

## Abstrakt

Human papillomaviruses (HPV) are small non-enveloped DNA viruses that infect cutaneous and mucosal stratified epithelia. High-risk HPV types (HR-HPV) encode oncoproteins, E6 and E7, that can induce carcinogenesis. Persistent infections with HR-HPV types are responsible for nearly 100 % cases of cervical carcinoma in women and also for significant portion of other anogenital and head and neck cancers in men and women. HPV16 is the most frequently detected type in all HPV-positive tumors. HPV types are classified into intratype variants – lineages and sub-lineages. HPV16 is separated into four phylogenetic lineages (A, B, C, D) and sixteen sub-lineages (A1–4, B1–4, C1–4, D1–4). HPV16 phylogenetic variants differ in geographical distribution and risk of developing cervical precancerous lesion and invasive carcinoma. In addition, individual single nucleotide polymorphisms in HPV16 genome can impact disease development and progression.

**Key words:** papillomavirus, genome, variants, cancer