Human papillomavirus (HPV) are non-enveloped small DNA viruses with both high- and low-oncogenic risk subtypes. HPV infections are widespread among human population. It is the most common sexually transmitted infection. HPVs are a group of more than 200 viral strains of which at least 20 subtypes have been shown to infect the genital tract and were classified as carcinogenic. HPV16 and 18 genotypes are among the most carcinogenic type, classified as high risk HR-HPV and cause 96% of cervical cancers. Both host- and virus-related factors may affect the course of the HPV infection. The results suggested that HR-HPV genotypes might have been detected in ovarian cancer. In heterogenous group of ovarian tumor, serous ovarian carcinoma is most common and is divided into high-grade (HGSOC) and low-grade (LGSOC). It was found that majority of high-grade serous ovarian cancers originate from the fallopian tube cells. The frequency of HPV detection in ovarian cancer depends mainly on geographical location. Human cytomegalovirus (CMV) infections are widespread among human population. In Poland, specific anti-CMV antibodies are detected in 70-76% of the population. It is a major cause of multiorgan disease in immunocompromised patients. CMV establishes a life-long persistence in the host by way of a latent infection. CMV can cause severe disease in immunocompromised patients *via* reactivation of latent infection or *via* acquisition of primary CMV infection. There is no data available on the role of CMV reactivation in the development of the ovarian cancer.

Our preliminary results revealed that the presence of HR-HPVs and CMV in EOC samples is detected in the epithelial ovarian cancer (EOC) cases. We hypothesize that HPV infection might be localized in fallopian tube and associated with development of HGSOC. In addition, polymorphisms in oncogenes seem to contribute to virulence and viral pathogenesis. CMV can be reactivated and may affect cancer disease. Its potential role in cancer seems to be oncomodulatory, which imply that expression of CMV gene products may promote tumour growth. CMV and HPV infections can be potential risks for EOC development.

The general aim of the Project is to assess the molecular mechanisms that determine the development of the epithelial ovarian cancer caused by HPV infection and to determine the role of CMV in this process. The Project will identify viral and host factors involved in HPV infection and development of ovarian cancer. We will investigate the prevalence and genotyping of viruses, determine and understand risk factors, as well as processes and mechanisms at interface pathogen – host. We will try to determine the role of CMV and viral co-infection in the development of ovarian cancer. The results of these studies will provide information about the prevalence, genotype distribution, antigenic variation of the viral structures, potential correlations between viral genotype and pathogenicity, as well as intracellular signaling proteins and transcription factors that allow the induction of antiviral immunity or carcinogenic potential.

Genital HPV infections are sexually transmitted infections of increasing public health. The public health importance of HPV infection is attributed to its oncogenic potential and high frequency in human population. The studies that define the viral and the host factors associated with protection against chronic HPV infection and CMV reactivation on the ovarian cancer development are needed. Since most women infected are asymptomatic even during several years, comparing the virological and immunological markers of women with ovarian cancer caused by the HPV infection to those with disease from another reason is a high-priority area for research. The Project results may provide new insight into the pathogenesis of ovarian cancer, new strategies for the use of antiviral therapy in oncology patients, and development of interventions to help address this important public health problem.