

# New Therapeutic Strategies to Counter PA

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## Abstract

*Pseudomonas aeruginosa* (PA) is a kind of highly infectious opportunistic pathogen with innate multi-drug resistance and has ability to acquire drug resistance mechanisms furthermore. In chronic infections, PA forms biofilms to reduce the effectiveness of antibiotics, while secreting a range of virulence factors, many of which are regulated by the population effect system. Several new therapeutic targets such as biological membrane formation and group response systems are being developed, as well as phages and immunotherapy. With the development of next-generation sequencing technology and comparative genomics, we will be able to design new ideas for safer and more effective drugs, which will revolutionize our choice of treatment for PA infection.

## Keywords

Antimicrobial Resistance, Biofilm, Next-Generation Sequencing Technology, *Pseudomonas aeruginosa*, Quorum Sensing

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# 治疗绿脓感染的新策略

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## 摘要

铜绿假单胞菌是种高感染性的条件致病菌, 先天具有多药耐药性, 同时具备进一步获得耐药机制的能力。在慢性感染中, 绿脓形成生物膜以减少抗生素的效果, 与此同时分泌一系列的毒力因子, 许多毒力因子受群体效应系统调控。数种新的治疗策略如以生物膜的形成和群体效应系统为靶标正在研发当中, 还有噬菌体以及免疫治疗随之孕育而生。随着下一代测序技术和比较基因组学的发展, 将给我们设计更为安

全有效的药物指引新的思路, 使得我们治疗绿脓感染的选择方案发生革命性的变化。

## 关键词

细菌耐药性, 生物膜, 新一代测序技术, 绿脓杆菌, 群体感染

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## 1. 引言

铜绿假单胞菌是一种可利用各种碳源的革兰氏阴性菌, 可生活在包括土壤、水和化妆品在内的多种生态环境中的微生物[1] [2] [3]。感染的宿主范围非常广泛, 包括了植物和动物[4]。绿脓感染占有全球的院内感染的 10%~15% [5], 它是院内血液感染中除大肠杆菌和肺炎克雷伯菌外的第三大革兰氏阴性菌, 是血液感染导致死亡的第二大杀手。尽管随着科技的进步, 医疗水平有了显著地提高, 绿脓杆菌的预防和治疗仍是医疗工作者目前难于克服的困难, 绿脓杆菌的感染致死率高达 38% [6] [7], 在并发症病人、外科手术、尿道和其他体内插管中绿脓感染的致死率高达 60% [8]。感染健康的个体主要是再生加工用水引起的, 导致产生皮肤泡疹样皮炎[9]。这种条件致病菌可使免疫缺陷的病人(如艾滋病人)产生更为严重的并发症[10]。引起呼吸系并发症, 各种炎症的爆发, 如皮炎、胃肠炎、耳炎、心内膜炎和尿路感染[11] [12] [13] [14]。使烧伤创伤感染后发展成为败血症, 感染眼部发展成为溃疡性眼角膜[15]。绿脓杆菌是引起囊胞性纤维症(CF)病人发生慢性肺部感染最常见的病原菌, 发病率和死亡率还在不断地上升。在成人的血液中, 高达 85%的 CF 病人受到绿脓感染[16], 从而引起 CF 的支气管扩张病人和慢性阻塞性肺病病人的肺部感染[17]。慢性绿脓杆菌感染给治疗提出严格地挑战, 毒性和对抗生素产生耐药性都是制定长期治疗方案所要面临的难题。

本文将解释为什么当前的治疗策略的效果非常有限, 并概述慢性绿脓感染的全新治疗策略。

## 2. 细菌耐药性

细菌的耐药性无疑是抗生素治疗失败的主要原因。大部分抗生素必须通过病原菌的外膜进入细胞, 在靶点聚集从而发挥作用, 首先绿脓杆菌会使用一切手段降低其外膜的通透性。多糖藻朊盐能与带阳离子的抗生素(如氨基糖苷类)结合, 从而降低抗生素的扩散[18]。大部分  $\beta$  内酰胺抗生素和亲水性抗生素, 都需通过亲水性的孔蛋白将自身易位穿过外膜[19]。绿脓杆菌改变自身孔蛋白 OprD 降低外膜的通透性, 导致对大部分的  $\beta$  内酰胺和喹诺酮抗生素产生抵抗能力。外排泵系统可将抗生素排出致病菌细胞外, 绿脓杆菌中发现多种不同机制的外排泵, 这些系统能将除了多粘菌素外几乎所有抗生素排出, 例如 MexAB-OprM 能将  $\beta$  内酰胺和喹诺酮等抗生素随同一系列消毒剂排出细胞外[20], MC-207110 外排泵抑制剂在体外能明显地降低细菌对氟喹诺酮类药物的耐药性。外排泵在细菌感染、抵抗人类胆汁和免疫分子的过程中发挥着重要的作用[21]。由此表明外排泵抑制剂对临床耐药致病菌的治疗有很大地帮助[22]。然而, EPIs 抑制单一机制的外排泵, 而绿脓杆菌拥有多种不同的外排泵。人们期望一种抑制剂可应对所有的的外排泵, 但现实并非如此。另外, 抑制外排泵也有可能提高毒力因子的表达[23] [24]。

即使抗生素分子设法易位进入绿脓杆菌的外膜内, 并没被外排泵排出细胞外, 也将遭遇着细胞周质间隙的一系列降解酶的作用, 如绿脓杆菌拥有 ampC 等一系列  $\beta$  内酰胺基因,  $\beta$  内酰胺酶将打开  $\beta$  内酰胺

环,  $\beta$  内酰胺环是一大类抗生素的核心骨架, 超广谱的  $\beta$  内酰胺酶(ESBLs)赋予了绿脓杆菌对除了碳青霉烯类外的所有  $\beta$  内酰胺类抗生素产生耐药性。降解酶的基因都由质粒编码的, 因此可在细菌间迅速地传播。全球范围内含有 ESBLs 的菌株将越来越多[25]。

对喹诺酮类抗生素产生耐药主要是由于靶基因发生突变, 尤其是在 DNA 旋转酶基因 *gyrA* 中。其耐药程度通常取决于抗生素与 DNA 旋转酶的亲和力的大小。因此, 环丙沙星在多数情况下还是有效的, 它与其靶点的亲和力大于其他氟喹诺酮类抗生素[20] [26]。不过耐环丙沙星的菌株也有报道[27]。

随着感染的持续, 变成慢性感染时, 形成成熟生物膜和黏液状的表型, 这些都会增加对抗生素的抗性[28]。抗生素的耐药性评价存在巨大地困难, 因为绿脓杆菌生长比较缓慢, 黏液状的表型和其他表型的多样性等使结果产生偏差[21] [29]。细菌生长过程中形成的生物膜使得抗生素对其的药敏性要明显减弱。

尽管细菌的抗生素耐药性增长速度快于新的抗菌药物的发展速度, 但是还是不断有抗生素开发出来。如 NXL104(Novexel)、克拉维酸和他唑巴坦[30] [31], 联合已有的  $\beta$  内酰胺类抗生素(如头孢他啶)。一种模拟肽抗生素具有很强的抗绿脓杆菌的能力, 它作用的靶点是外膜生物合成中的 LptD 蛋白[32]。

绿脓杆菌主要是通过改变自身的表现型和基因型以获得或者发展出新的耐药能力, 这得益于其巨大的基因组[33]。因此治疗细菌感染的方法和药物已经陷入穷途末路的境地, 迫切需要新型的治疗策略。

### 3. 治疗策略

#### 3.1. 以生物膜和藻朊酸盐为靶点

绿脓杆菌感染可形成结构鲜明的生物膜, 使之相互依附或依附在物体的表面。随着细胞的扩增, 形成一簇, 开始发展成成熟的生物膜结构, 错综复杂的细菌群落被自身产生的多糖、蛋白质和 DNA 所包裹着[34]。生物膜形成后有若干个生态微环境生成, 底部微环境的代谢活动比较微弱, 与表面形成巨大地反差, 这种分层的出现与其可用的氧气的浓度有关[35]。生物膜的形成是由多种因子共同作用, 涉及了一个非常复杂的调控机制和多种诱因的效应物[36]。通过基因芯片检测, 比悬浮培养物多出超过 70 种不同的因子在生物膜中表达, 其中大部分是毒力因子[37]。形成生物膜的绿脓杆菌比悬浮培养物耐受抗生素的能力要高 100~1000 倍, 这主要是因为生物膜中胞外基质渗透性差和近乎休眠状态的代谢活动[38]。

为防止绿脓杆菌形成生物膜、避免交叉感染和早期抑制其克隆, 目前还是采用比较激进的抗生素疗法。一旦绿脓杆菌形成了生物膜, 可用慢性抑制抗生素疗法, 包括抗生素治疗的规范性(例如喷雾的氨基糖苷类抗生素), 联合应用 DNA 酶降解粘性生物膜中的 DNA [39]。此外, 可进一步深入了解绿脓杆菌生物膜的形成和维护的机制, 为我们寻找以生物膜为靶点的疗法带来灵感。

##### 3.1.1. 以黏附素为靶点

为开发抑制生物膜形成的化合物, 提高对生物膜的了解尤为重要。以黏附素(如凝集素)为靶点时, 需要适当的生物膜装配。凝集素是细菌外膜蛋白, 促使细菌细胞聚集形成生物膜[40]。绿脓杆菌表达 PA-IIL 和 PA-III 两种凝集素, 可结合气管纤毛, 辅助绿脓杆菌感染。凝集素受到 QS 系统调控, 凝集素与糖类的相互作用在疾病发生过程中起着重要的作用, 尤其在生物膜的形成过程中[41]。海藻糖和半乳糖等含糖部分竞争性抑制凝集素的体外结合, 与抗生素联合用药时可提高生物膜的降解[42]。这些新型的抗生物膜的药物在小规模的随机临床试验中有良好的效果, 可提高治疗耳鼻喉等呼吸道绿脓感染的效果[43]。

##### 3.1.2. 以藻朊酸盐为靶点

藻朊酸盐、Pel 和 PSL 等胞外多糖是绿脓杆菌胞外基质的重要组成成分, 藻朊酸盐是过量表达的甘露糖醛酸和葡萄糖醛酸的聚合物, 形成粘液样表型, 通常与 CF 病人的慢性感染有关[44]。藻朊酸盐与绿脓杆菌的发病机制的多方面有牵连, 这其中包括黏附、避免吞噬作用、抵抗抗生素的作用[45]和淬灭活化的

中性粒细胞释放的自由基[46]。

有研究发现,藻朊酸盐可阻止抗生素的扩散分布[18]。降解绿脓杆菌胞外多糖的酶,能破坏生物膜的整体性,以提高抗生素治疗的效果。藻朊酸盐的聚合物骨架可被藻朊酸盐裂解酶(AlgL)解离糖苷键。Alkawash 和 Alipour 等人应用从 CF 病人中分离到的黏液样的绿脓杆菌建立体外生物膜模型[47] [48],已经证明,AlgL 可促进抗生素杀死与生物膜相关联的细胞,Bayer 等人的兔子心内膜炎模型验证了其结果,AlgL 和阿米卡星联合用药时无毒副作用[49]。最近 Lamppa 等人通过改造的半胱氨酸,在特定的位点融合了鞘氨醇单胞菌的藻朊酸盐裂解酶(AlgL-III)和聚乙二醇,提高药物药效的同时,减小了免疫反应性[50]。

### 3.1.3. 信号干扰

许多 QS 抑制剂具有抗生物膜活性,从而确定了自身诱导信号分子在生物膜形成和维持的过程中起着重要的作用。此外,修饰的核苷酸如环化二 GMP 在控制生物膜形成的调控机制中扮演着非常重要的角色,例如它可提高黏附因子的产生水平[51]。利用特定靶点筛选可知,亚抑制浓度的磺胺噻唑抑制环化二 GMP 的生物合成和防止生物膜形成[52]。

另外,低水平的核苷酸生物合成抑制剂(氟尿嘧啶),在体外可阻止 DNA 复制,从而达到防止生物膜的形成[53]。但是,其毒副作用比较大,不能用于临床治疗绿脓杆菌的感染,却给抑制生物膜形成带来的新的灵感。即抑制核苷酸的生物合成,达到阻止环化二 GMP 生成和生物膜的形成[54]。

### 3.1.4. 促进生物膜裂解

成熟的生物膜可以一种协调的方式裂解,释放出大量的悬浮的细菌。生物膜裂解是很正常的自然的过程,是由营养因子[55]、氧气[56]和一氧化氮[57]水平等环境因素引起的。绿脓杆菌分泌一系列的化合物,如 AlgL、单一不饱和脂肪酸和顺式-2-癸烯酸,组合形成生物膜结构[58]。所有这些化合物被看成是裂解绿脓杆菌生物膜的切入点。另外,丝状的噬菌体 Pf1 在生物膜裂解和扩散过程中发挥着重要作用[59]。促进生物膜裂解的化合物可与抗生素等现有的治疗策略联合应用。如亚致死浓度的一氧化氮供体亚硝酸铁氰化钠可诱导生物膜的裂解[57],也可显著地提高抗菌化合物(如妥布霉素、过氧化氢和十二烷基硫酸钠)裂解成熟的生物膜。

另外,从海洋生物体中筛选到引起革兰氏阴性菌生物膜脱落的天然化合物[54],还通过高通量筛选到许多具有抗绿脓生物膜活性的小分子化合物,这些小分子化合物属于不同的结构骨架,很多化合物的靶点还不明确[60]。高丽参和银等天然化合物都可用来治疗和抑制绿脓杆菌生物膜[61]。Dean 等人研究揭示人类的抗菌肽(AMP)LL37 具有抗绿脓生物膜的潜能,此肽为预防体内大蜡螟感染的多肽[62]。AMPs 作为抗菌药而又被重新得到重视,当前所面临的瓶颈主要是其稳定性和效价都不高,毒性较大[63]。

蛭弧菌是一种很常见的通过敏捷的鞭毛捕食固体表面的细菌,通过缓慢的滑行[64]在体内减少沙门氏肠炎 PT4 的克隆[65]。此菌与 *Micavibrio aerug-nosavorus* 同时存在时可在体外抑制包括绿脓杆菌在内的多种病原菌,这种捕食行为在氧气不足时就消失了[66]。由此推断,进一步研究这种捕食微生物,可寻找到新的有效的使绿脓杆菌生物膜裂解的候选物。

## 3.2. 调控系统

### 3.2.1. 群体效应

群体感染(QS)系统广泛地存在于许多细菌生物体中,以菌体密度依赖的方式全面调控基因的表达,使得细菌的群体行为更为协调。绿脓杆菌拥有 *las*、*rhl* 和 *pqs* 等多种 QS 系统分子[67]。QS 信号分子可自由地扩散出膜外,或者通过外排泵排出膜外。当细胞数目到一定浓度时,周围环境的信号分子达到临界浓度,能被细胞内的转录激活因子(LasR、RhlR 和 PqsR)检测到,这些激活因子通过结合保守的 DNA 元

件, 调节多种靶基因的表达[68]。

绿脓杆菌的 QS 调节网络相当复杂, 基因芯片检测到有 300 个 QS 控制基因[69], 绿脓杆菌基因组 10% 的基因受 QS 机制调节的[70]。QS 系统调节弹性蛋白酶、碱性蛋白酶、外毒素 A、绿脓菌素、氰化氢、脂肪酶、重要分泌途径组成元件[67]和 rpoS 编码的压力诱导的  $\sigma$  因子的表达[71], 促成一些细菌的生物膜的形成[72]。转录组学研究表明, QS 在整个调控体系中扮演着不可或缺的作用, QS 缺失的菌株毒性明显要比正常菌株小[73]。以 QS 调节系统为靶点, 通过干扰 QS, 细菌对抗菌化合物的敏感性明显增加, 特别是妥布霉素[74]。与绿脓的 QS 系统相互作用的几种不同治疗策略, 包括已有的抗生素、植物提取物、疫苗和酶。

大蒜萃取物无论在体外还是体内, 都能提高已有抗生素的治疗效果。在小鼠感染模型中, 应用大蒜萃取物治疗时可提高初期的炎症反应, 使得提高肺部的细菌清除率[75]。呋喃酮等化学合成化合物已经用来干扰 QS, 也可加速肺部细菌的清除率[76]。一些已有抗生素的浓度在 MIC 值以下时, 表现出抑制 QS 的作用, 例如阿奇霉素、头孢他啶和环丙沙星等抗生素[77]。用抗生素治疗 CF 病人时肺部的通常能达到亚抑制浓度, 这也是应用阿奇霉素等药物治疗的过程经常出现的结果[78]。

### 3.2.2. 双组份调控系统

双组份调控系统(TCSs)使细菌感受到外部环境的刺激, 并做出反应。这种普遍存在的信号转运系统控制基因簇的表达, 这些基因簇参与细胞生长和致病等生物过程[79]。往往一种病菌中有多种 TCSs, 在外部环境中的 pH、营养水平、抗生素选择性压力等不同条件下, TCSs 可刺激出不同的反应。此系统为许多细菌必不可少的系统, 也是将来治疗细菌感染的理想靶标。许多真菌病原菌也有 TCSs, TCSs 抑制剂可用作广谱的治疗药物[80]。TCSs 作为治疗干预的靶标已经得到了 Gotoh 等人的验证[81]。

### 3.3. III 型分泌系统

绿脓杆菌具有多种分泌机制, 其中包括将细胞毒素(ExoS、ExoU、ExoT 和 ExoY)直接传递给宿主靶细胞的 III 型分泌系统(TTSS)。有趣的是, TTSS 组成元件本身也是毒力因子, 正常表达 TTSS 而无效应分子的突变体也具有细胞毒性[82]。因此, TTSS 组成元件是个非常具有潜力的治疗的靶点。有研究显示提高抗 TTSS 的中心蛋白 PcrV 的血清, 能阻止外毒素向哺乳细胞中转运[83], 抗 PceV 的单克隆抗体(mAb 166)已经开发出来了, 并成功地应用于小鼠和大鼠的绿脓感染模型当中[84]。

### 3.4. 铁离子螯合作用

铁载体是可使好氧细菌占据有限的可用铁离子的微环境中的分子, 该微环境中绝大多数铁离子是  $Fe^{3+}$  的形式, 这种形式的铁离子是不溶的, 也不能被细菌所利用。分泌的铁离子载体通过螯合作用把铁离子与外界环境隔离。非荧光铁载体是铁离子有限的环境中绿脓杆菌释放的, 具高亲和力的铁载体。这两者都有结合铁离子的能力, 能将铁离子转化成可利用的形式, 并传输给细菌, 细菌的外膜上有特异性的受体。在小鼠模型中, 铁载体的产生直接影响着绿脓杆菌的毒力[85]。有研究发现, 非荧光载体可调节外毒素 A 等毒力因子的分泌, 就如同调节自身的分泌一样[86]。非荧光载体介导的铁离子吸收可成为新型药物或疫苗的靶点。此外, 铁离子螯合性质可融入药物制剂中, 例如, 镓和庆大霉素的联合制剂可提高抗绿脓活性[87]。

### 3.5. 细菌素

细菌素是小型毒性分子, 如绿脓杆菌的细菌素是绿脓菌素, 产绿脓菌素的菌株通常是耐受自身产生的绿脓菌素。这些毒力因子结合外膜的特定的蛋白, 所以他们的作用是特异性的。绿脓有三种类型的绿

脓菌素, 分别为 R、F 和 S 型, R 型可耐受核酸酶和蛋白酶, 阻止生物大分子的合成, 使细胞在 20 分钟内死亡[88]。F 型同样是耐受核酸酶和蛋白酶, 但是其拥有更为广谱的活性, 能够杀死一些其他的革兰氏阴性菌[89]。S 型绿脓菌素是可溶的, 蛋白酶敏感的, 通过破坏 DNA 和抑制磷脂合成诱导细胞死亡[88]。绿脓菌素的确切的功能还不清楚, 有研究者提出有形成微生态的作用[90], 此外, 临床分离菌株相比环境中分离得到的菌株, 绿脓菌素更为常见, 由此说明其与感染有关[91]。

R 型绿脓菌素已经成功地应用在致死小鼠腹膜炎模型中, 结果显示, 次微克级绿脓菌素可抑制 90%~100%绿脓菌素敏感的绿脓杆菌[92]。肠球菌可产生一系列细菌素具有抗革兰氏阴性菌和阳性菌作用, 包括有肠沙门氏菌、小肠结肠炎耶尔森菌、肺炎克雷伯菌、金黄色葡萄球菌、弧形杆菌和绿脓杆菌。E-760 肠道菌素在广泛的 pH 和热处理调节下都很稳定, 加入鸡饲料中, 可明显减少鸡体内弯曲杆菌的克隆[93]。苏云金芽孢杆菌产生的细菌素(Entomocin 9)具有抗单核细胞李斯特菌属、绿脓杆菌和多种真菌的活性[94]。PAO1 菌株产生的 S5 绿脓菌素浓度为 0.2 $\mu$ M 时, 具有抗临床绿脓杆菌的作用[95]。

应用绿脓菌素作为治疗手段, 已经在一系列的微生物疾病中完成了评价[96], 被看成是一种益生菌的治疗机制[97]。然而, 还是有许多问题有待解决, 单个的绿脓菌素作用的范围窄, 具有潜在的毒性和免疫原性[98]。

### 3.6. 噬菌体治疗

噬菌体是感染细菌的病毒, 是世界上最为丰富的生物个体。Felix d'Herelle 1917 年首次发现噬菌体, 裂解性噬菌体被用做抗菌药物的潜能随即就得到了开发, 然而, 在抗生素发现后, 噬菌体治疗策略在欧洲和美国几乎被遗忘, 可符合美国和欧洲临床标准的有效性和安全性研究报告极少, 噬菌体仅在分子和诊断领域应用的比较多[99]。随着多药耐药病原菌的比例不断提高, 裂解性噬菌体治疗方法的优势进一步突显[100], 一种快速有效的筛选噬菌体活性和细菌耐药性的高通量筛选已经建立[101]。

#### 3.6.1. 裂解假单胞噬菌体

噬菌体在裂解宿主细菌细胞时, 释放大量活跃的子代噬菌体, 应用噬菌体抑制感染被视为一种极具潜力的新型治疗的策略, 也包括抑制生物膜[99]。绿脓杆菌细胞被生物膜中的胞外多糖所包裹着, 导致许多抗菌药物无法到达作用的靶位。许多裂解绿脓杆菌噬菌体产生多聚糖降解聚合酶, 此酶可降解藻酸盐, 以自由扩散形式穿过藻酸盐[102], 噬菌体可破坏生物膜基质, 辅助药物穿过生物膜, 噬菌体治疗作为抗生素治疗的辅助疗法[103]。

噬菌体治疗绿脓杆菌的有效性已经应用多种动物模型进行评价, Debarbieux 等人应用无创伤技术, 实时分析急性小鼠肺部感染中噬菌体清除生物标记的绿脓杆菌的数量, 噬菌体可短期预防绿脓杆菌感染[104]。在感染了从 CF 病人分离的黏液样的多耐药的绿脓杆菌的小鼠模型中, 噬菌体可起到同样的治疗效果。在体外持续共培养噬菌体和 CF 病人中分离的绿脓杆菌, 可提高其在体内的裂解作用, 多种噬菌体复合物的单次给药, 可显著地降低感染绿脓杆菌的小鼠烫伤模型的死亡率[105]。

有个应用噬菌体治疗感染了绿脓杆菌的狗的临床试验, 48 小时后, 噬菌体效价提高了 100 倍, 而细菌数目减少了 30%, 没有出现毒副作用[106]。在随机双盲以安慰剂作对照的 24 例感染多药耐药绿脓杆菌的耳炎病人中, I/II 临床试验噬菌体治疗有很好疗效和安全性[107]。Goshahi 等人将抗假单胞裂解性噬菌体  $\phi$ KZ 冻干, 而其生物活性无明显降低或丧失[108], 再把粉末制成喷雾状将噬菌体传递给肺部, 以治疗感染了 CF 病人。但是, 这种噬菌体制剂商品化还远。开发抗假单胞菌噬菌体的试验还在不断地进行, Harper 和 Enright 提出, 他们可能将在欧美首先推出噬菌体治疗, 提供一个全新的有价值治疗顽疾的策略[99]。

### 3.6.2. 基因工程改造的噬菌体

经过基因改造的裂解大肠杆菌噬菌体可表达降解生物膜的酶，感染的同时可攻击带生物膜和生物膜基质的细菌细胞[109]。改造的噬菌体过量表达 *lexA*，*lexA* 可抑制 SOS 反应[110]。将其与抗生素联合应用时，可显著地增加杀死耐药大肠杆菌的能力，这种治疗策略可用来直接抵抗绿脓杆菌生物膜。应用噬菌体治疗时所面临的最大的问题是，大规模的细菌溶解会破坏炎症反应。Hagens 等人改造丝状绿脓杆菌噬菌体 Pf3，应用限制性内切酶敲出输出蛋白基因，构建无复制能力的非裂解型噬菌体(Pf3R)。改造后的噬菌体在体外能有效地杀死野生型宿主，外毒素释放保持在较低的水平。此外，经过噬菌体 Pf3R 治疗试验感染的小鼠，比裂解性噬菌体治疗的存活率要明显提高，存活率的提高与 Pf3R 治疗可减弱炎症反应有关[111]。

### 3.6.3. 噬菌体产物

如细胞溶解酶等纯化的噬菌体产物，是抗生素外另一种可控的治疗选择。溶解酶是噬菌体在裂解循环中可在细菌的肽聚糖层上穿孔，最终导致细胞裂解[112]。纯化的溶解酶的酶促反应非常迅速，几秒钟内纳克级的纯化溶解酶可减少 6 数量级的细菌细胞[113]。Briers 等人联合噬菌体细胞内溶素(EL188)和外膜渗透剂抑制多药耐药绿脓杆菌[114]。此外，纯化的来源于  $\pi$ KZ 噬菌体的细胞内溶素 gp144 在体外可裂解绿脓杆菌，这种溶菌糖苷转移酶可与细菌生物膜相互作用并破坏该膜，在噬菌体治疗中可作为抗假单胞菌制剂[115]。

细胞溶解酶在体内的活性受到限制，主要是因为酶的免疫原性。已经证明抗体会与酶发生作用，这种情况出现的比较少，且不会干扰其抗菌活性[115]。蛋白质因其半衰期短，阻碍其应用静脉注射，合理使用细胞溶解素，可减少粘膜表面的克隆数。另外，目前还没有出现细胞溶解素的抗性，因其受体是细胞活性所必须的[116]。

## 3.7. 免疫治疗与免疫作用

理想的治疗方案是在细菌定植以前就清除或预防，一些学者应用免疫治疗和免疫作用等策略，开发免疫系统使其成为一种治疗手段起初。脂多糖(LPS)被看成是一种极具潜力的疫苗，但是纯化的 LPS 具有毒性和引起发热[117]，应用 LPS 制作成疫苗并不成功，病人接种疫苗后，病情更为严重[118]。将 LPS 的脂质部分去除后，对宿主的毒性显著地降低，将抗原多糖制成个八价抗原多糖的结合疫苗(Aerugen)[119]。肌肉注射和鼻腔给药都可明显地抑制感染，接种疫苗 10 年后，给药组和对照组之间有明显的不同[120]。尽管试验数据令人欢欣鼓舞，但是在 2006 年其三期临床试验终止，主要原因是空白对照组和给药组的结果没有什么区别[117]。一种具有广泛前景的鞭毛疫苗(A 型)已经完成了三期临床试验，试验结果显示其可使 34%的人远离初次感染绿脓杆菌，保护了 51%的 CF 病人免受慢性感染[121]。

当病人出现重度感染，找不到理想的主动免疫候选物时，可用被动免疫作为替代手段。这种方式可直接抵抗绿脓杆菌，所以应用抗体治疗越来越受到重视。但是，目前抵抗细菌性病原菌的单克隆抗体批准上市的极少[122]。

目前有两个抗绿脓的单克隆抗体正在研究，且正处于二期临床研究，其中一个单抗的靶点是与毒力相关的 III 型分泌系统的 PcrV 蛋白，另一个的靶点是细菌细胞表面的 O 型抗原，尤其是以 O11 型血清为主[123]。兔子的抗重组 A 型鞭毛蛋白多克隆抗体 IgG，可提高小鼠烧伤感染模型存活率，主要是因为提高了吞噬作用和抑制了细菌的运动[124]。

有研究报道，CF 病人的硫氰酸盐分泌受到阻碍，推测可能由于 CF 跨膜蛋白参与其运输。硫氰酸盐在产生活性氧自由基(ROS)的先天性免疫机制中起着非常重要的作用，通过生成 ROS，氧化的宿主防御系统可清除支气管中的革兰氏阴性和阳性菌。提供外源的硫氰酸盐进入 CF 病人的支气管中，可修复氧

化的防御系统，增强病人抵御细菌感染的能力[125]。

### 3.8. 以基因表达为靶点

反义和反基因抑制剂(ASI)可阻止某些基因的转录和翻译，找到合适的靶点，这种方式可使耐药的细菌对抗生素敏感。这种治疗方法要广泛地用到分子生物学技术，联合应用已有的抗生素可延长当前的寿命，耐受良好的疗法。证据至今仍然有限。和许多其他细菌和病毒一样，应用大肠杆菌和肠球菌在体外进行了原理验证[126]。应用这种新型技术所面临的阻碍是，ASI 如何穿过绿脓杆菌相对不可渗透的外膜。ASIs 可联合一个穿膜肽、脂质体或噬菌体载体。应用传统的和下一代快速测序技术确定健康细菌基因组，为确定 ASI 的区域提供帮助[127]。

### 3.9. 下一代测序技术

在最近的五年中，下一代焦磷酸测序技术应用的不断普及，许多公司正在寻找更为快速更为经济的测序技术，以获得更为详尽的序列信息，其中就包括基因组测序和转录组测序。这种技术的革新使序列数据信息获得更为经济的同时，开辟了许多新的研究的方向。技术瓶颈也由样品的准备和序列数据的获得向生物信息学转变，在复杂的数据中挖掘详尽有用的数据至今还是个缓慢的过程，尤其是将序列数据转化为有意义的治疗靶点[128]，目前这些都只是个构想。此外，可用于质量控制检测，序列信息可使噬菌体的定向设计改变如宿主范围等特性，或者加入生物膜降解酶[109]。焦磷酸测序可应用于基因挖掘，鉴定不同物种基因组编码的新生物活性化合物，并应用于药物研发。这些方法可辅助鉴定治疗药物和靶点，也只有到后基因组时代才会出现。

#### 3.9.1. 比较基因组学

比较基因组学可深入了解，一些绿脓杆菌菌株比其他的菌株更致命原因。许多绿脓杆菌的基因组已经测序[129]，确定了一些流行病菌株在病人之间有不寻常的传递能力[130]。检测利物浦流行的绿脓杆菌菌株的基因组，发现了迁移遗传成分的新型区域，尤其是插入了溶原性噬菌体的基因组中后[131]。此外，大鼠的慢性肺部感染的模型中，噬菌体原会影响这些菌株的竞争性。因此，比较基因组学可鉴定新型的候选的治疗靶点[132]。

随着新一代测序技术的提高，此技术可用作快速准确的诊断工具，推出更为敏捷更为详尽的治疗方案，在早期就可检测出任何即将爆发的传染病的菌株。比较同一类细菌不同菌株的基因组序列，特别是慢性感染中，更清楚地了解绿脓杆菌种内间基因型和表现型的差异[133]。传统的鉴定和表征技术应用一个具有代表性的克隆代表整个群体，应用新一代测序技术可分性整个群体，利用 DNA 测序，可找出突变部位，能确定基因表达中转录组的变化。这种方法可揭示敏感菌株中有微弱耐药性的菌株，而应用传统的培养方法是不能实现的，披露经过治疗后种群多样性和种群结构发生的改变。最终根据病人所感染的细菌种群，制定个性化的治疗方案。

#### 3.9.2. 微生物组学

人体是个具有多种微生物的微环境，应用 16S rRNA 的焦磷酸测序确定这些种群的特征，可展示其多样性的水平，先前的 DNA 测序是无法实现的[134]。由此颠覆传统的观念，感染取决于种群的水平，而非单个的病原菌或隔离群。宏基因组学让我们对微生物种群了解存在缺陷，应用最为先进的科学技术，降低了我们的成本，弥补先前的缺陷，深入了解微生物组学的实时变化和从群体水平理解感染的发生。Caporaso 等人已经展开了一项研究，在人体的四个位点检测超过 396 个时间点的两个个体的序列，结果显示，在每个位点，微生物都是相对不稳定，若干天后微生物的种群动态会出现巨大地变化，种群的许多成员也非永恒的[135]。



长期以来,绿脓杆菌被认为是 CF 病人感染最重要的病原菌,然而,种群的多样性分析可知,在感染的部位是个非常复杂的多种微生物的群落,有着大量的厌氧菌[136]。这将引出一系列的问题,例如:在病情加重时,CF 病人肺部的微生物群落是否会发生改变;CF 病人肺部中其他微生物在临床症状中是否发挥了作用;在这种多种微生物环境中,微生物相互作用的水平如何。

最近有些学者应用新一代测序技术回答了这些问题,Cox 等人研究显示,CF 病人随着年龄的增加,肺部中微生物的多样性逐渐减少[137],因此,益生菌能否用于治疗 CF 肺部疾病的争论会更加激烈。

#### 4. 结论

尽管最近十年治疗和控制绿脓感染的水平有很大地提高,在临床中,这种条件致病菌引起的发病率仍然急剧上升。新型的治疗策略可辅助抗生素治疗,应对不断增加的多药耐药性。然而,近期它们距离真正的临床应用还很远。新的测序技术还正在降低成本,使更多的研究者可以应用这项技术。大量的信息帮助我们开发新颖的基因特异的治疗药物,使之持续地抵制耐药细菌的感染。这种测序方法不仅仅是确立靶标和潜在的抑制剂,也可实时追踪病原菌,监控疫苗引起的免疫反应,评价抗药性。以前应用单一的,广谱的药物治疗,将来的治疗方法相对比较昂贵,但是作用范围更窄的联合作用,例如,有信号干扰、抗生物膜活性和抗菌活性,更加追求治疗的个性化。

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