C50  Differential gene expression patterns in HER2 positive metastatic breast cancer patients according to hormone receptor status

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Background: HER2 positive breast cancer (HER2+ BC) is a heterogeneous disease. Presenting features, patterns of recurrence and survival of HER2+ BC can differ according to hormone receptors (HR) status. The purpose of this study is to highlight different gene profile and molecular pathways between HR+ and HR- metastatic HER2+ BC.

Abstract:

The study demonstrated that a LNR was effective in neoadjuvant setting especially in triple negative BC. p53 expression doesn’t affect by the type of anticancer drugs associated with antracyclines. Also, both carotid PWV and Troponin I, BNP, mociety assay showed that STS, in association with doxorubicin appears to protect healthy breast cells from chemotherapeutic treatment. Microarray approaches restricting food intake, including Short Term Starvation (STS), may exert a dietary restriction showed significant anticancer effects able to pre-
Materials and methods: 34 HER2+ metastatic BC patients were included: 18 patients with HR+/HER2+ and 14 with HR-/HER2+. Data regarding tumor characteristics, treatment information and clinical outcomes were collected. The expression of 770 genes and 13 molecular pathways were evaluated by means of NanoString PanCancer pathway panel performed on BC formalin-fixed paraffin-embedded tissues from diagnostic core biopsy or surgical resection specimen.

Results: Gene expression analysis identified 118 genes with significantly different expression in the two cohorts. All but one of these genes were over-expressed; only the gene CACNG6 was down-regulated in HR+/HER2+ group. In particular, 93 genes were over-expressed in HR-/HER2+ while 24 were overexpressed in HR+/HER2+. Most of these genes encoded growth factors, pro- or anti-inflammatory interleukins and DNA repair factors. 62% of these genes were involved in PI3K, MAPK and RAS pathways (32, 22 and 18, respectively). PI3K, MAPK and NOTCH pathways were differentially expressed between HR+/HER2+ and HR-/HER2+ (p = 0.003, p = 0.0018, p = 0.02, respectively). All these three pathways were overexpressed in HR-/HER2+ BC. In particular, all the significantly different expression genes in NOTCH pathways were overexpressed in HR-/HER2+ group.

Conclusions: This genome expression analysis identified a gene expression profile able to differentiate HR+ versus HR- HER2+ metastatic BC. The overexpression of PI3K, MAPK and NOTCH pathways in HR-/HER2+ BC could justify its more aggressive behaviour. The validation of this HER2+ BC profile needs further investigation.