DIFFERENTIAL MEMBRANE PROTEOME ANALYSIS OF HCC-1954 AND MCF-7 BREAST CANCER CELL LINES

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Introduction:
Breast cancer aggressiveness is associated with differential protein expression resulting in poor outcome, disease recurrence and death. The molecules closely associated with these processes are predominantly present at the cell surface. The HCC1954 is a hormone receptor negative, ERBB2 positive, poorly differentiated cell line. MCF7 is differentiated cell line that expresses estrogen receptor and is negative for ERBB2 receptor. We aimed to compare and characterize the relative quantification of membrane proteins present in both HCC1954 and MCF7 cell lines that can be involved in invasive ability and metastases.

Material and Methods:
Membrane proteins were biotinylated and fractionated using the cell surface protein isolation kit (Pierce®). Following trypsin/LysC digestion the peptides were analyzed by label free LCMS on a 2-D SCX/RP chromatography system coupled to a Synapt HDMS mass spectrometer (Waters, Farmington, MI, USA). For mass spectra processing and data analyses, ProteinLynx Global Server v.3.0 and Progenesis QI software v. 2.0 were used. GO analyses were done with Panther Classification System v10.0.

Results and Discussion:
More than 800 proteins of the HCC1954 and MCF7 breast cancer cell lines were identified. Among them, CD44, CD166, integrins α-v, cadherin-1 were fifty fold more expressed in HCC1954 than in MCF7 cell line. These molecules play important roles in cell migration, cell adhesion, cell junction and cell-cell interactions. GO analyses also showed that the activity of the integrin and cadherin pathways was higher in HCC1954. Moreover, the expression levels of ERBB2 and GRB7 were more than 300 times higher in HCC1954 than in MCF7 cell line.

Conclusions:
The expression levels of proteins involved in invasive and proliferative mechanisms are higher in HCC1954 than in MCF7 cell line. Further analyses will be performed to validate these results.

Key Words: HCC-1954, MCF-7, proteome
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