Conclusion These results show that the piRNA composition seen in pre-diagnostic serum samples may contain potential biomarkers that can lead to accurate classification of whether a patient was at increased risk of testicular cancer before the initial diagnosis. Preliminary results should be further expanded with different sncRNA datasets and lifestyle covariates.

Susceptibility Genes

PO-075 STUDY OF THE BIOMARKER POTENTIAL OF LONG NON-CODING RNAS HULC IN BREAST CANCER

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Introduction Recent reports show that long non-coding RNAs play major role in cancer initiation and progression. Here, we studied the potential role of lncRNA HULC in invasive ductal carcinoma of the breast.
Material and methods Quantitative real-time PCR was employed to investigate the expression of HULC in tumour tissues from 50 patients with breast cancer and 50 corresponding non tumoral margins as well as in cancer cell lines including MCF-7, MDA-MB231 and ZR-75. The correlation between HULC expression and clinic-pathological features was also evaluated. Furthermore, HULC expression was knocked down in cell lines by using siRNA.
Results and discussions Our data showed that HULC is over-expressed in tumour tissues and cancer cells compared to controls ($p \leq 0.05$, CI=95%). ROC curve analysis demonstrated the biomarker potential of HULC for breast invasive ductal carcinoma (AUC=0.71). However, there was no significant correlation between HULC and clinic-pathological characteristics. The results are in accordance with previous reports illustrating the biomarker potential of HULC in cancers including hepatocarcinoma, glioma and osteosarcoma.
Conclusion Token together, the data suggest that HULC may play an important role in breast cancer and could be considered as diagnostic biomarker for further investigations.

PO-076 MOLECULAR ANALYSIS OF BRCA-NEGATIVE BREAST AND/OR OVARIAN CANCER FAMILIES BY MULTIGENE PANEL TESTING

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Introduction About 5%–10% of the hereditary breast and/or ovarian cancer (BC/BOC) is associated with an autosomal dominant genetic susceptibility due to highly penetrant mutations of the *BRCA1/2* genes. In particular, *BRCA1/2* gene mutations are found in 25%–30% of the BC families subjected to genetic testing. These numbers suggest the possible involvement of other genes in BC/BOC genetic predisposition and a fraction of these cases remains to be assigned to specific genetic factors. Here we report on the application of the NGS multigene panel to a group of *BRCA1/2* mutation negative BC/BOC cases, in order to identify germline mutations that could further explain BC/BOC genetic susceptibility.
Material and methods We selected a group of 27 *BRCA1/2* negative BC and BOC families on the basis of a clear dominant inheritance pattern and/or a moderate/high BRCAPro score. We performed a genomic screening by a comprehensive multi-gene custom panel of 29 cancer-related genes, using Ion Torrent platform (Thermo Fisher Scientific).
Results and discussions In three cases (11%) we found mutations described as pathogenic (https://www.ncbi.nlm.nih.gov/clinvar/) in *ATM*, *MUTYH* and *PALB2* genes. In the series analysed, the most frequently altered genes were *APC* and *ATM* (15%) but were also identified mutations in *MSH6* and *TP53* (11%), *MUTYH* and *RAD51B* (7%), *MRE11, EPCAM, BRIP1, CHEK2, PALB2, BARD1,* STK11 and RAD50 (4%). In particular, we found six genomic variants of uncertain significance (VUS) in *MSH6, ATM, BRIP1, RAD50* and *APC* genes; nine genomic variants of conflicting interpretations of pathogenicity in *MUTYH, MRE11, TP53, APC, MSH6, CHEK2, EPCAM* and *ATM* genes and eight genomic variants not reported in ClinVar in *APC, RAD51B, STK11, TP53, ATM* and *BARD1* genes predicted deleterious by *in silico* analysis. Their biological significance and involvement in the development of the pathology is still unknown today. Only six patients were negative for the presence of mutations in the 29 genes analysed.
Conclusion Preliminary results of this study suggest that NGS could offer a great contribution to identify the genetic component of susceptibility to BC/BOC and could potentially be used with implications for clinical management and counselling of patients and their families. Moreover, our results suggest that multigene testing approach may benefit appropriately selected patients, especially those with increased risk of BC/BOC development.

Poster Presentation: Prevention and Early Detection

Preclinical Prevention Studies, Markers and Prevention

PO-077 TOBACCO USE AND CANCER AWARENESS AMONG IRULA TRIBES, NILGIRI HILLS, TAMILNADU, INDIA

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Introduction Tea is an important agro-industry of India, which contributes immensely to the countries economy. Tea garden population constitutes approximately 1/12th of tea growing state's population. Poor socio-economic conditions, ignorance due to illiteracy, over-crowded and unhygienic living conditions in the residential colonies make tea garden population vulnerable to various communicable diseases and malnutrition. Hence this study was contemplated with an aim to assess the oral health status, tobacco use and cancer awareness among tea plantation workers (Irula tribes), Nilgiri Hills, Tamil Nadu, India.
Material and methods A cross-sectional descriptive study was conducted to assess the tobacco use and cancer awareness among tea plantation workers, Nilgiri Hills.Data was collected using a