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SP8.07 Expression of Matriptase-2 and TMPRSS serine enzymes and the connection with bone metastasis in clinical breast cancer

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Aims: The present study investigated the connection between the matripase/TMPRSS (Transmembrane Serine Protease) protein enzyme family, a type II serine transmembrane enzymes, and bone metastasis in clinical breast cancer.

Methods: Six members of the TMPRSS family including Matriptase-1, -2, -3, TMPRSS-3, -5, -7, and -9 were evaluated for their gene expression by way of quantitative transcript analysis in a cohort of breast cancer and mammary tissues. The levels of expression were assessed against the presence of bone metastases of the patients who had a ten year followup. Statistical analysis was based on Receiver operating characteristic (ROC) method and student t test.

Results: Breast cancer tissues had a significant aberrant expression of matriptase-1 (p=0.01), matriptase-2 (p=0.047) and TMPRSS5 (p=0.031), when compared with normal mammary tissues. There was not significant difference for other members between tumour and normal tissues. When the expression levels were analysed against the presence of bone metastasis, it was found that matriptase-2 was the only TMPRSS member that had a significant value in predicting bone metastasis (AUC=0.716, p=0.013) with a hazard ratio at 6.13 (95% confidence interval 1.598-23.525. p=0.008). Multifactorial model analysis demonstrated that amongst the clinical factors and key hormone receptors (including ER and ERBB family members), matriptase-2 was the only factor that independently predict bone metastasis.

Conclusions: Matriptase-2, amongst the TMPRSS serine protein family members, is an independent factor in predicting bone metastasis from breast cancer. The protein which is a regulator factor for some pro-metastasis factors, thus has important value in bone metastasis.