

Laryngeal cancers belong to a large and heterogeneous group of tumors localized in the region of head and neck. Annually, the incidence of new cases concerns about 3% of Polish population. This tumor type reveals a striking male predominance (up to 8:1). This disease is associated with the occurrence of physical ailments that hinder vital functions such as breathing, eating and speech. Larynx cancer tumors are often accompanied by cervical lymph node metastases. They constitute the largest mechanism of tumor spreading in head and neck - lymph nodes are usually the first place where metastases appear. This problem concerns nearly 50% of patients at the time of diagnosis and is associated with a very unfavorable prognosis for these patients. Distant metastases are rarely seen during the course of disease. The process of metastasis formation is complex, multi-stage, involving a number of genes engaged in different processes, such as: apoptosis, adhesion, invasion, migration, neoangiogenesis, and so on. Unfortunately, none of the currently available imaging techniques is able to confirm clearly the presence of metastases in small, non-enlarged lymph nodes. Despite improvements in diagnostics and therapeutics there is still no obvious marker/s indicating an increased risk of lymph node metastasis development in laryngeal cancers.

In recent years, the use of high throughput whole genome microarray techniques has allowed to obtain a number of novel information related to genetic alterations found in different types of tumors. For the purposes of this project, data obtained from the expression microarray study performed in larynx cancer cell lines and normal controls were used. This array encompassed nearly 55 thousand points that correspond to respective sequences or genes in human genome. We selected 24 genes whose expression differed between tumors metastasizing to lymph nodes and those which did not reveal metastases. None of these genes have been up to now associated with the process of lymph nodes metastasis formation in carcinomas of the larynx. In this project we plan to check whether the differences in the expression of these genes are also found in the primary laryngeal samples. For 10 most interesting genes the presence and expression of encoded proteins will also be verified. The expression of proteins will be analyzed on tissue microarrays prepared from non-metastasizing tumors of the larynx as well as from metastasizing tumors and their corresponding lymph node metastasis.

We expect that the planned studies will confirm that the selected genes/proteins may play a role in the development of lymph node metastases in larynx cancer. This will not only expand the knowledge of this process but also become a starting point for further research on the mechanism of genes aberrant expression and for functional studies. This approach provides an opportunity to identify marker/s of lymph node metastasis formation.