P247

建立快速高分辨熔點分析法檢測急性骨髓性白血病 NPM1 突變檢驗方法

蘇揚迪[1]，林建佑[1]，劉素卿[1,2]，林彩秀[1]，王秀娟[1]，何承懋[1]，楊淑芬[1]，盧章智[3]，彭慶添[2]，張建國[1]
中國醫藥大學附設醫院[1]檢驗醫學部,[2]兒童醫學中心
林口長庚紀念醫院[3]檢驗醫學科

Establishment of rapid high-resolution melting analysis to detect NPM1 mutation in acute myeloid leukemia

Yang-Di Su[1], Chien-Yu Lin[1], Su-Ching Liu[1,2], Tsai-Hsiu Lin[1], Shiow-Jain Wang[1], Cheng-Mao Ho[1], Shu-Fen Yang[1], Jang-Jih Lu[3], Ching-Tien Peng[2], and Jan-Gowth Chang[1]
[1] Department of Laboratory Medicine, [2] Children's Medical Center, China Medical University Hospital, Taichung, Taiwan.
[3]Department of Laboratory Medicine, Chang-Gung Memorial Hospital, Linkou, Taoyuan, Taiwan

BACKGROUND: Nucleophosmin mutations of exon 12 (NPM1 mutations) represent the most frequent molecular aberration in about 35% of acute myeloid leukaemia (AML) patients. High resolution melting (HRM) is a novel screening method that enables rapid identification of mutation positive DNA samples.
METHODS and MATERIALS: We developed HRM assays to detect NPM1 mutations. Twenty-one AML patients were enrolled. The research project was reviewed and approved by the IRB committee of our hospital (DMR99-IRB-108). All mutations are confirmed with directly sequencing.
RESULTS: Herein, we established molecular diagnosis of NPM1 mutation assays for AML. Analysis of a series of 32 patient specimens revealed 11 positive for NPM1 mutation and 21 negatives. In additional, NPM1 positive mutation is referred to as c.960 ins TCTG (Type I) were 9 patients and c.960 ins GTCG and c.962 ins TGCA heterozygote insertion were 1 patients, respectively.
CONCLUSIONS: This study demonstrates that HRM is a rapid and efficient method of screening NK-AML samples for NPM1 mutations. We expect to set up the molecular diagnostic technique for clinical laboratory service

P248

乳房微鈣化組織檢體之 UBE2C 腫瘤生物標記之分析

莊淑貞[1,2,5]、潘慧本[3]、周春平[3]、彭南靖[4]、陳錦翠[5]、張聰賢[1]
[1]高雄榮民總醫院教學研究部,[2] 高雄榮民總醫院病理檢驗部,[3]高雄榮民總醫院放射線部,[4]高雄榮民總醫院核醫科,[5]中山大學生物科學所

Analysis of UBE2C tumor biomarker in breast microcalcifications tissue

Shu-Jhen Jhuang[1,2,5], Huay-Ben Pan[3], Chen-Pin Chou[3], Nan-Jing Peng[4], Jiin-Tsuey Cheng[5], Tsung-Hsien Chang[1]#
[1]Department of Medical Education and Research, [2]Department of Pathology and Laboratory Medicine, [3]Department of Radiology, [4]Section of Nuclear Medicine, Kaohsiung Veterans General Hospital, [5]Department of Biological Sciences, National Sun Yat-Sen University

Breast microcalcification is an important feature of early breast cancer. The data of ammography and histology reveal that 15% of breast calcification could be furthure defined as breast carcimnoma. UBE2C, an ubiquitin conjugation E2 enzyme, is a newly identified biomarker candidate expressed in various solid tumor and cancer cells. It contributes to the process of ubiquitin-mediated proteasome degradation in cell cycle. To evaluate the clinical application of UBE2C in diagnosis of early breast cancer, we measured the UBE2C mRNA expression level from 28 sets of breast biopsy samples; each set contains normal and microcalcification tissue from individual. The quantitative PCR indicated that approximately 70% microcalcification samples with UBE2C mRNA expressed were detected; immunohistochemistry also revealed 68% of microcalcification tissues were UBE2C positive. In addiction, UBE2C over expressed breast cancer cells of MCF-7 and MDA-MB-231were rapid proliferation. Contrarily, reduced cell growth rate and increased cell death were observed in UBE2C knockdown cells. Our data suggest that the UBE2C promoted cell proliferation may contribute to breast ontogenesis. The molecular mechanism of UBE2C in breast cancer will be further investigated.