微生物学通报

Microbiology China tongbao@im.ac.cn http://journals.im.ac.cn/wswxtbcn







细菌胞外多糖生物合成转录调控因子研究进展

杜心恬 宋馨 刘欣欣 夏永军 艾连中 熊智强*

上海理工大学医疗器械与食品学院 上海食品微生物工程研究中心 上海 200093

摘 要: 细菌胞外多糖(Exopolysaccharide, EPS)因其独特的理化特性和生理活性,在食品、制药和 化工等领域广泛应用。在食品行业中,黄原胶、结冷胶和热凝胶等细菌 EPS 备受青睐。转录调控因 子能在转录水平上调控 eps 基因的表达,影响细菌 EPS 的生物合成。目前细菌 EPS 转录调控因子的 研究报道较少,且多数已知的 EPS 转录因子调控机制尚未阐明。本文总结了近年来细菌 EPS 调控因 子的研究进展,重点介绍其研究方法和调控机制,以期为细菌 EPS 转录调控研究提供借鉴。

关键词:细菌胞外多糖,生物合成,转录调控因子,调控机制

Advances in transcription regulators of bacterial exopolysaccharides biosynthesis

DU Xintian SONG Xin LIU Xinxin XIA Yongjun AI Lianzhong XIONG Zhiqiang *

Shanghai Engineering Research Center for Food Microbidogy, School of Medical Instrument and Food Engineering, University of Shanghai for Science and Technology, Shanghai 200093, China

Abstract: Bacterial exopolysaccharides (EPS) are widely used in food, pharmaceutical, and chemical fields due to their unique physicochemical properties and physiological activities. Bacterial EPS such as xanthan gum, gellan gum, and thermal gel are widely applied and favored in food industry. Transcriptional regulators can regulate the expression of *eps* genes at transcription level to affect bacterial EPS biosynthesis. Moreover, the regulatory mechanism of most reported EPS transcriptional regulators has not been elucidated. This review summarizes the progress of bacterial EPS transcriptional regulators in recent years and focuses on the research methods and regulatory mechanisms, in order to provide reference for transcription regulation research of bacterial EPS.

Keywords: bacterial exopolysaccharides, biosynthesis, transcription regulators, regulation mechanism

	细菌	胞外多	\$糖(Exc	opolysaccl	haride,	EPS)	是细
菌	自身合	成并分	泌到细	胞外的糖	善类化合	物,	包括
粘泽	夜多糖	和荚膜	氢糖。	根瘤菌、	乳酸菌	f和假	单胞

菌等细菌是常见的 EPS 来源菌。作为一种备受青睐的天然食品添加剂^[1],细菌 EPS 可作为增稠剂和稳定剂用于改变产品的质构^[2-3]。细菌 EPS 也是安

Foundation items: National Natural Science Foundation of China (31871776, 31972101); Shanghai Natural Science Foundation (18ZR1426800)

^{*}Corresponding author: E-mail: xiongzq@hotmail.com

Received: 01-03-2020; Accepted: 15-05-2020; Published online: 10-08-2020

基金项目: 国家自然科学基金(31871776, 31972101); 上海市自然科学基金(18ZR1426800)

^{*}通信作者: E-mail: xiongzq@hotmail.com

收稿日期: 2020-03-01; 接受日期: 2020-05-15; 网络首发日期: 2020-08-10

全的"粘性"发酵剂^[4],能在发酵过程中显著改善乳制品的风味和品质^[5]。其中,黄原胶、结冷胶和热凝胶等细菌 EPS 由于产量高、成本低等优点在食品工业中广泛应用。

根据单糖组成,细菌 EPS 可分为同型多糖和 异型多糖。同型多糖(如热凝胶、葡聚糖和果聚糖) 在胞外直接合成,无须脂载体参与,主要通过对 应的糖基转移酶完成 EPS 的合成; 而异型多糖(如 黄原胶和结冷胶)都是脂载体依赖型胞内合成,需 要糖核苷酸前体、酶催化系统、酰基供体、脂载 体和糖基受体,其合成包括糖核苷酸前体的胞内 合成、重复单元的合成和多糖的延伸、聚合及输 出^[6]。细菌 EPS 生物合成由 eps 基因簇控制,包括 调控基因、链长决定基因、重复单元合成基因、 聚合和输出基因,而且不同细菌中 eps 基因簇的数 量和种类有所差异^[7-8]。Song 等^[9]发现干酪乳杆菌 (Lactobacillus casei) eps 基因簇中 3 个关键基因对 EPS 生物合成至关重要。Xiong 等^[10-11]完成了嗜热 链球菌(Streptococcus thermophilus) S-3 的 EPS 及其 前体生物合成基因簇和表型分析。Kong 等^[12]利用 强组成型启动子同时表达了嗜热链球菌 eps 基因簇 中 2 个关键基因, 显著提高了 EPS 的合成。细菌 eps 基因簇的深入研究为探索 EPS 生物合成的转录 调控奠定了基础。

转录调控因子是一类具有转录调节活性的蛋 白质,参与调控细菌内糖、脂和碳代谢等重要生 理活动^[13]。调控因子与 *eps* 基因簇中靶基因位点结 合,启动 *eps* 基因的转录及控制其转录效率,从而 调控细菌 EPS 的生物合成^[14]。但目前仅少数细菌 EPS 调控因子被鉴定,且调控机制尚未阐明,尚有 大量未知的 EPS 调控因子亟待研究。本文主要从 细菌 EPS 调控因子的研究方法和调控机制展开综 述,为深入研究细菌 EPS 转录调控提供参考。

1 细菌 EPS 生物合成转录调控因子的信号 传导调控机制

转录因子调控 EPS 生物合成的过程中,调控 蛋白对靶基因的识别和结合是调控机制的核心。 调控蛋白含有特殊构象的结构域,能特异性识别 并结合靶基因中对应的结合位点(保守短序列片 段,Motif)^[14],调控靶基因表达。许多调控蛋白家 族有相似的结合结构域,与 EPS 生物合成密切相 关(表 1)。通过信号分子传导,调控因子影响 RNA 聚合酶识别特定短序列片段,对下游编码基因的 转录表达进行正/负调控。EPS 转录因子调控机制 中,存在 3 类经典的信号传导机制:群体感应系 统、双组分系统和第二信使分子传导系统。

1.1 群体感应系统

群体感应(Quorum Sensing)是细菌因自身种群 密度变化,利用信号分子调控基因表达的机制, 参与调控 EPS 生物合成、抗生素合成和生物膜发 育等代谢过程。群体感应系统中,细菌合成的信

表1 细菌中常见的调控因子

Table 1	Common regulatory factors in bacteria						
Family	Action	Binding domain conformation	Regulation function	References			
LuxR	+	HTH	Quorum sensing, biofilm formation, and metabolism	[15-17]			
TetR	-	HTH	Antibiotic synthesis, biofilm formation, and osmotic stress	[18-19]			
GntR	-	HTH	General metabolism, CPS synthesis, and virulence	[20-21]			
LacI	-	НТН	Carbon source utilization, virulence, cell activity, and carbohydrate metabolism	[22-24]			
DeoR	-	HTH	Antibiotic synthesis and carbohydrate metabolism	[25-27]			
ArsR	-	HTH	Metal and acid resistance	[28-30]			
LysR	+/	НТН	Carbon and nitrogen metabolism, biofilm formation, and flagellar movement	[31-33]			
OmpR	+	Winged helix	Heavy metal, CPS synthesis, and virulence	[34-35]			

号分子及其感应机制可分为3类:G⁻细菌的酰基高 丝氨酸内酯类信号分子 (N-Acyl-Homoserine Lactones, AHL)系统、G⁺细菌的寡肽类信号分子 (Autoinducing Peptides, AIP)系统和细菌通用信号 分子 AI-2 系统。Licciardello 等^[17]在波纹假单胞菌 (Pseudomonas corrugata) 中发现,信号系统 PcoI/AHL 和 LuxR 家族调控因子 PcoR 组成群体感 应系统,调节海藻酸钠生物合成。在苜蓿根瘤菌 (Rhizobium meliloti)中, 信号系统 SinI/AHL 与调控 因子 ExpR 组成的群体感应系统,调控细菌内多种 EPS 的生物合成^[36]。此外,一些细菌中同时存在 多种不同的信号分子调节机制。例如, 霍乱弧菌 (Vibrio cholerae)中存在3种参与调控因子 LuxO调 控细菌 EPS 合成和生物膜形成的群体感应系统: CqsA/CAI-1 (AHL 类信号分子)、LuxS/AI-2 和一种 未知的信号系统^[37]。

1.2 双组分调控系统

双组分系统是细菌适应体内外环境变化的重要信号传导系统,一般由组氨酸激酶与应答调控 蛋白组成,通过双组分蛋白磷酸化传递信号,调 控胞内基因表达(图1)^[38-39]。Black等^[40]在黄色粘球

菌(Myxococcus xanthus)中发现途径特异性 EPS 调 控因子 EpsW 和组氨酸激酶 DifE, EpsW 被 DifE 激 活后调控 EPS 合成。转录调控因子 RcsB 与激酶 RcsC 组成双组分系统,协同 LuxR 家族调控因子 RcsA 共同激活大肠杆菌(Escherichia coli)荚膜多糖 基因簇的表达^[41]。淀粉液化芽孢杆菌(Bacillus amyloliquefaciens) SQR9 中存在双组分调控系统 ResDE, ResD 被激酶 ResE 激活后促进生物膜形 成, 潜在调控 EPS^[42]。VicRK (调控因子 VicR 和激 酶 VicK)、ComDE (调控因子 ComE 和激酶 ComD) 和 CiaRH (调控因子 CiaR 和激酶 CiaH)等双组分系 统在乳酸菌中调控多糖合成等多种代谢过程^[43]。 此外,细菌中也存在非典型的 EPS 双组分调控系 统,如 Minic 等^[44]发现嗜热链球菌 eps 基因簇上的 酪氨酸激酶 EpsD 可激活调控蛋白 EpsE,调控 EPS 合成。本课题组过表达嗜热链球菌 eps 基因簇上关 键基因 epsA 和 epsE, 能显著提高 EPS 的合成, 其中 epsA编码途径特异性调控因子 EpsA^[12]。此外,我们 利用构建的 CRISPR-Cas9 基因编辑系统解析了干酪 乳杆菌 LC2W 中 EPS 合成关键基因^[45],也发现基因 簇上存在途径特异性调控因子 LC2W 2170^[9]。



图 1 经典双组分调控体系

Figure 1 Classical two-component regulation system

1.3 第二信号分子传导系统

第二信使分子与细胞表面的受体结合后,通 过受体信号的转导形成信号通路, 调控胞外蛋白 和 EPS 分泌。其中,环二鸟苷酸(c-di-GMP)和环磷 酸二腺苷(c-di-AMP)在细菌 EPS 调控中最为常见。 Schäper 等^[46]在草木樨中华根瘤菌(Sinorhizobium meliloti)中发现, AraC 家族调控因子 CuxR 的二聚 体在 c-di-GMP 的作用下调控细菌 EPS。恶臭假单 胞菌(P. putida) KT2440 中, c-di-GMP 抑制调控因 子 FleQ 与 EPS 合成基因 bcs 启动子的结合^[47]。铜 绿假单胞菌(P. aeruginosa)中, c-di-GMP 抑制 FleQ 负调控 EPS 基因簇上 pel 在内的多个基因^[48]。Fazli 等^[49]发现 c-di-GMP 在新生伯克霍尔德菌 (Burkholderia cepacia)中通过转录调控因子级联调 节 EPS 合成: c-di-GMP 首先激活 BerB-RpoN 体系 控制 berA 编码调控因子 BerA, BerA 再与 c-di-GMP结合,促进EPS合成基因bep转录表达。 与已鉴定出数百种结合蛋白的 c-di-GMP 不同, 迄

与C 鉴定田数日种结合蛋白的 c-dl-GMP 不问, 迄 今为止在细菌中只发现了少数与 c-di-AMP 作用的 EPS 调控因子。在变形链球菌中, c-di-AMP 与受 体蛋白 CabPA 相互作用,影响转录因子 VicR 调控 EPS 合成中关键基因 *gtfB* (编码葡萄糖基转移酶)的 表达^[50]。同样在变形链球菌(*S. mutans*)中, Cheng 等^[51]和 Rismondo 等^[52]发现调控因子 CdaR 调控单 二磷酸环化酶CdaA 的合成,并通过 c-di-AMP 信号 网络调控氧化反应和 EPS 生物合成。金黄色葡萄 球菌 KdpDE 双组分系统中的组氨酸激酶 KdpD 也 是 c-di-AMP 受体蛋白,参与调控荚膜多糖生物合 成与生物膜形成^[53]。

2 细菌 EPS 生物合成转录调控因子的研究 方法

在基因调控过程中,转录调控因子作用的本 质是蛋白质-DNA 相互作用。研究调控因子常见的 方法及其优缺点见表 2。目前染色质免疫沉淀、 DNA 亲和层析技术和凝胶阻滞实验在细菌 EPS 调 控因子的研究中应用最为广泛。

2.1 染色质免疫沉淀

染色质免疫沉淀技术 (Chromatin Immunoprecipitation Assay, ChIP)在体内研究调控 因子-靶 DNA 相互作用, 与微阵列芯片 (ChIP-on-chip)或高通量测序(ChIP-seq)结合,能准 确分析细菌内调控因子的靶基因位点,构建基因 表达调控网络。Partridge 等^[54]利用 ChIP-on-chip 分 析得到大肠杆菌调控因子 NsrR 的结合位点 (AANATGCATTT),该位点存在于细胞膜发育基因 mqsR-ygiT 的启动子区域,潜在调控 EPS 合成。 ChIP-seq 识别伤寒沙门氏菌(Salmonella typhi)与渗 透压响应调控因子 OmpR 相互作用的靶点,其中包 括 gltA (柠檬酸合酶基因)、sdhC (琥珀酸脱氢酶基 因)和tviA(Vi多糖生物合成蛋白基因)等多个与EPS 生物合成相关基因^[55]。在假单胞菌中, ChIP-seq 证明全局调节因子 AlgR 不仅直接调控海藻酸钠合 成和毒力因子表达,还能与 c-di-GMP 相互作用间 接调控 EPS 生物合成^[56]。

2.2 DNA 亲和层析技术

DNA 亲和层析能分离与特定 DNA 序列作用的 蛋白质,利用细菌 eps 基因启动子片段可寻找未知 的 EPS 调控因子^[57]。Wu 等^[58]在肺炎链球菌(S. pneumoniae) D39 中用 5′生物素化的荚膜多糖基因 簇启动子 cpsp 亲和层析,筛选得到6个候选调控因 子,其中 CpsR 通过结合 cps 基因簇阻遏荚膜多糖 的生物合成。在金黄色葡萄球菌(Staphylococcus aureus)中,生物素化的 psm (酚溶性模块蛋白基 因,参与细胞膜形成)操纵子亲和层析筛选出调控 蛋白 MgrA, MgrA 通过抑制 psm 表达阻遏生物膜 形成,潜在调控 EPS 合成^[59]。在铜绿假单胞菌 中,细胞分裂基因 ftsZ 启动子区域亲和层析得到调 控因子 LexA,并通过 DNase I 足迹法分析出其 DNA 结合位点(LexA Box),该位点存在于多个 EPS 合成基因中^[60]。

研究方法		缺点		
Methods	Advantages	Disadvantages		
凝胶阻滞实验	体外快速研究 DNA 与蛋白质相互作用, 特异性强	不能真实反映体内情况,不能确定靶序列,结论单一		
EMSA	Rapid detection in vitro, strong specificity	Cannot reflect the situation <i>in vivo</i> and identify the target motif		
DNA 微阵列技术	有效确定下游靶基因	不能直观体现作用机制,昂贵且分析要求高		
DNA microarray	Effective determination of downstream target genes	Cannot directly reflect the mechanism of action, expensive and high analysis requirements		
酵母单杂交技术	确定 DNA-蛋白质相互作用,提供蛋白前体的折叠	非酵母体系中准确率低		
Yeast one hybrid	和修饰	Low accuracy in the non-yeast system		
	Identification of DNA-protein interaction with folding and modification of protein precursors			
染色质免疫沉淀技术	显示 DNA-蛋白质在体内动态作用情况,确定靶基	难以获得特异性蛋白质抗体;调控蛋白的基因限制在		
ChIP	因结合位点	特定来源		
	Determination of dynamic action between DNA and protein <i>in vivo</i> and identification of the binding sites of tarret games	Difficult to obtain specific protein antibody and limited sources of specific gene for regulator		
DNA 亲和层析技术	活性物质纯度高、性质稳定、步骤简单有效	配基要求高,不可避免非特异性结合		
DNA affinity	High purity of active substances, property stability,	High requirements for ligand and inevitable non-specific		
RNA-seq	and simple operation 今其田组水亚的其田圭壮羊县研究 宁景准确	DINGING 左左按糖体 DNA 影响 天能直测体和相互作用		
num seq	可重复性高、检测范围广	Ribosomal RNA interference and cannot directly reflect		
	Gene expression differences at the genome level, quantitative accuracy, high repeatability, and wide-range detection	the interaction		
噬菌体展示技术	大量快速检测、蛋白结构和活性稳定	噬菌体文库的容量和遗传多样性有限制		
Phage display	Fast and simultaneous test, stability of protein structure and activity	Limited capacity and genetic diversity of phage library		
荧光素酶实验	靶动子和调控因子作用过程光信号强、信噪比高,	仅适用于转录激活检测,无法检测转录抑制		
Luciferase assay	同时分析多个信号转导通路	Only suitable for transcriptional activation detection,		
	Strong light signal and SNR for promoter-regulator interaction, multiple analysis of signal transduction nathways	inapplicable for transcriptional inhibition		
生物膜干涉技术	利用光干涉原理检测小分子间相互作用,灵敏度	样本纯度要求严格,易受非特异性结合影响		
Biolayer interferometry	高. 样本容量大	Limited sample purity, and easily affected by non-specific		
	Detection of molecular interaction based on light	binding		
	interference, large sample size			
扫描探针显微技术	原子级分辨率检测调控因子与靶基因作用,准确	检测环境和样本纯度要求高,不适用于大样本筛选		
Scanning probe microscope	率高	High requirements on test environment and sample purity,		
	Detection of DNA-regulator by atomic resolution, high accuracy	and unsuitable for large sample screening		
凝胶阻滞实验	体外快速研究 DNA 与蛋白质相互作用, 特异性强	不能真实反映体内情况,不能确定靶序列,结论单一		
EMSA	Rapid detection in vitro, strong specificity	Cannot reflect the situation <i>in vivo</i> and identify the target motif		

表 2 细菌 EPS 调控因子研究方法的优缺点

 Table 2
 Advantages and disadvantages of research methods for bacterial EPS regulators

2.3 凝胶阻滞实验

凝胶阻滞实验(Electrophoretic Mobility Shift Assay, EMSA)可以直观显示调控因子和 eps 基因

的相互作用,灵敏度高且特异性强。Zhou 等^[61]通 过 EMSA 证明调控因子 OpaR 和 AphA 与副溶血弧 菌(*V. parahaemolyticus*)荚膜多糖基因 *cpsQ* 启动子 区域有特异性结合。利用 EMSA 证明全局调控因 子 CcpA 能与肺炎链球菌 *cps* 启动子区域特异性结 合,参与调控细菌 EPS^[62]。转录抑制因子 NigR 经 EMSA 表明可特异性结合变形链球菌中糖转运和代 谢相关基因,潜在调控细菌 EPS^[63]。

3 问题和展望

目前细菌 EPS 转录调控研究仍有较大的局限 性,已报道的调控因子多集中在肺炎链球菌、金 黄色葡萄球菌和铜绿假单胞菌等毒力强的致病菌 中^[33,64-66], 而在乳酸菌、地衣芽孢杆菌(B. licheniformis) 和枯草芽孢杆菌(B. subtilis)等益生菌中鲜有报 道^[67-69],而且鉴定的多为荚膜多糖调控因子,粘液 多糖调控因子的报道较少。此外,细菌中还存在大 量 EPS 潜在或未知的调控因子亟待研究。例如,在 乳杆菌中发现的蔗糖代谢调节因子 ScrR^[70]和中枢 糖酵解基因调节因子 CggR^[71]可能与 EPS 生物合成 相关,但并未实验证实。我们在干酪乳杆菌和嗜热 链球菌 EPS 转录调控研究中,利用其 eps 启动子区 域 DNA 亲和层析发现多个不同类型的潜在调控因 子,包含未知调控因子和尚未证明与 EPS 合成相关 的调控因子,因此还需利用 EMSA 和 DNAase I Footprinting 等体内和体外技术方法进一步证实和 研究其调控机制。将荧光素酶实验、生物膜干涉技 术和扫描探针显微技术等分子生物学方法应用于 EPS 调控因子研究,有望鉴定出更多新颖的细菌 EPS 调控因子,为深入解析 EPS 生物合成调控网 络奠定基础。

REFERENCES

- Anadón A, Martínez-Larrañaga MR, Arés I, Martínez MA. Prebiotics and probiotics: an assessment of their safety and health benefits[A]//Watson RR, Preedy VR. Probiotics, Prebiotics, and Synbiotics[M]. London: Academic Press, 2016: 3-23
- [2] Dong YQ, Tuo YF, Mu GQ, Jiang SJ, Qian F, Song YL. Screening of exopolysaccharide-producing *Lactobacillus* strains and study of exopolysaccharide properties[J]. Modern Food Science & Technology, 2017, 33(2): 61-68 (in Chinese)

董阳勤, 妥彦峰, 牟光庆, 姜淑娟, 钱方, 宋莹龙. 产胞

外多糖乳杆菌的筛选及多糖功能的研究[J]. 现代食品科技, 2017, 33(2): 61-68

- [3] Zivkovic M, Miljkovic M, Ruas-Madiedo P, Strahinic I, Tolinacki M, Golic N, Kojic M. Exopolysaccharide production and ropy phenotype are determined by two gene clusters in putative probiotic strain *Lactobacillus paraplantarum* BGCG11[J]. Applied and Environmental Microbiology, 2015, 81(4): 1387-1396
- [4] Ale EC, Perezlindo MJ, Pavón Y, Peralta GH, Costa S, Sabbag N, Bergamini C, Reinheimer JA, Binetti AG. Technological, rheological and sensory characterizations of a yogurt containing an exopolysaccharide extract from *Lactobacillus fermentum* Lf2, a new food additive[J]. Food Research International, 2016, 90: 259-267
- [5] Zhang H, Ren W, Guo QB, Xiong ZQ, Wang GQ, Xia YJ, Lai P, Yin BX, Ai LZ. Characterization of a yogurt-quality improving exopolysaccharide from *Streptococcus thermophilus* AR333[J]. Food Hydrocolloids, 2018, 81: 220-228
- [6] Kong LH, Zhao LS, Xia YJ, Zhang H, Ai LZ, Xiong ZQ. Research advance in the exopolysaccharide biosynthesis of *Streptococcus thermophilus*[J]. Journal of Food Safety and Quality, 2019, 10(2): 284-290 (in Chinese) 孔令慧,赵林森,夏永军,张汇,艾连中,熊智强. 嗜热 链球菌胞外多糖生物合成的研究进展[J]. 食品安全质量 检测学报, 2019, 10(2): 284-290
- [7] Schmid J. Recent insights in microbial exopolysaccharide biosynthesis and engineering strategies[J]. Current Opinion in Biotechnology, 2018, 53: 130-136
- [8] Lebellenger L, Verrez-bagnis V, Passerini D, Delbarre-Ladrat C. Comparative genomics reveals a widespread distribution of an exopolysaccharide biosynthesis gene cluster among *Vibrionaceae*[J]. BMC Research Notes, 2018, 11(1): 102
- [9] Song X, Xiong ZQ, Kong LH, Wang GQ, Ai LZ. Relationship between putative *eps* genes and production of exopolysaccharide in *Lactobacillus casei* LC2W[J]. Frontiers in Microbiology, 2018, 9: 1882
- [10] Xiong ZQ, Kong LH, Meng HL, Cui JM, Xia YJ, Wang SJ, Ai LZ. Comparison of gal-lac operons in wild-type galactose-positive and -negative Streptococcus thermophilus by genomics and transcription analysis[J]. Journal of Industrial Microbiology & Biotechnology, 2019, 46(5): 751-758
- [11] Xiong ZQ, Kong LH, Lai PFH, Xia YJ, Liu JC, Li QY, Ai LZ. Genomic and phenotypic analyses of exopolysaccharide biosynthesis in *Streptococcus thermophilus* S-3[J]. Journal of Dairy Science, 2019, 102(6): 4925-4934
- [12] Kong LH, Xiong ZQ, Song X, Xia YJ, Zhang N, Ai LZ. Characterization of a panel of strong constitutive promoters from *Streptococcus thermophilus* for fine-tuning gene expression[J]. ACS Synthetic Biology, 2019, 8(6):

1469-1472

- [13] Ikawa Y, Tsuge S. The quantitative regulation of the *hrp* regulator HrpX is involved in sugar-source-dependent *hrp* gene expression in *Xanthomonas oryzae* pv. *oryzae*[J]. FEMS Microbiology Letters, 2016, 363(10): fnw071
- [14] Elmas A, Wang XD, Samoilov MS. Reconstruction of novel transcription factor regulons through inference of their binding sites[J]. BMC Bioinformatics, 2015, 16: 299
- [15] Subhadra B, Kim J, Kim DH, Woo K, Oh MH, Choi CH. Local repressor AcrR regulates AcrAB efflux pump required for biofilm formation and virulence in *Acinetobacter nosocomialis*[J]. Frontiers in Cellular and Infection Microbiology, 2018, 8: 270
- [16] Kleinman CL, Sycz G, Bonomi HR, Rodríguez RM, Zorreguieta A, Sieira R. ChIP-Seq analysis of the LuxR-type regulator VjbR reveals novel insights into the *Brucella* virulence gene expression network[J]. Nucleic Acids Research, 2017, 45(10): 5757-5769
- [17] Licciardello G, Caruso A, Bella P, Gheleri R, Strano CP, Anzalone A, Trantas EA, Sarris PF, Almeida NF, Catara V. The LuxR regulators PcoR and RfiA co-regulate antimicrobial peptide and alginate production in *Pseudomonas corrugata*[J]. Frontiers in Microbiology, 2018, 9: 521
- [18] Liu JL, Stone VN, Ge XC, Tang M, Elrami F, Xu P. TetR family regulator *BrpT* modulates biofilm formation in *Streptococcus sanguinis*[J]. PLoS One, 2017, 12(1): e0169301
- [19] Taylor DL, Ante VM, Bina XR, Howard MF, Bina JE. Substrate-dependent activation of the *Vibrio cholerae vexAB* RND efflux system requires *vexR*[J]. PLoS One, 2015, 10(2): e0117890
- [20] Taw MN, Lee HI, Lee SH, Chang WS. Characterization of MocR, a GntR-like transcriptional regulator, in *Bradyrhizobium japonicum*: its impact on motility, biofilm formation, and soybean nodulation[J]. Journal of Microbiology, 2015, 53(8): 518-525
- [21] Tsypik O, Makitrynskyy R, Bera A, Song LJ, Wohlleben W, Fedorenko V, Ostash B. Role of GntR family regulatory gene SCO1678 in gluconate metabolism in Streptomyces coelicolor M145[J]. BioMed Research International, 2017, 2017: 9529501
- [22] Fillenberg SB, Grau FC, Seidel G, Muller YA. Structural insight into operator *dre*-sites recognition and effector binding in the GntR/HutC transcription regulator NagR[J]. Nucleic Acids Research, 2015, 43(2): 1283-1296
- [23] Kuge T, Teramoto H, Inui M, Zhulin IB. AraR, an L-arabinose-responsive transcriptional regulator in *Corynebacterium glutamicum* ATCC 31831, exerts different degrees of repression depending on the location of its binding sites within the three target promoter regions[J]. Journal of Bacteriology, 2015, 197(24): 3788-3796
- [24] Wilson CM, Klingeman DM, Schlachter C, Syed MH, Wu

CW, Guss AM, Brown SD, Parales RE. LacI transcriptional regulatory networks in *Clostridium thermocellum* DSM1313[J]. Applied and Environmental Microbiology, 2016, 83(5): e02751-16

- [25] Kaznadzey A, Shelyakin P, Belousova E, Aleksandra E, Shvyreva U, Bykova D, Emelianenko V, Korosteleva A, Tutukina M, Gelfand MS. The genes of the sulphoquinovose catabolism in *Escherichia coli* are also associated with a previously unknown pathway of lactose degradation[J]. Scientific Reports, 2018, 8(1): 3177
- [26] Hirooka K, Kodoi Y, Satomura T, Fujita Y. Regulation of the *rhaEWRBMA* operon involved in L-rhamnose catabolism through two transcriptional factors, RhaR and CcpA, in *Bacillus subtilis*[J]. Journal of Bacteriology, 2016, 198(5): 830-845
- [27] Turner SE, Pang YY, O'Malley MR, Weisberg AJ, Fraser VN, Yan Q, Chang JH, Anderson JC. A DeoR-Type transcription regulator is required for sugar-induced expression of type III secretion-encoding genes in *Pseudomonas syringae* pv. tomato DC3000[J]. Molecular Plant-Microbe Interactions, 2020, 33(3): 509-518
- [28] Sai R, Li QM, Xie LX, Xie JP. Molecular mechanisms underlying the function diversity of ArsR family metalloregulator[J]. Critical Reviews in Eukaryotic Gene Expression, 2017, 27(1): 19-35
- [29] Servetas SL, Carpenter BM, Haley KP, Gilbreath JJ, Gaddy JA, Merrell DS, Silhavy TJ. Characterization of key *Helicobacter pylori* regulators identifies a role for ArsRS in biofilm formation[J]. Journal of Bacteriology, 2016, 198(18): 2536-2548
- [30] Li QM, Li CY, Xie LX, Zhang CH, Feng YH, Xie JP. Characterization of a putative ArsR transcriptional regulator encoded by *Rv2642* from *Mycobacterium tuberculosis*[J]. Journal of Biomolecular Structure and Dynamics, 2017, 35(9): 2031-2039
- [31] Mao DN, Bushin LB, Moon K, Wu YH, Seyedsayamdost MR. Discovery of *ScmR* as a global regulator of secondary metabolism and virulence in *Burkholderia thailandensis* E264[J]. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114(14): E2920-E2928
- [32] Park H, Do E, Kim M, Park HJ, Lee J, Han SW. A LysR-type transcriptional regulator LcrX is involved in virulence, biofilm formation, swimming motility, siderophore secretion, and growth in sugar sources in *Xanthomonas axonopodis* pv. glycines[J]. Frontiers in Plant Science, 2019, 10: 1657
- [33] Yang XJ, Zhang ZQ, Huang ZW, Zhang XX, Li DH, Sun L, You JJ, Pan XW, Yang HJ. A putative LysR-type transcriptional regulator inhibits biofilm synthesis in *Pseudomonas aeruginosa*[J]. Biofouling, 2019, 35(5): 541-550
- [34] Zhang Y, Xia L, Lin LP, Tang H, Osei-Adjei G, Xu SG,

Zhang YQ, Huang XX. Reciprocal regulation of OmpR and Hfq and their regulatory actions on the Vi polysaccharide capsular antigen in *Salmonella enterica* Serovar Typhi[J]. Current Microbiology, 2018, 75(6): 773-778

- [35] Tipton KA, Rather PN. An ompR-envZ two-component system ortholog regulates phase variation, osmotic tolerance, motility, and virulence in Acinetobacter baumannii strain AB5075[J]. Journal of Bacteriology, 2017, 199(3): e00705-16
- [36] Charoenpanich P, Meyer S, Becker A, Matthew M. Temporal expression program of quorum sensing-based transcription regulation in *Sinorhizobium meliloti*[J]. Journal of Bacteriology, 2013, 195(14): 3224-3236
- [37] Solano C, Echeverz M, Iñigo L. Biofilm dispersion and quorum sensing[J]. Current Opinion in Microbiology, 2014, 18: 96-104
- [38] Haag AF, Bagnoli F. The role of two-component signal transduction systems in *Staphylococcus aureus* virulence regulation[A]//Bagnoli F, Rappuoli R, Grandi G. Staphylococcus Aureus[M]. Cham: Springer, 2017: 145-198
- [39] Wei CF, Tsai YH, Tsai SH, Lin CS, Chang CJ, Lu CC, Huang HC, Lai HC. Cross-talk between bacterial two-component systems drives stepwise regulation of flagellar biosynthesis in swarming development[J]. Biochemical and Biophysical Research Communications, 2017, 489(1): 70-75
- [40] Black WP, Wang LL, Davis MY, Yang ZM. The orphan response regulator EpsW is a substrate of the DifE kinase and it regulates exopolysaccharide in *Myxococcus xanthus*[J]. Scientific Reports, 2016, 5: 17831
- [41] Pannen D, Fabisch M, Gausling L, Karin S. Interaction of the RcsB response regulator with auxiliary transcription regulators in *Escherichia coli*[J]. The Journal of Biological Chemistry, 2016, 291(5): 2357-2370
- [42] Zhou X, Zhang N, Xia LM, Li Q, Shao JH, Shen QR, Zhang RF. ResDE two-component regulatory system mediates oxygen limitation-induced biofilm formation by *Bacillus amyloliquefaciens* SQR9[J]. Applied and Environmental Microbiology, 2018, 84(8): e02744-17
- [43] Monedero V, Revilla-Guarinos A, Zúñiga M. Physiological role of two-component signal transduction systems in food-associated lactic acid bacteria[J]. Advances in Applied Microbiology, 2017, 99: 1-51
- [44] Minic Z, Marie C, Delorme C, Faurie JM, Mercier G, Ehrlich D, Renault P. Control of EpsE, the phosphoglycosyltransferase initiating exopolysaccharide synthesis in *Streptococcus thermophilus*, by EpsD tyrosine kinase[J]. Journal of Bacteriology, 2007, 189(4): 1351-1357
- [45] Song X, Huang H, Xiong ZQ, Ai LZ, Yang S. CRISPR-Cas9^{D10A} nickase-assisted genome editing in *Lactobacillus casei*[J]. Applied and Environmental Microbiology, 2017, 83(22): e01259-17
- [46] Schäper S, Steinchen W, Krol E, Altegoer F, Skotnicka D,

Sogaard-Andersen L, Bange G, Becker A. AraC-like transcriptional activator CuxR binds c-di-GMP by a PilZ-like mechanism to regulate extracellular polysaccharide production[J]. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114(24): E4822-E4831

- [47] Xiao YJ, Nie HL, Liu HZ, Luo XS, Chen WL, Huang QY. c-di-GMP regulates the expression of *lapA* and *bcs* operons via FleQ in *Pseudomonas putida* KT2440[J]. Environmental Microbiology Reports, 2016, 8(5): 659-666
- [48] Baraquet C, Harwood CS. FleQ DNA binding consensus sequence revealed by studies of FleQ-dependent regulation of biofilm gene expression in *Pseudomonas aeruginosa*[J]. Journal of Bacteriology, 2015, 198(1): 178-186
- [49] Fazli M, Rybtke M, Steiner E, Weidel E, Berthelsen J, Groizeleau J, Wu B, Zhi BZ, Zhang YM, Kaever V, et al. Regulation of *Burkholderia cenocepacia* biofilm formation by RpoN and the c-di-GMP effector BerB[J]. MicrobiologyOpen, 2017, 6(4): e00480
- [50] Peng X, Zhang Y, Bai GC, Zhou XD, Wu H. Cyclic di-AMP mediates biofilm formation[J]. Molecular Microbiology, 2016, 99(5): 945-959
- [51] Cheng XQ, Zheng X, Zhou XD, Zeng JM, Ren Z, Xu X, Cheng L, Li MY, Li JY, Li YQ. Regulation of oxidative response and extracellular polysaccharide synthesis by a diadenylate cyclase in *Streptococcus mutans*[J]. Environmental Microbiology, 2016, 18(3): 904-922
- [52] Rismondo J, Gibhardt J, Rosenberg J, Kaever V, Halbedel S, Commichau FM. Phenotypes associated with the essential diadenylate cyclase CdaA and its potential regulator CdaR in the human pathogen *Listeria monocytogenes*[J]. Journal of Bacteriology, 2016, 198(3): 416-426
- [53] Moscoso JA, Schramke H, Zhang Y, Tosi T, Dehbi A, Jung K, Gründling A. Binding of cyclic di-AMP to the *Staphylococcus aureus* sensor kinase KdpD occurs via the universal stress protein domain and downregulates the expression of the Kdp potassium transporter[J]. Journal of Bacteriology, 2016, 198(1): 98-110
- [54] Partridge JD, Bodenmiller DM, Humphrys MS, Spiro S. NsrR targets in the *Escherichia coli* genome: new insights into DNA sequence requirements for binding and a role for NsrR in the regulation of motility[J]. Molecular Microbiology, 2009, 73(4): 680-694
- [55] Perkins TT, Davies MR, Klemm EJ, Rowley G, Wileman T, James K, Keane T, Maskell D, Hinton JCD, Dougan G, et al. ChIP-seq and transcriptome analysis of the OmpR regulon of *Salmonella enterica* serovars Typhi and Typhimurium reveals accessory genes implicated in host colonization[J]. Molecular Microbiology, 2013, 87(3): 526-538
- [56] Kong WN, Zhao JR, Kang HP, Zhu M, Zhou TH, Deng X, Liang HH. ChIP-seq reveals the global regulator AlgR mediating cyclic di-GMP synthesis in *Pseudomonas aeruginosa*[J]. Nucleic Acids Research, 2015, 43(17):
- Tel: 010-64807511; E-mail: tongbao@im.ac.cn; http://journals.im.ac.cn/wswxtbcn

8268-8282

- [57] Zhang QH, Huang Q, Fang Q, Li HT, Tang H, Zou G, Wang D, Li SQ, Bei WC, Chen HC, et al. Identification of genes regulated by the two-component system response regulator NarP of *Actinobacillus pleuropneumoniae* via DNA-affinity-purified sequencing[J]. Microbiological Research, 2020, 230: 126343
- [58] Wu KF, Xu HM, Zheng YQ, Wang LB, Zhang XM, Yin YB. CpsR, a GntR family regulator, transcriptionally regulates capsular polysaccharide biosynthesis and governs bacterial virulence in *Streptococcus pneumoniae*[J]. Scientific Reports, 2016, 6: 29255
- [59] Jiang Q, Jin ZY, Sun BL. MgrA negatively regulates biofilm formation and detachment by repressing the expression of *psm* operons in *Staphylococcus aureus*[J]. Applied and Environmental Microbiology, 2018, 84(16): e01008-18
- [60] Honda T, Morimoto D, Sako Y, Yoshida T. LexA binds to transcription regulatory site of cell division gene *ftsZ* in toxic cyanobacterium *Microcystis aeruginosa*[J]. Marine Biotechnology, 2018, 20(4): 549-556
- [61] Zhou DS, Yan XJ, Qu F, Wang L, Zhang YQ, Hou J, Hu Y, Li J, Xin SJ, Qiu JF, et al. Quorum sensing modulates transcription of *cpsQ-mfpABC* and *mfpABC* in *Vibrio parahaemolyticus*[J]. International Journal of Food Microbiology, 2013, 166(3): 458-463
- [62] Wang LB, Xu HM, Wu KF, Zheng YQ, Wang JM, Ma F, Zhang XM, Yin YB, Zhang Q. Regulation effect of CcpA protein on the biosynthesis of capsular polysaccharide in *Streptococcus pneumoniae*[J]. Acta Microbiologica Sinica, 2015, 55(6): 732-738 (in Chinese)

王丽滨,徐红梅,吴凯峰,郑玉强,王建敏,马峰,张雪梅,尹一兵,张群. 肺炎链球菌糖代谢蛋白 CcpA 对荚膜 多糖的调控作用[J]. 微生物学报,2015,55(6):732-738

[63] Vujanac M, Iyer VS, Sengupta M, Ajdic D. Regulation of *Streptococcus mutans* PTS^{Bio} by the transcriptional repressor NigR[J]. Molecular Oral Microbiology, 2015, 30(4): 280-294

- [64] Peng D, Li X, Liu P, Zhou XP, Luo M, Su KW, Chen S, Zhang ZS, He Q, Qiu JF, et al. Transcriptional regulation of galF by RcsAB affects capsular polysaccharide formation in *Klebsiella pneumoniae* NTUH-K2044[J]. Microbiological Research, 2018, 216: 70-78
- [65] Yang Y, Luo MJ, Zhou HK, Li C, Luk A, Zhao GP, Fung K, IP M. Role of two-component system response regulator *BceR* in the antimicrobial resistance, virulence, biofilm formation, and stress response of group B Streptococcus[J]. Frontiers in Microbiology, 2019, 10: 10
- [66] Huertas-Rosales O, Romero M, Heeb S, Espinosa-Urgel M, Cámara M, Ramos-González MI. The *Pseudomonas putida* CsrA/RsmA homologues negatively affect c-di-GMP pools and biofilm formation through the GGDEF/EAL response regulator CfcR[J]. Environmental Microbiology, 2017, 19(9): 3551-3566
- [67] Vastano V, Perrone F, Marasco R, Sacco M, Muscariello L. Transcriptional analysis of exopolysaccharides biosynthesis gene clusters in *Lactobacillus plantarum*[J]. Archives of Microbiology, 2016, 198(3): 295-300
- [68] Li BL, Ding XY, Evivie SE, Jin D, Meng YY, Huo GC, Liu F. Short communication: genomic and phenotypic analyses of exopolysaccharides produced by Streptococcus thermophilus KLDS SM[J]. Journal of Dairy Science, 2018, 101(1): 106-112
- [69] Dertli E, Mayer MJ, Colquhoun IJ, Narbad A. EpsA is an essential gene in exopolysaccharide production in Lactobacillus johnsonii F19785[J]. Microbial Biotechnology, 2016, 9(4): 496-501
- [70] Teixeira JS, Abdi R, Su MSW, Schwab C, Gänzle MG. Functional characterization of sucrose phosphorylase and *scrR*, a regulator of sucrose metabolism in *Lactobacillus reuteri*[J]. Food Microbiology, 2013, 36(2): 432-439
- [71] Rud I, Naterstad K, Bongers RS, Molenaar D, Kleerebezem M, Axelsson L. Functional analysis of the role of CggR (central glycolytic gene regulator) in *Lactobacillus plantarum* by transcriptome analysis[J]. Microbial Biotechnology, 2011, 4(3): 345-356