

脓毒血症早期诊断血清学标志物及预测模型研究进展

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摘要: 脓毒血症是危重患者死亡的主要原因,早期识别感染类型是决定患者治疗和预后的关键。目前,血培养作为脓毒血症诊断的金标准,但因其培养周期长且阳性率较低等局限性,而无法为临床早期开展抗感染治疗提供病原学依据。血清学标志物因其在体外检测方便快捷,且可作为早期推断感染的有益实验室指标而受到广泛关注。近年来,随着各领域对脓毒血症的深入研究,许多新型血清学标志物被发现在诊断脓毒血症方面具有潜在应用价值。因此,该文就近年报道的脓毒血症的新型血清学标志物的特点及应用价值进行探讨,以期发现有价值的早期诊断脓毒血症的新型血清学标志物,并结合相关预测模型进行综述,为临床早期诊断脓毒血症带来新思路。

关键词: 脓毒血症; 血清学标志物; 感染; 诊断; 预测模型

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Research Progress on Serological Markers and Prediction Models for Early Diagnosis of Sepsis

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Abstract: Sepsis constitutes a predominant cause of mortality in critically ill patients, and early determination of the type of infection is crucial for influencing patient management and forecasting outcomes. Currently, blood culture serves as the gold standard for diagnosing sepsis. Yet, its limitations, such as a lengthy culture period and low positivity rate, hinder its ability to provide a microbiological basis for early initiation of antimicrobial therapy in clinical practice. Serological markers have engendered significant interest due to their convenience and rapid detection in vitro, emerging as indispensable laboratory indices for early inference of infection. In recent years, with extensive research on sepsis across diverse academic domains, numerous novel serological markers exhibit promise in diagnosing sepsis. Therefore, this review explores the characteristics and application value of new serological markers for early diagnosis of sepsis, and reviews them in combination with relevant predictive models, bringing new ideas for early clinical diagnosis of sepsis.

Keywords: sepsis; serological markers; infection; diagnosis; prediction model

脓毒血症是宿主对感染反应失调而引起的危及生命的器官功能障碍^[1],也是危重症患者死亡的重要原因,具有高发病率和高死亡率特点。基于国内一项调查报告显示,重症监护病房(ICU)患者脓毒血症的发病率约为21%,90天死亡率为35.5%,对于脓毒性休克患者,90天死亡率高达52%左右^[2]。此外,对于脓毒血症或脓毒性休克患者,每延迟1h给予靶向抗生素治疗,其死亡率就会增加7.6%^[3]。因此,早期识别脓毒血症及其严重程度,进而选择合适的抗生素治疗,对提高患者的生存率至关重要。目前,血培养(blood culture, BC)仍作为诊断脓毒血症的金标准,但通常需要3~5天才能获得病原体鉴定及药敏结果,可能导致治疗延迟。因此,临床迫切需要新的实验室指标作为早期正确开展抗感

染治疗的参考依据。相比其它病原体检测技术,如基质辅助激光解吸电离飞行时间质谱(matrix-assisted laser desorption/ionization time-of-flight mass spectrometry, MALDI-TOF MS)、宏基因组二代测序(metagenomics next-generations sequencing, mNGS)等,血清学标志物检测方便快捷,应用于临床可以早期推断感染存在及感染类型,为临床诊治脓毒血症带来新方向。因此,本文从实验室角度出发,结合临床常见评分系统,就有助于脓毒血症早期诊断或对疾病严重程度和预后评估具有潜在应用价值的新型血清学标志物及相关预测模型进行综述。

1 脓毒血症血清学标志物

1.1 急性期蛋白

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1.1.1 降钙素原(PCT): PCT 是一种由甲状腺 C 细胞产生的降钙素前体激素，其在感染发生后 3~6 h 内升高，6~8 h 后达到峰值^[4]，与 C 反应蛋白(CRP)相比，PCT 水平在刺激后升高更快，达到峰值更快，感染消退后下降也更快^[5]。有研究表明，当临界值 > 2 ng/ml 时，PCT 可作为细菌性脓毒血症患者早期诊断的有益血清学标志物^[6]。同时，宁熙等^[7]人通过探讨 PCT、CRP 及白细胞介素 -6(IL-6) 在脓毒血症与全身炎症反应综合征(systemic inflammatory response syndrome, SIRS) 患者中的差别，发现患者入 ICU 24 h 内，当 PCT < 4.18ng/ml 时，可排除约 97% 的脓毒血症阴性患者；当 PCT>0.5 ng/ml 时，其诊断脓毒血症的敏感度和特异度分别为 95.83%，100.00%，且 PCT 在鉴别脓毒血症和 SIRS 方面优于 IL-6 和 CRP。但 PCT 在机体发生应激、创伤、过敏或局部感染(如呼吸道感染、肠道感染)时也会相应升高。因此，PCT 用于诊断脓毒血症时，需要联合其他指标并结合患者临床症状综合判断，以提高对脓毒血症诊断的准确度。

1.1.2 肝素结合蛋白(heparin-binding protein, HBP): HBP 也称 azurocidin 或阳离子抗菌蛋白 CAP37，是中性粒细胞受到免疫原刺激后释放的颗粒蛋白^[8]，已被证明与血管舒张和脓毒血症的发展密切相关。LINDER 等^[9]发现在循环衰竭发生前 12 h，HBP 水平已显著升高，当临界值为 15 ng/ml 时，HBP 预测脓毒性休克的敏感度和特异度分别为 87.1%，95.1%。一项荟萃分析^[10]结果显示，HBP 诊断脓毒血症合并敏感度为 85% (95%CI: 0.79~0.90)，合并特异度为 91% (95%CI: 0.82~0.96)，均高于 PCT 和 CRP。然而，XUE 等^[11]研究发现，HBP 虽然可以诊断细菌感染，但在革兰阳性菌和革兰阴性菌感染之间无显著差异，且难以区分单一感染和混合感染，因此 HBP 在临床抗感染指导方面仍存在一定局限性。

1.1.3 胰石蛋白(pancreatic stone protein, PSP): PSP 主要由胰腺泡细胞分泌，确切的生理作用尚不清楚，但已被证明能激活中性粒细胞^[12]，其变化程度与脓毒血症的病程密切相关。基于一项 meta 分析^[13]结果表明，PSP 诊断脓毒血症的敏感度和特异度分别为 66%，83%，其受试者工作特征(ROC) 曲线 - 曲线下面积(AUC) 为 0.81，优于 CRP (0.77) 和 PCT (0.78)。当 PSP 与 CRP 联合时，其诊断脓毒血症的敏感度和特异度分别为 81%，84%，AUC 可提高至 0.90。此外，在一项前瞻性研究^[14]中，通过动态监测疑似脓毒血症患者 PSP、CRP 及 PCT 的变化，发现 PSP 在脓毒血症确诊前 5 天就已经开始升高，而 PCT 和 CRP 在脓毒血症确诊前 2

天开始升高，且脓毒血症发生前 72 h 内，PSP 已开始明显升高，可升高 3.3~5.5 倍^[15]。以上研究表明，PSP 在早期诊断脓毒血症方面具有良好潜能，但仍需大样本进一步验证其诊断效能。

1.1.4 钙卫蛋白(Calprotectin, Cal): Cal 是由两个蛋白质亚基组成的异二聚体，以高浓度存在于中性粒细胞的细胞质中，也称为 S100A8 和 S100A9，属于 S100 蛋白家族^[16]。研究发现，Cal 可在数小时内伴随细菌或内毒素而增加^[17]。与 PCT 和 CRP 相比，Cal 在炎症刺激下快速释放，可以更早地在循环中检出^[18]。因此，Cal 被证明是早期发现感染的有益血清学标志物。基于一项荟萃分析^[19]显示，将 Cal 作为早期诊断脓毒血症的血清学标志物，其合并敏感度和特异度分别为 77% 和 85%。此外，有研究^[20]发现，Cal 在诊断脓毒血症及区分脓毒血症与非脓毒血症方面优于 PCT。

1.2 细胞因子 过度的炎症反应和细胞因子风暴被认为是脓毒血症发生发展的重要机制之一。细胞因子作为参与免疫调节的组成部分，存在于几乎所有有核细胞中。目前作为血清学标志物的细胞因子，如血清 IL-6, IL-1, IL-18 和肿瘤坏死因子 α (TNF- α) 等升高是细胞因子风暴的典型特征，特别是 IL-6 水平升高是细胞因子风暴的标志^[21]。

IL-6 正常情况下表达量极低，在感染、创伤及应激状态下 1~3h 迅速上升，在 24~48h 达到峰值^[22]。IL-6 与脓毒血症患者的炎症严重程度、器官功能障碍和死亡率有关。基于一项荟萃分析^[23]，发现 IL-6 诊断脓毒血症的并发敏感度为 72% (95% CI: 0.65~0.78)，并发特异度为 70% (95% CI: 0.62~0.76)，AUC 为 0.77 (95% CI: 0.73~0.80)。此外，有研究通过探讨细胞因子及其他指标在脓毒血症患者早期诊断及预后评估中的价值，发现 IL-8, PCT, IL-17 和中性粒细胞/淋巴细胞比值(NLR) 预测脓毒血症的能力较强，其诊断敏感度分别为 70%，84%，66% 和 72%，特别当联合检测四种指标时，其诊断敏感度可提高至 86%，AUC 可达到 0.90 (95% CI: 0.85 ~ 0.93)，优于单独检测 [IL-8 (0.78), NLR (0.81), PCT (0.83) 和 IL-17 (0.86)]。同时，IL-6 表达水平的升高可以有效预警脓毒性休克的发生，而对脓毒血症患者死亡结局有较好预测价值的细胞因子为 IL-10, IL-2 和 IL-5^[24]。综上，细胞因子可作为脓毒血症早期诊断及预后评估的有用指标，当与其他血清学标志物联合检测时，有助于脓毒血症的早期鉴别诊断。相信随着脓毒血症的深入研究，细胞因子家族会有更多新的标志物被应用于脓毒血症的诊断和预后评估。

1.3 膜蛋白与受体蛋白

1.3.1 可溶性 CD14 亚型(soluble CD14 subtype, sCD14-

ST): sCD14 也称 Presepsin, 为脂多糖受体的片段之一, 存在于单核细胞、巨噬细胞及中性粒细胞表面。Presepsin 在感染后 2 h 开始上升, 并在 3 h 后达到峰值, 使其成为脓毒血症潜在的早期血清学标志物^[25-26]。有研究^[27]表明, 血清 sCD14-ST 水平可作为脓毒血症敏感的指示器, 当临界值为 249.5 时, 其诊断敏感度和特异度分别为 88.5%, 86.7%。sCD14 水平与疾病严重程度 (SIRS, 败血症、感染性休克) 的相关性已被证实, 并且多次比较强调了与 PCT 相似的平均诊断性能。然而, 基于一项荟萃分析表明^[28], sCD14 目前还没有临床使用的明确临界值。因此, 建议将其作为临床评估脓毒血症的一部分, 而不是独立的血清学标志物。

1.3.2 中性粒细胞白细胞分化抗原 64(neutrophil cluster of differentiation 64, nCD64): nCD64 是一种高亲和力的免疫球蛋白 Fc-γ 受体 I, 其表达开始于由细菌感染引起的免疫反应的早期阶段, 并在 1 h 内增加^[29]。在一项系统综述和荟萃分析中, YEH 等^[30]通过比较 nCD64, PCT 和 CRP 对脓毒血症的诊断效能, 发现 nCD64 诊断脓毒血症的合并敏感度和特异度分别为 87% (95% CI: 0.80~0.92) 和 89% (95% CI: 0.82~0.93)。且 nCD64 诊断脓毒血症的 AUC (95%CI) 值大于 CRP[0.89(95% CI: 0.87~0.92) vs 0.84 (95%CI: 0.80~0.88), $P<0.05$] 或 PCT[0.89(95% CI: 0.84~0.95) vs 0.84 (95%CI: 0.79~0.89), $P<0.05$], 表明 nCD64 诊断准确度优于 CRP 和 PCT 测定。综上, nCD64 可作为脓毒血症早期诊断的血清学标志物。

表 1

几种血清学标志物在脓毒血症诊断中的文献评价

项目		动力学特点	临界值	敏感度 (%)	特异度 (%)	诊断价值	参考文献
单独检测	PCT	3~6 h 开始上升, 6~8 h 达到峰值	0.5 ng/ml	95.83	100.00	较高	[7]
	HBP	循环衰竭发生前 12 h, 显著升高	15 ng/ml	87.10	95.10	较高	[9]
	PSP	脓毒血症发生前 72 h, 显著升高	-	66.00	83.00	中等	[13]
	Cal	感染后数小时内增加	-	77.00	85.00	中等	[19]
	IL-6	1~3 h 开始上升, 24~48 h 达到峰值	-	72.00	70.00	中等	[23]
	sCD14-ST	2 h 开始上升, 3 h 达到峰值	-	88.50	86.70	较高	[27]
	nCD64	感染后 1 h 内增加	-	87.00	89.00	中等	[30]
	sTREM-1	-	-	85.00	79.00	中等	[32]
	MR-proADM	-	1~1.5 nmol/L	83.00	90.00	较高	[36]
联合检测	miR-223-3p + PCT + IL-6 + CRP	-	-	92.00	83.40	较高	[37]
	PCT + IL-6	-	-	87.50	90.90	较高	
	Presepsin+IL-6	-	-	92.10	98.20	较高	
	Presepsin+PCT	-	-	94.40	98.40	较高	[38]
	Presepsin + PCT + IL-6	-	-	97.60	99.20	较高	

1.5 其他血清学标志物

1.5.1 外泌体: 外泌体是细胞间通讯的重要媒介, 其介导的 mRNA 和微小 RNA (micro RNA, miR) 转移不仅使细胞间的遗传物质交换^[39-40], 还可作为脓

毒血症诊断的标志物^[41]。miRNA 是内源性基因编码的长度为 21 ~ 25 个核苷酸的单链非编码 RNA, 可在炎症、感染和脓毒血症期间由细胞释放到循环中^[42]。既往研究表明, 循环 miRNAs 的表达在脓

毒血症早期受到调控，并与疾病严重程度和进展呈正相关^[43]。TIAN等^[41]发现血清外泌体中circRNA的表达在脓毒血症患者与健康个体间存在差异，其中hsa_circRNA_104484和hsa_circRNA_104670的升高可作为脓毒血症新型诊断标志物和分子治疗靶点。基于一项meta分析^[44]显示，miRNA，特别是miRNA-155-5p，在诊断脓毒血症时，其合并敏感度和特异度分别为71%，82%，AUC为0.85，因而可将miRNA-155-5p作为脓毒血症诊断的有用指标。此外，邓颖云等^[45]发现，脓毒血症患儿血浆miR-455-5p和miR-483-5p表达水平明显升高，且miR-455-5p和miR-483-5p表达水平随疾病进展（健康对照组、脓毒血症组及脓毒性休克组）依次升高。当联合PCT检测时，miR-455-5p，miR-483-5p对儿童脓毒血症的诊断及预后评估价值显著提高，其敏感度和特异度分别高达94.7%和86.5%。然而，目前国内关于血浆外泌体用于脓毒血症诊断方面的研究仍相对较少，且血浆外泌体在评估脓毒血症危重患者器官衰竭的严重程度和预测死亡率方面还需要进一步大规模验证。

1.5.2 微生物毒素：微生物毒素包括内毒素（细菌细胞壁的结构成分）和外毒素（合成和分泌的蛋白质）^[46-47]，致病菌的毒力强度依赖于能侵入目标真核细胞的毒素产生。越来越多的证据表明，脓毒血症期间严重失调的发病机制背后的关键在于微生物毒素的全身传播，而不是菌血症本身^[48-49]。脂多糖被认为是一种高致病性的内毒素，可导致脓毒血症患者的器官功能障碍^[50-51]，在一定程度上反映机体由革兰阴性菌感染的程度。研究发现，相比健康人群，血清内毒素在脓毒血症患者中表达水平更高（ $P < 0.05$ ），其中细菌血流感染致脓毒血症患者和健康人群的血清内毒素水平分别为 $11.39 \pm 4.39\text{ng/L}$ 和 $0.05 \pm 0.02\text{ng/L}$ ，且血清内毒素水平在革兰阴性菌感染中表达高于革兰阳性菌感染（ $15.20 \pm 4.14\text{ng/L}$ vs $6.77 \pm 3.95\text{ng/L}$ ），差异具有统计学意义^[52]。因此，通过对不同微生物毒素的检测，在区分感染类型及评估患者感染严重程度方面有重要价值。

2 脓毒血症临床常见评分系统及相关预测模型

2.1 脓毒血症临床常见评分系统

2.1.1 序贯器官衰竭评估评分：序贯器官衰竭评估（sequential organ failure assessment, SOFA）评分是一种常用评分系统，用于检查与器官系统相关的危重疾病并发症的顺序，包括肝、肺、血液、血流动力学、肾脏和神经系统。每个器官系统的评分范围从0（正常）到4（高度功能障碍/衰竭）^[53]，评分越高反映器官功能障碍越严重。qSOFA即快速脓毒症相关器官衰竭评估，是在SOFA基础上优化的一种评分，

包括3项指标：低血压（收缩压≤100 mmHg），呼吸急促（呼吸频率≥22次/分）及精神状态改变（格拉斯哥昏迷量表评分≤13分），每项指标赋值1分，qSOFA≥2分的患者患脓毒血症的危险性明显增加^[54]。

2.1.2 APACHE II评分 急性生理学与慢性健康状况评分II（acute physiology and chronic health evaluation II, APACHE II）是一种基于12个当前生理变量、既往健康状况和年龄的疾病严重程度测量。总分在0~71分之间，对应院内死亡风险的增加^[55]。

2.2 相关预测模型 在一项单中心回顾性研究^[56]中，采用Logistic回归模型，发现性别（OR=0.504, 95%CI: 1.008~1.059），NLR（OR=1.030, 95%CI: 1.008~1.059）和SOFA评分（OR=1.179, 95%CI: 1.073~1.308）是ICU患者发生脓毒血症的独立危险因素。将三者联合预测ICU患者发生脓毒血症的AUC为0.722（95%CI: 0.637~0.807）。表明基于性别、NLR、SOFA评分构建的列线图用于预测ICU重症患者发生脓毒血症的预测性能较好。此外，范昊等^[57]将PCT，IL-6等多种细胞因子和APACHE II评分联合后发现，判断脓毒血症患者短期预后具有较好的效果。以上研究表明，在诊断脓毒血症方面，单一的临床评分系统或血清学标志物往往存在局限性，通过将多种血清学标志物和临床评分系统联合建立预测模型，可以更好地实现对脓毒血症患者的早期诊断及危险度分级，进而改善患者预后。

3 总结与展望

综上所述，血清学标志物对脓毒血症早期的发现、发展及预后评估中都具有重要的应用价值，但鉴于没有任何单一血清学标志物可以准确评估脓毒血症，同时满足诊断脓毒血症的高敏感度和特异度，故通常需要联合多种血清学标志物及临床评分系统以提高脓毒血症诊断及疗效评估的准确度，实现 $1+1>2$ 的效能。血清学标志物为临床诊治脓毒血症带来新希望，然而新的血清学标志物可能因以下问题降低其临床可信度或应用价值，如缺少与传统生物标志物的比较、缺乏临床大规模验证、没有统一的评估标准或评估过程不严格、不同标志物具体临界值如何界定等。随着医疗水平的不断提高，新兴检测技术或方法不断涌现，未来期望借助基因组学和代谢组学等方法发现诊断价值更高的血清学标志物，结合临床评分系统，找到更佳血清标志物组合，为脓毒血症的早期诊治、预后评估带来新的参考价值。

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