・综述・

液体活检在胶质瘤诊断中的意义

李峰平,李志强 武汉大学中南医院神经外科, 湖北 武汉 430071

摘 要:随着对胶质瘤发生发展机制的深入研究,越来越多的肿瘤标志物被用于胶质瘤的精准诊断,包括循环肿瘤细胞(CTCs)、循环肿瘤 DNA(ctDNA)、微小 RNA(miRNAs)、外泌体等。有别于病理组织活检,应运而生的液体活检技术,通过检测血液、脑脊液等体液中存在的特异性肿瘤标志物,不仅降低了侵入性,而且对于诊断胶质瘤,阐明肿瘤侵袭和播散的机制,揭示肿瘤异质性,设计个体化治疗和评估改善疗效意义重大。

关键词:胶质瘤;循环肿瘤细胞;循环肿瘤 DNA;微小 RNA;外泌体

中图分类号: R739.41

DOI: 10.16636/j. cnki. jinn. 2020. 05. 014

Diagnostic value of liquid biopsy in glioma

LI Feng-Ping, LI Zhi-Qiang. Department of Neurosurgery, Zhongnan hospital of Wuhan University, Wuhan, Hubei 430071, China Corresponding author: LI Zhi-Qiang, (1975 –), male, doctor of medicine, chief physician and professor of neurosurgery; doctoral supervisor; current deputy dean of Zhongnan Hospital of Wuhan University, specializing in the comprehensive treatment of glioma and metastasis. Email: lizhiqiang@ whu. edu. cn

Abstract: As research in the mechanism of glioma development and progression advances, more and more tumor markers are used for the precise diagnosis of glioma, including circulating tumor cells, circulating tumor DNA, microRNA, and exosome. The newly emerging technique, liquid biopsy, shows features differing from pathological tissue biopsy. Through detecting specific tumor markers in body fluids like blood and cerebrospinal fluid, liquid biopsy provides a less invasive but valuable way to diagnose glioma, clarify how it spreads, unravel its heterogeneity, design individualized treatment, and evaluate therapeutic effect.

Key words: glioma; circulating tumor cells; circulating tumor DNA; microRNA; exosome

胶质瘤是最常见的中枢神经系统原发性恶性肿瘤,每100000人中约有7.3例患者,其中高级别胶质瘤约占85%,低级别胶质瘤约占15%,多发于成年人[1]。胶质瘤细胞可以起源于不同的前体细胞,少突细胞前体细胞(oligodendrocyte precursor cells,OPCs)是重要的原始细胞之一,将p53和NF1基因敲除后,大部分时间处于稳定状态来源于成年人的OPCs将会被重新激活、增殖直至发生恶变。哺乳动物类雷帕霉素靶蛋白(mammalian target of rapamycin,mTOR)信号通路等参与了胶质瘤的发生

发展^[2]。由于胶质瘤的发生机制非常复杂,绝大部分胶质瘤早期不易发现,确诊胶质瘤仍然面临极大的挑战。传统的诊断技术主要包括病理组织活检和颅脑影像学检查,但两者均有一定的局限性:前者作为侵袭性手段,患者依从性不高;后者鉴别诊断仍有困难而可能延误最佳治疗时机^[3-5]。目前,在肿瘤检测的临床研究中,科学家对无创诊断技术即液体活检技术表现出极大兴趣。该技术通过分离检测来自体液的循环肿瘤细胞(circulating tumor cells, CTCs)、循环肿瘤 DNA(circulating tumor DNA,

基金项目:国家自然科学基金项目(81573459);国家卫计委医药卫生科技发展研究中心"重大疾病防治科技行动计划":神经系统肿瘤精准诊疗技术的研发及推广应用研究(2018ZX - 07S - 011)。

收稿日期:2020-04-16;修回日期:2020-08-07

作者简介:李峰平(1998-),男,武汉大学中南医院神经外科博士,主要从事胶质瘤发病机制的研究。

通信作者:李志强(1975 -),男,医学博士、神经外科主任医师、教授;博士生导师;现任武汉大学中南医院副院长,擅长脑胶质瘤与转移瘤的综合治疗。Email:lizhiqiang@whu.edu.cn。

ctDNA)、微小 RNA(miRNAs)、外泌体等为肿瘤学的临床决策提供丰富信息,它的应用能够较好地弥补传统诊断技术的不足。本文围绕胶质瘤的液体活检技术及新型肿瘤标志物进行综述,探讨其在临床中的巨大应用前景。

1 CTCs

通过激活信号通路,表达细胞外黏附分子等机 制,来自原发肿瘤的胶质瘤细胞和胶质瘤干细胞 (glioma stem cells, GSCs)可进入血管成为 CTCs^[6], 因 CTCs 具有干细胞的特性,对放化疗和循环应激 诱导的细胞凋亡也具有一定的的耐受性[7]。在 GSCs 中,增殖细胞核抗原相关因子(proliferating cell nuclear antigen-associated factor, PAF)的过度表达影 响了 DNA 的复制和嘧啶代谢通路, PAF 与增殖细 胞核抗原(proliferating cell nuclear antigen, PCNA)相 互作用并能够调节 DNA 的跨损伤修复(trans-lesion synthesis, TLS), 因此 GSCs 拥有强大的自我更新能 力,并导致胶质母细胞瘤(glioblastoma multiforme, GBM)患者对放疗不敏感,具有 PAF 类似作用的还 有 Akt 家族基因以及磷脂酰肌醇 3-激酶 (phosphoinositide 3-kinase, PI3K)/蛋白激酶 B (protein kinase B, Akt)信号通路^[8-10]。Krol等首次证实了胶 质母细胞瘤患者 CTCs 簇的存在[11]。为了筛选分 析 CTCs, Müller 等利用胶质细胞原纤维酸性蛋白 (glial fibrillary acidic protein, GFAP)作为标志,通过 比较基因组杂交技术(comparative genomic hybridization, CGH)、序列分析和荧光原位杂交(fluorescence in situ hybridization, FISH),进一步证明 CTCs 来源于 GBM,但是,在这一研究中,通过 GFAP 的免疫染 色,仅有 20.6% 的 GBM 患者在外周 血检测到了 CTCs^[12]。利用原位杂交技术,同样可以检测 CTCs 的 miRNAs, Ortega 等利用 MishCTC 在上皮来源的循 环肿瘤细胞中检测到 miRNA-21[13]。因此,利用这 项技术有可能让胶质瘤得到早期诊断。由于CTCs 获得率和纯度较低、获得的 CTCs 与原始肿瘤细胞间 的异质性等有待研究,所以,该技术真正应用于临床 还须进一步探索[14-16]。为了降低背景噪音,提高胶 质瘤诊断技术的特异性,有科学家在尝试从脑脊液 中分离 CTCs,期望能够从中获得胶质瘤细胞[17]。

2 ctDNA

循环血液中存在着一种 DNA, 称之为血浆游离 DNA (cell-free DNA, cfDNA), 其中来源于肿瘤细胞的称之为 ctDNA。ctDNA的获取方法无创, 利于

GBM 诊断和分型,可以协助制定治疗方案并检测 患者对治疗的反应。对获取的 ctDNA 可以开展包 括微滴式数字 PCR (droplet digital PCR, ddPCR) 定量 分析,突变基因检测,基因组、表观基因组和蛋白 质组分析等[18-19]。在一项研究中,19位脑脊液中 分离检测到 ctDNA 的患者,仅有3位的 cfDNA 检测 到 35 个 突 变 位 点,包括 1p/19q 共 缺 失 、突 变 型 IDH1/IDH2 和生长因子受体信号通路的改变等, cfDNA 的这些突变位点的平均变异等位基因分数远 低于脑脊液来源的 ctDNA(0.58% vs 23.96%),且 大多数肿瘤组织中的克隆突变也存在于脑脊液 中[20]。随着更多特异性突变位点被发现,这些位 点的联合检测可以使肿瘤 DNA 诊断胶质瘤的特异 性高达 100% [21]。尽管如此,不同体液来源的 ctD-NA 方法学特征和提供的信息仍然具有差异,脑脊 液来源的 ctDNA 提供的信息更加精确,更具有代表 性,获得成本更低,相比 cfDNA,脑脊液来源的 ctD-NA 突变位点的检测敏感性更高(100% vs 38%)[22],它的优势得益于检测分析手段的更新,即 将体拷贝数改变(somatic copy number alteration, SC-NAs)的分析与配对端测序确定的 DNA 片段模式相 结合,借助 sWGS 数据检测 CSF 中的肿瘤细胞游离 DNA (cell -free tumor DNA, cftDNA) [23-25], 同时将 DNA 分子片段长度测定联合特异性片段基因测序能够进 一步提高 ctDNA 相关检测技术在胶质瘤诊断中的准 确性,将受试者操作特征曲线下面积(area under curve, AUC) 从小于 0.5 提高至大于0.91^[26]。鉴于脑 脊液中 ctDNA 的密度低于外周血液, Mair 等研究发 现循环肿瘤线粒体 DNA (circulating tumor mitochondria DNA, tmtDNA)有助于提高胶质母细胞瘤的检 测率,可以替代核 ctDNA(82% vs 24%),在脑脊液 和尿液中也可以检测到,因此 tmtDNA 有更加广泛 的应用前景[27-28]。

miRNA

miRNA 是长约 22 nt 的非编码 RNA,广泛存在于从病毒到人类的各种生物中,通过与 mRNA 的3'-UTRs 结合抑制 mRNA 表达或促进 mRNA 降解,防止蛋白合成^[29-30]。许多研究表明 miRNA 在人类疾病的发生发展扮演重要的角色,如胶质瘤等肿瘤^[31-37]。由于恶性肿瘤细胞具有异质性,ctDNA 并不会拥有完全相同的序列^[38],相比之下,miRNAs 的一致性更高。Zhou 等通过荟萃分析得出,在胶质瘤的诊断中,miRNAs 的整体检测灵敏度达 85%

(95% CI:0.81~0.89),特异性为90%(95% CI: 0.85 ~ 0.93), AUC 是 93% (95% CI: 0.91 ~ 0.95),其中来自血液标本的分别是84%(95%CI: $0.80 \sim 0.88$), 85% (95% CI: $0.81 \sim 0.89$) π 92% (95% CI:0.89~0.94),来自脑脊液标本的 分别是 89% (95% CI: 0.73~0.96),98% (95% $CI: 0.87 \sim 1.00$), 98% (95% $CI: 0.96 \sim 0.99$); 同时检测一组 miRNAs 可以提高灵敏度,如(miR-NA-93, miRNA-590-3p, miRNA-454); (miRNA-15b, miRNA-21) 等组合^[39]。不仅如此,通过测序 以及信号通路分析发现 miRNA 可以用于评估胶质 瘤细胞的放化疗敏感性[40]。对患者临床资料的分 析结果表明,低表达 miRNA-221 和 miRNA-222 的 患者预后更好[34]。而且, miRNAs 与胶质瘤的侵袭 性密切相关,通过慢病毒转导 miRNA-1270 的 LN-18 细胞系在雄性裸鼠体内的生长速度和体积得到 了抑制; miRNA-605 的高表达可以抑制胶质瘤细胞 系 U251 和 T98 细胞系增殖、迁移和侵袭的进 展^[32,35]。相比于肿瘤组织来源的 miRNA,基于脑脊 液的 miRNA 因对核糖核酸酶和物理化学条件的耐 受性更高,所以更加稳定、精确性也可能更高[41-43], 并可以用于 CNS 其他恶性病变的鉴别诊断[44]。但 是,由于 miRNA 序列较短,目前的探针不能很好分 析 pri-, pre-以及成熟形式的区别,而且相关技术只 能进行相对定量,因此,需要找到更加标准的内源 性对照[41]。除了 miRNA,其他细胞外 RNA(extracellular RNA, exRNA)在胶质瘤检测中的标记作用也 有待进一步挖掘,如 Y RNA 和 tRNA 等^[43]。其中, tRNAs 的产生离不开 RNA 多聚酶 Ⅲ (polymerase III, Pol III) 的指导和转录因子 III B 和 III C (transcription factor II B/C, TF II B/C) 的控制, 对于 mRNA 的表 达至关重要,被证明与包括黑素瘤、GBM 在内的多 种癌症密切相关,其关键在于癌基因和肿瘤抑制信 号通路可以调节 Pol III 和 tRNAs 的合成,进而影响 细胞的生物学行为[4547]。 Yang 等发现 SOX4 通过 结合特异的 tRNAs,如 tRNAiMet 等,阻碍 TATA box 结合蛋白和 Pol III 对 tRNAs 基因的募集,从而抑制 其表达以及 GBM 细胞的增殖^[48]。

4 外泌体

外泌体是由多种细胞产生的脂双层分泌体,直径30~100nm,包含 miRNAs 以及蛋白质等多种物质,参与细胞间信息传递和肿瘤微环境的形成^[49-51]。在胶质瘤中,外泌体的产生与间充质干细

胞和胶质瘤干细胞密切相关[52-54],如:来源于 GBM 的外泌体包含有凝血因子 TF/VIIa 复合体,进而诱 导形成乏氧环境、促进血管生成、增强侵袭性[55]。 Sun 等证明 GBM 干细胞通过分泌产生包含 Notch1 蛋白的外泌体促进 GBM 的侵袭转移^[56]。外泌体凭 借其提供的丰富信息可以用于胶质瘤的诊断,预后 和治疗[57-58]。Santangelo 等发现血浆来源的外泌体 包含的 mi-21/222/124-3p 与胶质瘤的分级和预 后有关[59]。表皮生长因子受体(epidermal growth factor receptor, EGFR)与胶质母细胞瘤某一亚型密 切相关,以突变型 EGFRvIII 为例,47% 左右的 GBM 患者 EGFRvIII 为阳性,它可以调控外泌体生物发 生、细胞间转运和生物学效应[60-61]。大部分胶质瘤 患者存在 EGFRvIII 突变体,利用脑脊液来源的外泌 体检测 EGFRvIII 突变体,在诊断胶质瘤中特异性高 达98%,敏感性只有61%[62]。当分离检测血浆来 源的包含长链非编码 RNA-HOX 转录反义基因间 RNA (hox transcript antisense intergenic RNA , HOTAIR) 的外泌体时,灵敏度为86.1%,特异性为87.5%, AUC 为 0.913 (95% CI: 0.845 ~ 0.982, P < 0.0001)[63]。然而由于分离检测方法步骤多耗时 长,外泌体的纯度得不到保证,甚至有污染的风 险[18]。为了提高临床应用价值, Lobbr 等报道了一 种有效可重复,室温下能够维持外泌体足够稳定的 方法[57]。同样的,经过人工设计的外泌体作为载 体,可以顺利的通过血脑屏障,将纳米材料、化学 药物和 miRNAs 靶向运输到病灶,甚至大脑小胶质 细胞来源的外泌体也可以作为纳米治疗剂,用于诊 断和治疗[53,64-65]。

通过筛选分析与肿瘤密切相关的细胞、分子与基因等物质,液体活检技术拓展了对肿瘤发生发展机制的认识,提高了诊断治疗的特异性,因其微侵袭性而更容易被患者接受。随着各项研究的开展,越来越多的循环肿瘤标志物被发现,但是由于灵敏度或特异性的限制,能够应用到临床的标记十分有限。更大的挑战在于如何找到合适的标记组合,收集分析不同信息,为胶质瘤的早期诊断分型、治疗方案的制定实施和疗效判定等提供科学依据;如何将基础研究和临床应用相结合,使丰富的生物标志更多地转化为胶质瘤的临床检测方法;如何降低高昂的检测成本,使液体活检技术能够在临床广泛开展。相信随着研究的深入进展,液体活检技术将在胶质瘤的临床应用中大放异彩。

参考文献

- [1] Rasmussen BK, Hansen S, Laursen RJ, et al. Epidemiology of glioma: clinical characteristics, symptoms, and predictors of glioma patients grade I-IV in the Danish Neuro-Oncology Registry [J]. J Neurooncol, 2017, 135 (3): 571-579.
- [2] Galvao RP, Kasina A, McNeill RS, et al. Transformation of quiescent adult oligodendrocyte precursor cells into malignant glioma through a multistep reactivation process [J]. Proc Natl Acad Sci U S A, 2014, 111 (40): E4214-E4223.
- [3] Bogsrud TV, Londalen A, Brandal P, et al. 18F-Fluciclovine PET/CT in suspected residual or recurrent high-grade glioma [J]. Clin Nucl Med, 2019, 44(8): 605-611.
- [4] Thust SC, Heiland S, Falini A, et al. Glioma imaging in Europe: a survey of 220 centres and recommendations for best clinical practice [J]. Eur Radiol, 2018, 28(8): 3306-3317.
- [5] van Dijken BRJ, van Laar PJ, Holtman GA, et al. Diagnostic accuracy of magnetic resonance imaging techniques for treatment response evaluation in patients with high-grade glioma, a systematic review and meta-analysis [J]. Eur Radiol, 2017, 27 (10): 4129-4144.
- [6] Diksin M, Smith SJ, Rahman R. The molecular and phenotypic basis of the glioma invasive perivascular niche [J]. Int J Mol Sci, 2017, 18(11); 2342.
- [7] Liu TR, Xu HN, Huang MG, et al. Circulating glioma cells exhibit stem cell-like properties [J]. Cancer Res, 2018, $78\,(\,23\,):\,6632-6642\,.$
- [8] Ong DST, Hu B, Ho YW, et al. PAF promotes stemness and radioresistance of glioma stem cells [J]. Proc Natl Acad Sci U S A, 2017, 114(43): E9086-E9095.
- [9] Turner KM, Sun Y, Ji P, et al. Genomically amplified Akt3 activates DNA repair pathway and promotes glioma progression [J]. Proc Natl Acad Sci U S A, 2015, 112 (11): 3421-3426.
- [10] Wei YY, Jiang YZ, Zou F, et al. Activation of PI3 K/Akt pathway by CD133-p85 interaction promotes tumorigenic capacity of glioma stem cells [J]. Proc Natl Acad Sci USA, 2013, 110 (17): 6829-6834.
- [11] Krol I, Castro-Giner F, Maurer M, et al. Detection of circulating tumour cell clusters in human glioblastoma [J]. Br J Cancer, 2018, 119(4): 487-491.
- [12] MMüller C , Holtschmidt J , Auer M , et al. Hematogenous dissemination of glioblastoma multiforme [J] . Sci Transl Med , 2014 , 6(247) ; $247 \, \mathrm{ra} \, 101$.
- [13] Ortega FG, Lorente JA, Garcia Puche JL, et al. miRNA in situ hybridization in circulating tumor cells--MishCTC [J]. Sci Rep, 2015, 5: 9207.
- [14] Shen ZY, Wu AG, Chen XY. Current detection technologies

- for circulating tumor cells [J] . Chem Soc Rev , 2017 , 46 (8) : 2038-2056 .
- [15] Watanabe M, Kenmotsu H, Ko R, et al. Isolation and molecular analysis of circulating tumor cells from lung cancer patients using a microfluidic chip type cell sorter [J]. Cancer Sci, 2018, 109 (8): 2539-2548.
- [16] Yu M, Bardia A, Aceto N, et al. Cancer therapy. Ex vivo culture of circulating breast tumor cells for individualized testing of drug susceptibility [J]. Science, 2014, 345 (6193): 216-220.
- [17] Madhankumar AB, Mrowczynski OD, Patel SR, et al. Inter-leukin-13 conjugated quantum dots for identification of glioma initiating cells and their extracellular vesicles [J]. Acta Biomater, 2017, 58; 205-213.
- [18] Campos CDM , Jackson JM , Witek MA , et al. Molecular profiling of liquid biopsy samples for precision medicine [J] . Cancer J , 2018 , 24 (2) : 93-103 .
- [19] Panditharatna E, Kilburn LB, Aboian MS, et al. Clinically relevant and minimally invasive tumor surveillance of pediatric diffuse midline gliomas using patient-derived liquid biopsy [J]. Clin Cancer Res, 2018, 24(23): 5850-5859.
- [20] Miller AM, Shah RH, Pentsova EI, et al. Tracking tumour evolution in glioma through liquid biopsies of cerebrospinal fluid[J]. Nature, 2019, 565 (7741): 654-658.
- [21] Zacher A, Kaulich K, Stepanow S, et al. Molecular diagnostics of gliomas using next generation sequencing of a gliomatailored gene panel [J]. Brain Pathol, 2017, 27 (2): 146-159.
- [22] Pan C, Diplas BH, Chen X, et al. Molecular profiling of tumors of the brainstem by sequencing of CSF-derived circulating tumor DNA [J]. Acta Neuropathol, 2019, 137 (2): 297-306.
- [23] De Mattos-Arruda L, Mayor R, Ng CKY, et al. Cerebrospinal fluid-derived circulating tumour DNA better represents the genomic alterations of brain tumours than plasma [J]. Nat Commun, 2015, 6: 8839.
- [24] Mouliere F, Mair R, Chandrananda D, et al. Detection of cell-free DNA fragmentation and copy number alterations in cerebrospinal fluid from glioma patients [J]. EMBO Mol Med, 2018, 10(12): e9323.
- [25] Ramalingam N, Jeffrey SS. Future of liquid biopsies with growing technological and bioinformatics studies: opportunities and challenges in discovering tumor heterogeneity with single-cell level analysis [J]. Cancer J, 2018, 24 (2): 104-108.
- [26] Mouliere F, Chandrananda D, Piskorz AM, et al. Enhanced detection of circulating tumor DNA by fragment size analysis [J]. Sci Transl Med, 2018, 10 (466); eaat4921.
- [27] Mair R, Mouliere F, Smith CG, et al. Measurement of plas-

- ma cell-free mitochondrial tumor DNA improves detection of glioblastoma in patient-derived orthotopic xenograft models [J]. Cancer Res , 2019 , 79 (1) : 220-230.
- [28] Pan WY, Gu W, Nagpal S, et al. Brain tumor mutations detected in cerebral spinal fluid [J]. Clin Chem, 2015, 61 (3): 514-522.
- [29] Masamha CP, Xia Z, Yang J, et al. CFIm25 links alternative polyadenylation to glioblastoma tumour suppression [J].
 Nature, 2014, 510 (7505): 412-416.
- [30] Wang JX , Gao J , Ding SL , et al. Oxidative modification of miR-184 enables it to target Bcl-xL and bcl-w [J] . Mol Cell , 2015 , 59 (1) : 50-61.
- [31] He QR, Zhao LN, Liu XB, et al. MOV10 binding circ-DICER1 regulates the angiogenesis of glioma via miR-103a-3p/miR-382-5p mediated ZIC4 expression change [J]. J Exp Clin Cancer Res, 2019, 38(1):9.
- [32] Jia JW , Wang J , Yin MF , et al. microRNA-605 directly targets SOX9 to alleviate the aggressive phenotypes of glioblastoma multiforme cell lines by deactivating the PI3 K/Akt pathway [J] . Onco Targets Ther , 2019 , 12 : 5437-5448.
- [33] Lu J, Getz G, Miska EA, et al. MicroRNA expression profiles classify human cancers [J]. Nature, 2005, 435 (7043): 834-838.
- [34] Swellam M, Ezz El Arab L, Al-Posttany AS, et al. Clinical impact of circulating oncogenic MiRNA-221 and MiRNA-222 in glioblastoma multiform [J]. J Neurooncol, 2019, 144 (3): 545-551.
- [35] Wei L, Li P, Zhao CJ, et al. Upregulation of microRNA-1270 suppressed human glioblastoma cancer cell proliferation migration and tumorigenesis by acting through WT1 [J]. Onco Targets Ther, 2019, 12: 4839-4848.
- [36] Yang ZY , Wang Y , Liu Q , et al. microRNA cluster MC-let-7a-1 \sim let-7d promotes autophagy and apoptosis of glioma cells by down-regulating STAT3 [J] . CNS Neurosci Ther , 2020 , 26(3): 319-331.
- [37] Zheng J, Liu XB, Xue YX, et al. TTBK2 circular RNA promotes glioma malignancy by regulating miR-217/HNF1β/Derlin-1 pathway [J]. J Hematol Oncol, 2017, 10(1): 52.
- [38] Schroeder B , Shah N , Rostad S , et al. Genetic investigation of multicentric glioblastoma multiforme : case report [J] . J Neurosurg , 2016 , 124 (5) : 1353-1358.
- [39] Zhou Q, Liu J, Quan J, et al. MicroRNAs as potential biomarkers for the diagnosis of glioma: a systematic review and meta-analysis [J]. Cancer Sci, 2018, 109(9): 2651-2659.
- [40] Guo XY, Luo ZG, Xia T, et al. Identification of miRNA signature associated with BMP2 and chemosensitivity of TMZ in glioblastoma stem-like cells [J] . Genes Dis, 2020, 7

- (3):424-439.
- [41] Detassis S, Grasso M, Del Vescovo V, et al. microRNAs make the call in cancer personalized medicine [J]. Front Cell Dev Biol, 2017, 5:86.
- [42] Qu K, Lin T, Pang Q, et al. Extracellular miRNA-21 as a novel biomarker in glioma: evidence from meta-analysis, clinical validation and experimental investigations [J]. Oncotarget, 2016, 7 (23): 33994-34010.
- [43] Wei Z, Batagov AO, Schinelli S, et al. Coding and noncoding landscape of extracellular RNA released by human glioma stem cells [J]. Nat Commun, 2017, 8(1): 1145.
- [44] Pentsova EI, Shah RH, Tang J, et al. Evaluating cancer of the central nervous system through next-generation sequencing of cerebrospinal fluid [J]. J Clin Oncol, 2016, 34 (20): 2404-2415.
- [45] Birch J, Clarke CJ, Campbell AD, et al. The initiator methionine tRNA drives cell migration and invasion leading to increased metastatic potential in melanoma [J]. Biol Open, 2016, 5(10): 1371-1379.
- [46] Graczyk D, Cieśla M, Boguta M. Regulation of tRNA synthesis by the general transcription factors of RNA polymerase III - TFII-IB and TFIIIC, and by the MAF1 protein[J]. Biochim Biophys Acta Gene Regul Mech, 2018, 1861(4): 320-329.
- [47] Macari F, El-Houfi Y, Boldina G, et al. TRM6/61 connects PKCα with translational control through tRNAi (Met) stabilization: impact on tumorigenesis [J]. Oncogene, 2016, 35 (14): 1785-1796.
- [48] Yang JJ, Smith DK, Ni HQ, et al. SOX4-mediated repression of specific tRNAs inhibits proliferation of human glioblastoma cells [J]. Proc Natl Acad Sci U S A, 2020, 117(11): 5782-5790.
- [49] Guo XF, Qiu W, Liu QL, et al. Immunosuppressive effects of hypoxia-induced glioma exosomes through myeloid-derived suppressor cells via the miR-10a/Rora and miR-21/Pten pathways [J]. Oncogene, 2018, 37(31): 4239-4259.
- [50] Huang K, Fang C, Yi KK, et al. The role of PTRF/Cavin1 as a biomarker in both glioma and serum exosomes[J]. Theranostics, 2018, 8(6): 1540-1557.
- [51] Shao NY, Xue L, Wang R, et al. miR-454-3p is an exosomal biomarker and functions as a tumor suppressor in glioma [J]. Mol Cancer Ther, 2019, 18(2): 459-469.
- [52] Figueroa J, Phillips LM, Shahar T, et al. Exosomes from gliomaassociated mesenchymal stem cells increase the tumorigenicity of glioma stem-like cells via transfer of miR-1587[J]. Cancer Res, 2017, 77(21): 5808-5819.
- [53] Lang FM, Hossain A, Gumin J, et al. Mesenchymal stem cells as natural biofactories for exosomes carrying miR-124a in the treatment of gliomas [J]. Neuro Oncol, 2018, 20(3): 380-390.
- [54] Wang ZF, Liao F, Wu H, et al. Glioma stem cells-derived exosomal miR-26a promotes angiogenesis of microvessel endothelial

- cells in glioma[J]. J Exp Clin Cancer Res, 2019, 38(1): 201.
- [55] Svensson KJ, Kucharzewska P, Christianson HC, et al. Hypoxia triggers a proangiogenic pathway involving cancer cell microvesicles and PAR-2-mediated heparin-binding EGF signaling in endothelial cells[J]. Proc Natl Acad Sci U S A, 2011, 108 (32): 13147-13152.
- [56] Sun Z, Wang L, Zhou YL, et al. Glioblastoma stem cell-derived exosomes enhance stemness and tumorigenicity of glioma cells by transferring notch1 protein [J]. Cell Mol Neurobiol, 2020, 40 (5): 767-784.
- [57] Lobb RJ, Becker M, Wen SW, et al. Optimized exosome isolation protocol for cell culture supernatant and human plasma[J]. J Extracell Vesicles, 2015, 4: 27031.
- [58] Ricklefs FL, Alayo Q, Krenzlin H, et al. Immune evasion mediated by PD-L1 on glioblastoma-derived extracellular vesicles [J]. Sci Adv, 2018, 4(3); eaar2766.
- [59] Santangelo A, Imbrucè P, Gardenghi B, et al. A microRNA signature from serum exosomes of patients with glioma as complementary diagnostic biomarker[J]. J Neurooncol, 2018, 136(1): 51-62.
- [60] Choi D, Montermini L, Kim DK, et al. The impact of oncogenic

- EGFRvIII on the proteome of extracellular vesicles released from glioblastoma cells [J]. Mol Cell Proteomics, 2018, 17 (10): 1948-1964.
- [61] Skog J, Würdinger T, van Rijn S, et al. Glioblastoma microvesicles transport RNA and proteins that promote tumour growth and provide diagnostic biomarkers [J]. Nat Cell Biol, 2008, 10 (12): 1470-1476.
- [62] Figueroa JM, Skog J, Akers J, et al. Detection of wild-type EGFR amplification and EGFRvIII mutation in CSF-derived extracellular vesicles of glioblastoma patients [J]. Neuro Oncol, 2017, 19 (11): 1494-1502.
- [63] Tan SK, Pastori C, Penas C, et al. Serum long noncoding RNA HOTAIR as a novel diagnostic and prognostic biomarker in glioblastoma multiforme [J]. Mol Cancer, 2018, 17(1): 74.
- [64] Jia G, Han Y, An YL, et al. NRP-1 targeted and cargo-loaded exosomes facilitate simultaneous imaging and therapy of glioma in vitro and in vivo[J]. Biomaterials, 2018, 178: 302-316.
- [65] Murgoci AN, Cizkova D, Majerova P, et al. Brain-cortex microglia-derived exosomes: nanoparticles for glioma therapy [J]. Chemphyschem, 2018, 19(10): 1205-1214.