Human papillomavirus in the etiology of oropharyngeal carcinoma

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Aim: The aim of this retrospective survey was to investigate the association of HPV status in patients with oropharyngeal cancer with tumour staging and other clinical features.

Introduction: Infection by human papillomavirus (HPV) stands for the most frequent viral carcinogenesis in the world. Over-expression of cell oncprotein p16 is routinely diagnosed by immunohistochemistry (IHC) as the surrogate marker of viral activity.

Methods: Records from the oropharyngeal cancer patients treated in the Department of Otorhinolaryngology-Head and Neck Surgery in Bratislava from January 2013 to December 2016 were retrospectively analysed. Patients were divided, according to IHC results on oncprotein p16, into p16 positive, considered HPV-positive, and p16 negative as HPV-negative. The incidence of oropharyngeal carcinoma, location, T and N staging, age, gender of patients was compared based on HPV status.

Results: From 129 oropharyngeal cancer patients with p16 examination were 52 (40%) considered as HPV positive. HPV positive group consisted of 45 (86.5%) men and 7 (13.5%) women. The primary tumour in HPV-positive patients originated from the palate tonsil and base of the tongue in 96% of cases. The peak of occurrence of HPV-associated carcinoma was found between 50 and 59 years of age. HPV positive tumours were diagnosed in early T stage (T1/2) in 52%. Both HPV positive and negative patients were predominantly diagnosed with advanced-stage cancer, 90.4% in HPV-positive and 87% in HPV-negative group.

Conclusion: Early T stage in HPV positive carcinomas was approved, as well as more advanced regional spreading and prevalence of men and non-smokers. Wide variations in numbers of diagnosed patients during years of study may be caused by relatively small size of the studied group. Survey is focusing at HPV status as the most important prognostic factor in oropharyngeal cancer and systematized introduction of HPV status examination as progressive approach to effective and targeted therapy.

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References

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The effects of cannabinoids in exemestane-resistant breast cancer cells

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Aim: Considering that the development of resistance is the main reason for endocrine treatment failure, our group decided to explore the ability of three cannabinoids, Δ9-tetrahydrocannabinol (THC), cannabidiol (CBD) and anandamide (AEA), to reverse resistance to exemestane. The THC and CBD are phytocannabinoids derived from the plant Cannabis sativa (marijuana) whereas AEA is an endocannabinoid. For that, it was used LTEDaro cells, a long-term estrogen deprived ER+ breast cancer cell line that mimics resistance to exemestane.¹ These cells were treated with exemestane in combination with two phytocannabinoids, CBD and THC, and the endocannabinoid AEA.

Introduction: Exemestane is one of the aromatase inhibitors (AI) used as first line treatment for estrogen-receptor positive breast cancer in post-menopausal women. Exemestane acts by inhibiting aromatase, the enzyme responsible for the conversion of androgens to estrogens² and also by promoting apoptosis of breast cancer cells.³ Nevertheless, despite its therapeutic success, this AI, after prolonged treatment, can induce acquired resistance, which causes tumor relapse. Therefore, it is important to find new strategies to overcome resistance in order to improve breast cancer treatment.

Methods: The presence of CB1 and CB2 in LTEDarO cells was confirmed by Western blot analysis and the effects of the combination of cannabinoids with exemestane were evaluated by MTT and LDH assays. Cell morphology was analyzed by Giemsa and Hoechst staining.

Results: Our results demonstrate that all the cannabinoids induce a decrease in viability of exemestane-resistant cells, in a dose- and time-dependent manner, without LDH release. These results indicate that the studied cannabinoids, mainly THC and AEA, revert the resistance to exemestane, probably by inducing apoptosis, as observed in Giemsa/Hoechst stain by the presence of typical morphological features of apoptosis.

Conclusion: This study highlights the efficacy of using cannabinoids as a potential adjuvant treatment to revert resistance to AIs.

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However, these cellular processes require high lipophilicity in chemical molecules. These group of compounds act as non-nucleoside reversed transcriptase inhibitors (NNRTIs) to predict their logP which is the most commonly used measure (QSPR) of 66 thiazolidin-4-one derivatives was examined in order to predict their logP. Numbers of descriptors which showed high correlation with each other were removed by MATLAB software. The model between structures and their LogP was built for both methods with performing Multiple Linear Regression (MLR) in Spss package.

Results: Statistical results and application of developed model to the test set demonstrates that the DFT model is reliable with good predictive accuracy, (R2cal = 0.90, R2cv = 0.88) The lack of significant difference between the original and modeled values of logP reveals the validity of the built model which was built with 2D and 3D descriptors. The coefficients of model are statistically significant.

Conclusion: QSPR models can be used to predict molecular properties such as LogP. That will be beneficial in drug design processes. In this research, MLR model was built in order to correlate structure of 66 compounds with their LogP. Molecules that were optimized by DFT method showed better correlation than HF method that indicates the accuracy of the built model with 2D and 3D descriptors.

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