Abstract
The current condition of epidemiological and genetic knowledge of the cervical cancer (CC), as well as the development of probabilistic algorithms, allows the approximation of holistic diagnosis of the CC. It is necessary to consider the interactions between the genome of the host, the viral genomes and the clinical factors of epidemiological risk. This review is divided into four sections: 1) the holistic tools for multivariate model of CC are described; 2) the genetic markers associated with susceptibility to malignant progression of cervical squamous intraepithelial lesions to CC development are explored; 3) the Human Papillomavirus (HPV) as the essential element for CC development is exposed; finally, 4) the clinical factors of risk associated with CC development are considered, such as smoking, sexual habits and risky sexual behavior, sexually transmitted infections and multiparity.

Keywords
Cervical cancer, multivariate model, algorithm, genetic markers, holistic diagnosis.