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<td>Guan, XY; Zhou, H; Sham, JST; Zhang, H; Trent, JM</td>
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338 Cytogenetics in Breast Ductal Carcinoma. M.L. Soto-Alvarez, A. Rojas-Al-
 etoclo, F. Alvarez-Nava, K. Urdaneta, L. Gonzalez, A. Boesean. Unidad de Genetica
Medica, Universidad del Zulia, Maracaibo, Zulia, Venezuela.

The breast cancer research is one of the old problems of public health in our society, from the past decade an improvement in him has been observed diagnosis, as well as in the identification of parameters prognostic that permit a better evaluation of these patients. The objective of this work is to report, the chromosomal anomalies in 22 breast ductal carcinoma (BCD). In this report, we present the chromosomal abnormalities found in 32 primary breast ductal carcinomas. The tumor samples were studied us-
ing the technique for short-term culturing and cytogenetic analysis with G-band. Only one tumor with normal cytogenetics was observed. Thirty one (99%) of the tumors had chromosomal abnormalities including 21t (65.9%) in which chromosome 1 was in-
volved (trisomy, monosomy or structural abnormalities of the type t(1q2p) and
9q13.4). Other recurrent anomalies such as del(12p), del(4p), 7q-, 8q-, 7p-, 3q-. The signifi-
cance of these findings and their role in tumorigenesis will become more evident with close follow-up of women who have tumors with an abnormal kary-
type.

340 Physical and hematopoietic transcript map of a 5q31 "critical subregion" associ-
ated with the 5q-syndrome. S. Kamakari1, V. Konstantinopolou1, N.P. Angounou1-
2, 1 Institute of Molecular Biology and Biotechnology, 2 University of Crete School of
Medicine, Heralon, Greece.

The 5q31 syndrome represents a preleukemic state, exhibiting an acquired interstitial
5q31 (5q-31) for which a predisposition to secondary myelodysplastic syndromes and
leukemia. The delineation of the role of one of these subregions, we constructed a YAC con-
ting along the GM-CSF-IL3 and TCF-1 genes. Enzymatic PCR screening of the CEPH and ICI
YAC libraries, resulted in the isolation of twelve YACs: three YACs (B546, 67B8, 14DG110) pos-
tive for the GM-CSF-IL3 genes, five YACs (B546, 67B8, 14DG110, 14B86, 15A23, 14B86
28B11, positive for 7pYACs (51575B, 52508, bacs50065, bacs7755, 53225, 53427
and 53695), STS content mapping of all twelve YACs resulted in the construction of the first
complete YAC contig of the subregion and documented the expression in a bone marrow
cDNA library. Two of them, namely 777380 and W92884, mapping proximal and distal to the IL3 gene, respectively, were further ana-
lysed. Human RNA dot blot analysis of the EST 777380, exhibited expression in kidney,
heart, small intestine and lung. Northern blot analysis also documented its expression in a
variety of tissues, including bone marrow, with a transcript size of approximately 4 kb.
Following the technique of 5' and 3' rapid amplification of cDNA ends (RACE) for this
EST, using a bone marrow CDNA library as a template, two overlapping clones, cover-
ing a total length of 3.8 kb were isolated and sequenced. Characterisation of the full
length cDNA is in progress. RACE amplification of the EST W92884 resulted in a 500
bp PCR product, currently used as a probe in a bone marrow cDNA library hybridisation
screening.

342 Characterization of a Complex Chromosome Rearrangement involving 6q in a
Melanoma Cell Line: Isolation of a Candidate Tumor Suppressor Gene Interrupted
by the Breakpoint at 6q16. X.X. Guan1, H. Zhou4, J.S.T. Shih1, H. Zhang5, J.M.
Templ1. 1 Dept Clinical Oncology, Univ Hong Kong, Hong Kong, China; 2 Cancer Ge-
netics, Colorado State University, USA.

The incidence of human malignant melanoma has increased dramatically in many
parts of the world. Deletion of 6q is one of the most frequent chromosomal alterations
in malignant melanoma with a breakpoint cluster at 6q11-32. Recently, we used G-
banding analysis and micro-FISH technique to detect a complex chromosome rear-
arrangement involving 6q and 17p in a melanoma cell line UACC-353. The rearrangement
includes an inversion involving 6q, inv(6q53qq13) (16q21), and a translocation involving
the inserted 6q and 17p13. A BAC clone covering the breakpoint 6q16 was identified
by a FISH screen. A novel gene (named BIM1, broken in melanoma 1) interrupted by
the breakpoint was isolated by partial sequencing analysis of the BAC clone. Full-length
and 3'-rapid amplification of cDNA ends (RACE) analysis of BIM1 with two isoforms has been isolated. Sequence analysis identified a sig-
nificant similarity of BIM1 and prenyl transferase gene, which is required for the can-
cer-associated, malignant Ras gene. Expression of BIM1 was also detected in 1021 melanoma
lines. Our results indicate BIM1 may play an important role in the development of mal-
nignant melanoma.