Detection of High-risk Human Papillomaviruses Type Frequency and Viral Load in Latvian Patients with Laryngeal / Oropharyngeal Cancer

Lība Sokolovska [1], ***Maksims Čistjakovs*** [1], ***Alīna Sultanova*** [1], ***Andrejs Lifšics*** [2], ***Svetlana Čapenko*** [1], ***Modra Murovska*** [1]

Rīga Stradiņš University, Latvia
[1] *A. Kirhenšteins Institute of Microbiology and Virology*
[2] *Department of Surgery*

Introduction. Human papillomavirus (HPV) can be classified as high-risk (HR-HPV) and low-risk (LR-HPV) oncogenic types due to their association with cancer. HR-HPVs are considerable risk factors evaluating the risk of laryngeal or oropharyngeal cancer development. HPV 16, one of the HR-HPV types, has just recently been recognised as an emerging risk factor for oropharyngeal squamous cell carcinoma by the International Agency for Research on Cancer, and in the recent decades a lot of research has been done to determine the role of HPV in laryngeal cancer development. Results on HPV prevalence in laryngeal cancer are very diverse, ranging from 0 % to 79 %; therefore, more research is needed in this particular field of study.

Aim, Materials and Methods. The aim of this study was to compare the frequency and HR-HPV load in laryngeal and oropharyngeal cancer patients' post-surgical material DNA samples with that in mouth swabs' DNA samples of individuals without any pathology as a control.

Biopsy tissue samples from 27 patients (median age 61; IQR 56–68), ranging from 43 to 80) and 18 mouth swab samples from control group (median age 47; IQR 37–64) were used in this study. DNA was extracted using the phenol-chloroform method. To evaluate the quality of the extracted DNA polymerase chain reaction for β-globin was performed. Initial testing for high range of HPV types was done with polymerase chain reaction using consensus primers MY9/11. Commercial HPV High Risk Screen Real-TM Quant qPCR kit was used for quantitative detection of HR-HPV 12 types (16, 18, 31, 33, 35, 39, 45, 51, 52, 56, 58, and 59) in HPV positive DNA samples.

Results. Initial testing with consensus primers MY9/11 showed presence of HPV DNA in 5 of 27 (18.5 %) patients' tissue samples. However, results of quantitative PCR showed that 24 of 27 (88.8 %) tissue samples contained HR-HPV genomic sequences. Five samples which were previously positive on HPV genomic sequences with consensus primers showed clinically significant viral loads (> 3 log viral copies/10^5 cells) when in other samples the copy number was low. In contrast, none of the DNA samples obtained from the mouth swabs of control group individuals contained HR-HPV genomic sequences.

Conclusions. Presence of HR-HPV genomic sequences and high viral loads only in laryngeal and oropharyngeal cancer patients' DNA samples indicate on important role of these virus types in development of cancer. Several methods should be applied for more precise HR-HPV genomic sequences detection.