Head and neck squamous carcinoma (HNSCC) is the **sixth most prevalent cancer worldwide**, representing over half million of the new cases every year. Due to high genetic and histologic diversity of head and neck cancers, their molecular pathogenesis is based on complex process including disorders driven not only by accumulation of genetic alterations, but also changes in epigenetic landscape. The epigenetic variations in HNSCC include DNA methylation, histone modifications, non-coding RNA activity and **poorly described RNA methylation.** Some of the epigenetic alterations promote cancer formation and progression by controlling the expression machinery. Consequently, those modifications can be used **as biomarkers for clinical detection and surveillance of cancer** and **will reveal new therapeutic opportunities for cancer patients**.

Methylation of the nitrogen sixth of adenosine (m^6A) in RNA play a key role **in regulating RNA transcription, processing event, splicing, RNA stabilities and translation.** RNA methylation-related effects are results of cooperation of multiprotein complexes divided into ‘writers’- enzymes which set methylation marks, ‘erasers’- enzymes that remove them, and ‘readers’- proteins which recognize chemical modifications of RNA. Consequently, **there is growing evidence that variations in RNA methylation process may lead to tumor growth and progression of cancer, contribute to invasion, migration of cancer cells** and can be involved in **chemo- and radioresistance.**

The main aim of this project is **determination of RNA methylation profile and characterization of its function in HNSCC pathogenesis.** Authors of the project predict that disturbances in RNA methylation may lead to tumor growth and progression of HNSCC. To verify this hypothesis, we propose three highly important and challenging aims:

1. To determine RNA methylation quantitative profile in head and neck squamous cell carcinoma patients and *in vitro* model.

2. To identify the role of RNA methylation process in HNSCC pathogenesis by down-regulation of key components involved in this process.

3. To deliver new knowledge of RNA methylation in cancer development.

This study will be performed using tumor tissue and healthy adjacent epithelial tissues collected from postoperative margin of the same patient during surgical intervention in The Greater Poland Cancer Centre and *in vitro* model (established Head and Neck Cancer Cell Lines Panel).