植物与微生物之间的跨界信号调控

阚金红^{1,2,3}, 方荣祥^{1,2*}, 贾燕涛^{1,2*}

1. 中国科学院微生物研究所, 植物基因组学国家重点实验室, 北京 100101;

2. 国家植物基因研究中心, 北京 100101;

3. 中国科学院大学, 北京 100049

* 联系人, E-mail: fangrx@im.ac.cn; jiayt@im.ac.cn

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摘要 依靠信号分子的交流方式广泛存在于原核生物和真核生物之间, 在此交流过程中, 相互联络的生物之间产生并释放小分子化合物, 从而建立原核生物和真核生物交流的通道, 影响彼此基因的表达, 这个过程即为跨界信号交流。跨界信号交流广泛发生在病原菌或益生菌与其宿主之间, 其产生的生理效应主要取决于特异信号在生物个体中所激发的信号通路。揭示跨界信号调控的信号分子或语言, 并阐明其作用机理具有很大的挑战性。已有研究表明, 细菌和植物能产生多种多样的信号分子, 解析这些信号分子并探讨其作用机理逐渐成为该领域研究热点, 其研究成果将有助于发掘新的植物抗病策略, 例如, 通过干扰跨界信号调控途径而不是直接杀死病原细菌达到抗病的效果; 而益生菌中的信号分子的作用机理的研究, 也利于农业上的应用。这篇综述总结了植物与细菌之间跨界信号调控的最新研究进展, 以及植物相关细菌群体感应系统的LuxR类的转录调控因子在跨界信号调控过程中的作用机制。

关键词 跨界信号调控, 细菌, 宿主植物, 信号分子

1 细菌的群体感应信号分子及对植物的影响

群体感应(quorum sensing, QS)是细菌之间的一种交流方式, 主要依赖于细菌的群体密度, 通过感应细菌产生的信号分子的浓度从而调控细菌的行为。这种现象首次发现于费氏弧菌(*Vibrio fischeri*)中, 当细菌密度达到一定阈值时细胞产生荧光^[1,2]。在革兰氏阴性细菌中, 第一个被鉴定的QS信号分子(又称为自诱导子)是N-酰基高丝氨酸内酯(N-acyl homoserine lactone,

AHL)^[3]。QS系统的存在使细菌能够产生协同调控行为, 类似于多细胞生物的反应, 从而提高对复杂营养及环境条件的适应性。到目前为止, 革兰氏阴性细菌中的AHLs是研究最为深入的信号分子^[4,5]。许多AHL衍生物在细菌中被发现, 它们的分子结构差异主要在于酰基侧链的长度及酰基侧链上C3的氧化状态(发生羟基化或者发生甲基或酮基的添加)的不同^[6]。通常, 经典的AHL-QS系统包含LuxI和LuxR蛋白, 分别作为AHL合成酶和信号分子受体起作用^[7,8]。QS系统调控

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多种生理过程,包括细菌的毒性、竞争、结合及抗菌次级代谢物的产生^[9]. QS信号分子也参与细菌的种间交流,因为很多细菌进化出“偷听”其他细菌产生的信号分子的能力^[10~12].近年来的研究发现, QS信号分子也可以被微生物的真核生物宿主感应,从而建立跨界信号交流^[12~16].

跨界信号调控的发现,使人们认识到QS信号分子的作用并不只局限于细菌中,其在植物与细菌相互作用过程中还具有独特的功能(图1).细菌产生的AHL可被植物感应,从而影响植物的免疫、生长和发

育等过程(表1)^[12,16,18,36~42].研究发现,施加AHL可以增强菜豆(*Phaseolus vulgaris*)叶片气孔的电导率及蒸腾作用,使植物对根际菌提供更多营养^[19].中华根瘤菌(*Sinorhizobium meliloti*)产生的3-oxo-C14-HSL,使藜苳苳(*Medicago truncatula*)的结瘤数量增加,其作用依赖乙烯信号途径^[33].在大麦(*Hordeum vulgare* L.)中,3种AHL分子(C6-, C8-和C10-)能影响大麦解毒酶的活性,包括谷胱甘肽转移酶和脱氢抗坏血酸还原酶;但在豆薯(*Pachyrhizus erosus*)中,解毒酶的活性虽然不受这3种AHL的影响,但叶绿素含量在C10-HSL处理后降

图1 植物与细菌之间的跨界信号调控示意图^[17]

细菌产生的AHL群体感应信号分子影响植物的生长发育和免疫反应. AHLs能够引发基于植物MAP激酶及WRKY型转录调控因子的防御相关级联反应. 以AHLs处理局部叶,可诱导系统叶中氧化脂类(*cis*-OPDA)、水杨酸及植物生长素的积累,导致依赖于NPR1, LOX2及TGA2/5/6转录调控因子的防御反应的发生. AHLs也影响植物根的形态建成及结瘤数量. 植物产生和分泌的AHL类似物或内酯酶能阻断或操纵受体感应调控的细菌行为

表 1 群体感应信号分子对植物的影响, 依据参考文献[18]修改

信号分子类型	植物的反应	植物种类	参考文献
Short chain length HSL	Increased transpiration, stomatal conductance	<i>Phaseolus vulgaris</i>	[19]
C4-HSL	Intracellular Ca^{2+} elevation	<i>Arabidopsis thaliana</i>	[20]
C4-HSL, C6-HSL	Primary root elongation	<i>A. thaliana</i>	[21]
C6-HSL	Upregulation of metabolism, transport and transcriptional regulation	<i>A. thaliana</i>	[21]
C6-HSL	Herbivore susceptibility	<i>N. attenuata</i>	[22]
C4-HSL, C6-HSL (<i>S. liquefaciens</i>)	Upregulation of defense genes	<i>Lycopersicon esculentum</i>	[23]
C6-HSL, C8-HSL, C10-HSL	Lactonase induction	<i>Pachyrhizus erosus</i>	[24]
3-oxo-C6-HSL, 3-oxo-C8-HSL	G-protein coupled receptors for root growth	<i>A. thaliana</i>	[25,26]
3-oxo-C6-HSL (<i>S. plymuthica</i>)	Triggering plant immunity, increased SA level	<i>Cucumis sativa</i> , <i>L. esculentum</i>	[27]
C6-HSL, C8-HSL, C10-HSL	Root and shoot growth	<i>Hordeum vulgare</i>	[24]
3-oxo-C10-HSL	Adventitious root formation via H_2O_2 and NO dependent cGMP signaling	<i>Vigna radiata</i>	[28]
C10-HSL	Altering root system architecture, inhibiting primary root elongation, promoting lateral root formation, altering root hair development	<i>A. thaliana</i>	[29]
C12-HSL	Root hair development	<i>A. thaliana</i>	[29]
3-oxo-C12-HSL (<i>P. aeruginosa</i>)	Defense and stress management genes, phytohormones, and metabolic regulation	<i>M. truncatula</i>	[30]
3-oxo-C12-HSL	Resistance induction	<i>A. thaliana</i>	[31]
3-oxo-C14-HSL	Systemic resistance against <i>G. orontii</i>	<i>A. thaliana</i>	[31]
3-oxo-C14-HSL	Systemic resistance against <i>B. graminis</i>	<i>H. vulgare</i>	[31]
3-oxo-C14-HSL	Priming plants for enhanced callose deposition, accumulation of phenolic compounds, and lignification of cell walls	<i>A. thaliana</i>	[32]
3-oxo-C14-HSL (<i>S. meliloti</i>)	Increasing nodule numbers	<i>M. truncatula</i>	[33]
3-oxo-C16-HSL (<i>S. meliloti</i>)	Defense and stress management genes, phytohormones and metabolic regulation	<i>M. truncatula</i>	[30]
DSF (<i>Xcc</i>)	Reverting stomatal closure, eliciting plant innate immunity	<i>A. thaliana</i> , <i>N. benthamiana</i> , rice	[34,35]

低^[43]. 在其他的研究中发现, 细菌产生的AHLs对藻类也有影响. 例如, 大型藻类相关细菌*V. anguillarum*产生的AHLs, 能够作用于藻类游动孢子, 诱导孢子中钙离子内流, 从而促进孢子与细菌的黏附作用^[44-46]. 而短链的C4-和C6-HSL能够刺激绿藻石莼*Ulva*和红藻江

藻*Gracilaria*中果孢子的释放^[47].

在拟南芥(*Arabidopsis thaliana*)中, AHLs对根的形态发育的影响与其酰基侧链的长度(4~14个碳原子)有关. 其中, C10-HSL是改变根的形态结构最为有效的分子, 能促进侧根的形成; 而其他AHL虽然对根的影响

并不明显, 但影响根部细胞分裂和分化相关基因的表达, 该调控并不依赖生长素信号通路^[29]. 以C6-HSL处理拟南芥可改变其生长素和细胞分裂素的比值, 导致植物组织中基因表达谱的不同^[21]. 另外, C6-和C8-HSL介导主根伸长的一些植物组分已得到鉴定, 例如, G蛋白偶联受体GCR1, G蛋白 α 亚基GPA1及G蛋白偶联候选受体Cand2, Cand7^[25,26]. C4-HSL处理拟南芥, 导致胞质钙离子浓度瞬时增加, C6-HSL则诱导钙调蛋白水平的增加^[48]. 这些研究结果表明, 钙离子信号通路在植物响应细菌AHLs的过程中发挥重要作用^[20]. 在拟南芥中, 3-oxo-C6-HSL能够激活转录因子AtMYB44的表达, 并通过调控细胞分裂素和生长素相关基因的表达介导主根的生长, 促进分生区细胞的分裂及伸长区中的细胞伸长^[49]. 在绿豆(*Vigna radiata* (Linn.) Wilczek)中, 3-oxo-C10-HSL促进不定根的形成, 主要通过H₂O₂和NO依赖的cGMP信号通路发挥作用^[28].

诱导性的系统抗性(induced systemic resistance, ISR)是通过微生物在植物的局部诱导, 而使整株植物形成的广谱的抗病能力^[50]. 除了已发现的众多微生物因子, AHLs在激发ISR过程中也发挥作用^[51-53]. 利用能分泌AHL的根际细菌处理植物, 从而诱导植物的系统抗性的生物防控方法, 称为AHL-启动^[23]. 例如, 沙雷氏菌属(*Serratia*)产生的AHL衍生物(C4-和C6-HSL)能够增加豆类和番茄(*Lycopersicon esculentum* Mill.)对叶际病原真菌的系统抗性^[23,27,54], 这种现象的发生是因为AHLs系统性的诱导了水杨酸(salicylic acid, SA)及乙烯依赖的防御基因(如*PR1a*)的表达^[23]. 长链AHLs也可以激活植物的抗性反应. 例如, 两种由共生菌苜蓿中华根瘤菌(*Sinorhizobium meliloti*)及病原菌绿脓杆菌(*Pseudomonas aeruginosa*)产生的AHL分子, 3-oxo-C16-HSL和3-oxo-C12-HSL能够诱导苜蓿防御和胁迫相关蛋白的大量积累^[30]. 将黏质沙雷氏菌(*Serratia marcescens*)中的AHL合成和降解基因分别转化烟草(*Nicotiana tabacum*), 含有AHL合成基因的转基因烟草中ISR被激活, 能有效防御细菌病原菌的侵染, 但是含有AHL降解基因的转基因烟草由于ISR未被激活, 而无法防御病原菌^[55]. Oxo-C14-HSL能增强拟南芥对专性活体营养型真菌(*Golovinomyces orontii*)及半活体营养型细菌丁香假单胞菌(*P. syringae* pv. *tomato* DC3000)的系统抗性; oxo-C14-HSL诱导大麦对活体营养型的大麦白粉菌(*Blumeria graminis* f. sp. *hordei*)的

系统抗性^[31]. Oxo-C14-HSL激活拟南芥防御相关组分如丝裂原激活蛋白激酶AtMPK3和AtMPK6、转录调控因子WRKY22和WRKY29以及防御相关基因*PR1*的表达^[31]. 同时oxo-C14-HSL还能影响植物抗病相关的生理变化, 包括胼胝质的沉积、酚类化合物的积累、植物细胞壁的木质化、氧化脂类的含量变化, 以及丁香假单胞菌刺激植物SA介导的气孔关闭^[32,41]. 用能产生oxo-C14-HSL的苜蓿中华根瘤菌接种宿主植物时, 能增强宿主对真菌病原菌的抗性^[56]. 因此, 利用产生AHL的细菌来提高植物抗性, 是一种新的保护作物的方式.

另一种具有代表性的QS信号分子DSF(扩散性的信号因子), 其分子结构为顺-11-甲基-2-十二碳烯酸, 是一种新的 α,β -不饱和脂肪酸分子, 最初在植物病原菌野油菜黄单胞菌(*Xanthomonas campestris* pv. *campestris*, *Xcc*)中发现, DSF影响细菌的致病力、生物膜的形成及毒素的产生^[57,58]. 葡萄糖作为底物为DSF提供碳骨架, 激活*Xcc*中DSF家族信号分子的合成^[59]. 在*Xcc*中被称为调控致病因子(regulation of pathogenicity factors, *rpf*)的基因簇参与DSF的合成及应答^[60-62]. *Rpf*基因簇及DSF信号分子也存在于黄单胞菌属的其他细菌中, 例如, 水稻(*Oryza sativa*)白叶枯病菌*X. oryzae* pv. *oryzae* (*Xoo*), 在几种农作物中均引起疾病的木质部难养菌(*Xylella fastidiosa*)、柑橘溃疡病菌(*X. axonopodis* pv. *citri*)、大豆斑疹病菌(*X. axonopodis* pv. *glycines* (*Xag*)), 人的条件致病菌嗜麦芽寡养单胞菌(*Stenotrophomonas maltophilia*)^[63-72]. 有趣的是, DSF的合成并不局限于黄单胞菌属的细菌中, DSF的衍生物在洋葱伯克霍尔德菌(*Burkholderia cenocepacia*)和铜绿假单胞菌(*P. aeruginosa*)中也有发现^[73-75], 此发现扩展了DSF家族的信号分子的种类^[42,76]. 一种细菌能产生不止一种DSF家族的信号分子, 几种不同的菌也可能产生同一种DSF家族的信号分子^[65,70,75]. DSF家族的信号分子在细菌种间及真核与原核生物之间的跨界信号调控过程中发挥重要作用^[42,57,76-78], 例如, 嗜麦芽寡养单胞菌产生的DSF能够调控铜绿假单胞菌的生物膜的形成及多黏菌素的产生^[68], 也干扰人体条件致病菌白色念珠菌(*Candida albicans*)的酵母型至菌丝型形态的转变及生物膜的形成^[79]. 而白色念珠菌本身产生的法尼酸和法尼醇, 作为QS的信号分子能够抑制酵母型至菌丝型形态的转变, 其中法尼酸是DSF的结构和功能类似

物^[80,81]. 洋葱伯克霍尔德菌产生的顺式-2-十二碳烯酸(*cis*-2-dodecenoic acid, BDSF, 一种DSF家族信号分子)能够恢复*Xcc*的DSF缺陷突变体的生物膜和胞外多糖的产生, 强烈抑制白色念珠菌萌发管的形成, 并干扰菌的形态转变^[73]. 铜绿假单胞菌产生的顺式-2-癸烯酸则诱导自身及其他微生物(包括白色念珠菌)生物膜的扩散^[74,82]. DSF家族的信号分子也影响植物的免疫反应. 在拟南芥中, DSF干扰细菌或脱落酸(abscisic acid, ABA)引起的气孔免疫反应^[34], 但是在其他研究中也发现DSF能激活植物的免疫反应^[35].

2 植物信号分子对细菌群体感应系统的影响

真核细胞能产生AHLs类似物, 可以通过激活或拮抗细菌的QS系统发挥作用^[13,36,38,83], 如藻类和高等植物通过分泌QS信号分子类似物影响细菌的功能. 海洋红藻(*Delisea pulchra*)产生的卤代呋喃酮, 与AHLs结构相似, 通过竞争结合到AHL受体促进受体降解, 从而抑制黏质沙雷氏菌及其他细菌中受AHL诱导的细菌行为^[84-86]. 单细胞衣藻(*Chlamydomonas reinhardtii*)产生的维生素B2及其衍生物光色素作为激动剂与QS受体LasR结合, 从而激活铜绿假单胞菌中靶标基因的表达^[87,88]. 高等植物产生的AHL类似物在调控QS信号通路上也具有双重作用. 例如, 豌豆(*Pisum sativum*)幼苗渗出物能够抑制AHL诱导的紫色杆菌中紫色杆菌素的合成, 使黏质沙雷氏菌AHL合成酶缺陷突变体的运动性提高, 及激活大肠杆菌QS报告菌株的荧光产生^[89]. 在AHL处理条件下, 藜蒺苜蓿及其他豆科植物分泌的AHL类似物, 能够抑制相关细菌的AHL反应, 达到抑制细菌行为的效果^[30]. 利用紫色杆菌及根癌农杆菌报告菌株作为生物检测器, 发现美国南佛罗里达的一些药用植物具有抗QS的特性^[90], 其中一种药用植物提取物抑制了铜绿假单胞菌中QS控制的毒力因子的产生^[91]. 大蒜(*Allium sativum* L.)提取物阻断了铜绿假单胞菌(能同时侵染植物和动物)的QS信号通路, 使得细菌对妥布霉素、呼吸爆发、多形核白细胞的吞噬作用更为敏感, 从而能够有效清除人体肺部细菌的侵染^[92]. 番茄、小冠花(*Coronilla varia*)、豆类和水稻等高等植物也能分泌具有AHL类似物活性的化合物^[89,93-95], 但是这些化合物的性质还未被鉴定.

植物产生的其他类型的特异化合物也能影响细

菌的QS系统. 例如, 黄烷儿茶酚是一种黄酮类化合物, 分布在一种风车子属植物(*Combretum albiflorum*)的叶和树皮中, 能够降低铜绿假单胞菌中关键的QS调控基因*lasI/lasR*和*rhlI/rhlR*(*luxI/luxR*同源物)及*lasB*和*rhlA*的表达^[96]. 因此, 儿茶酚通过影响QS信号通路而构成了防御病原菌的第一道屏障. *L*-刀豆氨酸是苜蓿及其他豆科植物大量产生的一种精氨酸类似物, 它能抑制紫色杆菌中紫色杆菌素的产生, 也能抑制中华根瘤菌QS系统(*sinI/sinR*)所调控的*exp*基因的表达, 其中*exp*基因负责胞外多糖的合成^[97]. 目前发现, 几乎所有QS抑制剂都能促进LuxR受体蛋白的水解^[86,98]. 因此, 利用QS抑制剂干扰病原菌的QS系统从而抑制其在植物中的生长, 在农业上具有潜在的应用价值.

有些植物产生的化合物也可能被细菌利用从而促进细菌的侵染. 例如, 迷迭香酸(rosmarinic acid, RA)是植物产生的化合物, 作为AHL类似物起作用. 它通过与C4-HSL竞争结合到铜绿假单胞菌QS受体蛋白RhlR上, 诱导QS调控的系列过程, 包括促进生物膜的形成, 两种毒力因子(绿脓菌素和弹性蛋白酶)的产生^[99]. 有些研究发现, 细菌侵染能引起植物产生迷迭香酸, 通过刺激细菌QS反应的过早发生而保护植物, 因此被认为是植物的一种防御机制^[100,101], 尽管迷迭香酸的有效浓度在不同的研究中不尽相同^[100,102]. 植物激素水杨酸处理水稻白叶枯病菌*Xoo*, 能引起*Xoo*分泌DSF和DF(扩散因子), 从而促进细菌黄原胶和胞外多糖的产生^[103]. 另外, 植物产生的对-香豆酸可以作为前体化合物, 由沼泽红假单胞菌中的合成酶合成对-香豆酰高丝氨酸内酯^[104]. 它是一种新型的酰基高丝氨酸内酯信号分子, 只有细菌靠近其真核宿主时才发挥作用.

根癌农杆菌和发根农杆菌能引起很多双子叶植物产生冠瘿瘤和毛状根^[105,106]. 农杆菌致癌DNA片段(又称为转移DNA, T-DNA)插入到植物基因组上并导致冠瘿碱的产生. 冠瘿碱参与调控农杆菌QS转录调控因子TraR^[107,108], TraR的抗激活子TrlR及AHL剪切酶编码基因*aiiB*的表达^[109,110].

3 LuxR孤儿蛋白介导的一种新型跨界信号调控模式

在很多变形细菌中, QS的LuxRs受体蛋白没有相应的LuxI信号分子合成酶, 这类LuxRs蛋白称为LuxR

solos或orphans^[111-113]. LuxR solos蛋白结构与经典的LuxR蛋白类似, 都含有两个结构域, 即: N-端的AHL-结合结构域和C-端的螺旋-转角-螺旋(HTH)DNA结合结构域. 但是, 在LuxR solo蛋白的AHL-结合结构域中, 一个或两个保守的氨基酸发生了改变^[116]. 推测这些LuxR solos蛋白可能与其响应不同信号分子有关, 他们既可以响应自身细菌细胞中其他信号分子合成酶合成的AHLs^[114], 或者通过偷听其他细菌产生的AHLs^[10,115,116], 或者响应跨界信号调控过程中真核生物产生的信号分子^[112], 从而实现调控功能. 一类植物相关细菌(plant associated bacteria, PAB)的LuxR solos蛋白能对植物产生的低分子量的化合物进行响应, 而对AHLs不响应, 这类蛋白在植物与细菌相互作用的过程中发挥重要作用, 包括细菌致病性, 生物防控及共生过程等^[16,21,22]. 对LuxR solos蛋白介导的跨界信号调

控机制的研究, 特别是破译跨界交流的化学语言成为人们的研究热点.

LuxR solos广泛存在于植物相关的细菌中, 包括 α -变形菌门的红螺菌属、柠檬胞菌、根瘤菌、中华根瘤菌、农杆菌, 以及 γ -变形菌门的黄单胞菌属、假单胞菌属和Dickeya属等^[16], 目前已发现的LuxR solos蛋白列在表2中. XccR是第一个被鉴定的植物病原菌LuxR solo蛋白, 它不直接结合AHLs, 却能响应植物体内的未知化学物质^[117]. 在Xcc基因组中LuxR缺乏相应的AHL合成酶基因*LuxI*, 取而代之的是脯氨酸亚氨基酸酶编码基因(*pip*), *xccR/pip*遗传位点是细菌致病性所必需的. *pip*的激活依赖于转录调控因子XccR, 植物体内细菌*pip*的表达水平显著高于丰富培养基上的表达水平, 表明植物信号分子参与了这个过程的调控. 负调控因子XerR对*xccR*的阻遏作用被植物体内未知的

表 2 植物相关细菌的LuxR solos蛋白, 依据参考文献[16]修改^{a)}

LuxR solo	来源生物	LuxR solo作用	结合的分子	相关的功能	参考文献
XccR	<i>Xcc</i>	Virulence	Plant signal molecule Cabbage (+)	<i>pip</i> gene expression; virulence on cabbage	[117]
OryR	<i>Xoo</i>	Virulence	Rice signal molecule Rice (+)	<i>pip</i> gene expression; virulence on rice, flagellation	[118-120]
NesR	<i>S. meliloti</i>	Symbiosis	Not determined	Nutritional and environmental stress response; plant nodulation	[121]
PsoR	<i>P. fluorescens</i> Pf-5/CHA0	Biocontrol	Plant signal molecule Rice (+) Wheat (+) Cucumber (-)	Antimicrobial agents 2,4-DAPG, chitinase	[122]
XagR	<i>Xag</i>	Virulence	Plant signal molecule Soybean (+) Rice (+) Cabbage (+)	<i>pip</i> gene expression; virulence on soybean; adhesion	[123]
PsaR2	<i>Psa</i>	Virulence	Plant signal molecule	Virulence on kiwifruit	[124]
XocR	<i>Xoc</i>	Virulence	Rice signal molecule	Virulence on rice; swimming motility; <i>recN</i> and <i>trpE</i> expression	[125]
PipR	<i>P. sp.</i> strain GM79	Endophyte	Eastern cottonwood tree signal molecule	<i>pipA</i> gene expression	[126]
LesR	<i>Lysobacter</i> <i>enzymogenes</i>	Biocontrol	Not determined	Regulation of biosynthesis of a novel antifungal factor (HSAF), cell aggregation, and a melanin-like pigment	[127]

a) (+) and (-) denote positive activation and no activation of promoter activity, respectively. 2,4-DAPG, 2,4-diacetylphloroglucinol.

信号分子解除^[128]. 作为XccR同系物, Xoo中的OryR能感应水稻提取物中的未知信号分子, 从而增加OryR蛋白的可溶性^[118~120]. Xoo也不产生AHLs, OryR蛋白通过响应植物信号分子调控*oryR*邻近的基因*pip*的表达^[120]. Xag是大豆(*Glycine max*)斑疹病的病原物, 也含有LuxR solo蛋白XagR. *xagR*和邻近*pip*两个基因是Xag致病所必需的, XagR是*pip*在植物体内诱导表达所必需的^[123]. 水稻条斑病菌Xoc也含有LuxR solo蛋白XocR, 它是细菌致病性所必需的, 通过检测尚未鉴定出的水稻信号分子参与调控细菌的运动性^[125].

除了黄单胞菌属的细菌外, 植物生长促进菌荧光假单胞菌产生的PsoR也能响应植物特异的信号分子, 如水稻和小麦(*Triticum aestivum*)的叶片提取物, 但PsoR对黄瓜(*Cucumis sativus* L.)叶片提取物没有响应. PsoR邻近的*pip*基因启动子区并不含有*lux-box*序列, 因此这可能是*pip*不受PsoR调控的原因^[122]. 中华根瘤菌也含有编码LuxR solo蛋白NesR的基因, 其邻近的上下游基因各有一个*pip*, *pip*基因启动子区都有*lux-box*元件^[121]. NesR增强细菌的胁迫适应以及竞争结瘤的能力, 但对宿主植物的信号分子无响应^[121]. 猕猴桃(*Actinidia chinensis*)病原菌*P. syringae* pv. *actinidiae* (Psa)含有3个LuxR solos蛋白, 对于细菌的致病性发挥有重要作用, 其中PsaR2属于PAB的LuxR solos蛋白亚家族, 能结合并响应未知的植物信号分子^[124]. 棉白杨的内生菌*P. sp.* strain GM79含有一个LuxR solo蛋白PipR, 当植物叶片浸渍液而非AHLs存在时, *pipR*邻近的基因*pipA*受到*pipR*诱导表达^[126]. 一种新的植物相关的生物防控菌产酶溶杆菌(*Lysobacter enzymogenes*), 也含有LuxR solo蛋白LesR, 过表达*lesR*影响热稳定性抗真菌因子(HSAF)的生物合成, 加速细胞的聚集及黑色素素的产生. LesR还影响DF介导的细胞-细胞之间的信号通路, 尽管LesR直接响应的信号分子尚不清楚^[127].

4 群体感应淬灭

干扰QS信号通路的方式称为群体感应淬灭^[129], 它可以抑制QS所调控的细菌与宿主之间的相互作用. 引起QS淬灭有很多种方式, 例如, 植物产生并分泌许多天然化合物, 通过模拟QS信号分子阻止细菌靶标基因的表达^[89,94]. 另外, 人工合成的AHLs结构类似物也

有相似的功能^[130]. 最近开发的一种高通量筛选AHL合成酶抑制剂的方法^[131], 可以直接观察候选化合物的效果, 为AHL-降解酶的研究提供了一种有效的检测方法. 依据AHLs的结构特征, AHLs的降解发生在4个位置^[132]: 内酯酶和脱羧酶介导酰基高丝氨酸内酯环的降解, 酰基转移酶和脱氨酶切开脂肪酸链部分^[132]. 目前已经鉴定的细菌AHL-内酯酶可分成两类: *aiiA*基因编码的内酯酶AiiA家族和AttM家族. 其中AiiA, 最初发现于芽孢杆菌中^[131], AttM家族蛋白起初在根癌农杆菌中得到鉴定^[133]. *aiiA*基因在铜绿假单胞菌中的表达, 能够影响铜绿假单胞菌的致病力及生物膜的形成^[134]. AHL酰基转移酶的活性在革兰氏阴性菌和革兰氏阳性菌中均有发现, 表明不同细菌产生的各种各样的酰基转移酶都有AHL降解能力^[135~139]. 红球菌属(*Rhodococcus*)不同于其他的细菌, 是因为它含有3种AHL-降解活性, 包括内酯酶、酰基转移酶和氧化还原酶^[140,141]. AHL-氧化还原酶将3-氧基-AHL转换成3-羟基衍生物. 在营养贫瘠的环境中, AHL降解产物为细菌的生长提供碳源和能量, 这也部分解释了无AHL产生能力的细菌中含有AHL-降解活性的原因. 植物产生的脂肪酸酰胺水解酶(fatty acid amide hydrolase, FAAH)可以将AHL降解成L-高丝氨酸, 低浓度的L-高丝氨酸通过激活植物的蒸腾作用促进生长, 而高浓度L-高丝氨酸通过激活乙烯产生抑制植物的生长^[142].

DSF调控系统是由*rpf*基因簇编码的产物构成的. RpfF同时含有酰基-ACP硫酯酶和脱水酶活性, 负责合成DSF信号分子及DSF衍生物^[143]. RpfB作为脂肪酰-CoA连接酶发挥作用, 催化脂肪酸的 β -氧化产生酰基-CoA, 参与DSF-家族信号分子的循环及脂类代谢^[143,144]. 这些研究表明, DSF-型的QS信号的精细调控对细菌适应变化的环境是非常重要的. 过表达*rpfB*能够抑制DSF的产生, 这是一种淬灭DSF信号的方法^[143].

5 通过分子对接预测LuxR蛋白新的配体化合物

虽然序列比对分析结果显示, 在QS系统LuxRs家族蛋白中有9个氨基酸是保守的, 但是LuxR受体蛋白在氨基酸序列上具有较低的相似性(18%~25%)^[5,145]. 所

有的LuxRs蛋白都包含自诱导子结合结构域和DNA结合结构域,表明它们可能作为信号分子开关调控基因的表达.根瘤农杆菌中TraR蛋白是第一个被解析出晶体结构的LuxR家族蛋白,通过结合自诱导子,并以二聚体形式结合到下游基因启动子的顺式作用元件发挥作用^[145,146].已有越来越多的LuxR蛋白的结构得到解析,数据存于PDB蛋白质数据库中^[147].这些LuxRs的3D晶体结构非常保守,其自诱导子结构域包括5个反向平行的 β -折叠片以及分布于两侧的每侧3个 α -螺旋.基于同源性的蛋白模式结构,对于尚未解析的LuxR蛋白的结构预测有重要价值.基于已知蛋白结构来推测未知蛋白结构的算法包括MODELLER, SWISS-MODEL, ModWeb, ModPipe和M4T^[148-152]等.预测的LuxR三维结构有利于通过分子对接的方法来分析蛋白与配体之间的相互作用,候选配体对接到蛋白的能力可利用Libdock^[153-155]方法进行评估.最近的在LuxR蛋白与其所识别的植物衍生信号分子的相互作用的研究中,对几种植物相关细菌的LuxRs蛋白可能结合的信号分子进行了预测^[156],其中迷迭香酸与铜绿假单胞菌的RhIR自诱导子结合结构域的生物信息学的对接预测已经得到实验验证^[99].生物信息学预测方法的发展,有助于深入挖掘更多的潜在信号分子.

6 结束语

共生和致病是植物与细菌相互作用的重要方面,跨界信号调控与该过程有关,而细菌的QS有利于细菌与植物之间的跨界信号交流.细菌的QS信号分子,如AHLs, DSFs影响植物的生长和免疫;植物产生的化学物质也可以被细菌的QS系统响应,影响细菌的生理过程.事实上,相互作用的植物和细菌面临相同的环境,两者均能产生大量低分子量的化学物质,而破译相互交流的化学语言在该领域未来研究中具有一定的挑战性.

包括LuxR solos在内的所有LuxRs蛋白,都包含保守的自诱导子结合结构域和DNA结合结构域,作为信号调节开关能够调控细菌的基因表达.最近的研究发现,植物相关细菌LuxR solos蛋白,特异地响应特定植物的信号分子而非经典的QS配体.利用生物信息学预测方法有望揭示与LuxRs家族蛋白直接相互作用的候选小分子.基于已知的LuxRs结构数据重塑未知蛋白的三维结构,并通过分子对接分析参与配体结合的直接位点,对于模拟蛋白与配体的相互作用研究有重要价值.在未来农业生产上,通过淬灭信号分子阻断跨界信号调控途径来控制植物细菌病害的方法具有广阔的应用前景.

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