using standard clonogenic assays, and counting individual colony survival post-exposure to increasing doses of x-ray radiation. Biological (siRNA) knockdown of AC was performed, and clonogenic assays were repeated to establish the impact of AC inhibition on radiosensitivity.

Results: Colorectal cancer cell lines with greater cellular AC protein expression (LIM 1215/MDST8) demonstrated higher colony survival compared to lower expressers (HT29/HCT 116) at specific radiation doses. Titrated siRNA concentrations (40 nM−80 nM) achieved >70% AC expression reduction. Three cell lines with differential AC expression (HCT 116/HT 29/LIM 1215) were treated with siRNA for AC. Clonogenic assays confirmed that siRNA knockdown reduced colony formation efficiency (colonies/number of cells plated − CFE) and improved radiosensitivity across all cell lines. HT29 (0.52 (CFE) *control* vs 0.13 (CFE) *knockdown* at 1 Gy); HCT (0.24 (CFE) *control* vs 0.09 (CFE) *knockdown* at 1 Gy); LIM 1215 (0.88 (CFE) *control* vs 0.43 (CFE) *knockdown* at 0.25 Gy).

Conclusion: High AC expression correlates with radio resistance in the colorectal cancer cell lines studied. In vitro analysis confirmed siRNA knockdown of AC levels in these cell lines improved their radiosensitivity. Further work is needed to determine the translational potential of AC to serve as a novel response biomarker in patients selected to undergo CRT in colorectal cancer.

https://doi.org/10.1016/j.ejso.2017.10.088

1042. Metabolic organization in HPV+ oropharyngeal squamous cell carcinoma

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Background: HPV positive (HPV+) oropharyngeal squamous cell carcinomas (OPSCC) are characterised by extensive nodal disease, but are associated with significantly better outcome than HPV negative OPSCC. In head and neck SCC, high levels of lactate are associated with subsequent nodal and distant metastases and a 'three compartment tumour metabolism' model has been proposed in oral cancer. We investigated the metabolic status of HPV+ OPSCC.

Method: The metabolic organization of 50 HPV +ve OPSCC was determined by histopathological staining using antibodies to Ki-67, TOMM20, MCT4 and MCT1.

Results: High, levels of Ki-67 reactivity were observed in carcinoma cells at both the tumour centre and the advancing front, but more highly differentiated cells did not express Ki67. TOMM20 expression was strongly positive in all carcinoma cells, while CAFs were always more weakly stained.

High MCT1 expression was observed in all carcinoma cells regardless of their position within the tumour but was negative or weak in the stromal compartment. Strong MCT4 immunoreactivity was found in more than 2/3 of carcinoma cells, but the unstained areas did not show consistent localisation. MCT4 expression was present at lower intensity in CAFs.

In general, where we observed TOMM20 staining, the cells also expressed MCT1 and a high proportion of the cells were Ki-67 positive.

Conclusion: We have identified that epithelial cancer cells in HPV+ OPSCC are highly proliferative, rich in mitochondria and consume mitochondrial fuels (Ki-67+/TOMM20+/MCT1+). These proliferating cells co-exist with a group of non-proliferating stromal cells which express MCT4. This contrasts with earlier data from oral SCC (Curry et al 2013) where a separate, non-proliferating, catabolic compartment of carcinoma cells also exists.

In summary, we show that the three-compartment tumour metabolism model is not present in HPV+ OPSCC, possibly due to the histological characteristics of these tumours.

https://doi.org/10.1016/j.ejso.2017.10.090

1051. Increased FABP12 expression in prostate cancer and its possible promoting role in malignant progression

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Background: FABPs are a family of 12 cytosolic proteins and their main function is to transport fatty acids into cells. FABP5 was proved to play an important role prostate cancer cells. The possible roles of other FABPs have not been fully studied. In this work, we investigated the expression status of FABP12 (a newly discovered member of FABPs) in prostate cancer cells and tissues. The possible promoting role of the elevated FABP12 in malignant progression was also assessed.

Method: The FABP12 mRNA was measured by qPCR. Western blot was performed to analyse FABP12 at the protein level. Immunohistochemical attaining was performed to analyze an archival set of benign and malignant human prostate tissues to assess the expression status of FABP12. The correlation of the increased FABP12 expression with patient survival is assessed with Kaplan Meier Survival curve and Log Rank test.

Results: FABP12 expression at both mRNA and protein levels were increased in malignant cell lines and the FABP12 increase is closely associated with increasing degree of malignancy. FABP12 was barely detectable in BPH, but its immunohistological staining in prostate carcinomas was significantly stronger than that in BPH. The staining intensity was increased as the increasing Gleason scores and the increased FABP12 is significantly associated with patient survival.

Conclusion: The results showed that FABP12 is overexpressed in highly malignant prostate cancer cells and tissues. Thus, FABP12 may play an important promoting role in malignant progression of prostate cancer.

https://doi.org/10.1016/j.ejso.2017.10.091

1059. Differences in risk factors for ductal carcinoma in situ and invasive breast cancer: A prospective cohort study

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Background: In the UK, ductal carcinoma in situ (DCIS) accounts for one fifth of all screen-detected breast cancers. Risk factors for DCIS have traditionally been thought to be the same as for invasive breast cancer (IBC), but few studies have examined this. We compared the effect of different lifestyle factors on the incidence of these two cancers.

Method: We undertook a prospective cohort study using data from UK Biobank. We included all women aged 50−69 years enrolled into UK Biobank between 2006 and 2010 from across the UK. We excluded women with a prior diagnosis of any cancer, except non-melanoma skin cancer. Women were followed from the date of entry into UK Biobank until the earliest of DCIS diagnosis, IBC diagnosis, death, loss to follow-up on 31/12/2015.

Results: During our study period, 456 women were diagnosed with DCIS without prior IBC and 2772 were diagnosed with IBC without prior DCIS. For both conditions, postmenopausal body mass index (BMI) was associated with an increased risk, and the number of live births was associated with a decreased risk. However, the magnitude of the effects differed between DCIS and IBC. The effect of postmenopausal BMI $\geq$35 kg/m^2 was larger for DCIS than for IBC (RR 2.35, 95% CI 1.14−4.82), and the decrease in risk with each additional live birth was greater for DCIS than for IBC ($p = 0.03$).

Conclusion: We present the most detailed comparison of risk factors for DCIS and IBC to date. Our results confirm similarities in the risk factors for these two conditions, but reveal differences in the magnitude of their effect. By doing so, these findings provide insights into the contribution of different factors at different stages in the process of carcinogenesis.

https://doi.org/10.1016/j.ejso.2017.10.092