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食源性致病细菌在土壤中的生存策略及其治理方式

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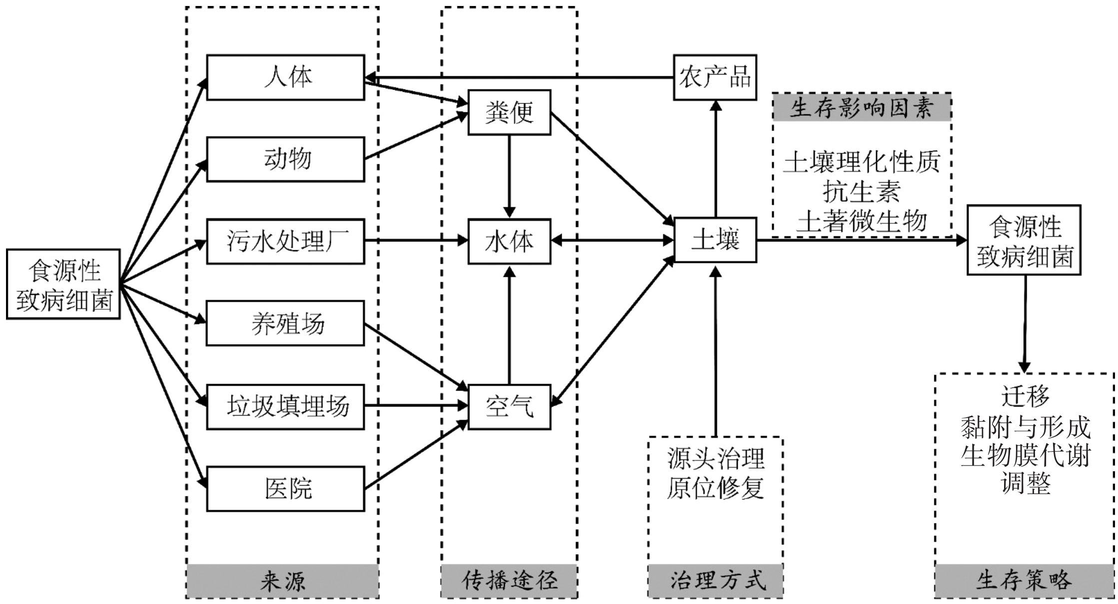

摘　要：土壤健康，特别是农业土壤的健康，与食品安全密切相关。然而，目前在土壤中已检出了大肠杆菌、肠沙门氏菌、单核增生李斯特氏菌等食源性致病细菌。某些食源性致病细菌能适应土壤中生物与非生物环境并可长期存活，其毒力基因与抗生素抗性基因可能会通过食物链传播，从而给土壤环境生物安全与消费者健康带来风险。本文综述了土壤中食源性致病细菌的主要来源及其生存策略，并介绍了源头治理和原位修复的方法。在此基础上，对土壤中食源性致病细菌治理的技术策略进行了展望，并从改善土壤化学环境和物理环境、切断传播途径、生物防治等方面讨论了未来研究重点关注的方向，以期为保障土壤健康和食品安全提供新思路。

关键词：土壤健康；食源性致病细菌；抗生素抗性；生物膜；微塑料

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Survival and decontamination strategies of food-borne bacterial pathogens in soil

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Abstract: Soil health, particularly agricultural soil health, is closely related to food safety. However, several food-borne bacterial pathogens, such as *Escherichia coli*, *Salmonella enterica*, and *Listeria monocytogenes*, have been detected in soil. Some bacterial pathogens have adapted to various biotic and abiotic environments to improve their survival in soil. Their virulence genes and antibiotic resistance genes may be transmitted via the food supply system, creating risks for both soil environmental biosafety and consumer health. In this review, we focused on the sources of food-borne bacterial pathogens in soil, factors that influence their survival, and decontamination technologies including source disinfestation and *in situ* remediation. Future studies are needed to evaluate pathogen decontamination technologies and strategies. Research directions are discussed from the perspectives of improving the soil′s chemical and physical environment, transmission blocking, and biocontrol to promote the development of methods for maintaining soil health and protecting food safety.

Keywords: soil health; food-borne bacterial pathogen; antibiotic resistance; biofilm; microplastic

食源性致病菌是一类可以引起食品腐败变质，并导致食源性疾病的微生物，主要包括细菌、真菌、病毒和寄生虫[1]。食源性致病菌是目前食源性疾病的主要诱因，其中由细菌引起的疾病占到了2/3[1]。这些食源性致病细菌会产生毒素，引起恶心、呕吐、腹痛、肠道功能菌群紊乱、腹泻、便血、败血症、菌血症等，甚至导致死亡，从而带来严重的健康风险[2-3]。动物及动物来源的食品，如肉制品、乳制品、蛋制品等，被认为是食源性致病细菌传播进入人体的主要途径[1-2]，另外，食源性致病细菌还存在于新鲜水果、蔬菜、饮用水、果汁等食品，以及土壤、空气等环境和动物粪便中，从而直接或间接通过食物链传播进入人体[2,4-6]。

作为一种重要的自然资源，土壤为人类活动提供了物理环境，为植物的生长提供了各种养分[7]。土壤中含有丰富的微生物资源，这些微生物参与了生物地球化学循环和土壤污染的生物修复，并且为人类提供了丰富的代谢物，如各种抗生素[8-10]。然而，由土壤微生物引起的人类疾病时有发生。一些土壤微生物会对人体健康造成伤害，导致球孢子菌病、真菌性脑膜炎等疾病；而一些食源性致病菌也可以在土壤中存活，并黏附到植物表面，进而通过食物链传播[11-12]。

目前，在城市土壤、农田土壤以及森林土壤中均发现了食源性致病细菌，且城市土壤中的食源性致病细菌浓度显著高于其他两种土壤[13]。土壤中含有包括单核增生李斯特氏菌（*Listeria monocytogenes*）、肠沙门氏菌（*Salmonella enterica*）、大肠杆菌（*Escherichia coli*）、空肠弯曲杆菌（*Campylobacter jejuni*）、肉毒梭菌（*Clostridium botulinum*）在内的多种食源性致病细菌[12,14]及其相关的毒力基因[15]。不仅在土壤表层，甚至在3 m的深层土壤中也发现有食源性致病细菌[16]。这些土壤中的食源性致病细菌可以通过直接接触传播到人体，也可以黏附到植物表面后进入植物内部[17-18]，或通过下雨溅起的水珠[19]、带菌灰尘[20]等方式到达植物地上部分，并随着这些农产品一起流入市场，造成疾病的暴发，危害人类健康。另外，土壤中的食源性致病细菌还可以进入地下水[21]，通过饮用水系统危害人体健康。随着“大健康”（One Health）概念的提出，土壤健康，特别是土壤中食源性致病细菌的治理，也成为了一个亟待研究的全球性课题[12]。

1　土壤中食源性致病细菌的主要来源

施用粪肥、灌溉等人类生产活动过程和降水等自然过程可以将动物粪便、水体、空气中的食源性致病细菌带入到土壤中，从而对环境生物安全及人体健康构成威胁。

施用粪肥能为植物的生长提供营养（如氮、磷、钾元素），增加土壤中的碳含量，中和酸性土壤，进而提高作物产量[5]。但人体肠道和动物肠道中含有大量的食源性致病细菌，这些食源性致病细菌会进入粪便，并通过施用粪肥直接进入土壤，或通过堆肥产品[5]间接进入土壤。食源性致病细菌在粪肥中的赋存情况不仅与来源有关，也与存放方式、禽畜年龄、饲料、季节等因素有关[5,22]。食源性致病细菌在粪便中的存活率具有菌种间差异，如：大肠杆菌和空肠弯曲杆菌的含量随存放时间的延长而降低，而单核增生李斯特氏菌的含量则比较稳定[23]；某些食源性致病细菌

在粪便中可存活5周以上[24]。因此,施用粪肥引起的食源性致病细菌感染时有发生[25]。尽管堆肥过程中会经历70 ℃以上的高温,但是在堆肥产品中依然能检测到残留的食源性致病细菌[26]。特别是在自然堆肥过程中,中心温度很高,但表面温度依然较低,这些食源性致病细菌仍然可以存活下来,然后进入农田土壤。另外,动物粪便中含有大量的抗生素及抗性基因[27],因此,动物粪便来源的有机肥产品可能成为抗生素污染和超级细菌的来源之一。

灌溉是农业生产中必不可少的环节。随着人口的增长,粮食需求越来越大,随之而来的是农业用水量的快速增长。灌溉用水的来源广泛,湖泊、河流、水库和地下水是常见水源[28]。近年来,由于缺水问题,污水经处理之后获得的再生水也被回用于农田,即再生水灌溉[29]。然而,这些灌溉水源中常含有食源性致病细菌[28,30-32]。在室温条件下,大肠杆菌可以在河水中存活60 d,沙门氏菌可以存活90 d,而在低温条件下能存活更长时间[33]。水体中的食源性致病细菌可以通过灌溉污染蔬菜,特别是贴地蔬菜,如生菜[34-35],而喷灌则可以将食源性致病细菌直接喷洒到植物地上部分[36]。食源性致病细菌在植物地上部分的存活时间可达20 d以上[37],给食物供应链相关人员和消费者带来了潜在风险。

空气污染也是土壤中食源性致病细菌的重要来源。空气中不仅含有$PM_{2.5}$、PM_{10}等颗粒物,二氧化硫(SO_2)等有害气体,而且还存在有大量的食源性致病细菌[6]。空气中的食源性致病细菌主要来源于某些环境,如鸡舍等养殖场、垃圾填埋场、医院[38-39]等,其可以通过降水进入土壤和水系[40],或通过风力传播到周围的环境中[41]。近年来新冠疫情的暴发,使食源性致病细菌在空气中的传播也受到了广泛关注。

食源性致病细菌通过上述途径进入土壤环境后的存活率差异较大。通过灌溉进入土壤的大肠杆菌能存活18 d以上[42],将污染牛粪添加到土壤,其中的大肠杆菌可以在土壤中存活56~70 d[25,43],沙门氏菌在土壤中可以存活75~77 d[24,43]。而在种植有萝卜或洋葱的土壤中,通过不同途径(粪肥或灌溉)进入土壤中的大肠杆菌的存活时间在154~196 d[44]。这些结果说明土壤中食源性致病细菌的存活率不仅受到了污染源的影响,而且也受到了其他环境因素的影响。

2 食源性致病细菌在土壤中生存的影响因素

食源性致病细菌在土壤中生存状况与存活时间受到多种非生物因素(如土壤理化性质与抗生素等)与生物因素(如微生物互作)的共同影响。

2.1 非生物因素

典型土壤理化性质(包括土壤质地类型、湿度、深度、电导率和有机质含量等),显著影响了食源性致病细菌在土壤中的存活率[14]。

土壤湿度会影响微生物的生长以及酶活性[45]。随着湿度的升高,土壤呼吸强度也呈现先升高后降低的趋势,其最适湿度为60%~70%持水量[46]。因此,合适的土壤湿度有助于食源性致病细菌的生存。土壤电导率代表了土壤中可溶性离子的浓度。电导率过高,说明土壤中离子浓度太高,渗透压过高,最终导致微生物细胞失水甚至裂解[47],食源性致病细菌的存活率下降[14]。

土壤中的有机质不仅可以为食源性致病细菌的生长提供营养[48],还可以作为食源性致病细菌在土壤中的黏附位点,较高的有机质含量可以促进其在土壤的存活[49]。在土壤中加入有机肥,也能提高食源性致病细菌的存活率[50]。另外,土壤中较高的总氮和水溶性碳含量促进了沙门氏菌和大肠杆菌等食源性致病细菌在土壤中的存活[51-52]。因此,土壤中的营养物质也是决定食源性致病细菌存活率的关键因素之一。BRENNAN等[53]的报道指出,在土壤中加入矿物质(蒙脱石、高岭石和伊利石)能提高食源性致病细菌的存活率。

土壤质地类型通过土壤颗粒大小的分布状况来表征。研究表明,食源性致病细菌在土壤中的存活时间与砂粒含量呈负相关,与黏粒/粉粒含量呈正相关[14,54-56]。土壤颗粒大小决定了土壤孔隙度,并且会影响气体(如氧气)在土壤中的扩散[57],而氧气含量会直接影响微生物的代谢和生长。另外,粒径越小的土壤颗粒比表面积越大,对土壤中水分的吸附作用越强,土壤中含水量越高[58],这也会影响到食源性致病细菌的生存。与砂土相比,黏土中凋落物降解速度较慢,因此土壤中有机质含量较高[59];土壤中有机碳的含量也与黏粒和粉粒的含量呈正相关,与环境温度呈负相关[60];而生物固氮效率与粉粒含量呈正相关,但与黏粒含量呈负相关[61]。因此,土壤质地类型通过影响其他土壤因素,间接影响了食源性致病细菌的存活率。

抗生素可以作用于DNA的复制、转录、蛋白质翻译、细胞壁合成、细胞膜合成等生物学过程,抑制细菌的生长或杀死细菌,在治疗感染中发挥了极其重要的作用[62]。土壤中的抗生素主要来自于含有粪便的有机肥[63]和灌溉水[64]。抗生素胁迫会导致抗性选择与敏感

细菌的死亡，促使抗性细菌及抗性基因的相对丰度升高，土壤微生物群落结构改变[65]，最终影响到生物地球化学循环[66]。抗生素抗性基因可以通过微生物从土壤中传播到蔬菜上[67]，在蔬菜上的抗生素抗性基因丰度甚至比土壤中高[68]。某些抗性基因在土壤中能存在2 a以上[69]，且这些抗性基因还能通过基因的水平转移[70-72]传播到其他土壤微生物乃至食源性致病细菌中，从而严重威胁到食品安全。目前在土壤中已经发现了能耐受多种抗生素的超级细菌[73]。

2.2 生物因素

微生物之间相互作用是影响食源性致病细菌在土壤中存活的因素之一。食源性致病细菌进入土壤中，可以视作一种"生物入侵"，土著微生物会对外源微生物的入侵产生一定的抵抗力[74]。研究发现，根际土著微生物能显著抑制食源性致病细菌的存活[75-76]。土壤中土著微生物多样性越高，食源性致病细菌的存活率越低[77-78]。进一步研究发现，多样性高的土壤，微生物对营养的竞争也更激烈，微生物的入侵则更加困难[79]。另外，微生物之间的竞争也可能会导致某些微生物的抑菌物质产量上升[80-81]，从而杀死入侵的食源性致病细菌。尽管如此，仍然在很多土壤中检测到食源性致病细菌，因此，土著微生物可以防止食源性致病细菌的大暴发，但不能完全杀死入侵的食源性致病细菌。

3 食源性致病细菌在土壤中的生存策略

3.1 被动迁移与主动迁移

食源性致病细菌在土壤中的迁移和扩散会扩大其生存环境，进而带来更严重的风险。真菌的生长方式为顶端生长，其菌丝可以在土壤中扩散，而细菌在土壤中的迁移分为被动迁移和主动迁移[82]。

食源性致病细菌可以借助水和风力在土壤中进行被动迁移。土壤中的食源性致病细菌可以沿灌溉水或雨水在土壤中进行水平方向和垂直方向的迁移。在含有食源性致病细菌的土壤上方空气中也含有大量的食源性致病细菌[83]，说明食源性致病细菌不仅可以通过空气进入土壤，也可以从土壤中进入空气。食源性致病细菌随气溶胶可以传播1 m左右[84]，而风力可以将食源性致病细菌传播到150 m以外的环境中[41]。

除了被动迁移，当土壤中含水量较高时，一些细菌可以借助鞭毛在水中游动；而当含水量不足时，鞭毛可以介导细菌沿真菌菌丝或植物根系在土壤中运动[82,85]。真菌菌丝表面可以形成一层水膜，辅助细菌的迁移[86]。革兰氏阴性菌的鞭毛由基体、钩形鞘和鞭毛丝3部分组成。鞭毛丝逆时针运动时，可以推动细菌细胞向前运动；顺时针运动时，可以拉动细菌细胞倒退运动[87]。鞭毛运动的方向主要由趋化性决定。一般来说，细菌的趋化性运动分为3步：(1)细胞膜上的趋化性受体蛋白识别环境中的信号，如根系分泌物；(2)信号通过信号转导途径，最终由CheY蛋白传递到鞭毛运动蛋白；(3)鞭毛调整运动方向[49,88]。细菌细胞内CheY的磷酸化和去磷酸化控制着鞭毛的运动方向，其磷酸化由CheA负责，而去磷酸化由CheZ负责[87-88]。沙门氏菌[49]、李斯特氏菌[89]也都有鞭毛结构和趋化性系统，也可能利用鞭毛在土壤中传播与扩散；在缺失鞭毛系统后，单增李斯特菌在土壤中的存活率显著下降[89]。

3.2 表面黏附与生物膜的形成

食源性致病细菌还可以通过表面黏附与生物膜形成提高存活率。例如：在与生菜叶片接触之后，单增李斯特菌可以迅速黏附到叶片表面[90]；沙门氏菌也可以黏附于苹果表面，形成生物膜[91]。生物膜的形成需要固体表面，如土壤颗粒[92]、根系[93]、菌丝[94]、塑料[95]及各种管道[96]的表面。特别是近年来，微塑料污染越来越严重，这些微塑料为食源性致病细菌生物膜的形成提供了大量的固体表面，因此带来了严重的健康风险[97-99]。生物膜的形成大致可分为3步，聚集与黏附、细菌生长和生物膜的成熟、解离[100]。在生物膜形成的过程中，细菌的运动能力下降[100]。胞外多糖可以促进细菌生物膜的形成，并且可以保护细菌免遭抗生素的攻击[101]，从而使食源性致病细菌的存活率提高。土壤中某些微生物甚至可以促进食源性致病细菌在植物根系的黏附[102]。生物膜中的微生物细胞相互紧密接触，为抗性基因的水平转移，特别是接合转移[103]，提供了便利条件，因此，生物膜还可以提高抗生素抗性基因的丰度[104-105]。

3.3 适应土壤环境的机制

研究发现，沙门氏菌在含有西红柿根系分泌物的培养基中，糖代谢相关的基因表达量显著提高[106]；而在含有生菜根系分泌物的培养基中，氨基酸合成相关的基因表达量提高最多[107]。李斯特菌在含有土壤提取物的培养基上，趋化性迁移相关基因和糖类转运蛋白的表达量显著提高[108]。因此，在进入土壤后，食源性致病细菌会响应周围的理化环境及生物环境，调整其基因的表达量和代谢途径的通量。

微生物对环境变化的响应需要双组分系统和转

录调控因子的参与。双组分系统由两部分组成：位于细胞膜的组氨酸激酶和位于胞内的应答调控蛋白。组氨酸激酶的胞外结构域可以感知环境信号的变化，然后催化胞内结构域中组氨酸的自磷酸化，该磷酸基团可以进一步转移到应答调控蛋白中保守的天冬氨酸残基上，而磷酸化的应答调控蛋白可以调控相关基因的表达[109]。单增李斯特菌中的双组分系统 LisRK[76]和 ArgA/ArgC[110]可以提高细菌在土壤中的存活率，而沙门氏菌中的 EnvZ/OmpR 系统可以提高细菌细胞在土壤颗粒表面的黏附[49]。转录调控因子 RpoS 参与了细菌对酸和渗透压等环境胁迫的耐受、毒力基因的表达、鞭毛蛋白的表达、抗生素的合成等多种生物学过程[111-112]。与野生型细菌相比，敲除 *rpoS* 基因的大肠杆菌和沙门氏菌在土壤中的存活率显著下降[51,113]。因此，通过双组分系统和转录调控因子对土壤环境进行快速响应，有助于食源性致病细菌在土壤中的生存。

4 土壤中食源性致病细菌的治理方式

土壤中食源性致病细菌的危害正受到人们的广泛关注，然而，其治理策略尚不成熟。目前对土壤中食源性致病细菌的治理，主要有源头治理和原位修复两种策略。

4.1 源头治理

堆肥、灌溉和空气污染是土壤中食源性致病细菌污染的主要来源。因此，对这些污染源进行治理，可以从源头上避免土壤中的食源性致病细菌污染。

如前所述，堆肥过程中的高温可以杀死一部分食源性致病细菌，但是依然会有食源性致病细菌的残留，因此需要进一步对堆肥工艺进行改进。有研究表明，在牛粪中加入米糠等有机废物进行堆肥，可以增加有机物含量，进而提高堆肥温度，提高对大肠杆菌的清除效率[114]。在碱性条件下，碳酸根阴离子和铵盐可以有效清除粪肥中的大肠杆菌和沙门氏菌[115]；而生防菌剂的应用，也能完全杀灭粪肥中的大肠杆菌[116]。一些表面活性剂，如鼠李糖脂和吐温80，也可以有效清除土壤中的抗生素抗性基因[117]。

水体中食源性致病细菌的治理，目前主要关注于污水处理。虽然活性污泥能清除污水中98%的食源性致病细菌[118]，紫外照射和臭氧也能使污水中的食源性致病细菌下降1.5~3.6个数量级[119]，但是依然会有残留。氯气[120]、巴比妥酸[121]、二氧化钛结合紫外照射[122]、生防细菌[123]、蚯蚓生物滤池[124]等方式均可以在一定程度上降低水体中的食源性致病细菌浓度，但是依然无法彻底消除隐患。相比之下，利用微藻进行污水处理，可以完全清除粪肠球菌和大肠杆菌[125]，而将噬菌体应用于污水处理，14 h之后即无法检测到水体中的大肠杆菌和伤寒沙门氏菌[126]，以上是两种非常高效的环境友好型污水处理方式。这些方法，也可以尝试引入到其他来源水体及对其他食源性致病细菌的处理中。另外，如前所述，沟灌可以将水中的食源性致病细菌转移到蔬菜的贴地叶面上[35]，喷灌可以将食源性致病细菌直接喷洒到植物地上部分[36]，而滴灌可以有效减少种植洋葱表面大肠杆菌的数量[127]。因此，改进耕作方式也可以减少食源性致病细菌的传播。

通风、紫外照射、过滤、二氧化钛结合光催化是室内空气杀菌的常用方法[84]，然而这些方法并不适用于室外空气的治理。空气中的食源性致病细菌来源于其他环境，因此，切断源头的传播，对养殖场、污水处理厂、垃圾处理厂等场所进行治理，是对空气中食源性致病细菌污染进行治理的最有效方法。

4.2 原位修复

4.2.1 传统方法

农田土壤不仅受到食源性致病细菌的污染，更重要的是会受到植物致病细菌的影响。因此，农业上经常利用化学法和物理法进行土壤消毒。前者会用到溴甲烷、威百亩、四氧化二氮等杀菌剂，采用熏蒸或灌溉的方式进入土壤；后者包括高温闷棚、蒸汽消毒。这些方法不仅能杀灭植物致病细菌，也能清除土壤中的食源性致病细菌污染[42,128]。然而，化学法用到的这些杀菌剂毒性较大、残留时间长，因此近年来逐渐被禁止使用；高温闷棚耗时较长，并且受到气候条件的影响；蒸汽消毒成本较高，因此也未能推广使用[128]。随着科技的发展，近年来兴起的一些环境友好型治理方式也有所报道，并取得了良好的效果。

4.2.2 生物炭

生物炭是生物质在无氧条件下经高温处理而获得的产品[129]。生物炭进入土壤后，能改变土壤的pH、元素组成、营养成分等土壤理化性质，进而影响微生物的生长代谢[129]。某些生物炭还可以促进大肠杆菌在土壤中的消亡[130]。进一步研究表明，生物炭可以吸附环境中的营养物质，从而抑制大肠杆菌的生长[131]；生物炭可以吸附环境中的游离DNA，从而抑制抗生素抗性基因的转化[132]。在生物炭表面加载铁离子，可以进一步提高其对食源性致病细菌的清除能

力[133]。另外，生物炭也可以导致食源性致病细菌ATP合成减少及细胞膜通透性降低，进而抑制抗生素抗性质粒的接合转移[134]。但也有研究表明，猪粪制成的生物炭能提高沙门氏菌在土壤中的存活率[135]；某些生物炭的添加也可能使部分抗生素抗性基因在土壤中的半衰期延长[69]；大肠杆菌能黏附于生物炭表面形成生物膜[131]，增加了杀灭难度。因此，需要进一步深入分析影响生物炭使用效果的因素，并优化生物炭的制作工艺，以期增强其对食源性致病细菌的清除效果。

4.2.3 新型生物材料

与传统的化学杀菌剂相比，新型生物材料毒性较小，是一种环境友好型产品。新型生物材料主要通过产生活性氧等途径抑制微生物活性。羟基磷灰石作为一种常见的无机改良剂，其载体已被广泛应用于空气、水体和土壤污染的治理[136]。大黄素是提取自中药的一种成分，具有多种生理功能，将其与羟基磷灰石载体合成大黄素-羟基磷灰石复合物，在光照条件下能产生活性氧，有效清除水体中的四环素和金黄色葡萄球菌[137]。生物炭表面加载钴作为一种新型生物材料，可以激活过硫酸氢盐，并进一步产生活性氧，30 min内即可清除粪肥中96.5%的环丙沙星[138]，从而可以减少土壤环境中的抗生素胁迫及抗性细菌的生长。因此，将这些新型生物材料应用于土壤中食源性致病细菌的治理，也具有良好的应用前景。

4.2.4 生物防治

生物防治近年来也受到了广泛关注。很多植物，特别是药用植物，可以产生抑菌物质，如禾本科香根草属 *Vetiveria zizanioides* 和 *Vetiveria nigritana* 根部产生的基油可以有效抑制革兰氏阳性食源性致病细菌的生长[139]，湖北旋覆花（*Inula hupehensis*）根部提取的麝香草酚衍生物可以抑制金黄色葡萄球菌和大肠杆菌的生长[140]，石竹科肥皂草属植物 *Saponaria cypria* 产生的皂苷和酚类化合物可以抑制大肠杆菌、金黄色葡萄球菌、粪肠球菌和肠炎沙门氏菌的生长[141]。而且一些植物的根系内生菌也会产生抑菌物质，如禾本科金须茅属 *Chrysopogon zizanioides* 根系内生的枯草芽孢杆菌可以抑制大肠杆菌的生长[142]。将这些植物应用于生物修复，可以清除土壤中的食源性致病细菌。例如，在种植有新西兰植物 *Metrosideros robusta* 的土壤中，14 d后大肠杆菌数量下降了90%[143]。

某些土壤生物，如植物根系、细菌、真菌产生的挥发性抑菌物质可以扩散到空气中，从而可以在大尺度上杀灭食源性致病细菌。这些生物应用于土壤生物熏蒸，可以代替化学熏蒸[128,144]。强还原土壤灭菌也是目前应用较多的土壤消毒方法。该方法是在土壤中添加易分解有机物后立即进行灌溉，然后覆盖塑料薄膜，从而创造出还原状态，以利于这些有机物的厌氧分解，在此过程中，氧气含量减少，好氧菌生长受到抑制，厌氧菌快速生长。厌氧条件下还可以发酵产生有机酸等对食源性致病细菌有致死作用的物质[145-146]，从而杀灭食源性致病细菌。

5 总结与展望

目前，土壤中食源性致病细菌带来的潜在风险已经受到了广泛的关注。污水与人体或动物肠道中的食源性致病细菌可以通过施用粪肥、灌溉、降水等多种方式进入土壤，影响环境生物安全，并可以通过食物链危害消费者的健康。土壤理化性质、抗生素、土著微生物的多样性、食源性致病细菌的迁移能力、生物膜形成能力等多种环境因素及生物因素均会影响食源性致病细菌在土壤中的存活率，进而决定了其带来的风险程度。然而，影响食源性致病细菌在土壤中存活率的分子机制尚待深入研究。

土壤中食源性致病细菌的清除与治理是保障食品安全的重要环节。虽然多种源头治理和原位修复方法可以应用于土壤中食源性致病细菌的清除，但其实际应用效果仍有待进一步验证。下一步应该从以下几个方面加强对食源性致病细菌治理方式与技术策略的关注与研究：

（1）生物膜可以促进食源性致病细菌在土壤中的存活。土壤化学环境如何影响食源性致病细菌生物膜的形成，如何改善土壤化学环境，进而干预乃至抑制食源性致病细菌生物膜的形成值得深入研究。

（2）食源性致病细菌可以黏附于微塑料、管道等人造物体表面形成生物膜。如何改进这些材料及清除土壤中的微塑料污染，改善土壤物理环境，从而防止食源性致病细菌生物膜的形成，成为一个亟待解决的重大科学技术问题。

（3）食源性致病细菌可以在食品-水源-土壤-空气等环境中传播，其在大尺度空间的迁移规律尚不明确，加强源头治理、切断传播途径的治理方式值得进一步研究。

（4）生防细菌、噬菌体已经应用于堆肥和污水中食源性致病细菌的清除，而生防细菌、生防真菌也已经应用于土壤中植物致病细菌的防治。生防菌剂是否可以应用于土壤中食源性致病细菌的治理，如何提

高生防菌剂的治理效果，需要进一步探索。

参考文献：

[1] ABEBE E, GUGSA G, AHMED M. Review on major food-borne zoonotic bacterial pathogens[J]. *Journal of Tropical Medicine*, 2020:1-19.

[2] HEREDIA N, GARCIA S. Animals as sources of food-borne pathogens: A review[J]. *Animal Nutrition*, 2018, 4(3):250-255.

[3] SARAVANAN A, KUMAR P S, HEMAVATHY R V, et al. Methods of detection of food-borne pathogens: A review[J]. *Environmental Chemistry Letters*, 2021, 19(1):189-207.

[4] YOON J H, LEE S Y. Review: Comparison of the effectiveness of decontaminating strategies for fresh fruits and vegetables and related limitations[J]. *Critical Reviews in Food Science and Nutrition*, 2018, 58(18):3189-3208.

[5] BLACK Z, BALTA I, BLACK L, et al. The fate of foodborne pathogens in manure treated soil[J]. *Frontiers in Microbiology*, 2021, 12:781357.

[6] MA Q X, QI Y, SHAN Q L, et al. Understanding the knowledge gaps between air pollution controls and health impacts including pathogen epidemic[J]. *Environmental Research*, 2020, 189:109949.

[7] 李奕赞, 张江周, 贾吉玉, 等. 农田土壤生态系统多功能性研究进展[J]. 土壤学报, 2022, 59(5):1177-1189. LI Y Z, ZHANG J Z, JIA J Y, et al. Research progresses on farmland soil ecosystem multifunctionality[J]. *Acta Pedologica Sinica*, 2022, 59(5):1177-1189.

[8] 朱永官, 彭静静, 韦中, 等. 土壤微生物组与土壤健康[J]. 中国科学：生命科学, 2021, 51(1):1-11. ZHU Y G, PENG J J, WEI Z, et al. Linking the soil microbiome to soil health[J]. *Scientia Sinica Vitae*, 2021, 51(1):1-11.

[9] NAZARI M T, MACHADO B S, MARCHEZI G, et al. Use of soil actinomycetes for pharmaceutical, food, agricultural, and environmental purposes[J]. *3 Biotech*, 2022, 12(9):232.

[10] SOKOL N W, SLESSAREV E, MARSCHMANN G L, et al. Life and death in the soil microbiome: How ecological processes influence biogeochemistry[J]. *Nature Reviews Microbiology*, 2022, 20(7):415-430.

[11] BANERJEE S, VAN DER HEIJDEN M. Soil microbiomes and one health[J]. *Nature Reviews Microbiology*, 2022.

[12] SAMADDAR S, KARP D S, SCHMIDT R, et al. Role of soil in the regulation of human and plant pathogens: Soils' contributions to people[J]. *Philosophical Transactions of the Royal Society B-Biological Sciences*, 2021, 376(1834):20200179.

[13] GERKEN T, WIEGNER T N, ECONOMY L M. A comparison of soil *Staphylococcus aureus* and fecal indicator bacteria concentrations across land uses in a Hawaiian watershed[J]. *Journal of Environmental Quality*, 2022, 51(5):916-929.

[14] PIVETEAU P, DRUILHE C, AISSANI L. What on earth? The impact of digestates and composts from farm effluent management on fluxes of foodborne pathogens in agricultural lands[J]. *Science of the Total Environment*, 2022, 840:156693.

[15] SU Y F, LIU S, DONG Q, et al. Tracking virulence genes and their interaction with antibiotic resistome during manure fertilization[J]. *Environmental Pollution*, 2022, 840:156693.

[16] PONGMALA K, PIERRET A, OLIVA P, et al. Distribution of *Burkholderia pseudomallei* within a 300-cm deep soil profile: Implications for environmental sampling[J]. *Scientific Reports*, 2022, 12:8674.

[17] STANDING T A, DU PLESSIS E, DUVENAGE S, et al. Internalisation potential of *Escherichia coli* O157:H7, *Listeria monocytogenes*, *Salmonella enterica* subsp. *enterica* serovar Typhimurium and *Staphylococcus aureus* in lettuce seedlings and mature plants[J]. *Journal of Water and Health*, 2013, 11(2):210-223.

[18] BURRIS K P, SIMMONS O D, WEBB H M, et al. Colonization and internalization of *Salmonella enterica* and its prevalence in cucumber plants[J]. *Frontiers in Microbiology*, 2020, 11:1135.

[19] LEE D, TERTULIANO M, HARRIS C, et al. *Salmonella* survival in soil and transfer onto produce via splash events[J]. *Journal of Food Protection*, 2019, 82(12):2023-2037.

[20] KUMAR G D, WILLIAMS R C, AL QUBLAN H M, et al. Airborne soil particulates as vehicles for *Salmonella* contamination of tomatoes[J]. *International Journal of Food Microbiology*, 2017, 243:90-95.

[21] ALEGBELEYE O O, SANT'ANA A S. Manure-borne pathogens as an important source of water contamination: An update on the dynamics of pathogen survival/transport as well as practical risk mitigation strategies[J]. *International Journal of Hygiene and Environmental Health*, 2020, 227:113524.

[22] HUTCHISON M L, WALTERS L D, AVERY S M, et al. Analyses of livestock production, waste storage, and pathogen levels and prevalences in farm manures[J]. *Applied and Environmental Microbiology*, 2005, 71(3):1231-1236.

[23] KLEIN M, BROWN L, TUCKER R W, et al. Diversity and abundance of zoonotic pathogens and indicators in manures of feedlot cattle in Australia[J]. *Applied and Environmental Microbiology*, 2010, 76(20):6947-6950.

[24] YOU Y, RANKIN S C, ACETO H W, et al. Survival of *Salmonella enterica* serovar Newport in manure and manure-amended soils[J]. *Applied and Environmental Microbiology*, 2006, 72(9):5777-5783.

[25] MUKHERJEE A, CHO S, SCHEFTEL J, et al. Soil survival of *Escherichia coli* O157:H7 acquired by a child from garden soil recently fertilized with cattle manure[J]. *Journal of Applied Microbiology*, 2006, 101(2):429-436.

[26] GURTLER J B, DOYLE M P, ERICKSON M C, et al. Composting to inactivate foodborne pathogens for crop soil application: A review[J]. *Journal of Food Protection*, 2018, 81(11):1821-1837.

[27] WANG G Y, LI G X, CHANG J L, et al. Enrichment of antibiotic resistance genes after sheep manure aerobic heap composting[J]. *Bioresource Technology*, 2021, 323:124620.

[28] GARTLEY S, ANDERSON-COUGHLIN B, SHARMA M, et al. *Listeria monocytogenes* in irrigation water: An assessment of outbreaks, sources, prevalence, and persistence[J]. *Microorganisms*, 2022, 10(7):1319.

[29] LYU S D, WU L S, WEN X F, et al. Effects of reclaimed wastewater irrigation on soil-crop systems in China: A review[J]. *Science of the Total Environment*, 2022, 813:152531.

[30] KOCZURA R, MOKRACKA J, BARCZAK A, et al. Association between the presence of class 1 integrons, virulence genes, and phyloge-

netic groups of *Escherichia coli* isolates from river water[J]. *Microbial Ecology*, 2013, 65(1): 84–90.

[31] GU G Y, STRAWN L K, OTTESEN A R, et al. Correlation of *Salmonella enterica* and *Listeria monocytogenes* in irrigation water to environmental factors, fecal indicators, and bacterial communities[J]. *Frontiers in Microbiology*, 2021, 11: 557289.

[32] RASEALA C M, EKWANZALA M D, MOMBA M. Multilocus–based phylogenetic analysis of extended–spectrum beta–lactamase *Escherichia coli* O157: H7 uncovers related strains between agriculture and nearby water sources[J]. *Journal of Infection and Public Health*, 2020, 13(12): 1899–1906.

[33] IBRAHIM E, EL–LIETHY M A, ABIA A, et al. Survival of *E. coli* O157: H7, *Salmonella* Typhimurium, HAdV2 and MNV–1 in river water under dark conditions and varying storage temperatures[J]. *Science of the Total Environment*, 2019, 648: 1297–1304.

[34] STEELE M, ODUMERU J. Irrigation water as source of foodborne pathogens on fruit and vegetables[J]. *Journal of Food Protection*, 2004, 67(12): 2839–2849.

[35] OLIVEIRA M, USALL J, VINAS I, et al. Transfer of *Listeria innocua* from contaminated compost and irrigation water to lettuce leaves[J]. *Food Microbiology*, 2011, 28(3): 590–596.

[36] KISLUK G, YARON S. Presence and persistence of *Salmonella enterica* serotype Typhimurium in the phyllosphere and rhizosphere of spray–irrigated parsley[J]. *Applied and Environmental Microbiology*, 2012, 78(11): 4030–4036.

[37] ERICKSON M C, LIAO J Y, PAYTON A S, et al. Survival of *Salmonella enterica* and *Escherichia coli* O157: H7 sprayed onto the foliage of field–grown cabbage plants[J]. *Journal of Food Protection*, 2019, 82(3): 479–485.

[38] LAI K M, EMBERLIN J, COLBECK I. Outdoor environments and human pathogens in air[J]. *Environmental Health*, 2009, 8: S15.

[39] FACCIOLA A, PELLICANO G F, VISALLI G, et al. The role of the hospital environment in the healthcare–associated infections: A general review of the literature[J]. *European Review for Medical and Pharmacological Sciences*, 2019, 23(3): 1266–1278.

[40] KAUSHIK R, BALASUBRAMANIAN R, DE LA CRUZ A A. Influence of air quality on the composition of microbial pathogens in fresh rainwater[J]. *Applied and Environmental Microbiology*, 2012, 78(8): 2813–2818.

[41] BAI H, HE L Y, WU D L, et al. Spread of airborne antibiotic resistance from animal farms to the environment: Dispersal pattern and exposure risk[J]. *Environment International*, 2022, 158: 106927.

[42] IBEKWE A M, GRIEVE C M, YANG C H. Survival of *Escherichia coli* O157: H7 in soil and on lettuce after soil fumigation[J]. *Canadian Journal of Microbiology*, 2007, 53(5): 623–635.

[43] ONGENG D, MUYANJA C, GEERAERD A H, et al. Survival of *Escherichia coli* O157: H7 and *Salmonella enterica* serovar Typhimurium in manure and manure–amended soil under tropical climatic conditions in Sub–Saharan Africa[J]. *Journal of Applied Microbiology*, 2011, 110(4): 1007–1022.

[44] ISLAM M, DOYLE M P, PHATAK S C, et al. Survival of *Escherichia coli* O157: H7 in soil and on carrots and onions grown in fields treated with contaminated manure composts or irrigation water[J]. *Food Microbiology*, 2005, 22(1): 63–70.

[45] BOROWIK A, WYSZKOWSKA J. Soil moisture as a factor affecting the microbiological and biochemical activity of soil[J]. *Plant, Soil and Environment*, 2016, 64: 250–255.

[46] YAN N, MARSCHNER P. Previous water content influences the response of soil respiration to changes in water content in non–saline and saline soils[J]. *Biology and Fertility of Soils*, 2014, 50(7): 1129–1140.

[47] YAN N, MARSCHNER P, CAO W, et al. Influence of salinity and water content on soil microorganisms[J]. *International Soil and Water Conservation Research*, 2015, 3(4): 316–323.

[48] ZHANG T, HU S, YANG W. Variations of *Escherichia coli* O157: H7 survival in purple soils[J]. *International Journal of Environmental Research and Public Health*, 2017, 14(10): 1246.

[49] KARMAKAR K, NAIR A V, CHANDRASEKHARAN G, et al. Rhizospheric life of *Salmonella* requires flagella–driven motility and EPS–mediated attachment to organic matter and enables cross–Kingdom invasion[J]. *FEMS Microbiology Ecology*, 2019, 95(8): fiz107.

[50] YAO Z Y, YANG L, WANG H Z, et al. Fate of *Escherichia coli* O157: H7 in agricultural soils amended with different organic fertilizers[J]. *Journal of Hazardous Materials*, 2015, 296: 30–36.

[51] SHAH M K, BRADSHAW R, NYARKO E, et al. *Salmonella enterica* in soils amended with heat–treated poultry pellets survived longer than bacteria in unamended soils and more readily transferred to and persisted on spinach[J]. *Applied and Environmental Microbiology*, 2019, 85(10): e00334–19.

[52] MA J, IBEKWE A M, CROWLEY D E, et al. Persistence of *Escherichia coli* O157: H7 in major leafy green producing soils[J]. *Environmental Science & Technology*, 2012, 46(21): 12154–12161.

[53] BRENNAN F P, MOYNIHAN E, GRIFFITHS B S, et al. Clay mineral type effect on bacterial enteropathogen survival in soil[J]. *Science of the Total Environment*, 2014, 468: 302–305.

[54] WANG H, ZHANG T, WEI G, et al. Survival of *Escherichia coli* O157: H7 in soils under different land use types[J]. *Environmental Science and Pollution Research International*, 2014, 21(1): 518–524.

[55] WANG H Z, WEI G, YAO Z Y, et al. Response of *Escherichia coli* O157: H7 survival to pH of cultivated soils[J]. *Journal of Soils and Sediments*, 2014, 14(11): 1841–1849.

[56] HAN Z M, HUANG G N, LIAO J F, et al. Disentangling survival of *Escherichia coli* O157: H7 in soils: From a subpopulation perspective[J]. *Science of the Total Environment*, 2020, 749: 141649.

[57] NEIRA J, ORTIZ M, MORALES L, et al. Oxygen diffusion in soils: Understanding the factors and processes needed for modeling[J]. *Chilean Journal of Agricultural Research*, 2015, 75(Suppl 1): 35–44.

[58] CHEN C, ARTHUR E, TULLER M, et al. Estimation of soil specific surface area from adsorbed soil water content[J]. *European Journal of Soil Science*, 2020, 72(4): 1718–1725.

[59] ANGST G, POKORNÝ J, MUELLER C W, et al. Soil texture affects the coupling of litter decomposition and soil organic matter formation

[J]. *Soil Biology and Biochemistry*, 2021, 159:108302.

[60] ZHANG Y, LI P, LIU X, et al. The response of soil organic carbon to climate and soil texture in China[J]. *Frontiers of Earth Science*, 2022.

[61] YANG Z, CHEN X, HOU J, et al. Soil texture and pH exhibit important effects on biological nitrogen fixation in paddy soil[J]. *Applied Soil Ecology*, 2022, 178:104571.

[62] CYLKE C, SI F W, BANERJEE S. Effects of antibiotics on bacterial cell morphology and their physiological origins[J]. *Biochemical Society Transactions*, 2022, 50(5):1269-1279.

[63] LI J J, XIN Z H, ZHANG Y Z, et al. Long-term manure application increased the levels of antibiotics and antibiotic resistance genes in a greenhouse soil[J]. *Applied Soil Ecology*, 2017, 121:193-200.

[64] PAN M, CHU L M. Occurrence of antibiotics and antibiotic resistance genes in soils from wastewater irrigation areas in the Pearl River Delta region, southern China[J]. *Science of the Total Environment*, 2018, 624:145-152.

[65] ZHAO L, PAN Z, SUN B, et al. Responses of soil microbial communities to concentration gradients of antibiotic residues in typical greenhouse vegetable soils[J]. *Science of the Total Environment*, 2022, 855:158587.

[66] SEMEDO M, SONG B, SPARRER T, et al. Antibiotic effects on microbial communities responsible for denitrification and N_2O production in grassland soils[J]. *Frontiers in Microbiology*, 2018, 9:2121.

[67] WANG F, SUN R, HU H, et al. The overlap of soil and vegetable microbes drives the transfer of antibiotic resistance genes from manure-amended soil to vegetables[J]. *Science of the Total Environment*, 2022, 828:154463.

[68] KEENUM I, WIND L, RAY P, et al. Metagenomic tracking of antibiotic resistance genes through a pre-harvest vegetable production system: An integrated lab-, microcosm-, and greenhouse-scale study[J]. *Environmental Microbiology*, 2022, 24(8):3705-3721.

[69] HE L, HE L, GAO F, et al. Dissipation of antibiotic resistance genes in manure-amended agricultural soil[J]. *Science of the Total Environment*, 2021, 787:147582.

[70] GARBISU C, GARAIYURREBASO O, LANZÉN A, et al. Mobile genetic elements and antibiotic resistance in mine soil amended with organic wastes[J]. *Science of the Total Environment*, 2018, 621:725-733.

[71] MENG M, LI Y, YAO H. Plasmid-mediated transfer of antibiotic resistance genes in soil[J]. *Antibiotics(Basel)*, 2022, 11(4):525.

[72] ZHANG Y, GUO Y, QIU T, et al. Bacteriophages: Underestimated vehicles of antibiotic resistance genes in the soil[J]. *Frontiers in Microbiology*, 2022, 13:936267.

[73] SURESH S, ADITYA V, DEEKSHIT V K, et al. A rare occurrence of multidrug-resistant environmental *Acinetobacter baumannii* strains from the soil of Mangaluru, India[J]. *Archives of Microbiology*, 2022, 204(7):422.

[74] MALLON C A, ELSAS J D V, SALLES J F. Microbial invasions: The process, patterns, and mechanisms[J]. *Trends in Microbiology*, 2015, 23(11):719-729.

[75] SHARMA R, GAL L, GARMYN D, et al. Plant growth promoting bacterial consortium induces shifts in indigenous soil bacterial communities and controls *Listeria monocytogenes* in rhizospheres of *Cajanus cajan* and *Festuca arundinacea*[J]. *Microbial Ecology*, 2022, 84(1):106-121.

[76] BRUNHEDE M Z, DOS SANTOS P T, GAL L, et al. LisRK is required for optimal fitness of *Listeria monocytogenes* in soil[J]. *FEMS Microbiology Letters*, 2020, 367(22):fnaa188.

[77] VAN ELSAS J D, CHIURAZZI M, MALLON C A, et al. Microbial diversity determines the invasion of soil by a bacterial pathogen[J]. *Proceedings of the National Academy of Sciences of the United States of America*, 2012, 109(4):1159-1164.

[78] SCHIERSTAEDT J, JECHALKE S, NESME J, et al. *Salmonella* persistence in soil depends on reciprocal interactions with indigenous microorganisms[J]. *Environmental Microbiology*, 2020, 22(7):2639-2652.

[79] MALLON C A, POLY F, LE ROUX X, et al. Resource pulses can alleviate the biodiversity-invasion relationship in soil microbial communities[J]. *Ecology*, 2015, 96(4):915-926.

[80] WESTHOFF S, KLOOSTERMAN A M, VAN HOESEL S F A, et al. Competition sensing changes antibiotic production in *Streptomyces*[J]. *mBio*, 2021, 12(1):e02729-20.

[81] LEE N, KIM W, CHUNG J, et al. Iron competition triggers antibiotic biosynthesis in *Streptomyces coelicolor* during coculture with *Myxococcus xanthus*[J]. *The ISME Journal*, 2020, 14(5):1111-1124.

[82] YANG P, VAN ELSAS J D. Mechanisms and ecological implications of the movement of bacteria in soil[J]. *Applied Soil Ecology*, 2018, 129:112-120.

[83] THIEL N, MUNCH S, BEHRENS W, et al. Airborne bacterial emission fluxes from manure-fertilized agricultural soil[J]. *Microbial Biotechnology*, 2020, 13(5):1631-1647.

[84] AHMADI Y, BHARDWAJ N, KIM K H, et al. Recent advances in photocatalytic removal of airborne pathogens in air[J]. *Science of the Total Environment*, 2021, 794:148477.

[85] YANG P, CALIXTO R, VAN ELSAS J D. Migration of *Paraburkholderia terrae* BS001 along old fungal hyphae in soil at various pH levels[J]. *Microbial Ecology*, 2018, 76(2):443-452.

[86] FURUNO S, PAZOLT K, RABE C, et al. Fungal mycelia allow chemotactic dispersal of polycyclic aromatic hydrocarbon-degrading bacteria in water-unsaturated systems[J]. *Environmental Microbiology*, 2010, 12(6):1391-1398.

[87] ARONEY S, POOLE P S, SANCHEZ-CANIZARES C. Rhizobial chemotaxis and motility systems at work in the soil[J]. *Frontiers in Plant Science*, 2021, 12:725338.

[88] SAMPEDRO I, PARALES R E, KRELL T, et al. *Pseudomonas* chemotaxis[J]. *FEMS Microbiology Reviews*, 2015, 39(1):17-46.

[89] MCLAUGHLIN H P, CASEY P G, COTTER J, et al. Factors affecting survival of *Listeria monocytogenes* and *Listeria innocua* in soil samples[J]. *Archives of Microbiology*, 2011, 193(11):775-785.

[90] KYERE E O, FOONG G, PALMER J, et al. Rapid attachment of *Listeria monocytogenes* to hydroponic and soil grown lettuce leaves[J]. *Food Control*, 2019, 101:77-80.

[91] GONZALEZ-LOPEZ C, MARTINEZ-PENICHE R A, ITURRIAGA M H, et al. Attachment and colonization of *Salmonella* on 'Rayada', 'Golden Delicious', and 'Red Delicious' apples[J]. *Journal of the Science of Food and Agriculture*, 2019, 99(3):1166-1171.

[92] KIM Y M, KWON T H. Entrapment of clay particles enhances durability of bacterial biofilm-associated bioclogging in sand[J]. *Acta Geotechnica*, 2022, 17(1):119-129.

[93] ZHANG H, QIAN Y Y, FAN D N, et al. Biofilm formed by *Hansschlegelia zhihuaiae* S113 on root surface mitigates the toxicity of bensulfuron-methyl residues to maize[J]. *Environmental Pollution*, 2022, 292:118366.

[94] GUENNOC C M, ROSE C, LABBE J, et al. Bacterial biofilm formation on the hyphae of ectomycorrhizal fungi: A widespread ability under controls?[J]. *FEMS Microbiology Ecology*, 2018, 94(7):fiy093.

[95] ARUTCHELVI J, JOSEPH C, DOBLE M. Process optimization for the production of rhamnolipid and formation of biofilm by *Pseudomonas aeruginosa* CPCL on polypropylene[J]. *Biochemical Engineering Journal*, 2011, 56(1/2):37-45.

[96] LIU B, SUN M H, LU F Y, et al. Study of biofilm-influenced corrosion on X80 pipeline steel by a nitrate-reducing bacterium, *Bacillus cereus*, in artificial Beijing soil[J]. *Colloids and Surfaces B-Biointerfaces*, 2021, 197:111356.

[97] CHEN Y, WANG X B, WANG X L, et al. Biofilm structural and functional features on microplastic surfaces in greenhouse agricultural soil [J]. *Sustainability*, 2022, 14(12):7024.

[98] YANG K, CHEN Q L, CHEN M L, et al. Temporal dynamics of antibiotic resistome in the plastisphere during microbial colonization[J]. *Environmental Science & Technology*, 2020, 54(18):11322-11332.

[99] ZHU D, MA J, LI G, et al. Soil plastispheres as hotspots of antibiotic resistance genes and potential pathogens[J]. *The ISME Journal*, 2022, 16(2):521-532.

[100] SAUER K, STOODLEY P, GOERES D M, et al. The biofilm life cycle: Expanding the conceptual model of biofilm formation[J]. *Nature Reviews Microbiology*, 2022, 20(10):608-620.

[101] LIMOLI D, JONES C, WOZNIAK D. Bacterial extracellular polysaccharides in biofilm formation and function[J]. *Microbiology Spectrum*, 2015, 3(3):223-247.

[102] SCHOENBORN A A, CLAPPER H, ECKSHTAIN-LEVI N, et al. Rhizobacteria impact colonization of *Listeria monocytogenes* on *Arabidopsis thaliana* roots[J]. *Applied and Environmental Microbiology*, 2021, 87(23):e0141121.

[103] WU S, WU Y C, CAO B, et al. An invisible workforce in soil: The neglected role of soil biofilms in conjugative transfer of antibiotic resistance genes[J]. *Critical Reviews in Environmental Science and Technology*, 2022, 52(15):2720-2748.

[104] LOISEAU C, SORCI G. Can microplastics facilitate the emergence of infectious diseases? [J]. *Science of the Total Environment*, 2022, 823:153694.

[105] YANG Y, LI T, LIU P, et al. The formation of specific bacterial communities contributes to the enrichment of antibiotic resistance genes in the soil plastisphere[J]. *Journal of Hazardous Materials*, 2022, 436:129247.

[106] ZARKANI A A, SCHIERSTAEDT J, BECKER M, et al. *Salmonella* adapts to plants and their environment during colonization of tomatoes[J]. *FEMS Microbiology Ecology*, 2019, 95(11):103833.

[107] JECHALKE S, SCHIERSTAEDT J, BECKER M, et al. *Salmonella* establishment in agricultural soil and colonization of crop plants depend on soil type and plant species[J]. *Frontiers in Microbiology*, 2019, 10:967.

[108] VIVANT A L, DESNEUX J, POURCHER A M, et al. Transcriptomic analysis of the adaptation of *Listeria monocytogenes* to lagoon and soil matrices associated with a piggery environment: Comparison of expression profiles[J]. *Frontiers in Microbiology*, 2017, 8:1811.

[109] PAPON N, STOCK A M. Two-component systems[J]. *Current Biology*, 2019, 29(15):R724-R725.

[110] VIVANT A L, GARMYN D, GAL L, et al. The Agr communication system provides a benefit to the populations of *Listeria monocytogenes* in soil[J]. *Frontiers in Cellular and Infection Microbiology*, 2014, 4:160.

[111] SCHELLHORN H E. Function, evolution, and composition of the RpoS regulon in *Escherichia coli*[J]. *Frontiers in Microbiology*, 2020, 11:560099.

[112] 李珅瑀. 5-8对稻瘟病菌的抑制作用及生防细菌FD6中*rpoS*对抗生素合成调控机制[D]. 扬州:扬州大学, 2021:41-42. LI S Y. Inhibitory effect of 5-8 on rice blast and regulation mechanism of *rpoS* on antibiotic synthesis in biocontrol bacterium FD6[D]. Yangzhou: Yangzhou University, 2021:41-42.

[113] DETERT K, SCHMIDT H. Survival of enterohemorrhagic *Escherichia coli* O104:H4 Strain C227/11fcu in agricultural soils depends on *rpoS* and environmental factors[J]. *Pathogens*, 2021, 10(11):1443.

[114] HANAJIMA D, KURODA K, FUKUMOTO Y, et al. Effect of addition of organic waste on reduction of *Escherichia coli* during cattle feces composting under high-moisture condition[J]. *Bioresource Technology*, 2006, 97(14):1626-1630.

[115] PARK G W, DIEZ-GONZALEZ F. Utilization of carbonate and ammonia-based treatments to eliminate *Escherichia coli* O157:H7 and *Salmonella* Typhimurium DT104 from cattle manure[J]. *Journal of Applied Microbiology*, 2003, 94(4):675-685.

[116] LIU G X, ALLY N M, DOOLY D D, et al. A study on the effectiveness of a defined microbial consortium to enhance the microbiological safety of cattle manure[J]. *Journal of the Science of Food and Agriculture*, 2021, 101(6):2614-2620.

[117] ZHANG Y J, LI H C, GU J, et al. Effects of adding different surfactants on antibiotic resistance genes and intI1 during chicken manure composting[J]. *Bioresource Technology*, 2016, 219:545-551.

[118] LI B, JU F, CAI L, et al. Profile and fate of bacterial pathogens in sewage treatment plants revealed by high-throughput metagenomic approach[J]. *Environmental Science & Technology*, 2015, 49(17): 10492-10502.

[119] TONDERA K, KLAER K, GEBHARDT J, et al. Reducing pathogens in combined sewer overflows using ozonation or UV irradiation[J]. *International Journal of Hygiene and Environmental Health*, 2015,

218(8):731-741.
[120] TANG M, LAU S. Strategy to evaluate changes in bacterial community profiles and bacterial pathogen load reduction after sewage disinfection[J]. *Frontiers in Microbiology*, 2022, 13:919207.
[121] TONDERA K, KLAER K, KOCH C, et al. Reducing pathogens in combined sewer overflows using performic acid[J]. *International Journal of Hygiene and Environmental Health*, 2016, 219:700-708.
[122] WANG H B, JIA P P, DING N, et al. Photocatalytical deactivation of pathogens for municipal wastewater reusing[J]. *Water, Air, and Soil Pollution*, 2015, 226(10):333.
[123] GAIKWAD G L, GUPTA P, WATE S R. Bio-control of waterborne pathogens using *Lactobacillus* spp. [J]. *Environmental Monitoring and Assessment*, 2012, 184(11):6627-6635.
[124] ARORA S, KAZMI A A. Reactor performance and pathogen removal during wastewater treatment by vermifiltration[J]. *Journal of Water Sanitation and Hygiene for Development*, 2016, 6(1):65-73.
[125] DELANKA-PEDIGE H, MUNASINGHE-ARACHCHIGE S P, CORNELIUS J, et al. Pathogen reduction in an algal-based wastewater treatment system employing *Galdieria sulphuraria*[J]. *Algal Research*, 2019, 39:101423.
[126] PERIASAMY D, SUNDARAM A. A novel approach for pathogen reduction in wastewater treatment[J]. *Journal of Environmental Health Science and Engineering*, 2013, 11:12.
[127] MOYNE A L, WAITE-CUSIC J, HARRIS L J. Water application method influences survival or growth of *Escherichia coli* on bulb onions during field curing[J]. *Journal of Food Protection*, 2022, 85(6):961-972.
[128] GURTLER J B. Pathogen decontamination of food crop soil: A review [J]. *Journal of Food Protection*, 2017, 80(9):1461-1470.
[129] TAN S M, NARAYANAN M, HUONG D, et al. A perspective on the interaction between biochar and soil microbes: A way to regain soil eminence[J]. *Environmental Research*, 2022, 214:113832.
[130] GURTLER J B, BOATENG A A, HAN Y X, et al. Inactivation of *E. coli* O157:H7 in cultivable soil by fast and slow pyrolysis-generated biochar[J]. *Foodborne Pathogens and Disease*, 2014, 11(3):215-223.
[131] HILL R A, HUNT J, SANDERS E, et al. Effect of biochar on microbial growth: A metabolomics and bacteriological investigation in *E. coil*[J]. *Environmental Science & Technology*, 2019, 53(5):2635-2646.
[132] FANG J, JIN L, MENG Q K, et al. Biochar effectively inhibits the horizontal transfer of antibiotic resistance genes via transformation [J]. *Journal of Hazardous Materials*, 2022, 423:127150.
[133] BOLSTER C H. Comparing unamended and Fe-coated biochar on removal efficiency of bacteria, microspheres, and dissolved phosphorus in sand filters[J]. *Biochar*, 2021, 3(3):329-338.
[134] WU Y J, YAN H C, ZHU X M, et al. Biochar effectively inhibits the horizontal transfer of antibiotic resistance genes via restraining the energy supply for conjugative plasmid transfer[J]. *Environmental Science & Technology*, 2022, 56(17):12573-12583.
[135] ZHANG T X, YU W, SHI Y Y, et al. Effects of biochar pyrolyzed at different temperatures on the survival of *Salmonella* in vegetable soils[J]. *Water, Air, and Soil Pollution*, 2020, 231(3):100.
[136] IBRAHIM M, LABAKI M, GIRAUDON J M, et al. Hydroxyapatite, a multifunctional material for air, water and soil pollution control: A review[J]. *Journal of Hazardous Materials*, 2020, 383:121139.
[137] ZHANG Y, WANG L J, LU L S, et al. Highly efficient decontamination of tetracycline and pathogen by a natural product-derived Emodin/HAp photocatalyst[J]. *Chemosphere*, 2022, 305:135401.
[138] LUO J M, BO S F, QIN Y N, et al. Transforming goat manure into surface-loaded cobalt/biochar as PMS activator for highly efficient ciprofloxacin degradation[J]. *Chemical Engineering Journal*, 2020, 395:125063.
[139] CHAMPAGNAT P, SIDIBE L, FORESTIER C, et al. Antimicrobial activity of essential oils from *Vetiveria nigritana* and *Vetiveria zizanioides* roots[J]. *Journal of Essential Oil Bearing Plants*, 2007, 10(6):519-524.
[140] ZHAO J, LI Y, LIU Q, et al. Antimicrobial activities of some thymol derivatives from the roots of *Inula hupehensis*[J]. *Food Chemistry*, 2010, 120(2):512-516.
[141] CHARALAMBOUS D, CHRISTOFOROU M, KITIRI E N, et al. Antimicrobial activities of *Saponaria cypria* Boiss. root extracts, and the identification of nine saponins and six phenolic compounds[J]. *Molecules*, 2022, 27(18):5812.
[142] MUNAKATA Y, HEUSON E, DABOUDET T, et al. Screening of antimicrobial activities and lipopeptide production of endophytic bacteria isolated from vetiver roots[J]. *Microorganisms*, 2022, 10(2):209.
[143] GUTIERREZ-GINES M J, ALIZADEH H, ALDERTON E, et al. Phytoremediation of microbial contamination in soil by New Zealand native plants[J]. *Applied Soil Ecology*, 2021, 167:104040.
[144] PENUELAS J, ASENSIO D, THOLL D, et al. Biogenic volatile emissions from the soil[J]. *Plant Cell and Environment*, 2014, 37(8):1866-1891.
[145] 蔡祖聪, 张金波, 黄新琦, 等. 强还原土壤灭菌防控作物土传病的应用研究[J]. 土壤学报, 2015, 52(3):469-476. CAI Z C, ZHANG J B, HUANG X Q, et al. Application of reductive soil disinfestation to suppress soil-borne pathogens[J]. *Acta Pedologica Sinica*, 2015, 52(3):469-476.
[146] LIU L L, HUANG X Q, ZHAO J, et al. Characterizing the key agents in a disease-suppressed soil managed by reductive soil disinfestation[J]. *Applied and Environmental Microbiology*, 2019, 85(7):e02992-18.

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