

斯氏线虫-致病杆菌共生体侵染昆虫的生物标志物



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摘要: 昆虫病原线虫是一类专性侵染和寄生昆虫的病原线虫, 是非常重要的生防资源。斯氏线虫属 *Steinernema* 和致病杆菌属 *Xenorhabdus* 通过形成共生体在侵染昆虫过程中共同完成生活史, 其中致病杆菌释放效应物质引发昆虫败血症是其重要机制。该文对斯氏线虫-致病杆菌共生体的侵染策略和在侵染过程中产生的免疫调节因子、释放的毒素蛋白和活性代谢物进行概述, 其中, 苯乙酰胺作为免疫抑制因子促进自身定殖, 脂多糖作为内毒素引起寄主血细胞裂解, Tc 毒素蛋白作为外毒素导致寄主中肠上皮细胞溶解, 活性代谢产物如 xenematinides、fabclavine 和 PAX 肽等具有抑菌、诱导细胞凋亡等活性。而斯氏线虫本身也能够产生表皮/分泌蛋白来抑制寄主免疫, 与共生菌协同致死寄主。因此, 通过对斯氏线虫-致病杆菌共生体产生的致病物质进行汇总分析, 为研究昆虫病原线虫致病机制提供理论参考, 同时也为新型绿色杀虫剂的开发和应用提供证据支持。

关键词: 昆虫病原线虫; 斯氏线虫; 致病杆菌; 侵染策略; 生物标志物

Biomarkers of insect septicemia caused by *Steinernema-Xenorhabdus* symbionts

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Abstract: Entomopathogenic nematodes (EPNs), which are obligate parasitic nematodes that infect a wide range of insects, are a valuable resource for biocontrol. During the process of infecting a host insect, the *Steinernema-Xenorhabdus* symbionts releases various pathogenic factors to complete their life cycle. In this paper, the pathogenic strategies employed by *Steinernema* spp. and *Xenorhabdus* spp. were reviewed. This includes utilizing phenylethylamides as immunosuppressive factors to facilitate colonization, lipopolysaccharide (LPS) as an endotoxin to cause host blood cell lysis, Tc proteins as exotoxins to kill host insects, and the production of special metabolites (e.g. fabclavine, PAX peptides, and other antibiotics) that have bacteriostatic and apoptosis-inducing activities. Additionally, some epidermal/secretory proteins can inhibit the host's immune system, work together with the symbiotic bacteria to kill the host, and cause a series of changes in the host insect's physiology and metabolism. Therefore, this review of the biochemical metabolism caused by *Steinernema-Xenorhabdus* symbionts can serve as both a theoretical guide for exploring the septicemia mechanism of EPN infestations and as evidence to support the creation of novel, environmentally friendly insecticides.

Key words: entomopathogenic nematodes; *Steinernema*; *Xenorhabdus*; infestation strategies; biomarker

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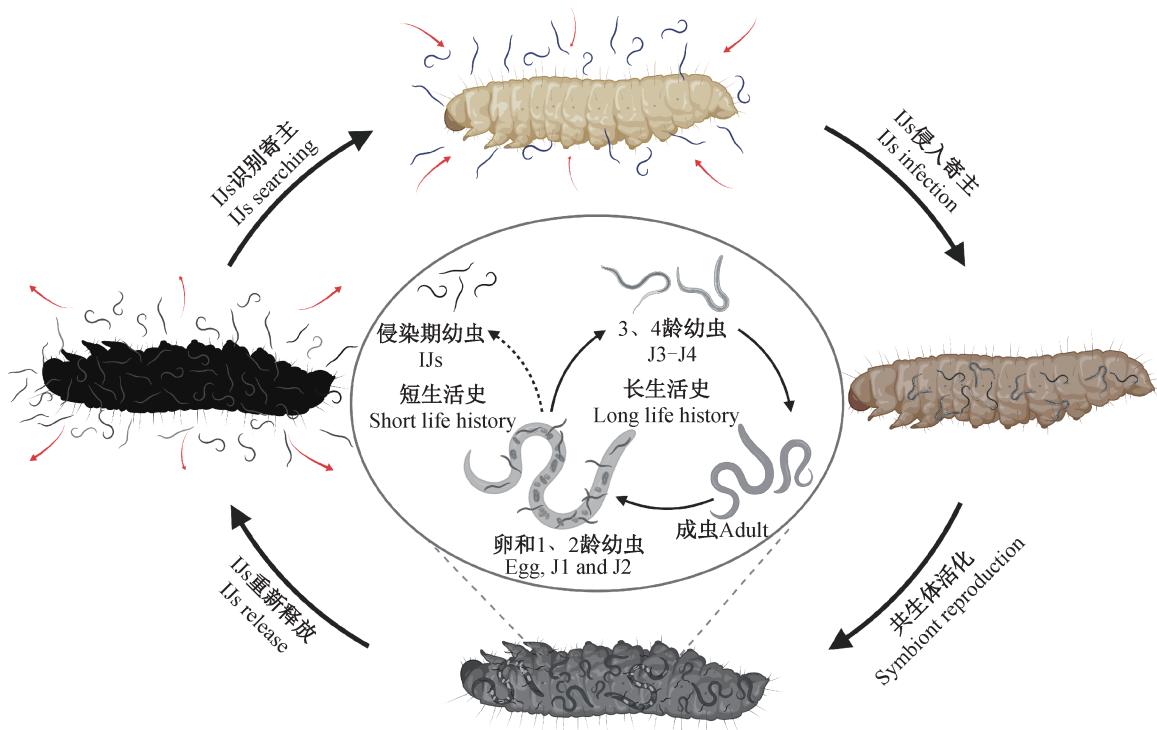
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昆虫病原线虫是一类专性侵染和寄生昆虫的病原线虫,斯氏科斯氏线虫属 *Steinernema* 线虫(简称斯氏线虫)是其中重要的一类,能够与体内细菌致病杆菌属 *Xenorhabdus* 细菌(简称致病杆菌)共生进而对昆虫形成复合侵染(武海斌等,2015;李而涛等,2022),但斯氏线虫和致病杆菌之间具有不完全的营养专化性,一种斯氏线虫只携带一种共生菌,但一种共生菌可以和多种斯氏线虫形成共生关系(Kämpfer et al., 2017)。侵染期斯氏线虫是侵染昆虫并造成寄主死亡的唯一虫态,其自由生活在土壤中并搜寻寄主,通过寄主体表的自然孔口,如口、肛门和气孔等或节间膜穿透体壁进入昆虫体内,并将致病杆菌释放到昆虫的血腔中(Strauch & Ehlers, 1998; 刘奇志等,2023),致病杆菌在血腔中繁殖并产生多种毒素分子,使寄主在24~48 h内患败血症而死亡。同时,致病杆菌通过产生胞外酶将昆虫组织分解,当寄主体内营养消耗殆尽,侵染期斯氏线虫从寄主体内爬出,并进入土壤中寻找新的寄主昆虫(Akhurst, 1980; 1983)。随着研究的不断深入,近年来有大量关于斯氏线虫和致病杆菌复合侵染昆虫过程中释放的生化代谢物的研究报道,如Tc毒素(Roderer et

al., 2020)、xenoamicin(Zhou et al., 2013)、fabclavine(Wenski et al., 2020)和PAX(peptide-antimicrobial-Xenorhabdus)肽(Fuchs et al., 2011)。因此,本文主要对斯氏线虫与致病杆菌复合侵染寄主昆虫过程中导致其死亡的致病生化物质进行综述,以期为深入挖掘昆虫病原线虫的生防潜力和分析致病机理提供参考,并为昆虫病原线虫杀虫因子的开发提供重要依据。

1 斯氏线虫-致病杆菌共生体侵染策略

斯氏线虫分为长生活史型线虫和短生活史型线虫,长生活史型线虫会经历卵、幼虫及成虫的完整发育阶段,当线虫密度过高和寄主食物供应不足时,转化为短生活史型线虫;短生活史型线虫的卵直接发育成侵染期线虫(丛斌等,1999;Gaugler,2002)。斯氏线虫-致病杆菌共生体的侵染分为4个阶段:侵染期线虫首先识别并定位寄主;穿透寄主体壁并侵入寄主体内;释放共生菌,引发寄主败血症并开始发育;食物耗尽后侵染期线虫重新形成并释放寻找新的寄主。线虫-共生菌共生体侵染是一种始于侵染期线虫侵染并以侵染期线虫形成为结束的周期性循环(图1)。



IJs: 侵染期线虫。IJs: Infective juveniles; J1, J2, J3, J4: indicate the 1st, 2nd, 3rd and 4th instar juveniles, respectively.

图1 斯氏线虫和致病杆菌共生体的生活史和侵染策略

Fig. 1 Life history and infestation strategies of symbionts of *Steinernema* and *Xenorhabdus*

1.1 侵染期斯氏线虫识别和定位寄主

侵染期斯氏线虫通过对昆虫分泌物、表皮或肠

道内容物进行识别,如CO₂、精氨酸和尿酸,并向寄主昆虫所在方向移动(杨秀芬和杨怀文,1998),如小

卷蛾斯氏线虫 *S. carpocapsae* 对红棕象甲 *Rhynchophorus ferrugineus* 的搜寻与嗅觉识别通路基因的表达相关(Santhi et al., 2021)。此外,侵染期线虫还可以回避已被侵染的寄主,避免资源的过度分配,利于线虫种群的繁衍(Baiocchi et al., 2017; 王杰等,2021)。除生物因素外,温湿度和渗透压等非生物因素也会影响线虫对寄主的识别(王杰等,2021)。线虫能够通过主动传播和被动传播进行扩散(Epsky et al., 1988),主动传播是借助水膜进行水平和垂直方向的短距离移动,被动传播则依靠风、雨、人类或昆虫活动进行长达数千米的长距离传播(Epsky et al., 1988; Timper et al., 1988)。

1.2 侵染期斯氏线虫穿透和侵入寄主

侵染期斯氏线虫能够通过昆虫的自然孔口直接侵入,也可以通过昆虫的伤口直接分泌蛋白酶破坏寄主的原表皮形成开口,进入寄主体内(AbuHatab et al., 1995)。线虫对不同寄主的侵入方式不同,其中昆虫的气门和肛门是重要的侵染途径,如夜蛾斯氏线虫 *S. feltiae* 通过气门侵入大蜡螟 *Galleria mellonella*,并在钻入后会将鞘及头部附器留在寄主昆虫体外,而侵入家蝇 *Musca domestica* 幼虫时则是通过肛门(Parkman et al., 1993; Renn, 1998)。

1.3 侵染期斯氏线虫共生体活化并致死寄主

侵染期斯氏线虫进入寄主昆虫血腔中恢复取食,并通过反刍将存在于肠道前端特殊囊泡中的致病杆菌释放到昆虫体内(Bird & Akhurst, 1983; Martens & Goodrich-Blair, 2005),致病杆菌繁殖并分泌一系列毒素因子和免疫抑制因子,在短时间内杀死寄主(Brивio & Mastore, 2018)。此外,致病杆菌还可以产生胞外酶,将昆虫的尸体转化成供自身和线虫利用的营养物质,同时线虫也可以通过取食共生菌完成自身生长、发育和繁殖(王立霞等,2000; Mucci et al., 2022)。

1.4 侵染期斯氏线虫重新形成并离开寄主

当斯氏线虫接收到营养资源匮乏的信号时,2龄幼虫重新将一个或几个致病杆菌储存在菌囊中,并繁殖形成50~100 CFU/侵染期斯氏线虫的稳定种群,进而形成侵染前期斯氏线虫和侵染期斯氏线虫(Martens et al., 2003; 王立婷等,2013)。新生成的侵染期斯氏线虫从昆虫尸体中钻出并向周围环境扩散,潜伏在土壤中进入半休眠状态,等待下一轮侵染。

2 斯氏线虫-致病杆菌共生体产生的致病生化物

斯氏线虫-致病杆菌共生体通过逃避或抑制免

疫在昆虫体内定殖,逃避免疫是通过合成或获得某些与寄主本身相关的物质附在线虫或细菌的表面,避免被寄主免疫系统识别(Brivo & Mastore, 2018);抑制免疫则是通过分泌一些物质来减弱寄主免疫系统对自身的攻击(Burman, 1982; 刘劲等,2012)。致病杆菌可以通过鞭毛附着在昆虫血腔中某些组织的表面,产生多种免疫抑制因子、毒素蛋白和特殊代谢物,使寄主迅速死亡(Moureaux et al., 1995)。

2.1 线虫表皮/分泌蛋白

斯氏线虫在复合侵染中除了起到载体作用外,还能利用自身表皮复合物逃避寄主免疫攻击,并产生一些物质来抑制昆虫的免疫反应,甚至合成毒素相关蛋白破坏寄主的中肠上皮细胞,导致昆虫停止进食,随后破坏寄主脂肪体、马氏管或消化道等组织(Wang et al., 1995; 常豆豆等, 2022)。斯氏线虫的外层表皮会直接与寄主免疫系统接触,但由于其幼虫蜕皮并且在生长发育过程中受多种因素的影响,其表皮成分存在一定差异,因此不同线虫在寄主昆虫中发挥作用的方式也不同(Shamseldean et al., 2007)。夜蛾斯氏线虫表皮中的脂类物质可以与大蜡螟血淋巴因子结合,在自身周围形成一层非特异性薄膜,逃避寄主免疫系统的识别,也可以通过抑制酚氧化酶活性、血细胞包埋反应和抗菌肽合成来抑制寄主的免疫攻击(Brivo et al., 2006; Mastore & Brivio, 2008)。格氏斯氏线虫 *S. glaseri* 的表皮蛋白不仅可以逃避日本金龟子 *Popillia japonica* 血细胞的识别,甚至还可以引起血细胞凋亡(Li et al., 2009),并且通过验证无菌线虫和携菌线虫对日本金龟子血细胞的包埋和黑化作用,发现这种烯醇化酶家族的免疫活性蛋白 Sg-ENOL(*S. glaseri* enolase)是由线虫自身产生的(刘华, 2012; 常豆豆等, 2022)。除表皮蛋白外,侵染期斯氏线虫还可以产生分泌蛋白,分泌蛋白对寄主免疫系统的抑制能力更强,毒性也更高(刘劲等,2012)。将小卷蛾斯氏线虫产生的分泌蛋白注射到大蜡螟体内,发现来自于线虫的分泌蛋白对大蜡螟具有相当高的细胞毒性(Lu et al., 2017),目前已鉴定了包括 Sc-CHYM(*S. carpocapsae* chymotrypsin)(Hao et al., 2009)、Trypsin-like protease(Balasubramanian et al., 2010)、Sc-AST(*S. carpocapsae* astacin metalloprotease)(Jing et al., 2010)和 Sc-KU-4(*S. carpocapsae* BPTI-Kunitz family inhibitor)(Toubarro et al., 2009)等在内的蛋白酶,这些成分通过降解寄主组织、促进线虫发育、抑制血细胞扩散、诱导血细胞凋亡、溶解纤维蛋白、抑制寄

主酚/原酚氧化酶活性和水解细胞外基质蛋白等方式抑制寄主的免疫系统,发挥毒性作用(常豆豆等,2022)。

2.2 致病杆菌的代谢产物

致病杆菌到达昆虫血腔后识别L-脯氨酸,从与线虫的共生型转换成对昆虫的致病型,调节多种毒力蛋白和代谢产物的合成(Herbert & Goodrich-Blair, 2007; Crawford et al., 2010)。致病杆菌在复合侵染过程中对寄主昆虫表现出强烈的致病力(杨秀芬和杨怀文,1998),其致病性主要体现在生成免疫因子逃逸或抑制寄主免疫系统的攻击,产生毒素蛋白使寄主昆虫患败血病迅速死亡,通过分泌具抑菌活性和细胞毒性的特殊代谢物质来抑制其他杂菌的生长并为线虫创造良好的生长发育环境,最终对寄主昆虫产生强烈的致病作用(Serczyńska & Bajan, 1975; 王立霞等,2000)。

2.2.1 免疫抑制因子

致病杆菌会被寄主的免疫系统识别并清除,但致病杆菌可以通过逃避或者抵抗寄主免疫系统的攻击在昆虫体内定殖(王立霞等,2000)。致病杆菌细胞壁中的脂多糖(lipopolsaccharide, LPS)类物质通过破坏酚氧化酶级联反应抑制血细胞免疫(Tang, 2009);也可以通过产生苯乙酰胺来抑制血清素受体介导的免疫反应,从而抑制寄主昆虫的免疫(Hasan et al., 2019);*X. hominickii*还可以通过抑制斜纹夜蛾*Spodoptera litura*体内类花生酸的合成来破坏昆虫免疫系统(Mollah et al., 2021)。

2.2.2 毒素蛋白

除了能够产生免疫因子逃避和抑制寄主的免疫外,致病杆菌产生的毒素才是导致寄主死亡的关键。致病杆菌对多种原生动物和昆虫表现出较高的毒性,但物种特异性很强,根据毒素存在的位置可分为内毒素和外毒素(王立霞等,2000)。

内毒素是致病杆菌细胞壁中的LPS类物质,由类脂A、核心多糖和O-抗原构成,毒性部分是类脂A,细菌裂解后将类脂A释放到寄主体内发挥毒性(Dunphy & Webster, 1988)。将LPS注射到家蚕幼虫体内后能诱导其中肠*BmToll9-2*基因的转录,激活昆虫的免疫相关Toll信号(廖文丽等,2017)。嗜线虫致病杆菌*X. nematophilus*将LPS释放到昆虫体内后通过D-氨基葡萄糖苷残基结合外源凝集素包围血细胞引起裂解,并导致脂肪体解离(Dunphy & Webster, 1988)。

外毒素是由致病杆菌产生并分泌到体外的一类

毒素,包括外毒素蛋白和一些胞外酶,其中外毒素蛋白可以直接杀死寄主(王立霞等,2000)。致病杆菌能产生具有极高杀虫活性的蛋白毒素复合物Xpts (*Xenorhabdus* protein toxins),每个活性蛋白复合体由A、B和C三个成分组成(Morgan et al., 2001; 崔龙等,2005),A作为毒素的核心元件促进毒素和受体相互作用,导致中肠上皮细胞顶端膨胀并加速生长、溶解,甚至穿越中肠到血腔中引发酚氧化酶反应(Roderer et al., 2020)。XhLA(*Xenorhabdus haemolysin*)是一种细胞表面相关的溶血素,可以溶解最常见的2种昆虫免疫细胞,在线虫逃避昆虫免疫过程中发挥了重要作用(Cowles & Goodrich-Blair, 2004)。Txp40(40 kD toxin from *Xenorhabdus*)是一种普遍存在于致病杆菌中的杀虫毒素蛋白,可导致中肠肠壁细胞间排列紊乱,降解周围的营养基质和脂肪体核(Brown et al., 2006)。Xax(*Xenorhabdus alpha-xenorhabdolysin*)二元毒素引起细胞凋亡并具有溶血活性,XaxA和XaxB对于Xax毒素发挥作用是必需的,每个单独表达时均不会产生溶血活性(Vigneux et al., 2007)。近几年,已从致病杆菌中分离鉴定到的SrfABC(Yang et al., 2019)、Tp40(杨君等,2008)、HipBA(Yadav & Rathore, 2020)和几丁质酶(Mahmood et al., 2020)等均具有不同程度的血腔毒性或口服毒性,甚至可以抑制抗菌肽活性(Vo et al., 2021)。除毒素蛋白外,致病杆菌还可以产生酯酶和蛋白酶等胞外酶,它们几乎没有杀虫活性,而是通过参与抑制寄主免疫反应和分解转化昆虫尸体为线虫生长发育提供营养,对致病起辅助作用(Caldas et al., 2002)。

2.2.3 具有抑菌活性和细胞毒性的特殊代谢物质

致病杆菌可以产生多种具有抗细菌、真菌、昆虫、线虫、原生生物和癌细胞的活性物质,防止寄主尸体被感染,从而维持自身特殊的环境生态位(McInerney et al., 1991a)。不同致病杆菌之间产生的代谢物存在较大差异,主要包括由聚酮合成酶(polyketide synthetase, PKS)和非核糖体肽合成酶(non-ribosomal peptide synthetase, NRPS)编码合成的多种肽,包括缩肽类、xenocoumacins、fabclavine、普那霉素(pristinamycin)、rhabdopeptides、bicornitun、PAX肽、cabanillasin和nemaucin;除此之外还可以产生由核糖体编码的细菌素、吲哚及其衍生物、氨基酸衍生物、亚苄基丙酮类、呋喃酮类和二硫吡咯类等具有抗菌和杀虫活性的代谢物质(表1)(Dreyer et al., 2018)。

表1 致病杆菌产生的特殊代谢物功能

Table 1 Functions of specialized metabolites produced by *Xenorhabdus* spp.

类别 Class	致病杆菌 <i>Xenorhabdus</i> spp.	特殊代谢物 Specialized metabolite	功能 Function	参考文献 Reference
聚酮合成酶和非核糖体肽合成酶编码的抗菌肽 Antimicrobial peptides encoded by polyketide synthetase/non-ribosomal peptide synthetase	<i>X. doucetiae</i> , <i>X. mauleonii</i> <i>X. indica</i> <i>X. nematophila</i> <i>Xenorhabdus</i> sp. <i>X. szentirmiai</i>	Xenoamicins Lipodepsipeptides Xenematides Xenobactin Szentiamide	抗细菌、真菌、原生动物和弱细胞毒性 Antibacterial, antifungal, antiprotozoal activities and weakly cytotoxic 抗原生动物和癌细胞 Antiprotozoal and anticancer cells activities 抗细菌, 弱杀虫性 Antibacterial and weak insecticidal activities 抗细菌 Antibacterial activity 抗原生动物 Antiprotozoal activity	Zhou et al., 2013 Kronenwerth et al., 2014 Lang et al., 2008; Crawford et al., 2011 Nollmann et al., 2012 Nollmann et al., 2012; Grundmann et al., 2013 McInerney et al., 1991a Fuchs et al., 2014; Wenski et al., 2020
嗜线虫致病杆菌 <i>X. nematophilus</i> <i>X. budapestensis</i> , Fabclavines <i>X. szentirmiai</i>	Xenocoumacins 普那霉素 Pristinamycin Xenortides <i>X. nematophilus</i> <i>X. nematophila</i>	Xenocoumacins 抗细菌、真菌和溃疡 Antibacterial, antifungal and antiulcer activities 抗细菌、真菌和原生动物 Antibacterial, antifungal and antiprotozoal activities 抗细菌 Antibacterial activity 抗细菌和原生动物 Antibacterial and antiprotozoal activities 抗细菌、原生动物、弱细胞和血腔毒性 Antibacterial and antiprotozoal activities, weakly cytotoxicity and haemotoxic	抗细菌、真菌和溃疡 Antibacterial, antifungal and antiulcer activities 抗细菌、真菌和原生动物 Antibacterial, antifungal and antiprotozoal activities 抗细菌 Antibacterial activity 抗细菌和原生动物 Antibacterial and antiprotozoal activities 抗细菌、原生动物、弱细胞和血腔毒性 Antibacterial and antiprotozoal activities, weakly cytotoxicity and haemotoxic	Brachmann et al., 2012 Reimer et al., 2014 Bi et al., 2018 Fuchs et al., 2012 Fuchs et al., 2011 Houard et al., 2013
核糖体编码的细菌素 Bacteriocins encoded by ribosomes	嗜线虫致病杆菌 <i>X. nematophilus</i> <i>X. nematophila</i>	Xenorhabdicin Xenocin	抗细菌 Antibacterial activity 抗细菌 Antibacterial activity	Morales-Soto et al., 2012 Singh & Banerjee, 2008
吲哚及其衍生物 Indole and its derivatives	伯氏致病杆菌、 嗜线虫致病杆菌 <i>X. bovienii</i> , <i>X. nematophilus</i> <i>X. nematophila</i>	吲哚 Indole 羟吲哚 Oxindole 伯氏致病杆菌 Xenocycloins 嗜线虫致病杆菌 Nematophin <i>X. nematophila</i>	抗细菌、真菌、溃疡和杀虫 Antibacterial, antifungal, and antiulcer insecticidal activities 抑制磷脂酶A ₂ Inhibition of phospholipase A ₂ activity 血腔毒性 Haemotoxic 抗细菌 Antibacterial activity 抑制酚氧化酶, 具杀虫活性 Inhibition of phenoloxidase and insecticidal activities	McInerney et al., 1991b; Sundar & Chang, 1993; Zhang et al., 2019 Shrestha & Kim, 2007 Proschak et al., 2014 Li et al., 1997 Crawford et al., 2012
氨基酸衍生物 Amino acid derivatives		<i>X. nematophila</i>	Rhabduscin	
亚苄基丙酮类 Benzylideneacetones		<i>X. nematophila</i>	苯亚甲基丙酮 Benzylideneacetonee	Spogliarich et al., 1989; Ji et al., 2004
呋喃酮类 Furanones		<i>X. szentirmiai</i>	Xenofuranones	Brachmann et al., 2006
二硫吡咯类 Dithiopyrroles	伯氏致病杆菌 <i>X. bovienii</i>	Xenorhabdins, Xenorrides	抗细菌、真菌、癌细胞和杀虫 Antibacterial, antifungal, anticancer cells and insecticidal activities	Oliva et al., 2001; Challinor & Bode, 2015

由PKS/NRPS编码的缩肽类物质是指多肽中的一个或多个酰胺基被羟基取代形成酯键,包括xenamicins、lipodepsipeptides、xenematides、xenobactin和sentiamide共5类,其中sentiamide对恶性疟原虫*Plasmodium falciparum*有较大的毒性,并对布氏锥虫*Trypanosoma brucei*和克氏锥虫*T. cruzi*均有一定的致死效果(Nollmann et al., 2012)。其他由PKS/NRPS合成的物质中,fabclavines和一些阳离子抗菌肽结构非常相似,可以抑制革兰氏阳性和阴性细菌、酿酒酵母*Saccharomyces cerevisiae*、恶性疟原虫、布氏锥虫和克氏锥虫的生长(Fuchs et al., 2014; Wenski et al., 2020)。在致病杆菌中共分离得到8种rhabdopeptide,不同rhabdopeptide的活性不同,rhabdopeptide 2对成肌细胞的毒性较弱,rhabdopeptide 2、7和8对原生动物有抗性,rhabdopeptide 7和8有微弱的血腔毒性,并在昆虫的生物转化和线虫繁殖阶段发挥着重要作用(Bi et al., 2018)。

除上述由PKS/NRPS基因簇控制编码合成的毒素物质外,致病杆菌还能产生由核糖体编码的细菌素、二硫吡咯类和吲哚类等特殊代谢物。核糖体编码的细菌素中xenocin的产生由低浓度铁离子触发,铁的消耗与一种铁抑制蛋白有关,该蛋白可能作为敏感菌株的毒素受体,因此这种细菌素在营养浓度较低且竞争加剧时在寄主幼虫中产生,进而发挥毒素作用(Singh & Banerjee, 2008)。在致病杆菌中分离的吲哚及其衍生物中,能发挥杀虫活性的有吲哚、羟吲哚和xenocycloins,其中吲哚是一种芳香族杂环化合物,通过增加核苷酸鸟苷四磷酸(guanosine-3',5'-(his) pyrophosphate, ppGpp)的合成来抑制细菌RNA的合成,表现出强烈的抑制细菌、真菌及溃疡活性和杀虫活性(McInerney et al., 1991b; Zhang et al., 2019);羟吲哚具有较弱的磷脂酶A₂抑制作用,可以抑制昆虫的免疫反应,使其更易受到微生物感染(Shrestha & Kim, 2007);xenocycloins对大蜡螟血细胞有血腔活性,有助于斯氏线虫-致病杆菌共生体发挥杀虫活性(Proschak et al., 2014)。rhabduscin是一种酪氨酸衍生物,通过将昆虫体内的酚氧化酶浓度控制在低纳摩尔水平实现其杀虫活性(Crawford et al., 2012)。苯亚甲基丙酮作为磷脂酶A₂的抑制剂调控类花生酸的合成,减弱寄主血细胞的吞噬作用,抑制昆虫免疫反应,间接参与线虫-共生菌共生体的毒力效应(Spogliarich et al., 1989)。二硫吡咯类物质具有典型的异双环吡咯酮二硫唑核,通过抑制RNA的合成发挥细胞毒性(Oliva et al.,

2001;Challinor & Bode, 2015)。Xiao et al. (2012)从*X. budapestensis*中分离到2种未命名的抗菌肽GP-19和EP-20,其对真菌和细菌均表现出广谱抗菌活性,但具体的作用模式尚未阐明。

致病杆菌产生的特殊代谢物不仅在保证线虫繁殖方面发挥着关键作用,还可以抑制昆虫免疫反应,发挥杀虫活性,在防治农业病害和人类疾病方面具有潜在价值。随着生物学技术的飞速发展与相关研究的不断深入,越来越多的新型抗生素被发现,例如siderophores、khoicin和xenopep(Boysen et al., 2021)。并且已有研究证明抗菌物质和具杀虫活性物质的运输与致病杆菌的VI型分泌系统密切相关,它们通过分泌系统将毒素分子运输到寄主细胞内并引发弥散性败血症的级联效应,但目前对其发挥毒力的作用机制研究还相对较浅,仍有巨大的研究空间(Kochanowsky et al., 2020; Pei et al., 2020)。

3 展望

昆虫病原线虫-共生菌复合侵染具有致病力高、特效期长和绿色安全等特点,已成为国际上生物防治研究领域的热点,致病杆菌也逐渐成为开发新型抗菌剂和杀虫剂的极佳资源。本文总结了斯氏线虫和致病杆菌共生体在复合侵染寄主昆虫过程中的生理变化和代谢变化,包括免疫抑制因子、表皮/分泌蛋白、毒素蛋白和活性次生代谢物的产生和作用机制。Dreyer et al. (2018)研究结果表明,*X. nematopila*的DSM 3370^T基因组包含多种编码生物合成的基因簇,据统计这种细菌产生的潜在毒力因子数量远远超过已知的所有抗生素代谢物的数量。此外,不同致病杆菌产生的代谢活性物质不同,因此致病杆菌不同种以及不同菌株几乎可以产生无限的新颖生物活性化合物。但由于多数活性代谢产物是由非核糖体编码产生,并非单一基因的产物,因此需要开发新的研究方法和技术进行深入挖掘。另外,昆虫病原线虫-共生菌-昆虫构成了一个可以用于研究寄生虫和寄主互作分子机制的独特系统,并且黑腹果蝇*Drosophila melanogaster*-致病杆菌模型已被广泛用于昆虫和共生细菌之间致病机制的研究。值得注意的是,黑腹果蝇的基因组和人类有60%的同源性,并且有75%的致病基因在黑腹果蝇中具有同源性。因此,深入研究昆虫病原线虫-共生菌的关键信号分子和生物标志物,不仅有助于推进新型生物农药的开发,而且还有助于推进对人类寄生虫病的理解和研究。

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