

AB063. 145. Identification and validation of circulating microRNA distinguishing metastatic from local breast cancer

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Background: Breast cancer is the leading cause of cancer related death in women, with metastasis the principle cause of morbidity and mortality. Non-invasive prognostic markers to expedite the early identification of metastasis are required, to optimise treatment decisions and improve patient outcomes. MicroRNA (miRNA) are small, non-coding RNAs that regulate gene expression and are implicated in a variety of cellular processes, including metastasis.

Methods: Analysis of subtype and age matched

plasma samples from metastatic disease or local disease (n=5 each) were profiled using next generation sequencing. Analysis revealed significantly dysregulated miRNAs that distinguished metastatic from local disease. Validation was performed on whole blood extracted RNA using TaqMan qRT-PCR. Mir-16 and mir-425 were used as endogenous controls. Data was analysed using SPSS v23, with P values <0.05 deemed significant.

Results: Mir-329, mir-331, mir-4433 and mir-181 were identified as potential biomarkers of metastasis and were validated on a large cohort of patients with local disease, patients with metastatic disease and healthy controls.

Conclusions: We identified and provisionally validated four circulating miRNAs that distinguish metastatic from local breast cancer. Validation could allow early identification of metastasis, informing clinical decisions and ultimately improving patient outcomes. Further research is required to identify if these miRNAs function as circulating biomarkers or play a direct role in the metastatic process.

Keywords: Breast cancer; metastases; biomarkers; micro RNA (miRNA); recurrence

doi: 10.21037/map.2018.AB063

Cite this abstract as: McAnena PF, Kahraman T, Curran C, Freedman J, Lowry A, Brown JA, Kerin MJ. Identification and validation of circulating microRNA distinguishing metastatic from local breast cancer. *Mesentery Peritoneum* 2018;2:AB063. doi: 10.21037/map.2018.AB063