Abstract

Molecular biology is one of the fastest developing technology areas. **Next Generation Sequencing** (NGS) and data science methods allow wide investigation of changes occurring on DNA and RNA level. They are revolutionising cancer research and are helping in understanding the disease allowing researchers to find novel ways of treatment and diagnosis. Ovarian cancer (OC) causes over 200 000 deaths every year. Its most common subtype is **High-Grade Serous Ovarian Cancer** (HGSOC). The disease is difficult to diagnose at the early stage, highly heterogenous, and despite a good first-line treatment response, most patients will develop drug resistance. Understanding the molecular dysregulation of the disease could help us find precise drug targets for effective and longstanding treatment. Transcriptome analysis allows for studying gene expression of protein-coding RNAs (mRNA) and noncoding RNAs (ncRNAs). **Combining the information of coding and noncoding RNAs is important in understanding the posttranscriptional mechanism that regulates cancer development.**

This work aimed to perform a comprehensive analysis of tissue-derived RNA profiles. This study included 33 primary HGSOC tumour tissues and 33 samples of ovary tissues removed during non-oncological procedures. The analysis focused on the crosstalk between competing endogenous RNAs (ceRNAs), including mRNA, long noncoding RNAs (lncRNAs) and microRNAs (miRNAs) and their interaction with transcription factors (TFs) in HGSOC patients. The key identified genes were used as a basis for the drug repurposing approach to predict drug candidates for HGSOC treatment. **PI-103 and ZSTK474, which are phosphoinositide 3-kinase (PI3K) pathway inhibitors, were identified as drug candidates.** The PI3K pathway, which is involved in developing drug resistance in OC, is closely associated with genes identified in the ceRNA network.

The research presented in this paper may contribute to the development of new treatment options for patients with HGSOC.