Histopathology

VOLUME 61 | SUPPLEMENT 1 | OCTOBER 2012

EDITED BY ALASTAIR D. BURT

Table of Contents | Author Index | Text Search

XXIXth Congress of the International Academy of Pathology

30 September – 5 October 2012
Cape Town, South Africa

NATIONAL HEALTH LABORATORY SERVICE

WILEY-BLACKWELL

Journal of the British Division of the International Academy of Pathology

ISSN 0309-0167
www.histopathologyjournal.com

ABSTRACTS
XXIXth Congress of the International Academy of Pathology

September 30 – October 5, 2012
Cape Town International Convention Centre
Cape Town, South Africa

Histopathology

48

Comparison of pathology of breast tissue and mammography

A Chotiyano[1], T Triamwittayanont[2,3], T Wongsiri[2,3], J Srinagarind[2,3], S Koonmee[2,3]

[1]Department of Pathology, Khon Kaen hospital, Khon Kaen, Thailand, [2]Department of Pathology, Srinagarind Hospital, Khon Kaen University, Khon Kaen, Thailand, [3]Department of Radiology, Srinagarind Hospital, Khon Kaen University, Khon Kaen, Thailand

Introduction: Evaluation of calcification in breast lesions is a major assessment criterion for breast mammography. The morphology and distribution of the calcification are related to the histology of the lesions. The Breast Imaging Reporting and Data system (BIRADS) were established to standardize mammographic interpretation. The objective of the study is to assess the pathologic outcome of BIRADS mammographic classification and the success of stereotactic biopsy of breast lesions.

Materials and Methods: A retrospective analysis of 250 consecutive patients undergoing breast biopsy for mammographic abnormalities from January 2004 to December 2008 was undertaken to identify biopsies done for indeterminate microcalcifications and breast lesions. Specimens were identified and reviewed by one pathologist. The BIRADS mammographic classification data was compared with histopathological data.

Results: Positive predictive value (PPV) of the BIRADS category five criteria in diagnosing breast cancer in the present study was 85% (46 in 54 patients). This PPV is compatible with the PPV advocated by the American cancer research (ACR), which proposed a PPV of at least 95%, and that of other published studies. PPV for mammographic BIRADS category five in published studies ranges from 80% to 97%.

Conclusion: A cancer detected by microcalcifications alone had a relatively low probability of being false negative, spiculate masses were the most common feature in both cancer groups. Poorly defined masses increased the risk of being false negative interval cancers.

49

Breast cancer stem cells in triple negative vs. non triple negative breast cancer

MV Comanescu, M Dobre, C Ardeleanu, G Butur, G. Bussolati

Victor Babes National Research Institute, Bucharest, Romania

Introduction: Triple negative breast cancers (TNBC) represent a subtype of breast cancer associated with poor prognosis and highly aggressive behaviour. This might be due as well to the fact that treatment options do not target cancer stem cells (CSC).

Materials and Methods: We evaluated tumor specimens of 20 breast cancer patients with known hormone receptor and Her2/neu status: 10 TNBC and 10 non TNBC. We initially performed immunohistochemistry analysis to determine CD44, CD24 and ALDH expression, as well as other markers of pluripotency and proliferation. We also investigated gene expression by real time PCR, using a stem cell PCR array from Qiagen.

Results: We identified significant differences between the percentage of cells with the immunophenotype of CSC (CD44+/CD24−/low, ALDH+) between TNBC and non TNBC. There were variations in patterns of expression of the other immunohistochemical markers. The level of expression differences measured by real-time PCR for the 84 genes showed stem cell differentiation markers and signalling pathways associated to each of the two categories studied.

Conclusion: The identification of factors involved in survival and self-renewal of cancer stem cells could highlight new molecular aberrations of TNBC and improve their therapy.

50

Pyrosequencing analyses of DNA methylation in breast cancer patients

I Zmetakova[1], L Danihel[2], B Smolkova[1], V Kajabova[1], T Krivulcik[1], V Repiska[3], I Fridrichova[1]

[1]Laboratory of Cancer Genetics, Cancer Research Institute of Slovak Academy of Sciences, Bratislava, Slovakia, [2]Institute of Pathological Anatomy, Faculty of Medicine, Comenius University, Bratislava, Slovakia, [3]Institute of Medical Biology and Genetics, Faculty of Medicine, Comenius University, Bratislava, Slovakia

Introduction: In breast cancer many tumour suppressor genes are inactivated by DNA hypermethylation, which could be utilized for identification of new epigenetic biomarkers.

Patients and Methods: We investigated relation between DNA methylation and breast cancer progression. The associations between methylation profiles in 10 genes (APC, ADAM23, CDH1, CXCL12, ESR1, PGRB, RASSF1A, SYK, SOCS1 and TIMP3) and clinico-pathological parameters were statistically evaluated. Paraffin embedded tumour and lymph node tissues, blood cells and plasma samples from 11 breast cancer patients and lymphocytes from 11 controls were analysed by new quantitative technology, pyrosequencing.

Results: The highest frequency of hypermethylation was found in RASSF1A (8/11), APC (6/11) and ADAM23 (6/11) genes. In eight DIC, two mucinous tumours and one LIC up to 5, 4 and 1 hypermethylated genes were observed, respectively. From three HR− cases, in one patient both HR genes were hypermethylated. In the most advanced case, a 56 year old patient with DIC, grade 3, stage IIIC, HR− and 41 positive LNs, 50% of investigated genes were hypermethylated from 27% to 86%. Four patients with positive LNs manifested high correlation between methylation levels in tumours and LNs in ADAM23, CXCL12, ESR1 and SYK genes. Methylation 'background' in healthy women was generally up to 3% except of CDH1 and PGRB genes (7–12%), where positive correlations between age and methylation levels were observed.

Conclusion: By introduction of pyrosequencing we obtained accurate and reproducible technology for quantification of DNA methylation in cancer patients. Preliminary results indicate the association of these epigenetic changes with invasion and metastasis.

This study is the result of the implementation of projects: no. APVV-0076-10 supported by the Slovak Research and Development Agency, no. 26240220058, Research and Development Operational Programme funded by the ERDF and no. 2/0065/10 funded by the Slovak Grant Agency VEGA.