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目 次

2017年11月18日 第25卷 第32期 (总第580期)

述评

2829 精准医学时代食管癌研究现状及展望

方一凡, 耿庆

2838 胃癌多药耐药在ABC转运蛋白、细胞凋亡和长链非编码RNA方面的研究进展

符兆英

2851 重症急性胰腺炎诊疗现状及主要问题

付杰, 刘强, 刘国兴, 徐迅迪

2858 显微镜结肠炎研究进展与现状

池肇春

2866 腹部手术止血方法的研究现状

王刚, 李宗倍, 曹成亮

临床研究

2873 个体化肠内营养支持对口腔颌面外科手术患者术后恢复的影响

赵存芳, 刘会香

2879 慢性乙型肝炎患者肝组织Toll样受体3、4表达及其临床意义

蒋福明, 李秀芬, 程书权, 曹亚昭, 黄成军, 杨景毅, 林君

2888 血清miR-21/miR-24表达及联合DNA定量分析对良恶性腹腔积液鉴别的临床价值

刘崇梅, 张雪纯, 余飞跃, 黄柳炎, 高亚

文献综述

2896 胃肠胰神经内分泌肿瘤的肿瘤微环境

魏亚玲, 柏建安, 何娜, 汤琪云

临床实践

2906 图文式健康教育对老年ERCP术患者的影响

陈艳

2911 锌剂剂量差异对轮状病毒性肠炎患儿血清炎性因子及心肌损伤的影响

贾彩华, 刘冬

2916 术前联合加温对腹部大手术患者体温及苏醒质量的影响

魏丽君, 徐培君, 祁伟

附 录

- 《世界华人消化杂志》投稿须知
- 2017年国内国际会议预告

志 谢

- 志谢《世界华人消化杂志》编委

消 息

- 2837 《世界华人消化杂志》性质、刊登内容及目标
2857 《世界华人消化杂志》修回稿须知
2865 《世界华人消化杂志》外文字符标准
2872 《世界华人消化杂志》消化护理学领域征稿启事
2878 《世界华人消化杂志》栏目设置
2887 《世界华人消化杂志》参考文献要求
2895 《世界华人消化杂志》正文要求
2910 《世界华人消化杂志》2011年开始不再收取审稿费

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EDITORIAL

2829 Research progress and prospects of esophageal cancer in era of precision medicine

Fang YF, Geng Q

2838 Role of ATP-binding cassette transporters, apoptosis, and long non-coding RNAs in gastric cancer multidrug resistance

Fu ZY

2851 Diagnosis and treatment of severe acute pancreatitis: Current status and main problems

Fu J, Liu Q, Liu GX, Xu XD

2858 Research progress and perspectives of microscopic colitis

Chi ZC

2866 Methods of hemostasis in abdominal surgery

Wang G, Li ZB, Cao CL

CLINICAL RESEARCH

2873 Effect of individualized enteral nutrition support on postoperative recovery in patients after oral and maxillofacial surgery

Zhao CF, Liu HX

2879 Clinical significance of expression of TLR3 and TLR4 in liver tissue of patients with chronic hepatitis B

Jiang FM, Li XF, Cheng SQ, Cao YZ, Huang CJ, Yang JY, Lin J

2888 Clinical value of serum miR-21/miR-24 detection combined with quantitative analysis of DNA content in differential diagnosis of benign and malignant ascites

Liu CM, Zhang XC, Yu FY, Huang LY, Gao Y

REVIEW

2896 Tumor microenvironment of gastroenteropancreatic neuroendocrine neoplasms

Wei YL, Bai JA, He N, Tang QY

CLINICAL PRACTICE

2906 Influence of graphic health education on elderly patients undergoing endoscopic retrograde cholangiopancreatography

Chen Y

2911 Effect of zinc dose difference on serum inflammatory factors and myocardial injury in children with rotavirus enteritis

Jia CH, Liu D

2916 Effect of preoperative combined warming strategy on body temperature and recovery quality in patients undergoing major abdominal surgeries

Wei LJ, Xu PJ, Qi W

APPENDIX - Instructions to authors
 Calendar of meetings and events in 2017

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胃癌多药耐药在ABC转运蛋白、细胞凋亡和长链非编码RNA方面的研究进展

符兆英

背景资料

对肿瘤化疗药耐药的认知已经有数十年的历史,并对耐药机制提出了数种假说,但耐药的机制尚未完全明了。

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Role of ATP-binding cassette transporters, apoptosis, and long non-coding RNAs in gastric cancer multidrug resistance

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Abstract

Cancer multidrug resistance refers to the cross resistance of cancer cells to a variety of anticancer drugs, which can be primary or secondary. Several mechanisms attribute to cancer multidrug resistance. In this paper, the recent progress in the understanding of the mechanisms of multi-drug resistance of gastric cancer cells with regard to the role of adenosine triphosphate binding cassette transporters, apoptosis, and long non-coding RNAs is reviewed.

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Key Words: Multidrug resistance; Gastric cancer; ATP-binding cassette transporter; Apoptosis; MicroRNA; Long non-coding RNAs

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摘要

肿瘤多药耐药指癌细胞对多种不同的抗癌药物的交叉性耐药, 可以是原发性的或继发性的, 耐药的机制有多种. 本文对胃癌细胞通过上调ABC转运蛋白超家族成员的表达使药物外排增加和抑制或逃避细胞凋亡而

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引起多药耐药以及长链非编码RNA在胃癌多药耐药形成中的作用的研究进展做了总结论述。

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关键词: 多药耐药; 胃癌; ABC转运蛋白; 细胞凋亡; MicroRNA; 长链非编码RNA

核心提要: 肿瘤多药耐药是肿瘤药物治疗中存在的一个严重问题, ABC转运蛋白超家族成员表达上调使药物外排增加和细胞凋亡受抑制是癌细胞耐药的两种重要机制。新近的研究发现, 长链非编码RNA在胃癌多药耐药的调节中起着重要的作用。

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0 引言

胃癌是全球常见的一种恶性肿瘤, 在东亚国家更为多见; 在中国, 其发病率和死亡率居所有恶性肿瘤之第2位^[1,2]。早期胃癌先行手术治疗, 术后进行化学治疗和其他辅助治疗, 而中晚期胃癌则以化疗为主要治疗手段; 但由于癌细胞往往对化疗药物产生多药耐药, 而使疗效不佳或肿瘤复发^[3,4]。癌细胞对化疗药的耐受可以是原发性的或天然性的耐受, 亦称内在性的耐受, 即有些癌细胞本身即携带有耐药的遗传特征; 也可能是继发性的或获得性的耐受, 即癌细胞在化疗药应用后被诱导产生耐药性。多种癌症都可以产生多药耐药; 一些胃肠道肿瘤对化疗药具有内在的耐受性^[5]。

肿瘤多药耐药是指肿瘤一旦对某一种化疗药物产生耐药, 就可以对多种化学性质不同和作用机制不同的化疗药物产生交叉性耐药^[3,4]。已发现癌细胞可经多种机制对化疗药产生耐药, 包括上调ABC转运蛋白(ATP-binding cassette transporter, ABC transporter)超家族某些成员的表达使药物外排增加、抑制细胞凋亡或对凋亡的敏感性降低、增强DNA修复能力、改变药物作用的靶分子、促进药物在细胞内的代谢和减弱药物的毒性等^[3-8]。不同的肿瘤可以

通过不同的机制耐药, 一种肿瘤可以通过数种机制耐药, 肿瘤对不同的药物可以通过相同的和/或不同的机制耐药。本文回顾论述了ABC transporter超家族成员过表达和细胞凋亡受抑制这两种机制引起胃癌多药耐药的研究进展, 并总结了近几年来长链非编码RNA(long non-coding RNA, lncRNA)在胃癌多药耐药形成中作用的研究成果。

研究前沿
长链非编码RNA和
microRNA调节
是近年来肿瘤多
药耐药机制研究
的热点。

1 ABC transporter超家族成员过表达与胃癌多药耐药

ABC transporter超家族是非常大的一个(膜)转运蛋白超家族, 该超家族成员的蛋白通常由多个亚基组成, 其中一个或两个为跨膜蛋白、另一个或两个为膜相关的腺嘌呤核苷三磷酸(adenosine triphosphate, ATP)酶。ATP酶利用ATP的结合和水解为多种物质的跨膜转运提供能量。原核生物的ABC transporter有向细胞内泵入和向细胞外泵出2种类型, 而真核生物的ABC transporter只有向细胞外泵出的作用^[9-13]。人类的ABC transporter共49个成员, 分为7个亚家族, 从ABCA到ABCG。ABC transporter具有生理作用, 但也可以介导细胞对药物的耐受。介导人类肿瘤多药耐药的ABC transporter超家族成员最主要的是ABCB1蛋白, 此外还有ABCC1/ABCC2蛋白以及ABCG2蛋白^[14-19]。

1.1 ABCB1蛋白与胃癌多药耐药 ABCB1(ATP-binding cassette sub-family B member 1)蛋白属ABC transporter超家族B亚家族的一个成员, 由ABCB1基因编码, 亦称P-糖蛋白(permeability glycoprotein, P-gp)或多耐药基因1(multidrug resistance gene 1, MDR1), 由12个跨膜结构域(N-端和C-端各6个)和一个大的主要位于细胞内的胞质结构域(在N-端和C-端之间)组成, 后者有ATP结合位点^[19-21]。进入细胞内的底物从ABCB1蛋白胞质结构域的开口处进入, 随着ATP分子与ATP结合位点的结合和ATP的水解, 底物被排出胞外; 同时, ATP水解产生的磷酸亦被释放; ATP结合位点的ADP被新的ATP分子置换, 从而可以开始下一个循环的底物泵出^[19,22,23]。ABCB1蛋白能将进入细胞的外源性物质(毒物、药物等)泵出细胞外; 多种正常细胞表达ABCB1蛋白, 但在耐药的癌细胞ABCB1蛋白呈超表达^[19]。ABCB1蛋白的底物非常广泛, 其中包括多种化

创新盘点

本文对胃癌多药耐药最重要的两种机制(ABC转运蛋白和细胞凋亡)以及长链非编码RNA和microRNA的调节作用近年来研究进展作了总结论述。

疗药物如阿霉素、道诺霉素(柔红霉素)、长春新碱、长春花碱、依托泊苷、替尼泊苷、紫杉醇和放线菌素D等。

胃癌标本的免疫组织化学染色发现^[24,25], ABCB1蛋白在胃癌细胞的细胞膜和细胞质中都有分布. Hu等^[25]发现, 59份未用化疗药治疗的胃癌组织标本中, ABCB1蛋白的表达率为86.4%, 这些组织中ABCB1蛋白的表达率与胃癌的病理组织(分化程度)类型没有关联性. 该结果支持胃癌对化疗药物具有内在的或固有的耐药性的观点. 研究^[24]还发现, ABCB1蛋白的表达在对阿霉素、高喜树碱等化疗药耐受的胃癌组织中显著性地比在对这些化疗药敏感的胃癌组织中高. Shi等^[26]用免疫组织化学染色发现, 69份胃贲门腺癌标本中ABCB1蛋白的表达率为49.2%, 而作为对照的正常组织ABCB1蛋白的表达率为0%; 有转移的胃癌ABCB1蛋白的表达率比没有转移的更高(67.5% vs 24.1%); ABCB1蛋白的表达率与胃癌的临床病理分期相关而与胃癌的分化程度无关。

近年来的许多研究表明, 微小RNA(microRNA, miRNA)在肿瘤多药耐药上起着重要的作用; 化疗药物的应用可以引起miRNA表达的异常上调或下调并进而经不同机制导致癌细胞的耐药; 多种miRNA可以通过调节ABCB1蛋白的表达而介导癌细胞多药耐药. Lu等^[27]发现, microRNA-129(miR-129)在耐顺铂的胃癌组织和细胞中呈低表达; 过表达miR-129可以减低胃癌细胞对顺铂的耐药性, 而敲低miR-129则减弱胃癌细胞对顺铂的敏感性; miR-129作用的靶分子是ABCB1蛋白; miR-129结合于ABCB1蛋白mRNA的3'末端非翻译区(3'-untranslated region, 3'-UTR)而下调其表达; 因此, 我们认为miR-129通过抑制ABCB1蛋白的表达而逆转胃癌对顺铂的耐药. 用实时定量聚合酶链反应(polymerase chain reaction, PCR)检测体外培养的胃癌传代细胞中ABCB1蛋白的表达发现, 下调miR-27a可以显著性地降低ABCB1蛋白的表达^[28]. 用实时定量PCR检测胃癌组织标本中ABCB1蛋白的表达的结果显示, 与癌旁正常组织相比, miR-27a在胃癌组织中明显高表达、miR-27a的高表达与胃癌的组织病理学分级显著相关; 在胃癌传代细胞, 下调miR-27a的表达可以明显增强抗肿瘤药派立福辛抑制细胞生

长的活性, 其机制可能是下调了P-gp的表达^[29]. Wang等^[30]报道, miR-19a/b在多药耐药细胞系中表达上调并降低胃癌细胞对化疗药的敏感性, miR-19a/b通过增加P-gp的表达水平而加速胃癌细胞对化疗药阿霉素的排出。

Shang等^[31]于2014年用高通量功能筛选技术找出11种调控胃癌多药耐药的miRNA, 其中的miR-508-5p能够最有效地逆转肿瘤多药耐药; 过表达miR-508-5p足以在体外逆转癌细胞对多种化疗药的耐药并在体内增强肿瘤对化疗的敏感性; 进一步的研究显示, miR-508-5p能够直接靶向于ABCB1基因和ZNRD1基因的3'-UTR从而抑制它们在mRNA和蛋白质水平的表达, 对ZNRD1的抑制同时导致ABCB1的降低; 以上发现提示, miR-508-5p/ZNRD1/ABCB1调节环在胃癌多药耐药的调节上起着关键性的作用. Shang等^[32]于2016年又研究了miR-508-5p在耐药胃癌细胞中被下调的机制, 他们发现, miR-27b能够直接靶向细胞周期蛋白(cell cyclin G1, CCNG1)的3'-UTR, 通过抑癌基因P53而上调miR-508-5p的表达(CCNG1是一种重要的细胞周期调控因子, 能够负性调节P53蛋白的稳定性); 因此miR-27b/CCNG1/P53/miR-508-5p轴在胃癌多药耐药的形成中起着重要的作用; 通过对胃癌组织中miR-27b和miR-508-5p表达的检测, 他们还发现, miR-27b和miR-508-5p都高表达的胃癌对化疗更敏感。

1.2 ABCC1/ABCC2蛋白与胃癌多药耐药 ABCC1和ABCC2(ATP-binding cassette sub-family C member 1, 2)蛋白为ABC transporter超家族C亚家族的两个成员, 分别由ABCC1基因和ABCC2基因编码, 二者与多种药物的耐受相关, 又分别称为多药耐药相关蛋白(multidrug resistance-associated protein, MRP)1和2(MRP1, MRP2)^[33-36]. ABCC1和ABCC2可以介导神经母细胞瘤、肺癌、乳腺癌、前列腺癌、肝癌、卵巢癌和结肠癌等^[37-43]对化疗药的耐药, 也有介导胃癌耐药的报道. Chen等^[44]在体外诱导分离出了对三氧化二砷耐受的胃癌细胞株SGC7901/AS, 发现该细胞株ABCB1蛋白和基因的表达升高最明显, 同时也有ABCC1和ABCC2蛋白和基因表达的升高. Yu等^[45]回顾了119例胃癌中MRP等的表达, 结果发现MRP的表达阳性率为42.9%. 靳胜^[46]用实时荧

光定量PCR检测了47例胃癌标本和17例正常胃组织的MRP、脂蛋白受体相关蛋白和*ABCB1*基因的表达, 结果发现, 3种基因在胃癌标本中的表达均高于正常胃组织, MRP在早期胃癌中的表达显著高于进展期胃癌, 在高、中分化腺癌中的表达显著高于低分化和未分化腺癌, 在病情恶化患者中MRP表达上调30%。Hu等^[25]检测了59例胃癌标本中*ABCB1*和MRP等的表达, 结果发现*ABCB1*和MRP的表达阳性率分别为86.4%和27.1%。以上两项研究的病人在术前均未使用化疗药。Ji等^[47]发现, 来自间充质干细胞的外泌体在体内和体外显著性地增加了胃癌细胞对5-氟尿嘧啶(5-fluorouracil, 5-Fu)的耐药, 其机制包括对抗凋亡和增强MDR1和MRP等蛋白的表达。Takegawa等^[48]发现胃癌细胞株N87-TDMR对T-DM1的耐药是因ABCC2和ABCG2表达异常使药物外排增加引起的: N87-TDMR中ABCC2和ABCG2表达上调, 用MK571抑制ABCC2和ABCG2能够恢复药物敏感性。

1.3 ABCG2蛋白与胃癌多药耐药 ABCG2(ATP-binding cassette sub-family G member 2)蛋白属ABC transporter超家族G亚家族的一个成员, 由*ABCG2*基因编码, 最初是在乳腺癌耐药细胞系中发现的, 故又称为乳腺癌耐药蛋白, 后来发现ABCG2蛋白与多种肿瘤包括胃癌的耐药相关^[49-58]。Wang等^[59]报道, ABCG2在胃癌患者频繁地异常表达, ABCG2在胃癌标本和胃癌细胞系均表达极度上调, 并与胃癌临床病理特征和预后不良相关。用ABCG2 siRNA转染MKN-45胃癌细胞, 能够抑制细胞增殖、阻滞细胞周期并诱导细胞凋亡。我们还发现, ABCG2与胃癌的一种关键性启动子CRKL相关, 用ABCG2 siRNA转染MKN-45细胞能使CRKL下调, 在MKN-45细胞中过表达CRKL可以恢复siRNA转染引起的ABCG2表型改变。Zhang等^[60]报道, miR-132在Lgr5阳性胃癌干细胞中表达上调, miR-132的高表达与胃癌患者对化疗药的耐药相关、与患者的预后相关。功能分析发现, miR-132在体内外均能促进Lgr5阳性胃癌干细胞对顺铂的耐药。用双荧光酶报告基因分析发现, SIRT1是miR-132的直接靶标。在胃癌标本中, miR-132表达与SIRT1表达呈反相关。进一步的研究发现, ABCG2是SIRT1的下游靶标; 过表达SIRT1可通过促进

转录因子CREB的去乙酰化而下调ABCG2表达; CREB结合于ABCG2启动子而诱导ABCG2的转录。Zhao等^[61]用含部分随机的 4×10^6 条siRNA的逆转录病毒文库转染胃癌SGC7901细胞寻找耐药相关基因, 得到12个耐药化疗药柔比星的细胞集落, 从这12个耐药集落中鉴定出两种基因: *GAS1*(growth arrest-specific 1)和*PTEN*(phosphatase and tensin homolog); *GAS1*的抑制导致SGC7901细胞对柔比星显著的耐药和对5-Fu和顺铂的交叉性耐药。*GAS1*基因的被抑制导致*ABCB1*和*ABCG2*的表达上调(但没有*ABCC1*表达上调)使药物外排增加所以细胞耐药, 敲低*ABCB1*和*ABCG2*能部分地逆转*GAS1*抑制导致的细胞耐药。IMMU-132是抗体与抗肿瘤药SN-38偶联的一种抗体-药物偶联物, 在治疗时往往由于ABC transporter介导的耐药而使治疗失败。Chang等^[62]研究了用ABC transporter抑制剂YHO-13351逆转耐药增强IMMU-132治疗效果的作用。他们建立了两个耐药细胞株: 来源于乳腺癌MDA-MB-231细胞的耐药细胞株MDA-MB-231-S120和来源于胃癌NCI-N87细胞的耐药细胞株NCI-N87-S120。他们发现, 这两个细胞株在体外对SN-38的敏感性下降(IC₅₀比未耐药的MDA-MB-231细胞和NCI-N87细胞分别上升约50倍), 这两株耐药细胞均发现有ABCG2表达升高但没有*ABCB1*表达升高, 用ABC transporter抑制剂YHO-13351处理这两株细胞可以恢复SN-38的细胞毒性, YHO-13351与IMMU-132合用能够增加NCI-N87-S120移植鼠的中位生存期。

2 细胞凋亡受抑制与胃癌多药耐药

化疗药物杀伤肿瘤细胞的重要机制, 是通过引起DNA损伤、干扰DNA合成、或阻遏有丝分裂而最终引起细胞凋亡^[63,64]。癌细胞对化疗药产生多药耐药的另一个重要机制是抑制或逃避细胞凋亡^[65,66]。细胞凋亡的始动主要有两条通路: 外源性通路和内源性通路。外源性通路亦称死亡受体通路, 通过细胞膜上的死亡受体如Fas(First apoptosis signal)和肿瘤坏死因子(tumor necrosis factor, TNF)而启动细胞凋亡, 该通路主要活化caspase-8。内源性通路亦称线粒体通路, 通过线粒体蛋白如SMACs(second mitochondria-derived activator of caspases)和细

应用要点
临床医生在选择化学治疗药物之前若能对患者癌细胞对相应化疗药的敏感性做一测试, 应该非常有助于合理选择药物和优化治疗效果。

□ 同行评价
该综述试图从P-糖蛋白、细胞凋亡以及长链非编码RNA三个角度探讨在胃癌多药耐药的发生机制. 文章具有一定的新颖. 此外, 论文的逻辑性强, 有较多作者的见解和评论. 对胃癌耐药研究的相关学者、研究人员的研究工作具有参考价值.

胞色素c向细胞浆的外溢而启动细胞凋亡, 该通路主要活化caspase-9. 活化的caspase-8和caspase-9引起caspase-3的连锁活化而最终导致细胞结构降解和细胞死亡^[67-70].

2.1 内源性凋亡通路与胃癌多药耐药 多种化疗药物可通过线粒体途径诱导细胞凋亡. 研究显示, 线粒体裂解能够诱发细胞凋亡, 而线粒体融合可以抑制细胞凋亡, 前者是因为线粒体裂解促进了细胞色素c的释放; Aung等^[71]发现, 在阿霉素作用下线粒体膜蛋白18(mitochondrial membrane protein 18, MTP18)可促进动力相关蛋白1在线粒体聚集并引起线粒体裂解或碎片化从而诱导胃癌细胞发生凋亡; 他们还发现, 在阿霉素治疗过程中, MTP18的表达下调, 故认为MTP18低表达是胃癌细胞通过细胞凋亡途径而耐药的一种机制. Liang等^[72]报道, 紫草素(一种天然萘醌)能通过增加细胞内的活性氧而使线粒体膜去极化最终诱发细胞凋亡, 其机制除了caspase依赖性的(通过细胞色素c的释放活化caspase酶)外, 还包括caspase非依赖性的, 后者介导凋亡诱导因子和内切酶G的核转运. 紫草素能在体内和体外增加胃癌细胞对化疗药5-Fu和奥沙利铂的敏感性. Tang等^[73]发现, 在对顺铂耐药的胃癌细胞中, 磷酸化的丝切蛋白呈过表达, 顺铂能使非耐药的胃癌细胞的丝切蛋白去磷酸化但不能使耐药细胞的丝切蛋白去磷酸化. 但是, 中药左金丸能诱导耐药胃癌细胞的丝切蛋白去磷酸化并促进该蛋白从细胞质进入线粒体, 最终经线粒体通路活化细胞凋亡. 向耐顺铂胃癌细胞转染丝切蛋白特异性siRNA能够抑制这一作用.

2.2 外源性凋亡通路与胃癌多药耐药 Yin等^[74]报道, 用外源性凋亡通路的Fas受体基因转染, 能够逆转人胃癌SGC7901/VCR细胞的多药耐药, 其机制可能是增敏了细胞凋亡和抑制了ABC1蛋白. Zhang等^[75]报道, α -生育酚琥珀酸酯与阿霉素合用, 能增加Fas蛋白表达水平并诱导胃癌细胞凋亡. Lim等^[76]研究了熊去氧胆酸对顺铂耐药细胞的作用, 结果发现, 熊去氧胆酸作用后, 死亡受体Fas转位于脂筏并诱发细胞凋亡. Li等^[77]研究了*Mcl-1*基因沉默对耐药胃癌细胞系的作用及其机制, 结果发现, 用siRNA能够有效地沉默*Mcl-1*基因的表达并阻滞细胞周期进展和促进细胞凋亡从而在一定

程度上逆转细胞对长春新碱、顺铂和5-Fu的耐药, 其机制是增强或减弱了Fas和Bcl-2等基因的表达. Na等^[78]报道, 对TRAIL(TNF-related apoptosis-inducing ligand)耐受的胃癌细胞经信号通路特异性抑制剂环巴胺作用后, 能通过上调死亡受体DR5的表达而增加对TRAIL诱导的凋亡的敏感性; survivin具有对抗DR5的作用, 而环巴胺能减弱survivin的表达.

2.3 Bcl-2家族蛋白与胃癌多药耐药 Bcl-2家族由进化上保守的含有Bcl-2同源结构域的多个成员组成, 在细胞凋亡的调控上发挥着非常重要的作用. 该家族的Bax是非常重要的凋亡促进蛋白, Bcl-2是非常重要的凋亡抑制蛋白. 耐药的肿瘤中Bax往往呈低表达而Bcl-2往往呈超表达, 使癌细胞对化疗药的敏感性下降并逃避凋亡.

Fan等^[79]发现, 锌指蛋白家族的成员ZNF139能够通过调节Bax和Bcl-2等凋亡相关基因而介导胃癌细胞对凋亡的耐受, 用siRNA抑制ZNF139的表达能够显著下调胃癌细胞中Bcl-2和survivin的表达、显著上调Bax和caspase-3的表达, 并引起胃癌细胞的凋亡率显著升高. 周露婷等^[80]用免疫组化检测了Bcl-2蛋白在胃癌组织中的表达, 结果发现, 胃癌组织中Bcl-2蛋白的阳性率为70.4%, 5-Fu、阿霉素和丝裂霉素对Bcl-2阳性表达胃癌的抑制率显著低于对Bcl-2阴性表达胃癌的抑制率, Bcl-2的阳性表达与上述3种药物的体外耐药相关, 故认为Bcl-2能介导胃癌耐药, 其高表达是胃癌产生多药耐药的一个原因. Ji等^[81]发现, CD133⁺胃癌细胞比CD133⁻细胞对化疗药更耐受, 骨髓间充质干细胞(BM-MSC)能够通过下调Bax表达和上调Bcl-2表达而增加CD133⁺胃癌细胞的抗凋亡能力和耐药性, 其机制是BM-MSC在CD133⁺胃癌细胞中诱发了PI3K/Akt信号, 阻断PI3K/Akt信号能够抑制耐药形成. Zhao等^[82]发现, 低氧诱导因子1 α siRNA转染耐药胃癌细胞OCUM-2MD3/L-OHP后, Bcl-2等表达下调而Bax等表达上调, 提示低氧诱导因子1 α 是通过调节这些凋亡相关基因而介导胃癌耐药的. Xu等^[83]报道, 曲克芦丁(在茶叶、咖啡、谷物和多种水果蔬菜中含有的一种黄酮类物质)与5-Fu合用能抑制Bcl-2表达和上调Bax表达并增加耐药胃癌细胞对5-Fu的敏感性. Zhao等^[61]的研究

发现, 胃癌SGC7901细胞对化疗药表柔比星、5-Fu和顺铂耐药的主要机制之一是*GAS1*基因被抑制导致Bcl-2/Bax比值升高使细胞凋亡受抑制, 抑制Bcl-2能够解除凋亡抑制。

许多种的miRNA可以通过调节Bax和Bcl-2表达而介导癌细胞耐药。Chen等^[84]发现, miRNA-200c能诱导E-钙黏素的表达并进而增加SGC7901/DDP细胞对化疗药顺铂的敏感性; E-钙黏素增加癌细胞对化疗药敏感性的机制是上调Bax表达和下调Bcl-2表达并促进细胞凋亡。智慧等^[85]发现, *Bcl-2*基因直接受miR-125b调控, 在耐药细胞株中上调miR-125b表达能显著抑制Bcl-2蛋白表达水平, 并显著增加耐药细胞对长春新碱、阿霉素、依托泊苷和顺铂的敏感性、显著增加耐药细胞在长春新碱诱导下的凋亡。Wang等^[86]研究了miR-503在胃癌对顺铂耐药中所起的作用, 结果发现, miR-503的高表达能够增加耐药细胞株SGC7901/DDP对顺铂的敏感性, miR-503的直接靶基因有胰岛素样生长因子-1受体(IGF1R)和Bcl-2, 在SGC7901/DDP细胞中增强miR-503的表达能够降低IGF1R和Bcl-2的表达从而增敏顺铂诱导的细胞凋亡。Zhuang等^[87]报道, miR-143在顺铂耐药细胞株中呈低表达, 同时伴有IGF1R和Bcl-2的高表达, miR-143的靶基因也是IGF1R和Bcl-2, 增强miR-143的表达能够降低IGF1R和Bcl-2的表达而增加顺铂诱导的SGC7901/DDP细胞的凋亡, 故认为miR-143通过靶向IGF1R和Bcl-2而介导了胃癌细胞对顺铂的耐药。Wang等^[30]报道, miR-19a/b在耐药胃癌细胞中表达上调, 其表达上调使胃癌对化疗药的敏感性下降, miR-19a/b除了能加快药物从细胞的排出外, 还能通过调节Bcl-2和Bax而抑制细胞凋亡, miR-19a/b通过靶向蛋白激酶B磷酸化的抑制因子PTEN而发挥作用。Wang等^[88]还发现, 参与染色体分离的中心粒蛋白Shugoshin1能通过调节Bcl-2和Bax等而抑制细胞凋亡并介导胃癌细胞对阿霉素的耐药。除上述miRNA外, miR-27a、miR-27b、miR-29、miR-34、miR-187、miR-203、miR-1271、miR-15b和miR-16也能通过靶向Bax和Bcl-2以及其他凋亡相关基因而调控胃癌多药耐药^[89-92]。

3 lncRNA在胃癌多药耐药形成中的作用

lncRNA指的是长度大于200 nt的lncRNA分子,

在非编码RNA转录组中占较大比例, 参与基因转录调控、转录后调控和表遗传调控^[93,94]。近几年来, lncRNA在肿瘤发生发展、肿瘤转移和肿瘤多药耐药形成中的作用被受到高度重视^[95-100]。lncRNAs能通过ABC transporter和细胞凋亡等而调节胃癌多药耐药。

3.1 lncRNA在耐药和非耐药胃癌细胞中的差异表达

王颖^[101]于2012年利用高通量lncRNA芯片比较了胃癌耐药细胞株SGC7901/ADR和SGC7901/VCR与亲本细胞SGC7901的lncRNA表达谱差异, 结果发现, SGC7901/ADR细胞和SGC7901/VCR细胞与SGC7901细胞lncRNA表达差异在2倍以上的分别有1499条和1420条; 其中627条为交集差异, 即在两种耐药细胞中均呈差异表达; 差异在4倍以上的有32种: 其中上调的和下调的各占16种; 差异最大的一种lncRNA(DMTF1v4)在SGC7901/ADR细胞中上调25.89倍, 在SGC7901/VCR细胞中上调21.42倍; 基因芯片差异倍数、邻近编码基因信息分析、phylo物种进化保守性评分、实时定量PCR表达水平验证等均提示, DMTF1v4可能是介导胃癌多药耐药的一种关键性lncRNA分子。Wang等^[102]于2015年又用高通量lncRNA微阵列分析发现, 胃癌细胞系SGC7901及其衍生的SGC7901/VCR和SGC7901/ADR耐药细胞株总共表达27833条lncRNA, 差异表达1637条(差异倍数 ≥ 2.0): 其中638条为表达上调, 999条为表达下调; 上调最高的差异倍数为146, 下调最大的差异倍数为59。通路分析显示, 有20条通路与lncRNA转录物的上调相关, 15条通路与lncRNA转录物的下调相关。张哲^[103]于2015年用高通量表达谱芯片筛选SGC7901/ADR和SGC7901/VCR相对于SGC7901的差异表达基因, 发现了一大批差异表达的lncRNA和miRNA分子。SGC7901/ADR细胞和SGC7901/VCR细胞相对于SGC7901细胞lncRNA分子表达上调4倍以上的分别有1811个和1571个, 其中有683个交集。SGC7901/ADR细胞和SGC7901/VCR细胞相对于SGC7901细胞lncRNA分子表达下调4倍以上的分别有2080个和1693个, 其中有885个交集。lncRNA分子在两株耐药细胞表达上调10倍以上的共有19个; 用qRT-PCR验证了从其中选出的10个lncRNA分子的表达水平, 结果显示, 所验证的分子都在两株耐药细胞中显著表达上调。

3.2 lncRNAs主要经ABC transporter对胃癌多药耐药的调节 王颖^[101]用高通量lncRNA芯片等技术筛选分析出胃癌耐药细胞株SGC7901/ADR和SGC7901/VCR与亲本细胞SGC7901差异表达最大、最可能介导胃癌多药耐药的lncRNA分子DMTF1v4后,进一步研究发现,DMTF1v4在原发性胃腺癌组织中的表达水平与癌组织在体外培养时对化疗药物的敏感率呈负相关;用siRNA下调DMTF1v4在SGC7901/ADR细胞和SGC7901/VCR细胞中的表达可以增加这些细胞对ABC B1蛋白相关化疗药物(如阿霉素、长春新碱、紫杉醇)的敏感性.阿霉素蓄积滞留实验显示,DMTF1v4表达水平的下调能使SGC7901/ADR中阿霉素的蓄积比例增加、外排比例减少. Western blot检测显示,下调DMTF1v4表达能使SGC7901/ADR细胞和SGC7901/VCR细胞的ABC B1蛋白表达下调,而多药耐药相关蛋白MRP的表达没有显著变化.裸鼠皮下异位移植瘤实验表明,DMTF1v4下调组肿瘤细胞的增殖被抑制.在SGC7901/ADR细胞中下调DMTF1v4的表达后,ABC B1蛋白表达水平也随之显著下降.双荧光素酶报告基因分析显示,DMTF1v4是通过增强子样作用而促进ABC B1蛋白的表达. *CASC9*(Cancer Susceptibility Candidate 9)是由染色体8q21.11编码的一种lncRNA, Shang等^[104]用微阵列技术发现, *CASC9*基因在胃癌组织中的表达比正常胃癌组织高出近8倍,进一步的研究发现,敲低*CASC9*基因后可以恢复多药耐药胃癌细胞BGC823/DR和SGC7901/DR对化疗药紫杉醇和阿霉素的敏感性,该作用与ABC B1蛋白的低表达相关. Lan等^[105]研究了lncRNA ANRIL(antisense non-coding RNA in the INK4 locus)在胃癌多药耐药中的作用,结果发现,ANRIL在对顺铂和5-Fu耐药的胃癌组织中呈高表达、在对顺铂和5-Fu耐药的胃癌细胞(BGC823/DDP和BGC823/5-Fu)中亦呈高表达,用ANRIL siRNA转染BGC823/DDP细胞和BGC823/5-Fu细胞后再分别用顺铂和5-Fu处理,可以降低细胞存活率和侵袭力并增加细胞凋亡率,用IC50分析发现,ANRIL敲低或沉默的BGC823/DDP细胞和BGC823/5-Fu细胞对顺铂和5-Fu的敏感性增加,用qRT-PCR和Western blotting检测发现, *ANRIL*基因敲低的BGC823/

DDP细胞和BGC823/5-Fu细胞中ABC B1蛋白呈低表达,回归分析显示, *ANRIL*基因的表达和ABC B1基因的表达呈正相关. *MRUL*(MDR-related and upregulated lncRNA)是位于ABC B1基因下游400 kb处的lncRNA基因, Wang等^[106]发现, *MRUL*能通过增强子样作用而上调阿霉素耐药细胞SGC7901/ADR和长春新碱耐药细胞SGC7901/VCR中ABC B1基因的表达. Hang等^[107]的研究发现,在对顺铂耐药的两株胃癌细胞(SGC7901/DDP和BGC823/DDP)中, *Notch 1*基因呈高表达,向不耐药的亲本细胞(SGC7901和BGC823)中转染*Notch 1*过表达的载体质粒,可使细胞中*Notch 1*基因高度表达;同时发现,这两种细胞中ABC B1蛋白和ABCC1蛋白亦呈高表达,而细胞凋亡受抑制;经筛选发现lncRNA AK022798参与了这一过程,用siRNA干扰AK022798的表达可上调ABC B1蛋白和ABCC1蛋白的表达并增强细胞凋亡,故我们认为,是*Notch 1*的高表达促进了AK022798的高表达从而导致了SGC7901/DDP细胞和BGC823/DDP细胞的耐药.

3.3 lncRNAs主要经细胞凋亡对胃癌多药耐药的调节 张哲^[103]在SGC7901/ADR和SGC7901/VCR两株耐药细胞筛选出19个表达上调10倍以上的lncRNA分子,用qRT-PCR验证显示,其中表达升高幅度最大的两个依次是AK127463和UCA1,但由于AK127463的干扰效果较差,所以选取了UCA1做进一步研究.在临床样本中检测UCA1的表达发现,UCA1在胃癌组织中的表达水平显著高于癌旁正常组织. UCA1可显著促进胃癌细胞对化疗药阿霉素、5-Fu和顺铂产生耐药,该作用与癌细胞的抗凋亡能力增强相关;下调UCA1表达可以逆转SGC7901/ADR细胞对化疗药的耐药性;裸鼠移植瘤试验亦显示,下调UCA1表达能够显著地增加胃癌细胞对化疗药的敏感性.荧光原位杂交和胞浆核分离实验证实,UCA1主要分布在细胞浆,细胞核中有少量分布,提示UCA1主要是在转录后水平发挥其调节作用. UCA1序列中包含有let-7家族miRNA的结合位点,其中以let-7e结合位点评分最高. Let-7e可降低UCA1双荧光素酶报告基因的荧光素信号强度, UCA1上let-7e结合位点的突变可部分抑制这一效应,表明UCA1可与let-7e直接结合、通过竞争内

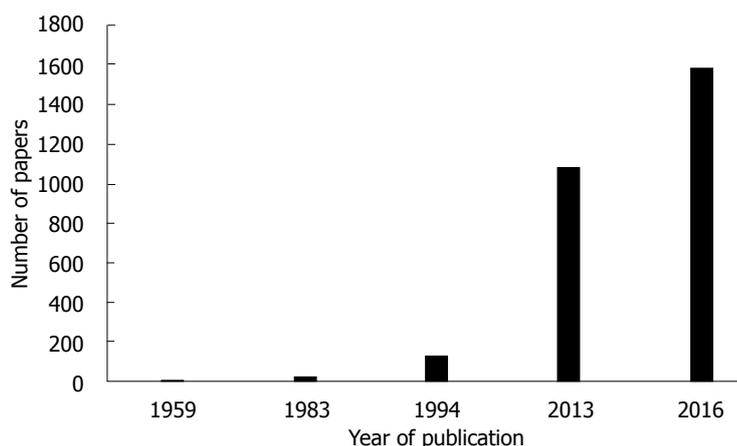


图1 肿瘤化疗耐药研究文献择年分布. 用((cancer[Title/Abstract])AND resistance[Title/Abstract])AND chemotherapy[Title/Abstract]在PubMed搜索所得结果.

表1 肿瘤化疗耐药研究文献分布情况

年代范围	论文数范围
1956 - 1982	1 - 9
1983 - 1993	23 - 93
1994 - 2012	126 - 952
2013 - 2016	1081 - 1585

源性RNA结合let-7e而发挥转录后调节作用. HMGA2是let-7e的下游靶分子. 在胃癌耐药细胞let-7e表达降低而HMGA2表达升高. 过表达let-7e或干扰HMGA2能降低阿霉素、5-Fu和顺铂对胃癌耐药细胞的IC₅₀, 并可使药物诱导的细胞凋亡增加. Let-7e可以负调控HMGA2蛋白的表达, 说明HMGA2是Let-7e的下游靶分子. UCA1可以促进HMGA2蛋白表达, 该作用依赖于结合let-7, let-7结合位点突变可以抑制这一作用. 综上所述, lncRNA UCA1通过与let-7 miRNA家族(主要是let-7e)结合, 降低let-7对耐药相关基因HMGA2的抑制作用, 使HMGA2的表达升高, 通过抗凋亡作用而促进胃癌细胞的多药耐药. Shang等^[108]研究了lncRNA UCA1对胃癌对阿霉素敏感性的影响, 结果发现, UCA1在胃癌中高表达, 沉默UCA1能够抑制Bcl-2表达并促进细胞凋亡. Zhang等^[109]发现, lncRNA NEAT1(Nuclear-enriched abundant transcript 1)在阿霉素耐药胃癌细胞中表达升高, 沉默NEAT1能够增加SGC7901/ADR对阿霉素的敏感性、促进阿霉素诱导的细胞凋亡. Yan等^[110]发现lncRNA HOTAIR(HOX antisense intergenic RNA)在对顺铂耐药的胃癌细胞和组织中明显上调, 过表达HOTAIR能增强细胞

增殖、减低细胞凋亡, 并发现HOTAIR通过直接结合于并抑制miR-126、促进VEGFA和PIK3R2表达并活化PI3K/AKT/ABCC1通路而介导胃癌细胞对顺铂的耐药. Zhang等^[111]报道了lncRNA GHET1过表达在促进胃癌多药耐药形成中的作用. 他们发现, GHET1在耐药胃癌患者和耐顺铂胃癌细胞(BGC823/DPP和SGC7901/DDP细胞系)中表达升高, 沉默GHET1能够抑制BGC823/DPP细胞和SGC7901/DDP细胞的耐药, 转染GHET1 siRNA能显著地降低这两株顺铂耐药细胞的IC₅₀. GHET1在亲代细胞BGC823和SGC7901中过表达能够降低细胞对顺铂的敏感性并减低细胞凋亡率, qRT-PCR和western blot检测发现, GHET1的过表达下调了BGC823和SGC7901细胞中Bax表达、上调了Bcl-2表达并上调了ABCB1和ABCC1表达. Zhang等^[112]还发现, lncRNA PVT-1(Plasmacytoma variant translocation 1)在顺铂耐药胃癌患者和顺铂耐药胃癌细胞BGC823/DDP和SGC7901/DDP中呈高表达, 用PVT-1 siRNA转染BGC823/DDP和SGC7901/DDP再用顺铂处理, 可见细胞存活率显著下降、细胞凋亡率显著升高; 此外, 用qRT-PCR和Western blot检测发现, PVT1的上调还能增加ABCB1和MRP等的表达.

4 结论

肿瘤多药耐药是肿瘤药物治疗的一大障碍. 对肿瘤对化疗药耐药的机制已经有数十年的历史^[113-119](图1, 表1), 并对耐药机制提出了数种假说, 但耐药的机制迄今尚未完全明了^[120]. 近几年来, lncRNA在肿瘤多药耐药形成中的调节作用被受到重视, 相关领域研究论文的数量迅

速增加。对肿瘤多药耐药机制的深入理解将有助于我们采取相应的措施应对或逆转耐药; 临床医生在选择化学治疗药物之前若能对癌细胞对相应化疗药的敏感性做一测试, 应该非常有助于合理选择药物和改善治疗效果。

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