expression adjacent to low grade tumours ($p = 0.047$) and for recurrence with significantly greater expression adjacent to tumours who remained recurrence free ($p = 0.006$). Survival analysis using Kaplan-Meier curves also revealed improved DFS associated with high ANCT IGFBP7 levels, which was statistically significant ($p = 0.004$). Results for IGFBP3 in either tumour or normal tissue or IGFBP7 in tumour tissue were not significant.

**Conclusions:** These data suggest that the level of local IGFBP7 adjacent to neoplastic breast tissue may act to restrict the progression of the malignant phenotype in a paracrine fashion, possibly even conferring a survival advantage. This needs to be evaluated further with larger series.

### O-84 Characterisation of specific micro-RNA expression profiles in fresh frozen human breast tissue

P.A. Davoren*, N. Miller, R. McNeill, M.J. Kerin. *National Breast Cancer Research Institute and University College Hospital, Galway, Ireland*

MicroRNAs negatively regulate the expression of specific mRNA targets at the post-transcriptional level and have been shown to display aberrant expression in several cancers including breast cancer. The expression profiles of miR-26b and miR-30a-3p were characterised in human breast tissue using real-time quantitative PCR. Significant deregulation of miR-26b has been shown in human breast tumour tissues. Transcripts targeted by miR-30a-3p include angiogenesis-related mRNAs. MiR-30a-3p has not previously been shown to be deregulated in breast cancer.

Following informed consent, malignant ($n = 33$) and benign ($n = 5$) primary breast tumour tissues and normal ($n = 5$) breast tissues were obtained at the time of surgery at University College Hospital, Galway. Malignant breast tumour samples were grouped according to the metastatic status of the patient five years from initial diagnosis into metastasis-free (MF, $n = 13$), bone-metastasis positive (BM, $n = 11$) and visceral and bone metastasis positive (VBM, $n = 9$) groups. Stem-loop gene-specific primers were used for cDNA synthesis and gene expression was measured using TaqMan® microRNA assays. Following relative quantification using qBASE software, statistical analysis was performed using Minitab (v.15).

The expression of miR-26b was significantly upregulated in BM versus MF groups ($P < 0.01$) suggesting a role for miR-26b in the bone-metastases process. There was a significant downregulation of miR-30a-3p in the VBM versus BM groups ($P < 0.05$). A significant relationship was not found between the expression levels of the individual microRNAs and prognostic factors such as nodal status, tumour grade and steroid hormone receptor status. This study confirms the potential of specific microRNAs in controlling outcome in breast cancer.

### O-85 Expression of the putative breast cancer gene BASE; relationship with microRNA 154* and estrogen receptor status

A.J. Lowery*, N. Miller, M.J. Kerin. *National University of Ireland, Galway, Ireland*

**Introduction:** It is estimated that 30% of human genes are regulated by non-coding micro-RNAs, many of which are cancer-related. One such potential gene, *BASE* has been shown by *in-vitro* studies to be estrogen responsive and breast cancer specific. Little is known, however, about the associations or precise regulation of *BASE* expression in breast cancer tissues.

**Aims:** To quantify expression of *BASE* and its putative targeting microRNA *miR-154** in breast cancers, and examine potential correlations with clinicopathological variables.

**Methods:** Microarray expression profiling of genes and miRNAs was performed in 16 early-stage, matched breast cancer specimens. Expression of selected differentially expressed micro-RNAs, including *miR-154**, was validated by real-time quantitative PCR in 52 breast tumour samples. Expression of *BASE*, a computationally predicted target of miR-154*, was also validated in 52 breast tumours and breast cancer cell lines. Associations between expression of *BASE*, *miR-154** and clinico-pathological variables were examined.

**Results:** *BASE* was expressed in 50% of tumour samples. A significantly higher proportion of tumours expressing *BASE* were estrogen receptor *(ER)* positive than *ER* negative ($p = 0.019$). *BASE* expression was also detected in the *ER+ve* cell lines but not in an *ER –ve* cell line. *MiR-154** was expressed in all breast tumour samples. *MiR-154** expression was significantly lower in *ER+ve* than *ER-ve* tumours ($p = 0.001$).

**Conclusions:** These findings suggest that the expression of both *miR-154** and putative target gene *BASE* correlate with ER status in breast tumours. This highlights the importance of these molecules in breast cancer. Functional analysis to elucidate interactions between these molecules is underway.

### O-86 Can differences in cellular antioxidant enzyme status predispose to breast cancer in women without a recognised increased risk?

G. Bermano*, S.D. Heys, M. Goua, E. Smyth, S. Chaturvedi, S. McIntosh, K.W.J. Wahle. *Department of Surgery, Aberdeen University and School of Life Sciences, The Robert Gordon University, Aberdeen, UK*

**Introduction:** Up to 10% of patients with breast cancer have a known genetic defect (eg. BRCA-1, BRCA-2) but the aetiological factors in the others remain unclear. We hypothesise that impaired expression of cellular antioxidant enzymes and subsequent reduction in the ability to counter DNA damage due to oxidative stressors could be, at least in part, important in the aetiology of breast cancer.

**Method:** We obtained whole blood and PBMNC from women with breast cancer ($n = 20$) and from an age matched control group without known risk ($n = 20$). Erythrocyte and plasma glutathione peroxidase-1 (GPX1) activity was determined in both groups using a spectrophotometric method. Aliquots of PBMNC were used to determine gene expression of redox enzymes in untreated, fresh cells using RT-PCR. Further aliquots of PBMNCs were incubated in autologus plasma for 24 hrs and stimulated with hydrogen peroxide (1 mM) for 15 minutes to assess inducibility of the selenium-dependent antioxidant enzymes (GPX1) and (GPX4).

**Results:** Neither GPX1 activity in plasma or erythrocytes nor mRNA expression in fresh, non-induced PBMNC differed significantly between groups although mRNA tended to be lower in the cancer group. However, GPX4 gene expression in fresh PBMNC was significantly (30%, $p < 0.004$) reduced in the cancer group. Percentage induction of mRNA by hydrogen peroxide was similar (30–40%) for GPX1 and GPX4 in both groups but absolute GPX4 induction was lower in the cancer group due to a lower un-stimulated, starting value.

**Conclusion:** Breast cancer patients do appear to have a lower redox enzyme expression than non-cancer patients which would be expected to impair their ability to counter free-radical damage to DNA resulting in greater risk of genetic mutations.