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Visual versus automatic measurement of mammographic breast density (MBD)

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Background: The study of the visual and automatic measurement of mammographic breast density (MBD) and its implications in diagnostic tumor size and tumor prognosis needs a thorough evaluation.

Material and methods: The comparison of Visual MBD and Automatic MBD shows that 70% of cases are matched in 40.6% (141/101), 58.4% (59/101) the MBD is 1, the visual MBD 3 matches with DMR automatic matches in 32.1% (9/28) in the MBD 3 automatic 64.3% (19/28) is lower (p < 0.001). When comparing Visual DMR and Automatic MBD, visual MBD 2 the MBD Automatic matches in 40.6% (41/101), 58.4% (59/101) the MBD is the one, the visual MBD 3 matches with MBD 3 automatic in 32.1% (9/28), in the MBD 3 automatic 64.3% (18/28) is lower (p < 0.001).

Results: The comparison of Visual MBD and Automatic MBD, visual MBD 2 the MBD Automatic matches in 40.6% (41/101), 58.4% (59/101) the MBD is 1, the visual MBD 3 matches with MBD 3 automatic in 32.1% (9/28), in the MBD 3 automatic 64.3% (18/28) is lower (p < 0.001).

Conclusion: Visual measurement overestimates MBD versus automatic measurement according BIRADs categories. Ultrasound and mammographic size and of the magnetic resonance, a regression is made to study which test values the size better, and the correlation of MBD with tumor size shows us a better estimate with less variability with ultrasound (RE, RP, HER2, Ki67, Histological Grade). Ultrasound and mammographic size and of the magnetic resonance, a regression is made to study which test values the size better, and the correlation of MBD with tumor size shows us a better estimate with less variability with ultrasound (RE, RP, HER2, Ki67, Histological Grade).

No conflict of interest.

Development of a multiplexed protein panel using a targeted mass spectrometry (MS)-based proteomics approach for the study of CDK4/6 inhibitors resistance in breast cancer.

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The aim of creating MRM assays to enable specific, sensitive and precise quantitation of these proteins in small amounts of samples. We developed a high resolution peptide fractionation system using high-pH micro-flow liquid chromatography (LC) which is required to overcome the problem of small samples amounts while improving analytical sensitivity in the analysis of complex biological matrices such as biopsies. The MCF-7 human breast cancer cell line was used as model during method development. Proteins from cell lysates were reduced, alkylated and digested with trypsin. The resulting peptides were micro-flow fractionated into 70 fractions and the developed nano-LC-MS MRM assays were used for peptide detection and quantification. Data were analyzed using Skyline.

We developed a highly specific MS-based multiplexed assay with peptide standards targeting 25 proteins relevant to CDK4/6 breast cancer treatment. Our micro-flow fractionation method increased assay sensitivity and allows for the analysis of small sample amounts. In the future we will apply this workflow to samples such as Patient Derived Xenografts models, breast cancer tissues and FFPE samples in order to identify the predictive value of these potential biomarkers for responsiveness to CDK4/6i.

No conflict of interest.

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No conflict of interest.

Development of a multiplexed protein panel using a targeted mass spectrometry (MS)-based proteomics approach for the study of CDK4/6 inhibitors resistance in hormone receptor positive breast cancer

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1. Hormone receptor positive breast cancer represents approximately 70% of all breast cancer cases. These patients are treated with endocrine therapies which improves survival and offers a cure in early stages. Recurrent disease, metastatic dissemination and drug resistance limit the survival of patients. The limitations regarding endocrine therapy have prompted the search for new therapeutic targets, such as CDK4/6 Inhibitors (CDK4/6i). Despite the improved disease control that CDK4/6i offer, not all patients respond to these drugs and most patients whose tumors respond to CDK4/6i eventually develop acquired resistance. No proven biomarkers of CDK4/6i efficiency exist to date, and there is a need for diagnostic tools that can stratify patients to save costs and the burden of unnecessary therapy. Our aim is to perform a quantitative evaluation of marker proteins with a developed multiplexed panel using targeted mass spectrometry (MS)-based proteomics for 25 proteins from the CDK4/6 pathway which have been shown in the literature to be central to CDK4/6i resistance.

2. We developed Multiple Reaction Monitoring (MRM) MS methods for the 25 target proteins using synthetic heavy-isotope-labeled standards with