Popular-scientific summary of the project

Cancer can be described as a disease of the genes. In the last years, thanks to the introduction of novel, high throughput techniques of DNA sequencing (the analysis of the sequence of nucleotides that build DNA; the sequence is the carrier of genetic information) called next generation sequencing, fast analysis of large fragment of the genome became available. Using the new technique in the last decades of intensive research conducted in many specialized laboratories multiple genes have been identified that if mutated contribute to the transformation of a normal cell to a malignant one. Doubtless, this approach has widely contributed the understanding of the complexity of genetic alterations in tumor cells.

Recently, attention is turned to regions of the genome that do not contain genes at all, such regions are also called gene deserts. It has been however shown that these regions harbor multiple regulatory sequences that despite the large distance separating them from genes still can regulate their functioning. Growing evidence suggest that mutations within such regulatory sequences can disturb proper functionality of genes and contribute to cancer development.

As regulatory sequences in laryngeal caner, one of the most common cancer type in the European Union, have not been analyzed yet, in this project we plan to use several advanced techniques one hand to identify mutations in such sequences and on the other to describe their effect on the neighboring genes. We will use the next generation sequencing to analyze regulatory sequences (mutation screen), the microarray based expression analysis of genes in the genome (expression analysis of genes neighboring regulatory sequences) and combine both analyses using bioinformatic tools. We assume that these analyses will allow the identification of multiple mutations in the regulatory sequences that can be of particular importance for the development of laryngeal tumors. We will assess the importance of the identified changes taking into account their frequency and by modeling their influence on the neighboring genes.

We think that this approach will result in better understanding of the genetic basis of laryngeal tumors that may help in early detection of the disease and the introduction of more effective therapies in the future.