

转录因子E2F1对急性单核细胞白血病新抗原基因MLAA-34的转录调控作用

《现代肿瘤医学》[ISSN:1672-4992/CN:61-1415/R] 期数: 2019年20期 页码: 3560-3565 栏目: 论著(基础研究) 出版日期: 2019-09-08

Title: Effects of transcription factor E2F1 on transcriptive regulation of acute monocytic leukemia-related gene MLAA-34

作者: 雷博; 张王刚; 何爱丽; 陈银霞; 曹星梅; 张鹏宇; 赵万红; 王剑利; 刘捷; 马肖容; 张彦平; 刘海玲
西安交通大学第二附属医院血液科, 陕西 西安 710004

Author(s): Lei Bo; Zhang Wanggang; He Aili; Chen Yinxia; Cao Xingmei; Zhang Pengyu; Zhao Wanhong; Wang Jianli; Liu Jie; Ma Xiaorong; Zhang Yanping; Liu Hailing
Department of Hematology, The Second Affiliated Hospital, Medical School of Xi'an Jiaotong University, Shaanxi Xi'an 710004, China.

关键词: 急性单核细胞白血病; MLAA-34; E2F1; 转录调控

Keywords: acute monocytic leukemia; MLAA-34; E2F1; transcriptional regulation

分类号: R733.71

DOI: 10.3969/j.issn.1672-4992.2019.20.004

文献标识码: A

摘要: 目的: 探讨转录因子E2F1对急性单核细胞白血病新抗原基因MLAA-34的转录调控作用。方法: 利用双荧光素酶报告基因检测系统及定点突变技术分析E2F1对MLAA-34基因启动子转录活性的影响。通过凝胶迁移实验(EMSA)和染色质免疫共沉淀(ChIP)实验,验证E2F1是否与MLAA-34启动子核心区直接特异性结合。构建E2F1真核表达载体和干扰载体,转染U937细胞,RT-PCR和Western Blot检测MLAA-34基因的转录和表达变化。结果: 转录因子E2F1对MLAA-34基因表达具有调控作用,E2F1结合序列点突变后,相对荧光素酶活性升高($P < 0.01$),绿色荧光蛋白的表达增高。EMSA和ChIP实验,从细胞内、外水平分别证明E2F1可与MLAA-34启动子直接结合而发挥调控作用。在过表达试验中,E2F1的增加可下调MLAA-34的表达($P < 0.05$);在干扰试验中,E2F1的降低可上调MLAA-34的表达($P < 0.05$)。结论: 转录因子E2F1可与MLAA-34基因启动子上的转录调控区结合,并抑制急性单核细胞白血病细胞中MLAA-34基因的转录。

Abstract: Objective: To investigate the transcriptional regulation of transcription factor E2F1 on acute monocytic leukemia-related gene MLAA-34. Methods: The effect of E2F1 on the transcriptional activity of MLAA-34 gene promoter was analyzed by luciferase reporter gene detection system and site-directed mutation technique. EMSA and ChIP assay were used to verify whether E2F1 directly and specifically binds to the core region of MLAA-34 promoter. The over-expression vector and interference vector of E2F1 were constructed to transfect U937 cells, and RT-PCR and Western Blot were used to detect the transcription and expression changes of MLAA-34 gene. Results: The transcription factor E2F1 had a regulatory effect on MLAA-34 gene expression, and the relative luciferase activity was increased after E2F1 binding point mutation ($P < 0.01$). EMSA and ChIP experiments demonstrated that E2F1 can directly bind to MLAA-34 promoter and play a regulatory role. In the over-expression test, the increase of E2F1 can down-regulate the expression of MLAA-34 ($P < 0.05$). In the interference test, the decrease of E2F1 can up-regulate the expression of MLAA-34 ($P < 0.05$). Conclusion: Transcription factor E2F1 can bind to the transcriptional regulatory region on the promoter of MLAA-34 gene and inhibit the transcription of MLAA gene in acute monocytic leukemia.

参考文献/REFERENCES

- [1] Estey E. Acute myeloid leukemia: 2016 update on risk-stratification and management [J]. Am J Hematol, 2016, 91(8): 824-846.
- [2] Chen G, Zhang W, Cao X, et al. Serological identification of immunogenic antigens in acute monocytic leukemia [J]. Leuk Res, 2005, 29(5): 503-509.
- [3] Zhang PY, Zhang WG, He AL, et al. Identification and functional characterization of the novel acute monocytic leukemia associated antigen MLAA-34 [J]. Cancer Immunol Immunother, 2009, 58(2): 281-290.

- [4] Zhang WJ, Zhang WG, Zhang PY, et al. The expression and functional characterization associated with cell apoptosis and proteomic analysis of the novel gene MLAA-34 in U937 cells [J]. *Oncol Rep*, 2013, 29(2): 491-506.
- [5] Zhao J, He AL, Zhang WG, et al. Quantitative assessment of MLAA-34 expression in diagnosis and prognosis of acute monocytic leukemia [J]. *Cancer Immunol Immunother*, 2011, 60(4): 587-597.
- [6] Lei B, Chen YX, He AL, et al. C59T mutation in exon 2 of monocytic leukemia-associated antigen-34 gene indicates a high risk of recurrence of acute myeloid leukemia [J]. *Oncol Lett*, 2017, 14(1): 55-62.
- [7] Lei B, Zhang WG, He AL, et al. Cloning of new antigen gene MLAA-34 promoter and identification of core region in acute monocytic leukemia [J]. *J Exp Hematol*, 2019, 27(3): 641-645.
- [8] Sutton MN, Huang GY, Zhou J, et al. Amino acid deprivation-induced autophagy requires upregulation of DIRAS3 through reduction of E2F1 and E2F4 transcriptional repression [J]. *Cancers (Basel)*, 2019, 11(5): 603.
- [9] Fabre B, Livneh I, Ziv T, et al. Modulation of the cell cycle regulating transcription factor E2F1 pathway by the proteasome following amino acid starvation [J]. *Biochem Biophys Res Commun*, 2019, 513(3): 721-725.
- [10] Meng P, Bedolla RG, Yun H, et al. Contextual role of E2F1 in suppression of melanoma cell motility and invasiveness [J]. *Mol Carcinog*, 2019:1-10.
- [11] Farra R, Dapas B, Grassi M, et al. E2F1 as a molecular drug target in ovarian cancer [J]. *Expert Opin Ther Targets*, 2019, 23(3): 161-164.
- [12] Qian L, Zhang W, Zhang P, et al. The anti-apoptosis effect of MLAA-34 in leukemia and the β -catenin/T cell factor 4 protein pathway [J]. *American Journal of Translational Research*, 2016(7): 2270-2278.
- [13] Chen J, Gong C, Mao H, et al. E2F1/SP3/STAT6 axis is required for IL-4-induced epithelial-mesenchymal transition of colorectal cancer cells [J]. *Int J Oncol*, 2018, 53(2): 567-578.
- [14] Song Y, Chen QT, He QQ. Identification of key transcription factors in endometrial cancer by systems bioinformatics analysis [J]. *J Cell Biochem*, 2019. doi:10.1002/jcb.28811.
- [15] Zhang L, Tan W, Zhou J, et al. Investigation of G-quadruplex formation in the FGFR2 promoter region and its transcriptional regulation by liensinine [J]. *Biochim Biophys Acta Gen Subj*, 2017, 1861(4): 884-891.
- [16] Iglesias-Ara A, Osinalde N, Zubiaga AM. Detection of E2F-induced transcriptional activity using a dual luciferase reporter assay [J]. *Methods Mol Biol*, 2018(1726): 153-166.
- [17] Koh KH, Jeong H. Electrophoretic mobility shift assay (EMSA) and supershift assay of cytochrome P450 2B6 in response to estrogen [J]. *Methods Mol Biol*, 2016(1366): 41-51.
- [18] Visa N, Jordán-Pla A. CHIP and CHIP-related techniques: Expanding the fields of application and improving CHIP performance [J]. *Methods Mol Biol*, 2018(1689): 1-7.
- [19] Bohaciakova D, Renzova T, Fedorova V, et al. An efficient method for generation of knockout human embryonic stem cells using CRISPR/Cas9 system [J]. *Stem Cells Dev*, 2017, 26(21): 1521-1527.
- [20] Oh KS, Ha J, Baek S, et al. XL-DNase-seq: Improved footprinting of dynamic transcription factors [J]. *Epigenetics Chromatin*, 2019, 12(1): 30.

备注/Memo: National Natural Science Foundation of China(No.8153000580) ; 国家自然科学基金资助(编号: 8153000580)

更新日期/Last Update: 1900-01-01