ottman et al., 2019). In the other, the highly diverse microbial soil was inactivated before introducing material to mice (González-Rodríguez et al., 2022).

González-Rodríguez et al. (2022) powdered and inactivated a microbially diverse mixture of commercially available soils. They showed that heat-inactivated soil powder stabilizes the gut microbiome of mice and decreases the pro-inflammatory cytokines IL-17F and IL-21 in serum. Additionally, splenocytes off mice treated with soil powder expressed less IL-1b, IL-5, IL-6, IL-13 and tumour necrosis factor (TNF) after cell activation compared to control mice without soil exposure (González-Rodríguez et al., 2022).

Using a murine asthma model, Ottman et al. (2019) observed that exposure to non-inactivated soil polarizes the immune system towards Th1 and a higher level of anti-inflammatory signalling, alleviating Th2- type allergic responses. The expression of IL-10, forkhead box P3 and cytotoxic T lymphocyte-associated protein 4 was upregulated in the mouse intestinal exposed to live soil compared to control group (Ottman et al., 2019). Furthermore, soil exposure changed the mouse gut microbiota towards a higher Bacteroidetes to Firmicutes ratio (Ottman et al., 2019). Zhou et al. (2016) made a similar observation that mice exposed to soil had more Bacteroidetes and less Firmicutes in the gut compared to mice living in a sterile pathogen-free animal room without soil contact. These phyla were also associated with total serum IgE levels and liver/body weight ratios that were higher in mice living under sterile conditions compared to mice

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TABLE 1 Summary of human intervention studies on the effect of soil microorganisms on the gut microbiota and indicators of immunological resilience.

Reference	Type of study	Intervention/exposure	Summary of results on gut microbiota	Indicators of immunological resilience
Nurminen et al. (2018)	Intervention control trial with soil-derived microbiota	The volunteers in the intervention group rubbed their hands with soil three times a day for a 2-week period: before breakfast, dinner and going to bed	Exposure was associated with an increase in gut bacterial diversity	The change in bacterial diversity both on skin and in stool was associated with the level of TGF-β expression
Brown et al. (2022)	Observational case-controlled cohort study among gardening and non-gardening families	Gut and soil samples, and diet history questionnaires were collected before and after the gardening season, and Healthy Eating Index (HEI-2015) scores and nutrient analysis were performed	Soil-derived bacteria were detected in the gut of 87% of gardeners. Gardening families had higher bacterial Faith's Phylogenetic Diversity and higher abundances of fibre-fermenting bacteria and relative abundances of Alphaproteobacteria, *Bacteroides ovatus*, *Eubacterium xylanophilum group* spp. and unclassified taxa compared to non-gardening families in the gardening season	Not direct indicators of immunological resilience. Gardening families had greater fibre intake, and higher self-reported intake of vitamin C and K, selenium and iron than non-gardening families during the gardening season, which can confound the gut microbiota results and affect immunological resilience
Roslund et al. (2020)	Intervention control trial in which urban environmental biodiversity was manipulated to examine its effects on commensal microbiota and immunoregulation among 3- to 5-year-old daycare children	The study included three treatments: intervention, standard urban (negative control), and nature-oriented daycares (positive control). Intervention daycare yards were modified with forest floor vegetation, sod and planting boxes. The intervention lasted 28 days	Exposure to microbial biodiversity affected the gut Ruminococcaceae community (including *Faecalibacterium*) community during the 28-day intervention	Plasma IL-10:IL-17A ratio increased among intervention children during the trial. A higher relative abundance of *Faecalibacterium prausnitzii* in the gut was associated with lower levels of IL-17A. The intervention diversified the gammaproteobacterial communities on the skin, which, in turn, were associated with increases in plasma TGF-β1 levels and the proportion of T_{reg} cells
Roslund et al. (2022)	Placebo-controlled double-blinded trial among daycare children	In the intervention group, children aged 3 to 5 years were exposed to playground sand enriched with microbially diverse soil ($n = 13$), or in the placebo group, visually similar, but microbially poor sand coloured with peat ($n = 13$). The research assistant organized activities twice a day for 20 min in the sandbox for 14 days. Bacterial changes were followed for 28 days	Gut proteobacterial diversity was lower among children exposed to enriched sand on day 14, but not anymore on day 28	The mean change in plasma IL-10 concentration and IL-10:IL-17A ratio supported immunoregulation in intervention treatment compared to placebo treatment. The Firmicutes to Bacteroidetes ratio in the gut was inversely associated, and the relative abundance of genus *Bacteroides* was directly associated with the IL-10 level. The change in the relative abundances of gut *Faecalibacterium* and *Roseburia* was directly associated, while the change in the relative abundance of *Romboutsia* was inversely associated with the change in the level of IL-10. Skin bacteria, Thermoactinomycetaceae 1, was associated with the higher proportion of total and memory T_{reg} cells

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TABLE 2 Summary of mammalian animal models that investigated the effect of soil eating on gut microbiota, immunological resilience and host health.

Reference	Type of study	Intervention/exposure	Summary of results on gut microbiota	Summary of results on immune markers and health
González-Rodríguez et al. (2022)	Intervention-control mouse study with inactivated soil material	The intervention group (8 mice) was exposed for 1 h to 50 mL of inactivated commercial soil on top of clean bedding. Exposure was repeated five consecutive days per week for 3 weeks. Control mice (8 mice) were kept in a new cage with clean bedding for 1 h	The gut microbial diversity and relative abundance of Proteobacteria and Deferribacteres were higher in the soil-exposed group compared to the control group after a week of soil exposure, but the difference levelled off after 3 weeks of exposure	Decreased level of pro-inflammatory cytokines IL-17F and IL-21 in the serum. Splenocytes expressed less IL-1b, IL-5, IL-6, IL-13 and tumour necrosis factor (TNF) after cell activation
Ottman et al. (2019)	Murine asthma model with commercial soil	BALB/c mice were housed on clean bedding ($n = 16$) or with the addition of 300 mL of soil ($n = 16$). After 6 weeks of contact with soil or clean bedding, 8 mice in each housing condition were exposed to the murine asthma model protocol	A higher proportion of Bacteroidetes relative to Firmicutes in the soil-exposed group compared to the control group	Exposure to soil polarizes the immune system towards Th1 and a higher level of anti-inflammatory signalling, alleviating Th2-type allergic responses. Upregulation of the immunoregulatory markers IL-10, forkhead box P3, cytotoxic T lymphocyte-associated protein 4
Zhou et al. (2016)	Comparative study between mice under three distinct environmental conditions with allergen sensitization assessment	BALB/c mice were housed under sterile grade pathogen-free conditions, or two soil-exposure conditions (animal room and a farm). The cage bedding in the animal room and farm was composed of decaying plants and local topsoil. Allergen sensitization was assessed by measuring total serum IgE levels after administration of 2-4-dinitrofluoro-benzene	A higher proportion of Bacteroidetes and a lower proportion of Firmicutes in the soil-exposed groups compared to sterile-grade group. Gut microbial diversity and richness were higher in the soil-exposed group compared to the sterile-grade group. Soil exposure also changed the gut microbiota at the genus level	The soil-exposed groups had lower levels of IgE and liver/body weight ratios that were associated with Bacteroidetes and Firmicutes in the gut
Liddicoat et al. (2020)	Comparative mouse study between high and low biodiversity soils and no soil exposure with anxiety-like behaviour assessments	Pathogen-free BALB/c mice were housed for 7 weeks in cages with 1.75 kg soil with high microbial diversity, low microbial diversity or no soil contact ($n = 18$ per treatment group)	The soil-derived anaerobic spore-forming butyrate producer, *Kineothrix alysoides*, was supplemented to a greater extent in the gut microbiomes of high biodiversity-treated mice	The increasing relative abundance of *Kineothrix alysoides* was correlated with reduced anxiety-like behaviour in anxious mice
Reber et al. (2016)	Murine model of chronic psychosocial stress with heat-killed soil-derived *Mycobacterium vaccae*	Male C57BL/6NCrl mice were immunized with *Mycobacterium vaccae* ($n = 97$) or vehicle injections ($n = 66$) during the 2-week period. Stress coping behaviour was evaluated with 2 h of chronic exposure of subordinate colony housing stressors on days 1, 8 and 15 after the *M. vaccae* immunization	Changes in the gut microbiota were observed; however, the stress-protective effects appear to be independent of changes in the diversity or community structure of the gut microbiota	Depletion of regulatory T cells negated the protective effects of immunization with *M. vaccae* on stress-induced colitis and anxiety-like or fear behaviours

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TABLE 2 (Continued)

Reference	Type of study	Intervention/exposure	Summary of results on gut microbiota	Summary of results on immune markers and health
Foxx et al. (2021)	Mouse cohort study with heat-killed soil-derived *Mycobacterium vaccae* in a 'two hit' stress exposure model	Seven consecutive cohorts of male C57BL/6NCrl mice ($n = 112$) were immunized with *M. vaccae* or borate buffered saline vehicle. Stress was assessed with the chronic disturbance of the rhythms model followed by acute social defeat. All mice were exposed to object location memory testing for 24 h	*M. vaccae* stabilized the gut microbiome, attenuating stress-induced reductions in alpha diversity and decreasing within-group measures of beta diversity	The results indicate that *M. vaccae* promotes resilience to stress and increases cognitive performance
Borruso et al. (2021)	Observational study of the links between soil eating, soil characteristics and gut mycobiome of lemur (*Indri indri*)	Gut mycobiome samples ($n = 9$) were obtained from indris (faecal material) and geophagic soils ($n = 7$) from Maromizaha forest (Madagascar). Indris has been the subject of ongoing ecological studies since 2009	Several same genera were found in soil and lemurs' faeces, including *Fusarium*, *Aspergillus*, *Penicillium*, *Apiotrichum*, *Ganoderma*, *Mortierella*, *Metarhizium*, *Tolypocladium* and *Chaetosphaeria*	The soil eaten by the lemur resulted in enriched secondary oxide-hydroxides and clays, together with a high concentration of specific essential micronutrients
Vo et al. (2017)	Intervention-control trial with soil-exposed piglets	Piglets from 20 litters were assigned to be in the control group ($n = 50$) or daily exposed to topsoil ($n = 50$) from 4 days post-partum (day 0) to the end of lactation (day 17). The control pigs were managed conventionally and the intervention group had approximately 1 kg of topsoil in flat containers in crates for the pigs	Soil exposure increased gut microbial diversity and decreased the abundance of potentially harmful bacteria. The gut microbiota was enriched in plant-degrading genera, accelerating the adaptation to the plant-based diet	Soil exposure modulates the gut microbiota towards improved fermentative potential, correlating with better growth performance

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exposed to soil. This study compared three different environmental conditions: a pathogen-free animal room with sterile-grade bedding, a general animal room with topsoil from the university campus area and a farmhouse with topsoil from the farm (Zhou et al., 2016). The general animal room and farmhouse bedding also contained house dust and decaying plants. Mice exposed to soil, dust and decaying plants had greater diversity and richness of the gut microbiota compared to mice living in sterile conditions. Taxonomic differences at the genus level included a higher relative abundance of *Staphylococcus*, *Desulfovibrio* and *Brachybacterium* in the gut of farm mice, while mice living under sterile conditions had a higher relative abundance of *Lactobacillus* in the gut (Zhou et al., 2016).

Mouse studies have also shown that exposure to highly diverse soil dust can change the gut microbiota with potential mental health benefits (Liddicoat et al., 2020). Liddicoat et al. (2020) compared the gut microbiota and anxiety of mice exposed to soils of high and low diversity or no soil exposure (control) ($n = 18$ mice per treatment). The study showed that the relative abundance of soil-derived butyrate producer, *Kineothrix alysoides*, increased more in the gut among mice with high diversity soil treatment, and was associated with reduced anxiety (Liddicoat et al., 2020).

Two murine studies investigated the role of soil-derived saprophytic *Mycobacterium* in the gut microbiome, immune regulation and stress resilience (Foxx et al., 2021; Reber et al., 2016). These studies suggest that immunization with heat-killed *Mycobacterium vaccae* has the potential to stabilize the gut microbiome and promote stress resilience (Foxx et al., 2021; Reber et al., 2016).

Vo et al. (2017) investigated whether early exposure to soil affects gut microbiota maturation with a piglet model. Their results suggested beneficial modulation of the gut microbiota relevant to human children. The soil exposure group had greater gut microbial diversity, more bacterial taxa producing short-chain fatty acids (SCFA), and faster maturation of the gut microbiota compared to a control group with no soil contact (Vo et al., 2017). Changes in the gut microbiota after exposure to soil were accompanied by depletion in several potentially harmful bacterial taxa in the gut and the improved growth performance of piglets (Vo et al., 2017).

Borruso et al. (2021) investigated the links between soil eating, soil characteristics and the lemur (*Indri Indri*) gut mycobiome. The study demonstrated how soil eating modulates the gut fungal community, including saprotrophs and plant-associated fungal taxa, which may have health benefits. Approximately 9% of the fungal taxa were found in both soil and gut samples, including *Fusarium*, *Aspergillus* and *Penicillium*. Soil eating was also associated with the enrichment of essential micronutrients and secondary oxide-hydroxides, and clays, which could explain the role of soil in gut detoxification and as a nutrient supply (Borruso et al., 2021).

3.3 | How risky is to eat soil?

The risks of soil eating cover consuming hazardous compounds, such as heavy metals (Gao et al., 2017), polyaromatic hydrocarbons (PAHs, Roslund et al., 2019), microplastics (Lu et al., 2019) and drug residuals (Wei et al., 2016) and biological risks, particularly parasites (Rosa et al., 2018), pathogens (George et al., 2015) and antibiotic resistant genes (Forsberg et al., 2012; Table 3; Figure 2). In addition to direct health risks, toxicants can change the microbial composition of the gut that is associated with immune regulation, metabolic pathways and endocrine signalling (Gao et al., 2017; Lu et al., 2019; Roslund et al., 2019).

Heavy metals have several acute and chronic toxic effects, including nervous, gastrointestinal and immune system disorders, deleterious effects on the liver and kidney, birth effects and cancer. Mouse model study using multiomics approaches showed that oral intake of lead induces changes in the gut microbiota and disrupts metabolic pathways, such as vitamin E, bile acids, nitrogen metabolism, energy metabolism, oxidative stress and the defence/detoxification mechanism (Gao et al., 2017). PAHs are mutagenic and carcinogenic compounds with endocrine-disrupting properties that pose a serious threat to human health. Study in daycare environment showed that PAHs in ambient air and playground soils are associated with altered skin microbiota of daycare children (Roslund et al., 2019). Furthermore, PAHs may interfere with endocrine signalling by gut microbiota (Roslund et al., 2019).

Microplastics are emerging environmental pollutants that are widely spread in soil and water ecosystems (Lu et al., 2019). Soil contamination of microplastics poses a serious threat to terrestrial organisms, including the microbial community of the soil, and important ecosystem functions, such as the biodegradation of harmful toxicants (Lu et al., 2019). Microplastics in the soil may also end up in the human gut through food chain networks or other pathways (Lu et al., 2019). Microplastics may interact with the gut microbiota, thus causing gut microbiota dysbiosis, intestinal barrier dysfunction and disrupt metabolic pathways (Lu et al., 2019).

Drug residuals, such as antimicrobial veterinary drugs, can enter soils through animal manure fertilizers and persist long time in soils (Wei et al., 2016). Antimicrobial veterinary drugs are biologically active substances that may inhibit microbial growth or kill microbes. Veterinary drugs are often poorly absorbed in the animal's gut and therefore can accumulate in soils, particularly in the deeper soil layers 20–60 cm (Wei et al., 2016). The accumulation of antimicrobial drugs in soils can lead to increased antibiotic resistance in bacteria, fungi, virus and parasites (Forsberg et al., 2012). Antibiotic resistance may be transferred to humans, thereby reducing the effectiveness of antimicrobial drugs against human diseases. Antibiotic resistance of soil bacteria is problematic if genes are shared with clinically relevant human pathogens (Forsberg et al., 2012).

Biological risks of soil eating include pathogenic microbes and parasites such as soil-transmitted helminths and the enteric pathogen *Escherichia Coli* (George et al., 2015; Rosa et al., 2018). Soil eating can lead to diarrheagenic *E. coli* infection and increase the risk of stunting and environmental enteropathy that is a disorder defined by malformed intestinal morphology, diminished intestinal barrier function and increased inflammation (George et al., 2015). Soil-transmitted

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TABLE 3 Summary of risk factors associated with soil eating.

Reference	Type of study	Risk factor	Summary of results
Roslund et al. (2019)	Observational study analysing associations between soil microbiota of the daycare yard and PAH levels, and the skin and gut microbiota of children	Polyaromatic hydrocarbons (PAHs)	PAHs may have indirect health consequences through microbial changes PAHs may change the functional properties of the gut microbiota that are associated with endocrine disruption
Gao et al. (2017)	Mouse model study using multiomics approaches, including 16S rRNA sequencing, whole genome metagenomics sequencing and gas chromatography mass spectrometry (GC–MS) metabolomics	Heavy metals	Lead exposure altered the gut microbiome and affected metabolic functions. Numerous metabolic pathways, including vitamin E, bile acids, nitrogen metabolism, energy metabolism, oxidative stress, and the defence/detoxification mechanism, were significantly disturbed by lead exposure
Forsberg et al. (2012)	A metagenomic protocol to assemble short-read sequence data after antibiotic selection experiments, using 12 different drugs in all antibiotic classes, and compared antibiotic resistance gene sequences between soil bacteria and clinically occurring pathogens	Antibiotic resistant genes	Sixteen sequences, representing seven gene products, were discovered in farmland soil bacteria within long stretches of perfect nucleotide identity with pathogenic proteobacteria
Wei et al. (2016)	The occurrence of 13 veterinary drugs was studied in soil fertilized with animal manure in eastern China	Drug residuals	Results showed that drugs accumulate easily and persist in the deeper soil layers 20–60 cm. The residuals of drugs in the soil were related to the animal species from which the manure was derived
Lu et al. (2019)	Review of interactions between microplastics, microorganisms and the gut microbiota	Microplastics	Studies indicate that microplastics could enter the gut and interact with microorganisms
Rosa et al. (2018)	A cross-sectional analysis identified conserved microbial signatures positively or negatively associated with soil-transmitted helminth infections across Liberia and Indonesia	Parasites	12 bacterial taxa in the gut were significantly associated with helminth infection. These included *Olsenella* associated with reduced gut inflammation and significantly reduced abundance following clearance of infection. Arachidonic acid metabolism in the gut was associated with helminth infection. Arachidonic acid is the precursor for pro-inflammatory leukotrienes that threaten helminth survival. Gut Lachnospiraceae was negatively associated with helminth infection
George et al. (2015)	Prospective cohort study of 216 children under 5 years of age in rural Bangladesh investigated the relationship between exposure to enteric pathogens through soil consumption	Pathogenic microbes	*Escherichia coli* was observed in soil samples (97%) from the outdoor courtyard area where the children played and 14% had diarrheagenic *E. coli*. Soil eating in young children may be an important risk factor for environmental enteropathy and stunting

helminth infections could also lead to alterations in the gut microbiota, which in turn may have a further influence on the immune system and other health implications, such as reduced ability to extract nutrients from food (Rosa et al., 2018). These infections may reduce the abundance of beneficial gut bacteria, such as *Lachnospiraceae*, while increasing the abundance of *Olsenella* and *Allobaculum* that are associated with gut inflammation (Rosa et al., 2018). Furthermore, soil-transmitted infections can alter the functional pathways of the gut microbiota, for example, arachidonic acid metabolism pathway that is a precursor for pro-inflammatory leukotrienes, was increased in the gut of soil-transmitted helminths infected individuals (Rosa et al., 2018).

4 | DISCUSSION

To our knowledge, the current review is the first attempt to understand the immunological benefits and risks of eating soil. Based on comparative studies and non-oral intervention trials, the potential health benefits of soil microorganisms include gut homeostasis, immunological resilience, prevention of allergies and autoimmune diseases, as well as benefits for mental well-being (Figure 2).

Although extensive literature considers soil eating among indigenous people, none of the publications filled our inclusion criteria since they neither determined the associations between

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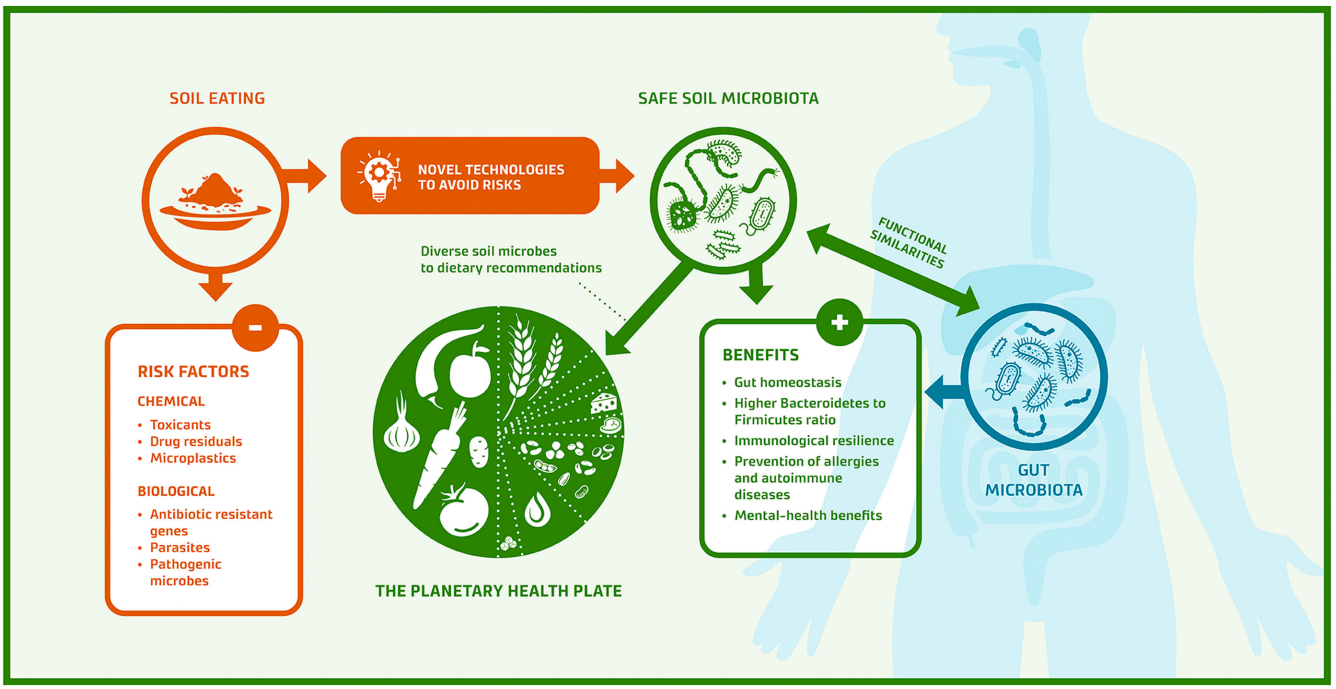

FIGURE 2 Graphical synthesis of results.

soil and gut microbial communities nor measured immunological resilience. Therefore, despite the apparently global interest on geophagy, clinical trials in which volunteers intentionally ingest microorganism-containing soil and gut microbiome and human health are monitored do not exist today. This points out to a remarkable research gap that needs to be filled to develop technologies that avoid the potential risks of soil eating. Despite this, the main findings of the currently available publications share characteristics that facilitate a basic understanding of the potential benefits and risks of geophagy. As the trials performed so far do not separate oral intake from effects via skin, further studies are needed to understand whether the immunological benefits are indeed a consequence of changes triggered by dirt on skin. Furthermore, it is not yet possible to state whether the benefits are widespread or restricted to species with an evolutionary history of soil eating. From the perspective of *Homo sapiens*, animal studies can serve as a model to investigate soil eating.

4.1 | Potential effects of soil microorganisms on gut microbiota composition and host immune regulation

Human intervention trials indicate that soil exposure enhances immunological tolerance for four reasons (Table 1). First, IL-10 is an anti-inflammatory cytokine and its blood levels reflect the activation of immunoregulatory pathways (Opal & DePalo, 2000). Second, TGF-β1 is a multifunctional cytokine that downregulates inflammatory processes in the gut-associated immune system (Opal & DePalo, 2000). Third, IL-17A is a pro-inflammatory cytokine that is associated with various immune-mediated diseases (Honkanen et al., 2010; Jin & Dong, 2013). Fourth, T_{reg} cells are essential regulators of the immune system, with important roles in maintaining self-tolerance and tolerance to the commensal microbiota, thus preventing autoimmune and chronic inflammatory diseases (Vignali et al., 2008).

Interestingly, three human intervention studies (Nurminen et al., 2018; Roslund et al., 2020, 2022) and three mouse studies (González-Rodríguez et al., 2022; Ottman et al., 2019; Zhou et al., 2016) had consistent results on how soil exposure affects immunological resilience. Additionally, the study by Vo et al. (2017) with piglets had consistent results with the human intervention trial with daycare children (Roslund et al., 2020) and with a comparative study with elderly people living in rural and urban environments (Parajuli et al., 2020). In detail, beneficial SCFA and butyrate producers, including Ruminococcaceae and *Faecalibacterium* genus, increased in the gut in soil exposure groups (Parajuli et al., 2020; Roslund et al., 2020; Vo et al., 2017). Importantly, butyrate has a crucial role in supporting immune tolerance and maintenance of the gut barrier (Parada Venegas et al., 2019). In the study by Roslund et al. (2020), the gut *Faecalibacterium* was also associated with higher levels of anti-inflammatory IL-10. The same association was found earlier by Sokol et al. (2008). Since Proteobacteria is a microbial signature of dysbiosis in gut microbiota (Pammi et al., 2017; Shin et al., 2015), the difference in gut Proteobacteria between the intervention and placebo arms in Roslund et al. (2022) may indicate that soil exposure balances gut microbial community. These results suggest that early exposure to various soil microbiota influences the maturation and homeostasis of the gut microbiota and potentially improves immunological resilience and overall health.

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The finding that soil exposure can shift the gut microbiota towards a higher Bacteroidetes to Firmicutes ratio (Ottman et al., 2019; Zhou et al., 2016) might be important since the higher Bacteroidetes to Firmicutes ratio is observed among lean people compared to obese people (Ley et al., 2006). However, the relative abundance of these phyla may vary between people for other reasons, and therefore, this ratio should not be considered as a hallmark of obesity (Magne et al., 2020). Zhou et al. (2016) showed that, in mice, a higher ratio of Bacteroidetes to Firmicutes is associated with lower levels of IgE and liver/body weight ratio, indicating that immunological resilience is related to the gut microbiota, which in turn was affected by soil exposure. Furthermore, the human intervention trial by Roslund et al. (2022) indicates that an increase in the Bacteroidetes to Firmicutes ratio is associated with higher levels of anti-inflammatory IL-10 in plasma.

In parallel with murine studies on consuming soil, a handful of in vivo studies with mice have investigated the role of soil-derived saprophytic *Mycobacterium* in health and immunological resilience (Foxx et al., 2021; Reber et al., 2016; Smith, 2020; Smith et al., 2019; Zuany-Amorim et al., 2002). The findings of these studies hint that soil bacteria are beneficial to mice; immunization with inactivated *Mycobacterium vaccae* had anti-inflammatory and immunoregulatory properties (Smith, 2020; Smith et al., 2019) and potential to stabilize gut microbiome and promote stress resilience (Foxx et al., 2021; Reber et al., 2016). Furthermore, inactivated *Mycobacterium vaccae* preparations prevented allergic airway inflammation in a murine model of allergic asthma (Zuany-Amorim et al., 2002). Since recent studies by González-Rodríguez et al. (2022) and Kummola et al. (2023) demonstrated the beneficial properties of inactivated soil material in in vivo settings, future attempts could substitute live soil consumption with inactivated material in oral studies.

4.2 | Challenges and research gaps related to soil eating

Although it was already known in the 19th century that immune tolerance may benefit from exposure to soil microorganisms (Graham-Rowe, 2011; Rook & Brunet, 2002; Strachan, 1989), there is no controlled human intervention trials that test the effect of soil eating on the human gut microbiome and immunological resilience. The reason may be in risks related to the biological and chemical characteristics of the soil (Figure 2). Soils may have traces of drugs, heavy metals, petroleum and PAH or other compounds that pose health risks (Cai et al., 2021; Cavazzoli et al., 2023; Gao et al., 2017; Lu et al., 2019; Roslund et al., 2019; Sinkkonen et al., 2013; Tan et al., 2022; Wei et al., 2016). Furthermore, the sensitivity, specificity and cost-effectiveness of molecular analytical technologies have partially limited soil-eating trials (Tan et al., 2018). However, today, technological advancements, followed by the completion of the Human Microbiome Project (The Human Microbiome Project Consortium, 2012) and comparative studies between patients with immune system disorders and healthy individuals (Brown et al., 2011; Hanski et al., 2012; Kondrashova et al., 2005; Nurminen et al., 2021; Stokholm et al., 2018; West et al., 2015), have extended the knowledge on the microbiota and its connections to human life and diseases.

Eggs of soil-transmitted helminths can remain viable in soil for several months, and these helminths contribute to malnutrition, iron deficiency anaemia and impaired cognitive performance (Savioli & Albonico, 2004). Besides potential risks, organisms such as helminths and environmental saprophytes have been recognized to be a crucial part of mammalian evolutionary history, and the so-called 'Old Friends' are thought to trigger normal functioning of the immune system (Elliott & Weinstock, 2012; Rook, 2009; Rook & Brunet, 2002). For example, products from helminth *Trichuris suis* promote Th2/Treg responses that dampen intestinal inflammation and have been proposed as therapy for Crohn's disease and ulcerative colitis (Summers, 2005).

Potential oral soil therapy has to overcome regional challenges as well; the use of antibiotics in animal farming has promoted natural selection for antibiotic resistance in farm soils (Wang et al., 2021). Human exposure to soil-borne antibiotic resistant genes has yet to be determined; a large cohort study on human gut microbiota revealed that human gut harbours more antibiotic resistance genes (0.26% of total human gut microbiome genes) compared to soil (farm soil: 0.05%, rainforest soil: 0.17% of total soil microbiome genes) (Hu et al., 2013). Because antibiotic resistance genes were naturally found in soil long before the discovery of antibiotics, it would be important to distinguish clinically relevant antibiotic resistant genes from those that do not confer resistance (Vasala et al., 2020; Wang et al., 2021).

Future studies and approaches should also take into account the dynamic and complex nature of soil. Soil-associated microbial feedstocks may be highly variable, including non-microbial organic material, partially decomposed microbial material, by-products of metabolism, inorganic compounds and minerals. These could provide additional effects on gut microbial homeostasis and immunological resilience. Soil consumption typically includes both microbes and their highly variable environmental feedstocks. In such mixtures, the complexity of interactions between microbes and with soil is high and there is a lack of knowledge about the functional roles of the different microbes in soil and in the gut. Therefore, the effects of soil consumption on gut microbial homeostasis and immunological resilience, for example, through prebiotics, nutrients and molecular patterns of immune signalling can be as complex as soil mixture and remain to be clarified. Therefore, future studies should consider the possibility of separate effects based on soil components, in addition to synergistic effects when soil components are combined. Most of the studies reviewed in this article used a metabarcoding approach, that is, 16S rRNA or ITS gene sequencing that targets only specific gene regions. To clarify the possible benefits of soil ingestion and obtain a more comprehensive understanding of the soil microbial community and its functional pathways and interactions, future studies should use metagenomic approaches, such as shotgun metagenomics, instead of metabarcoding that targets only specific gene regions.

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Since touching organic soil with high microbial richness reduces the relative abundance of pathogens on the skin and increases the diversity of Gammaproteobacteria, a class associated with a low risk of certain common non-communicable diseases (Grönroos et al., 2019; Hanski et al., 2012; Hui et al., 2019; Roslund et al., 2021), the richness and diversity of the soil microbial community have been used as an indicator of health-supporting microbial community. However, degraded urban environments with low microbial abundance may have high microbial diversity, simply because surviving species do not interact and compete. Therefore, it has been difficult to define what constitutes a beneficial and health-supporting microbial community. That is, are soil microbial diversity and richness important for immunological resilience or are there key taxonomies or functional groups that are important. Some studies have suggested that gammaproteobacterial diversity may play a special role in immunological resilience (Fyhrquist et al., 2014; Hanski et al., 2012; Riskumäki et al., 2021; Roslund et al., 2020). These studies demonstrated that environmental and soil biodiversity is directly associated with gammaproteobacterial genetic diversity on the skin, which in turn is associated with enhanced immune regulation (Roslund et al., 2020) and reduced risk of atopy and allergies (Fyhrquist et al., 2014; Hanski et al., 2012). Studies have also shown that certain gut bacteria play a special role in the development and maintenance of the gut homeostasis (Round & Mazmanian, 2009); however, for the immunological resilience, the detection of a wide spectrum of microbe-specific molecules and the discrimination between beneficial and pathogenic microbes is an important feature (Lee & Mazmanian, 2010). Therefore, it is likely that the high variety and richness of microbes in the soil activates a wide spectrum of pattern recognition receptors that play a fundamental role in the regulation of the immune system through the detection of microbe-specific molecules.

4.3 | Future approaches and limitations

As eating soil may create health benefits, there is an urgent need to research approaches and technologies suitable for large-scale use. These technologies must overcome the challenges discussed in this review. A potentially suitable approach is the sieving and careful mixing of various commercially composted soils, combined with careful selection and analysis of the raw materials (Hui et al., 2019; Nurminen et al., 2018; Roslund et al., 2022). This presumably aids in the even distribution of any potentially harmful biological agents. In case inactivation/sterilization of soil microbiota follows the thorough mixing, spores of potential pathogens, obliterated antibiotic resistance genes and other labile components will presumably be eliminated. The rationale in the first part of this approach is that after careful mixing and sieving, the frequency of potentially harmful agents is too low to cause an infection or toxification (Braciale et al., 2012; Paludan et al., 2021; Taylor & Latham, 2001). This finding facilitated human trials with homogenized soil that was shown safe for adults (Nurminen et al., 2018), 3- to 5-year-old children (Roslund et al., 2022) and ongoing trial with infants (Laiho et al., 2022). As stated earlier, these trials did not contain intentional soil eating.

Our review has two limitations. First, some studies may have been missed because we considered only English language publications. Second, to maximize our chances of screening all relevant studies, we used the general term 'Health'. Therefore, our search could have missed studies that focused specifically on immunology. However, specific immunological search terms would have been unlikely to produce additional studies, since the term 'health' covered all relevant immunological studies; we ensured that the use of specific immunological search terms, such as 'immune' and 'immunological' or other analogous search terms, would not have revealed additional studies, but rather irrelevant publications. Despite these two limitations, our review addressed an area of public health relevance. Based on available literature, exposure to the soil microbiota offers substantial promise for addressing a variety of health challenges, including immune disorders, obesity, depression and anxiety, which are public health priorities.

Sound science is essential to transfer geophagy from experimental research to everyday use. Although recent findings show how microbially live soil can be used to boost the immune system, an average citizen should not eat natural soil with unknown microbial, biochemical and physicochemical characteristics. Soils may have traces of inorganic particles, heavy metals, drug residuals, toxicants, pathogens, parasites, microplastics and antibiotic resistant genes, and all of these may have undesirable health effects. Therefore, it is not surprising that preventive oral treatments based on the soil microbiota do not exist today. In future clinical trials, it will be crucial to ensure safety while exposing humans to soil microbiota and to avoid chemical and biological risks associated with soil. If the results are in line with current findings, it might become realistic to consider soil-based microbiota as part of the planetary health plate. Before large-scale consumption of soil microbiota-based products, it will be necessary to satisfy the requirements of regulatory authorities, such as the European Food Safety Authority (EFSA) and the Food and Drug Administration (FDA) in the United States.

5 | CONCLUSIONS

Since more than 100 different immune-mediated diseases have been diagnosed so far and since they form the second highest cause of chronic illnesses, there is a huge unmet need for preventive approaches. As accumulating evidence supports the old friends, that is, the biodiversity hypothesis of immune-mediated diseases (Haahtela et al., 2021; Hanski et al., 2012; Rook & Lowry, 2022; Roslund et al., 2022), the benefits and trade-offs of consuming soil microbiota is a scientifically relevant research question. The available literature suggests that geophagy and the consumption of safe soil mixtures can provide immunological resilience. Importantly, clinical soil-eating trials are needed to test the prophylactic and anti-inflammatory potential of oral soil intake, and to understand the role

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of soil microbial assemblages in the gastrointestinal tract. The current scoping review encourages research initiatives to develop and investigate safe and diverse mixtures of soil microorganisms suitable for oral intake. Large clinical trials are necessary before soil microorganisms can be considered to the planetary health plate.

AUTHOR CONTRIBUTIONS

Marja I. Roslund designed and performed the review search, categorized reasons for exclusion and inclusions, analysed search results, wrote the manuscript, prepared the figures and tables and was the principal investigator of the project. Olli H. Laitinen checked a 20% sample of exclusion decisions and reviewed the manuscript. Aki Sinkkonen reviewed the manuscript and together with Marja I. Roslund performed a full-text screening and identified and categorized reasons for exclusion.

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CONFLICT OF INTEREST STATEMENT

Aki Sinkkonen and Olli H. Laitinen have been named inventors in a patent application 'immunomodulatory compositions' submitted by the University of Helsinki (Patent application number 20165932 at the Finnish Patent and Registration Office). Aki Sinkkonen and Marja I. Roslund have been named inventors in a patent application 'Immunomodulatory gardening and landscaping material' submitted by the University of Helsinki (Patent application number 20175196 at Finnish Patent and Registration Office). Aki Sinkkonen has received royalties from the European Patent Office patent originally submitted as FPRO 20165932. Aki Sinkkonen and Olli H. Laitinen are shareholders and board members of Uute scientific LtD that develops prophylactic treatments for topical use.

DATA AVAILABILITY STATEMENT

No original empirical data were used for this manuscript.

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