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BACKGROUND: In patients with newly presenting multiple myeloma (MM) immune paresis is often associated with intractable infections and recent evidence advocates the enumeration of bone marrow (BM) derived B cells and B cell maturation proteins for risk stratification of MM patients (1,2). The cellular measures of immune function (eg: B cell enumeration) are, however, seldom analysed in the peripheral blood (PB) of MM patients. This study was designed to enumerate T, T cell subset, B, NK and NKT cells at different stages of MM, and to determine if the PB B-cell component can act as a surrogate marker for B cell enumeration in the BM.

MATERIAL_METHODS: PB and BM lymphocyte subset analysis was performed on 102 samples obtained from a range of MM patients (n = 70) using multicolour flow cytometry. Uninvolved serum lg and paraprotein levels were also quantified.

RESULTS: Quantification of circulating lymphocyte subsets showed reduced, numbers of B cells (51/102), T cells (19/102), TH cells (32/102), CTLs (19/102), NK cells (28/102) and NKT cells (67/102). Furthermore, reduced B cell levels were more frequently seen in the MM-Diagnosis and MM-Treated groups (50% of samples) compared with the MGUS and SMM stages (10-25% of samples). A significant, positive, correlation was seen between relative numbers of B cells in paired PB and BM samples (p<0.0001, r2=0.94).

CONCLUSIONS: B lymphocyte and NKT cell subsets were the most frequently reduced in MM patients, in keeping with reduced levels of circulating uninvolved Ig levels, followed by T cells, particularly TH cells which have a crucial role in B cell Ig production. We suggest that monitoring of the B cell component in the PB of MM patients may serve as a surrogate assay for enumeration of B cell component in BM and also as a strategy for risk stratification and biomarker discovery in MM (1,2).

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Poster 10.

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SUBJECT: Biomarkers

TITLE: MicroRNAs In Prostate Cancer: Implications For Personalised Medicine.

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BACKGROUND: There is a clinical need for biomarkers that can help develop personalised medicine for prostate cancer. MicroRNAs (miRNAs) are small, non-coding RNA species which regulate gene expression by interacting with messenger RNAs (mRNAs). miRNAs are attractive candidates as biomarkers, since they are stably preserved in clinical samples, including FFPE tissues, serum and

urine, and can be readily detected by PCR (1, 2). In this study we highlight the potential of various miRNAs as biomarkers in prostate cancer

MATERIAL__METHODS: microRNAs of interest were selected by bioinformatics analyses performed on prostate cancer biopsy datasets held in The Cancer Genome Atlas (TCGA) repository. Expression of selected miRNAs (miR-205, miR-200c, miR-141, miR-24 and miR-210) were subsequently profiled by PCR in a panel of prostate cancer cell-lines and in a small cohort of clinical prostate biopsy specimens. Functional analysis, identification of targets and correlation with clinicopathological parameters were performed by in vitro bioassays and further in silico analysis.

RESULTS: TCGA analysis revealed several miRNAs that were significantly correlated with clinicopathological parameters (Gleason, TNM staging, PSA). Of these, we progressed to show in vitro that miR-210 is induced by hypoxia, an important factor in prostate cancer progression. In a small pilot dataset, we found miR-24 was down-regulated in tumour tissue compared to matched normal tissue. miR-200c and miR-141 displayed variable expression in these clinical samples, dependent on the methylation status of their shared promoter. mRNA targets and functional networks of each selected miRNA were identified, revealing the complex network of interactions that determine their functionality in prostate cancer.

CONCLUSIONS: In this study, we provide representative examples to illustrate that miRNAs play an important role in the pathogenesis of prostate cancer. Increasing our understanding of the functionality of specific miRNAs in prostate cancer will be instrumental in developing this exciting field of research so that it can inform precision medicine and improve patient outcome. REFERENCES: 1) Matin, F., Jeet, V., Clements, J.A., Yousef, G.M. and Batra, J., 2016. MicroRNA theranostics in prostate cancer precision medicine. Clinical chemistry, pp.clinchem-2015.

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Poster 11.

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SUBJECT: Digital Healthcare

TITLE: The effect of a digital chest image interpretation training tool on interpreter performance AUTHORS: 1Laura McLaughlin, 1Sonyia McFadden, 2Raymond Bond, 3Jonathan McConnell 4Nick Woznitza, 2Andrew Cairns, 3Ayman Elsayed, 2Dewar Finlay, 1Ciara Hughes

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BACKGROUND: There has been no research to date that evaluated training guides using eye tracking or no research that validates the use of training guides in chest image interpretation by measuring interpreter competency pre and post implementation. Using eye tracking technology and expert input we aim to provide reporting clinicians with a research informed training package for use in chest image interpretation and to test its effect on user performance.

MATERIAL_METHODS: A digital training platform has been developed to include: A) a search strategy training tool to assist reporters during their interpretation of images and B) an educational tool to communicate the search strategies to trainees using eye tracking technology.