Translational research/biomarkers

2022-RA-205-ESGO · **CIRCULATING HPV DNA IN CERVICAL CANCER: A MARKER FOR EARLY DETECTION OF RELAPSE**

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Introduction/Background Almost all cervical cancers (CC) are caused by human papillomavirus (HPV) and patients with advanced stage are at high risk for relapse. Studies has shown that most patients with HPV-associated tumors have detectable circulating HPV DNA (HPV ctDNA) in the blood at time of diagnosis, before treatment. Development in sensitive technologies led to the use of cell-free DNA for monitoring patients. In the present study, we investigated if HPV ctDNA may serve as a residual tumor marker at the end of chemo-radiation or to predict relapse during the follow-up period.

Methodology We analyzed serum samples from 94 HPV16- or HPV18-related CCs from the BioRAIDs (NCT02428842) prospective cohort. Samples were collected before and after treatment and during an 18-month follow-up period. Using digital droplet PCR (ddPCR), we assessed the relevance of circulating HPV E7 gene as a marker for residual disease. Finally, the prognostic impact of circulating HPV E7 gene was assessed with its prediction value of relapse.

Results Circulating HPV DNA (HPV ctDNA) was detected in 63% (59/94) of patients, before treatment. HPV ctDNA detection in serum sample was associated with high FIGO stage (p=0.02) and para-aortic lymph node involvement (p=0.01). The level of HPV ctDNA was positively correlated with HPV copy number in the tumor (R=0.39, p<0.001). Complete clearance of HPV ctDNA by the end of treatment was significantly associated with a longer PFS (p<0.0001). Patients with persistent HPV ctDNA in serum relapsed with a median time of 10 months (range, 2–15) from HPV ctDNA detection.

Conclusion HPV ctDNA detection is a useful marker to predict relapse in cervical cancer.

2022-RA-366-ESGO · **CALCIUM ACTIVATED POTASSIUM CHANNELS (KCNMA1) AS BIOMARKER OF PRE INVASIVE AND INVASIVE CERVICAL CANCER**

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Introduction With rising incidence of cervical cancer, novel biomarkers need to be developed. One such biomarker are ion channels and voltage gated channels which are known to be regulated by HPV oncogene and estradiol. Potassium channels including calcium- activated potassium channels (KCNMA1) are also involved in tumor cell proliferation, migration, invasion and angiogenesis and are over-expressed in cancers like glioma, breast, ovary and prostate. The primary objective was to study and compare the mRNA and protein expression of calcium-activated potassium channels (KCNMA1) in pre-invasive and invasive cervical cancer.

Methodology In a prospective comparative study women with biopsy proven diagnosis of CIN 1/2/3 and cervical carcinoma were recruited as cases (n=45). Cervical tissue from hysterectomy specimen done for benign gynaecological indication with normal cervical cancer screening tests were taken as controls (n=15). Women were allocated equally into four groups on the basis of histopathology, i.e. control (Group1), cervical intraepithelial neoplasia 1 (CIN1; Group2), CIN 2/3(Group 3) and invasive cervical carcinoma (Group 4). KCNMA1 mRNA level estimation was done by real-time quantitative PCR (RT-qPCR) and protein expression was studied by immunohistochemistry using anti- KCNMA1 rabbit polyclonal antibody against Maxi Potassium channel alpha. Main Outcome Measures estimated were KCNMA1 protein expression and mRNA expression in four groups: control, CIN1, CIN 2/3 and cervical cancer.

Results The mean KCNMA1 mRNA levels in Groups 1, 2, 3, 4 was 0.2253(SD±0.5798), 271.40(SD±1050.21), 298.84(SD±1153.33) and 326.545(SD±861.97) respectively; (p=0.039). Protein expression was positive in 34% in CIN1, 80% in CIN2/3 and 100% in the cervical cancer group(p≤0.001). On subgroup analysis in cancer, KCNMA1 channel mRNA levels and protein expression was higher in tumour size >4 cm, poorly differentiated tumours, deep stromal invasion and non keratinising squamous cell carcinoma.

Conclusion KCNMA1 channel expression has promising role as a biomarker of cervical precancer and cancer.

2022-RA-457-ESGO · **PROGNOSTIC ROLE OF TGF-β SIGNALLING PATHWAY ALTERATIONS IN ENDOMETRIAL CANCERS – A PROSPECTIVE CLINICAL STUDY**

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Introduction/Background Transforming growth factor-beta (TGF-β) has a crucial role in inducing endometrial cancer invasion and metastasis. Studies assaying this signalling pathway in endometrial cancers have been conflicting. Most of these have utilised cancer cell lines. Our research was to assess the TGF-β signalling pathway alterations in fresh tumour tissue specimens, including all subsets of endometrial cancers employing quantitative RNA assay techniques.

Methodology A prospective observational study was done on patients who underwent surgical staging for endometrial cancer from November 2020 to March 2021 at a tertiary cancer centre. Tumour samples from hysterectomy specimens