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糖尿病对泌尿系感染病原菌分布及耐药性的影响分析

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摘 要

【目的】分析2020~2024年本院糖尿病与非糖尿病患者泌尿系感染病原菌的分布特征及其对抗菌药物的耐药性差异，为临床个体化用药提供依据。【方法】回顾性分析青岛大学附属医院5217例中段尿培养阳性患者的菌株鉴定与药敏试验结果。采用SPSS 27.0进行统计分析，计数资料以例数(百分比)表示，组间比较采用χ^2检验，检验水准$\alpha = 0.05$。【结果】共检出病原菌5217株，两组均以革兰阴性菌为主(DM组74.19%，non-DM组74.05%)。DM组真菌占比高于non-DM组(10.24% vs 5.60%)。在大肠埃希菌中，DM组对左氧氟沙星的耐药率显著高于non-DM组(65.91% vs 62.27%, P = 0.049)，而对头孢噻肟(43.61% vs 51.27%, P < 0.001)、亚胺培南(0.45% vs 1.50%, P = 0.009)的耐药率显著低于non-DM组。在屎肠球菌中，DM组对四环素的耐药率显著低于non-DM组(32.33% vs 59.10%, P < 0.001)；在粪肠球菌中，DM组对莫西沙星的耐药率亦显著低于non-DM组(8.20% vs 19.66%, P = 0.038)。热带念珠菌中，DM组对伏立康唑的耐药率显著高于non-DM组(41.82% vs 22.22%, P = 0.038)。【结论】糖尿病与非糖尿病患者泌尿系感染病原菌谱存在差异，糖尿病患者真菌感染比例更高。糖尿病患者大肠埃希菌对氟喹诺酮类药物耐药形势更为严峻，临床应谨慎经验性使用；碳青霉烯类及部分头孢菌素类药物在糖尿病患者中仍保持较好敏感性，具有重要治疗价值。糖尿病患者肠球菌对四环素及莫西沙星的耐药风险较低，但热带念珠菌对伏立康唑的耐药风险显著升高，经验性抗真菌治疗时需注意菌种差异。

关键词

泌尿系感染，糖尿病，病原菌分布，耐药性，革兰阴性菌，抗菌药物

Effect of Diabetes Mellitus on Pathogen Distribution and Antimicrobial Resistance in Urinary Tract Infections

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Abstract

Objective: To analyze the distribution characteristics of pathogens causing urinary tract infections (UTIs) and the differences in antimicrobial resistance between diabetic and non-diabetic patients at our hospital from 2020 to 2024, providing evidence for clinical individualized medication. Methods: A retrospective analysis was conducted on bacterial identification and antimicrobial susceptibility test results from 5217 patients with positive midstream urine cultures at the Affiliated Hospital of Qingdao University. Statistical analysis was performed using SPSS 27.0. Enumeration data were expressed as numbers (percentages), and intergroup comparisons were made using the χ^2 test, with a significance level of $\alpha = 0.05$. Results: A total of 5217 pathogenic strains were detected, with Gram-negative bacteria predominating in both groups (DM group 74.19%, non-DM group 74.05%). The proportion of fungi in the DM group was higher than that in the non-DM group (10.24% vs 5.60%). Among *Escherichia coli*, the DM group showed a significantly higher resistance rate to levofloxacin (65.91% vs 62.27%, P = 0.049), but significantly lower resistance rates to cefotaxime (43.61% vs 51.27%, P < 0.001) and imipenem (0.45% vs 1.50%, P = 0.009) compared to the non-DM group. Among *Enterococcus faecium*, the DM group had a significantly lower resistance rate to tetracycline (32.33% vs 59.10%, P < 0.001); among *Enterococcus faecalis*, the DM group also showed a significantly lower resistance rate to moxifloxacin (8.20% vs 19.66%, P = 0.038). For *Candida tropicalis*, the DM group had a significantly higher resistance rate to voriconazole (41.82% vs 22.22%, P = 0.038). Conclusion: The pathogen profiles of urinary tract infections differ between diabetic and non-diabetic patients, with a higher proportion of fungal infections in diabetic patients. Diabetic patients face a more severe resistance profile of *E. coli* to fluoroquinolones, warranting caution in empirical use. Carbapenems and certain cephalosporins retain good susceptibility in diabetic patients, representing valuable therapeutic options. Diabetic patients show lower resistance risk of *Enterococcus* to tetracycline and moxifloxacin, but a significantly higher resistance risk of *Candida tropicalis* to voriconazole, which should be considered in empirical antifungal therapy.

Keywords

Urinary Tract Infection, Diabetes Mellitus, Pathogen Distribution, Drug Resistance, Gram-Negative Bacteria, Anti-Bacterial Agents

1. 引言

泌尿系感染(Urinary tract infection, UTI)是全球范围内最常见的感染性疾病之一，给医疗卫生系统带来了沉重负担。由于解剖结构差异，女性发病率显著高于男性[1]。UTI 病原菌谱多样，其中以大肠杆菌、肺炎克雷伯菌、奇异变形杆菌、粪肠球菌和腐生葡萄球等最为常见[2]。糖尿病患者是 UTI 的特殊高危人群。其高糖环境、免疫功能受损及神经源性膀胱等因素，共同导致其 UTI 发病率及并发症风险显著高于

非糖尿病人群[3]。抗菌药物是治疗 UTI 的基石，然而，随着全球抗菌药物耐药性的日益加剧，尤其是 UTI 主要病原菌对常用抗生素耐药率的不断攀升，使得对高危人群的经验性治疗，变得更为复杂[4]。本研究采用回顾性分析医院近 5 年泌尿系感染患者的临床资料，探讨糖尿病与非糖尿病患者中段尿细菌培养结果的菌谱特点及对抗菌药物耐药性的变化，为临床合理用药提供参考。

2. 资料与方法

2.1. 资料来源

回顾性分析 2020~2024 年青岛大学附属医院中段尿培养阳性的泌尿系患者的中段尿细菌培养鉴定和药敏试验结果。

2.2. 病原菌鉴定及其药敏试验

UTI 患者尿液标本留取参照《全国临床检验操作规程》及《尿路感染临床微生物实验室诊断》新标准[5]。用定量接种环取尿液 1 μl 接种血平板和中国兰或尿定位平板，放于 35℃培养 18~24 h，革兰阴性杆菌计数 $\geq 10^4$ CFU/ml，革兰阳性球菌$\geq 10^4$ CFU/ml，进行细菌鉴定及药物敏感性分析。菌株鉴定采用细菌鉴定药敏分析仪(德国西门子公司)进行，药敏部分采用最低抑菌浓度(MIC)值报告结果，由于同一患者不同时间分离的菌株可能存在耐药表型差异，因此对于同一患者多次送检标本检出的菌株，视为不同菌株分别计数。

2.3. 统计学方法

采用 SPSS27.0 软件进行数据分析不符合正态分布的计量资料以(p25, p75)表示，采用非参数检验；计数资料以例数或百分比表示，采用 χ^2 检验；双侧检验，检验水准 $\alpha = 0.05$。

3. 结果

3.1. 年龄与性别分布

本研究共纳入 5217 名患者，其中男性 1884 例，女性 3333 例。男性患者年龄(55.00，78.00 岁)岁，女性患者年龄(54.00，76.00 岁)。

3.2. 病原菌分布

3.2.1. 病原菌前五位来源科室

病原菌来源科室分布见表 1。其中，泌尿外科(20.57%)、肾内科(19.46%)、内分泌科(13.21%)、ICU (5.83%)及康复医学科(5.44%)是检出病原菌最多的五个科室，合计占比 64.50%。

Table 1. Top five source departments
表 1. 前五位来源科室

科室	检出病原菌	比例
泌尿外科	1073	20.57%
肾内科	1015	19.46%
内分泌科	689	13.21%
ICU	304	5.83%
康复医学科	284	5.44%
总数	3365	64.50%

3.2.2. 2020~2024 年 DM 组与 Non-DM 组泌尿系感染患者中段尿培养分离病原菌

患者样本中共检出病原菌 5217 株，其中 DM 组革兰阴性菌占 74.19% (1420/1914)，non-DM 组革兰阴性菌占 74.05% (2446/3303)；DM 组革兰阳性菌占 15.57% (298/1914)，non-DM 组革兰阳性菌占 20.35% (672/3303)；DM 组真菌占 10.24% (196/1914)，non-DM 组真菌占 5.60% (185/3303)；在病原菌构成分析中，我们观察到 DM 组与 non-DM 组存在差异，DM 组大肠埃希菌的构成比(57.63%)高于 non-DM 组(53.38)，见表 2。

Table 2. Pathogens isolated from midstream urine in urinary tract infection patients with and without DM
表 2. DM 组与 non-DM 组泌尿系感染患者中段尿分离病原菌

病原菌	DM 组(n = 1914)	non-DM 组(n = 3303)
革兰阴性菌	1420 (74.19%)	2446 (74.05%)
大肠埃希菌	1103 (57.63%)	1763 (53.38%)
肺炎克雷伯菌	169 (8.83%)	270 (8.17%)
奇异变形杆菌	32 (1.67%)	93 (2.82%)
铜绿假单胞菌	19 (0.99%)	92 (2.78%)
其他	97 (5.07%)	228 (6.90%)
革兰阳性菌	298 (15.57%)	672 (20.35%)
屎肠球菌(D 群)	133 (6.95%)	335 (10.14%)
粪肠球菌(D 群)	61 (3.19%)	178 (5.39%)
无乳链球菌(B 群)	33 (1.72%)	44 (1.33%)
金黄色葡萄球菌	23 (1.20%)	30 (0.91%)
咽峡炎链球菌	19 (0.99%)	23 (0.70%)
其他	29 (1.51%)	62 (1.88%)
真菌	196 (10.24%)	185 (5.60%)
白色念珠菌	80 (4.18%)	61 (1.85%)
热带念珠菌	55 (2.87%)	45 (1.36%)
光滑念珠菌	42 (2.19%)	25 (0.76%)
近平滑念珠菌	8 (0.42%)	34 (1.03%)
其他	11 (0.57%)	20 (0.61%)

3.3. 2020~2024 年 DM 组与 Non-DM 组常见革兰阴性菌对抗菌药物的耐药率比较

在大肠埃希菌中，氟喹诺酮药物中 DM 组对环丙沙星的耐药率显著高于 non-DM 组(75.43% vs 71.83%, OR = 1.17, 95% CI: 1.01~1.43, P = 0.035)。第三代头孢菌素的代表药物头孢噻肟呈相反趋势，DM 组耐药率 43.61%，显著低于 non-DM 组的 51.27% (OR = 0.74, P < 0.001)。尤为值得关注的是，DM 组对碳青霉烯类药物亚胺培南绝对值较低(0.45%)，但仍显著低于 non-DM 组(1.50%, OR = 0.30, P = 0.009)，见表 3。

Table 3. Comparison of antimicrobial resistance rates of *Escherichia coli* in midstream urine cultures between DM and Non-DM patients with urinary tract infections
表 3. DM 组与 non-DM 组泌尿系感染患者中段尿培养大肠埃希菌对抗菌药物的耐药率比较

	DM 组 (n = 1103)		non-DM 组 (n = 1736)		P 值	OR (95% CI)
	耐药株数	耐药率(%)	耐药株数	耐药率(%)		
环丙沙星	**832**	**75.43**	**1247**	**71.83**	**0.035**	**1.20 (1.01~1.43)**
替加环素	0	0.00	1	0.06	0.425	0.99 (0.99~1.00)
左氧氟沙星	**727**	**65.91**	**1081**	**62.27**	**0.049**	**1.17 (1.00~1.37)**
氨苄西林	**678**	**61.47**	**1152**	**66.36**	**0.008**	**0.81 (0.69~0.095)**
美罗培南	**2**	**0.18**	**1**	**0.06**	**0.008**	**0.17 (0.04~0.75)**
头孢哌酮/舒巴坦	41	3.72	84	4.84	0.156	0.76 (0.52~1.11)
头孢他啶	214	19.40	377	21.72	0.139	0.87 (0.72~1.05)
头孢噻肟	**481**	**43.61**	**890**	**51.27**	**<0.001**	**0.74 (0.63~0.86)**
头孢西丁	22	1.99	41	2.36	0.517	0.84 (0.50~1.42)
庆大霉素	**362**	**32.82**	**676**	**38.94**	**<0.001**	**0.77 (0.65~0.90)**
亚胺培南	**5**	**0.45**	**26**	**1.50**	**0.009**	**0.30 (0.12~0.78)**
阿莫西林/克拉维酸	**89**	**8.07**	**186**	**10.71**	**0.020**	**0.73 (0.56~0.95)**
厄他培南	**3**	**0.27**	**23**	**1.32**	**0.004**	**0.20 (0.06~0.68)**
哌拉西林/他唑巴坦	31	2.81	61	3.51	0.302	0.79 (0.51~1.23)
阿米卡星	18	1.63	47	2.71	0.062	0.60 (0.34~1.03)
氨曲南	332	30.10	562	32.37	0.204	0.90 (0.76~1.06)
头孢吡肟	155	14.05	257	14.80	0.579	0.94 (0.76~1.17)
头孢唑林	445	40.37	756	43.55	0.092	0.88 (0.75~1.02)

Notes：加粗字体表示两组间差异具有统计学意义 $P < 0.05$。

3.4. DM 组与 Non-DM 组常见革兰阳性菌对抗菌药物的耐药率比较

在屎肠球菌中，在屎肠球菌中，DM 组对四环素耐药率显著低于 non-DM 组(32.33% vs 59.10%, $P < 0.001$)，其耐药风险显著低于 non-DM 组(OR = 0.33, 95% CI: 0.22~0.51)。两组对替考拉宁、莫西沙星、青霉素、利奈唑胺、奎奴普丁、万古霉素、克林霉素、红霉素的耐药率无显著差异。见表 4。

在粪肠球菌中，DM 组对莫西沙星耐药率显著低于 non-DM 组(8.20% vs 19.66%, $P = 0.038$)，其耐药风险显著低于 non-DM 组(OR = 0.37, 95% CI: 0.14~0.98)。见表 5。

Table 4. Comparison of antimicrobial resistance rates of *Enterococcus faecium* in midstream urine cultures between DM and Non-DM patients with urinary tract infections
表 4. DM 组与 non-DM 组泌尿系感染患者中段尿培养屎肠球菌对抗菌药物的耐药率比较

抗菌药物	DM 组 (n = 133)		non-DM 组 (n = 335)		P 值	OR (95% CI)
	耐药株数	耐药率(%)	耐药株数	耐药率(%)		
替考拉宁	0	0.00	0	0.00	1.000	
莫西沙星	42	31.58	92	27.46	0.374	1.219 (0.79~1.89)
四环素	**43**	**32.33**	**198**	**59.10**	**<0.001**	**0.33 (0.22~0.51)**

续表

青霉素	127	95.49	304	90.75	0.086	2.16 (0.88~5.30)
利奈唑胺	0	0.00	2	0.60	0.372	0.99 (0.99~1.00)
奎奴普丁	2	1.50	4	1.94	0.788	1.26 (0.23~6.98)
万古霉素	1	0.75	0	0.00	0.112	1.01 (0.99~1.02)
克林霉素	0	0.28	1	0.38	0.528	1.00 (0.99~1.00)
红霉素	123	92.48	306	91.34	0.688	1.17 (0.55~2.46)

Notes：加粗字体表示两组间差异具有统计学意义 P < 0.05。

Table 5. Comparison of antimicrobial resistance rates of *Enterococcus faecalis* in midstream urine cultures between DM and Non-DM patients with urinary tract infections
表 5. DM 组与 non-DM 组泌尿系感染患者中段尿培养粪肠球菌对抗菌药物的耐药率比较

抗菌药物	DM 组 (n = 61)		non-DM 组 (n = 178)		P 值	OR (95% CI)
	耐药株数	耐药率(%)	耐药株数	耐药率(%)		
替考拉宁	0	0.00	0	0.00	1.000	
莫西沙星	**5**	**8.20**	**35**	**19.66**	**0.038**	**0.37 (0.14~0.98)**
四环素	47	77.05	142	79.78	0.651	0.85 (0.42~1.71)
青霉素	9	14.75	14	7.87	0.115	2.03 (0.83~4.96)
利奈唑胺	2	3.28	10	5.62	0.470	0.57 (0.12~2.68)
奎奴普丁	0	0.00	0	0.00	1.000	
万古霉素	0	0.00	0	0.00	1.000	
克林霉素	0	0.00	0	0.00	1.000	
红霉素	47	77.05	124	69.66	0.270	1.46 (0.74~2.88)

Notes：加粗字体表示两组间差异具有统计学意义 P < 0.05。

3.5. DM 组与 Non-DM 组常见真菌对抗菌药物的耐药率比较

DM 组与 non-DM 组分离白色念珠菌对两性霉素 B、伊曲康唑、氟康唑、氟胞嘧啶、伏立康唑耐药率均高度敏感(<2%)，两组对两性霉素 B、伊曲康唑、氟康唑、氟胞嘧啶、伏立康唑的耐药率无显著差异，见表 6。在热带念珠菌中，DM 组对伏立康唑的耐药率显著高于 non-DM 组(41.82% vs. 22.22%, P = 0.038)，其耐药风险约为 non-DM 组的 2.52 倍(OR = 2.52, 95% CI: 1.04~6.09)。见表 7。

Table 6. Comparison of antimicrobial resistance rates of *Candida albicans* in midstream urine cultures between DM and non-DM patients with urinary tract infections
表 6. DM 组与 non-DM 组泌尿系感染患者中段尿培养白色念珠菌对抗菌药物的耐药率比较

抗菌药物	DM 组 (n = 80)		non-DM 组 (n = 61)		P 值	OR (95% CI)
	耐药株数	耐药率(%)	耐药株数	耐药率(%)		
两性霉素 B	0	0.00	0	0.00	1.000	
伊曲康唑	1	1.25	0	0.00	0.381	1.01 (0.99~1.04)
氟康唑	1	1.25	0	0.00	0.381	1.01 (0.99~1.04)
氟胞嘧啶	0	0.00	0	0.00	1.000	
伏立康唑	0	0.00	1	1.64	0.250	0.98 (0.95~1.02)

Notes：加粗字体表示两组间差异具有统计学意义 P < 0.05。

Table 7. Comparison of antimicrobial resistance rates of *Candida tropicalis* in midstream urine cultures between DM and non-DM Patients with urinary tract infections
表 7. DM 组与 non-DM 组泌尿系感染患者中段尿培养热带念珠菌对抗菌药物的耐药率比较

抗菌药物	DM 组 (n = 55)		non-DM 组 (n = 44)		P 值	OR (95% CI)
	耐药株数	耐药率(%)	耐药株数	耐药率(%)		
两性霉素 B	0	0.00	0	0.00	1.000	
伊曲康唑	16	29.09	6	13.33	0.058	2.67 (0.94~7.53)
氟康唑	23	41.82	14	31.11	0.270	1.59 (0.70~1.60)
氟胞嘧啶	0	0.00	0	0.00	1.000	
伏立康唑	**23**	**41.82**	**10**	**22.22**	0.038	2.52 (1.04~6.09)

Notes：加粗字体表示两组间差异具有统计学意义 $P < 0.05$。

4. 讨论

本研究回顾性分析了 2020~2024 年青岛大学附属医院 5217 例泌尿系感染患者的病原菌分布及其耐药性，重点比较了糖尿病(DM)与非糖尿病(non-DM)患者之间的差异。结果显示，两组患者泌尿系感染仍以革兰阴性菌为主，占比均超过 74%，与既往研究[6] [7]报道一致。值得注意的是，DM 组中大肠埃希菌的构成比显著高于非 DM 组，提示糖尿病患者更容易感染该菌，其机制可能与高糖环境下尿路上皮细胞表面 AGEs 在尿路上皮蓄积后为I型菌毛提供了全新结合位点，增强了细菌黏附效率；此外，高糖环境可通过抑制中性粒细胞的趋化作用和吞噬活性，削弱宿主对定植菌的清除能力，为细菌增殖创造条件[8] [9]。

在耐药性方面，DM 组分离的常见革兰阴性菌的大肠埃希菌对环丙沙星和左氧氟沙星的耐药率显著高于 non-DM 组，这可能与糖尿病患者更常暴露于喹诺酮类药物有关，易诱导耐药基因的表达与传播[10] [11]，然而，本研究发现几个反常现象：DM 组大肠埃希菌对头孢噻肟、亚胺培南、美罗培南及厄他培南的耐药率反而显著低于 non-DM 组。这一现象与传统认知相悖，但可能并非由于糖尿病患者体内细菌本身更敏感，而是反映了 non-DM 组中存在更高比例的产超广谱 β-内酰胺酶(ESBL)或碳青霉烯酶的高耐药克隆株。non-DM 组患者可能更多来源于 ICU 或长期住院科室，这些环境中选择压力更大，更易筛选出多重耐药菌。此外，部分糖尿病患者因肾功能受损导致药物排泄减慢，体内药物浓度相对较高，可能抑制了耐药突变株的扩增，因此，在治疗 DM 合并复杂泌尿系感染时，碳青霉烯类及部分头孢菌素类药物仍具重要价值[12] [13]。

革兰阳性菌方面，屎肠球菌中 DM 组对四环素的耐药率显著低于 non-DM 组，其耐药风险显著低于 non-DM 组，粪肠球菌中 DM 组对莫西沙星的耐药率也显著更低，这与糖尿病通常促进耐药的传统认知[14]有所不同，其机制可能的解释包括：四环素和莫西沙星并非糖尿病合并感染经验治疗中的常用药物，DM 组患者对该类药物的暴露频率低于 non-DM 组，从而减少了获得性耐药的选择压力。此外，糖尿病患者的肠道微生态存在明显的群落结构改变，这种改变可能对整个肠球菌属的菌株丰度和克隆携带情况产生深远影响，这一点已有多项基于肠道宏基因组的研究加以证实[15] [16]。此外，两组中革兰阳性菌对万古霉素、利奈唑胺等保留药物仍保持高度敏感，这与既往研究数据相符[17]。

本研究还发现，DM 组与 non-DM 组分离白色念珠菌对两性霉素 B、伊曲康唑、氟康唑、氟胞嘧啶、伏立康唑耐药率均高度敏感，DM 组与 non-DM 组对伊曲康唑、氟康唑、伏立康唑均存在一定耐药性，在热带念珠菌中，DM 组对伏立康唑的耐药率显著高于 non-DM 组，其耐药风险约为 non-DM 组的 2.52 倍，高尿糖可通过多种途径促进真菌定植与感染：既往研究表明，在体外尿糖环境中，白色念珠菌不仅生长

加速，其对抗真菌药物的最小抑菌浓度也显著升高[18]。首先，高糖环境可通过 cAMP-PKA 和 MAPK 等葡萄糖敏感信号通路，促进白色念珠菌由酵母相向菌丝相转化，并增强生物膜的形成与稳定性，进而提高其对尿路上皮的黏附与侵入能力[19]；其次，高血糖可显著抑制中性粒细胞 NOX2 复合物的活化，导致活性氧(ROS)生成减少[20]。因此，在经验性抗真菌治疗中，需结合药敏结果合理选择药物，避免耐药进一步加剧。

年龄和性别是影响泌尿系感染的重要因素。本研究结果显示女性患者数量多于男性[21]，性别差异的根本原因主要在于解剖生理结构的差异。女性尿道较短(约 4~5 厘米)且直，且开口与肛门距离较近，使得肠道来源的病原菌更容易上行至膀胱，引发感染。本研究女性患者占比较高，与此普遍规律一致。相比之下，男性尿道较长，且前列腺液具有一定的抗菌作用，故年轻男性感染率较低。然而，本研究男性患者的中位年龄较高，提示其感染可能主要与老年男性前列腺增生等因素有关。前列腺增生可导致膀胱出口梗阻和尿液残留，为细菌繁殖提供了条件[22]。本研究患者的中位年龄在 54~78 岁之间，表明老年人是泌尿系感染的高危人群[23]。老年人易感原因复杂多样，此外，老年人常伴有糖尿病、神经系统疾病(如脑卒中后遗症、痴呆)导致的神经源性膀胱，以及营养不良等情况，这些均是泌尿系感染的明确危险因素[23]。

本研究存在一定局限性。本研究是一项单中心回顾性研究，可能存在选择偏倚和信息偏倚[24]。此外，本研究采用常规微生物学鉴定和药敏试验方法，未区分社区获得性与医院获得性感染，未能进行多位点序列分型(MLST)及耐药基因测序等分子生物学分析，限制了我们对耐药克隆的传播模式及其分子机制(如 ESBLs、碳青霉烯酶基因)的深入理解。为克服这些局限，未来研究应致力于开展多中心、前瞻性的协作研究，并整合基因组学(如全基因组测序 WGS)方法[25]，以更精确地追踪耐药菌的进化与传播。在此基础上，我们建议建立区域性的耐药监测网络，定期更新基于本地数据的抗菌药物应用指南。同时，必须加强碳青霉烯类等重要抗菌药物的科学化管理[26] [27]，并结合个体化真菌感染的防治策略。针对包括鲍曼不动杆菌在内的多重耐药菌[28] [29]，应深入开展其耐药机制研究。此外，积极探索并应用基于人工智能(AI)的预测模型和抗菌药物管理系统[30]，有望整合临床变量与微生物数据，实现感染性疾病更早期的精准诊断和治疗决策支持，从而改善患者预后。

声　明

本研究获得青岛大学附属医院伦理委员会批准：QYFY WZLL 550137，由于研究为回顾性分析且患者均已签署临床泛知情同意书，免除个人知情同意。

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