Methods: Protein expression of AURKA and KIF2C was investigated in 160 TNBC cases by immunohistochemistry and 23 normal breast epithelium. Overexpression of these biomarkers was correlated with RNA profiles (40-gene panel, established in previousstudies) assessed using a branched DNA assay to identify potential complimentary biomarkers related to AURKA and KIF2C expression. Protein expression of these biomarkers (CIP2A and PPME-1), was assessed on TNBC cell line (*n*=6) models treated with PP2A activator, FTY720 and TNBC patients (*n*=160).

Results: Sixty-five percent of TNBC patients overexpressed AURKA while 40% overexpressed KIF2C at a protein level. PPME-1 and CIP2A were found to be positively correlated with AURKA and KIF2C RNA and protein expression. Protein expression of these 4 biomarkers can predict FTY720 sensitivity in TNBC cell lines, which can be translated to a novel therapeutic group within TNBC patients.

Conclusion: Expression of these protein markers provides a biomarker signature signalling the deregulation of PP2A in TNBCs, hence classifying patients into a potential therapeutic group sensitive to PP2A reactivation.

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P.019

Profiling and characterisation of the p53 family as biomarkers for breast cancer

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Introduction: The p53 family of protein is comprised of p53, p63 and p73. p53 is traditionally known as a tumour suppressor and described as the guardian of the genome due to its role in preventing genome mutations. Mutations of the p53 gene increase the susceptibility to cancer. Over 50% of human cancers involve p53 loss of function. This study will focus on analysing p53 mutations in breast cancer. One of the results of a mutated p53 gene is the formation of amyloids. Amyloids are protein aggregates which form due to the distortion of the secondary structure of proteins.

Methods: Multiplexing assays will be used to profile the different mutations and combinations of isoforms from multiple breast cancer cell lines. Following the identification of mutations, protein aggregates within the cell lines will be studied. Subsequently, cloning of the observed isoforms and site-directed mutagenesis will be performed and studied in relation to protein expression. Properties of these proteins such as their predisposition to aggregate and form amyloids, the degree at which different combination of p53/p63/p73 proteins aggregate, and the rate at which this occurs will be studied.

Results: Recombinant human wild-type p53 together with isoforms and some mutants have been sub-cloned and purified from Escherichia coli.

Conclusion: Multiple types of breast cancers exist and characterisation of the isoforms and mutations of the p53 family may enable the development of a biomarker system for such tumours since each individual breast cancer type arises from a particular mutation which results in the gain of function of the oncogene activity.

P.020

Determining the genotype of the RH blood group system in the Maltese population

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Introduction: The Rh blood group system has a vital role in transfusion medicine therefore, by DNA typing important medical issues can be resolved when serological techniques are inconclusive. The main aim of this research was to determine the frequency of RHD and RHCE in the Maltese population so that in the future DNA typing can be employed to complement the routine serology techniques.

Methods: 400 blood donor samples and 397 neonatal blood samples were enrolled in this study. An allele-specific polymerase chain reaction (AS-PCR) method was used to determine the presence of RHD, RHCE*E and RHCE*e, while multiplex PCR was used to test for RHCE*C/c. 81 from these 400 blood donor samples were tested by serology for the RhD, C,c,E and e antigens, and the results were used for comparison with the results obtained by genotyping.

Results: Out of 797 samples, the most common allele was RHCE*e (98%), followed by RHD (91%). The lowest percentage was obtained for RHCE*E (23%). The most common haplotype in the study was DCe (49.7%). This is also expressed in the fact that DCcee and DCCee were the most common genotypes with a percentage of 38.27 and 24.46 respectively. In RHD negative samples, dccee was the most frequent (6.9%).

Conclusion: Like in previous studies, this research also concludes that the distribution of the RH genotype varies in different geographical areas. The molecular techniques used, offer a fast in-house testing system to obtain the RHD and RHCE genotype status. However this may merit further development to be used in a clinical setting.

P.021

Surgical ventricular restoration: A local experience.

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Introduction: Heart failure carries a high mortality, despite best medical therapy. Surgical ventricular restoration (SVR) is a technique whereby an attempt is made to restore the left ventricle's (LV) shape, size and function. The role of SVR in the treatment of heart failure has not yet been fully established, especially since there is no standardised procedure. Nonetheless studies have shown that with careful patient selection, SVR may be effective. This study retrospectively analyses data collected from patients who underwent SVR at Mater Dei Hospital, Malta over a 5 year period. An appropriately sized endoventricular mannequin was used as a template during surgery for all the patients.

Conclusion: While the number of patients who underwent this procedure was limited, our results mirror those from larger studies, showing that re-establishment of the LV size and geometry was related to a positive outcome.