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实时荧光定量PCR分析CML患者HMGA2基因的表达及其临床意义 点此下载全文

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摘要:

摘 要 目的:分析慢性髓系白血病(chronic myeloid leukemia, CML)患者外周血中高迁移率蛋白A2基因(high mobility group A2,HMGA2)mRNA的表达及其相关临床特征,探讨它们在CML演进中的作用及临床意义。方法:采集2006年1月至2008年2月在南方医科大学南方医院血液科就诊的24例CML和5例健康对照的骨髓和外周血标本(所有参与试验及贡献骨髓和外周血标本的患者均知情同意,并经伦理委员会批准),以荧光原位杂交(fluorescence in situ hybridization, FISH)技术检测CML骨髓标本间期细胞BCR/ABL融合基因的表达,实时荧光定量(real-time fluorescence quntitative)PCR(RTQ-PCR)技术对HMGA2 mRNA的表达进行相对定量分析,采用秩和检验比较CML患者不同阶段HMGA2转录水平,以Spaearman方法分别对HMGA2转录水平与BCR/ABL融合基因水平、外周血液学参数进行相关性分析。结果:12例CML-CP患者BCR/ABL阳性细胞率为(58.08±39.21)%,HMGA2相对定量为2.39±1.86;12例CML-AP/BP患者BCR/ABL阳性细胞率为(58.08±39.21)%,HMGA2相对定量为2.39±1.86;12例CML-AP/BP患者BCR/ABL阳性细胞率为(58.08±39.21)%,HMGA2相对定量为2.39±1.86;12例CML-AP/BP患者BCR/ABL阳性细胞率为(58.08±39.21)%,HMGA2相对定量为2.39±1.86;12例CML-AP/BP患者BCR/ABL阳性细胞率为(87.50±16.21)%,HMGA2相对定量为91.78±14.07。CML-AP/BP患者HMGA2转录水平与CML-CP患者之间的差异有统计学意义(Z=-4.157,P<0.01),CML-AP/BP患者HMGA2转录水平与为周血原幼细胞数呈正相关关系(r=0.636,P=0.017)。结论:CML患者HMGA2转录水平在AP/BP期显著高于CP期,HMGA2有可能成为预测CML疾病演变、判断预后和指导临床治疗的可靠指标。

关键词: 高迁移率蛋白A2基因(HMGA2) 慢性髓系白血病 慢性期 急变期 加速期 BCR/ABL 实时荧光定量PCR

Real-time fluorescence quntitative PCR in analysis of HMGA2 expression in CML patients and its clinical significance <u>Download Fulltext</u>

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Abstract:

Abstract Objective: To examine the expression of high mobility group A2 (HMGA2) mRNA in the peripheral blood of chronic myeloid leukemia (CML) patients and the related clinical characteristics, and to explore its role and clinical significance in CML progress. Methods: Peripheral blood samples of 24 CML patients and 5 volunteers, who had been diagnosed in our hospital from Jan. 2006 to Feb. 2008, were collected in the present study (all the patients and volunteers signed paper of informed consent and the study was approved by ethics committee). BCR/ABL fusion gene expression in CML bone samples was detected by fluorescence in situ hybridization (FISH). HMGA2 mRNA expression was examined by real-time fluorescence quantitative PCR (RTQ-PCR). Rank sum test was used to assess the HMGA2 gene transcription differences between CML-CP and CML-AP/BP patients. Correlation analyses were done using Spearman's correlation test to explore the correlation between HMGA2 expression, BCR/ABL fusion gene expression, and hematological parameters in peripheral blood of CML patients. Results: We found that (58.08±39.21)% leukemia cells were BCR/ABL fusion gene-positive in 12 CML-CP patients, and the relative quantitative expression of HMGA2 gene was 2.39±1.86. Meanwhile, (87.50±16.21)% leukemia cells were BCR/ABL fusion gene-positive in 12 CML-AP/BP patients, and HMGA2 gene relative quantitative expression was 91.78±14.07. HMGA2 gene transcriptions between CML-CP and CML-AP/BP patients were significantly different (Z=-4.157, P<0.01). HMGA2 gene transcription in CML-AP/BP patients was positively correlated with the numbers of blast cells in the peripheral blood (r=0.636, P=0.017). Conclusion: HMGA2 gene transcription level in CML-AP/BP patients is higher than that in CML-CP patients, indicating HMGA2 may be a reliable indicator in estimating the development, prognosis and clinical treatment outcome of CML patients.

Keywords: high mobility group A2 (HMGA2) chronic myeloid leukemia (CML) chronic phase accelerated phase blastic phase BCR/ABL real-time fluorescence quntitative PCR(RTQ-PCR)

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