Conclusions 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 IncRNA 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 ZK-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<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 Taken 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, BRIPI, CHEK2, PALB2, BARD1, STK11 and RAD50 (4%). In particular, we found six genomic variants of uncertain significance (VUS) in MSH6, ATM, BRIPI, 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...
pretested Questionnaire, which included Demographic data, tobacco habits, its frequency and form. The data collected was analysed using SPSS version 15.

**Results and discussions** Results showed that among 900 study population, showed 57% had no formal education, 34.5% had not visited dentist before. 64.5% had indigenous brushing habits. 52% of oral mucosal lesions and 6% malignant oral tumours were observed. A very high prevalence of periodontal disease, tobacco chewing, deep rooted beliefs and customs regarding dentition and dental treatment was observed in this community. Prevalence of oral mucosal lesions in the study population was due to tobacco usage and lack of awareness regarding the deleterious effects of the products used.

**Conclusion** The dangers from smoking and chewing tobacco are well documented within the literature but the public’s lack of knowledge of the risks is a concern. Health professionals are encouraged to ensure that the public is made aware of these risks, especially those within high-risk groups.

**PO-078** ABSTRACT WITHDRAWN

**PO-079** DYSREGULATION OF MIR-196B IN HEAD AND NECK CANCERS LEADS TO PLEITROPIC EFFECTS IN THE TUMOUR CELLS AND CAFS

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**Introduction** The miR-196 family members have been found dysregulated in different cancers. Therefore, they have been proposed as promising biomarkers and therapeutic targets. This study is the first to investigate the role of miR-196b in the development and progression of head and neck squamous cell carcinomas (HNSCC), and also the impact on the surrounding tumour microenvironment.

**Material and methods** The expression levels of miR-196a/b were analysed using Taqman miRNA assays in fresh tissue specimens from HNSCC patients (19 HNSCC samples and 11 patient-matched normal epithelia), in formalin-fixed paraffin-embedded tissue specimens from laryngeal dysplasia (17 non-progression and 23 progressing lesions, as the 23 patient-matched invasive tumours subsequently developed) and saliva samples from HNSCC patients (15 HNSCC samples and 11 healthy donors).

The pathobiological role of altered expression of miR-196a/b was assessed in HNSCC-derived cell lines (FaDu, UT-SCC-42B) and cancer-associated fibroblasts (CAFs), transiently transfected with specific pre-miR precursors, analysing their impact on cell proliferation, migration and invasion. We used a panel of validated and/or predicted miRNA target genes to identify the miR-196a/b targets in HNSCC and a phosphokinase array to study the activation status of multiple intracellular signalling pathways.

**Results and discussions** Increased miR-196b levels were detected in 95% of primary tumours and precancerous lesions, although no significant differences were observed between non-progressing versus progressing dysplasias. Furthermore, increased levels of both miR-196a and miR-196b were successfully detected in saliva samples from HNSCC patients. The functional consequences of altered miR-196 expression were investigated in both HNSCC cell lines and CAFs by transfection with specific pre-miR precursors. Results showed that both miR-196a and miR-196b elicit cell-specific responses in target genes and downstream regulatory pathways, and have a distinctive impact on cell proliferation, migration and invasion.

**Conclusion** These data reveal the early occurrence and prevalence of miR-196a/b dysregulation in HNSCC tumorigenesis, suggesting their utility for early diagnosis and/or disease surveillance and also as a non-invasive biomarker in saliva. The pleiotropic effects of miR-196a/b in HNSCC cell subpopulations and surrounding CAFs may complicate a possible therapeutic application.

**PO-080** PREVALENCE OF HUMAN PAPILLOMA VIRUS AND ITS PHYLOGENETIC ANALYSIS IN PATIENTS WITH HEAD AND NECK SQUAMOUS CELL CARCINOMA IN PAKISTAN

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**Introduction** HNSCCs are characterised by distinct phenotypic, aetiological, biological and clinical heterogeneity. It is a heterogeneous disease that can be roughly divided into human papillomavirus (HPV) positive and negative. HPV is a recently identified causative agent for a subset of head and neck cancers, primarily in the oropharynx but very little is known about the prevalence of specific HPV types in Pakistan.

**Material and methods** This cross sectional study was carried out in the Department of Immunology, University of Health Sciences, Lahore, Pakistan after approval from the Ethical Review Committee and Advanced Studies and Research Board, UHS Lahore. After an informed consent, tissue sections from a total of 72 patients with HNSCC were collected. The diagnosis of HNSCC was confirmed again on H and E staining and DNA was extracted from formalin fixed paraffin embedded tissue sections using DNA extraction kit. For the detection of HPV DNA, two universal primer sets GP5/GP6 and MY9/MY11 were used in the polymerase chain reaction. The samples, found to be positive for HPV on PCR, were sequenced for the phylogenetic analysis of HPV.

**Results and discussions** Among 72 cases of HNSCC, only 5 (14.4%) cases were found to be positive for HPV by using universal primers sets. The prevalence of HPV in HNSCC in many international studies from Europe and USA have documented a prevalence of 5%–50% in HNSCC cases. After confirming the presence of HPV in HNSCC cases, positive DNA samples have been transported to a well-known international laboratory for gene sequencing and molecular diagnosis. As soon as possible, we will receive the sequencing data, we will sketch a phylogenetic tree and further subtyping of HPV and the further results will be presented.

**Conclusion** The findings of current study will be helpful in launching public health awareness and future vaccination programs against specific HPV types in Pakistan to lessen the burden of HPV related HNSCC.