Evidence supporting the association of polyomavirus BK genome with prostate cancer.

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Abstract

Prostate cancer (PCA) is the most frequent cancer in men. Exposure to infectious agents has been reported to have a putative role in tumorigenesis. Among the infectious agents, convincing evidence has been accumulated about the human polyomavirus BK (BKV). Tissue fresh specimens, serum, and urine samples were collected from 124 consecutive patients, 56 with PCA and 68 with benign prostatic hyperplasia (BPH). Quantitative PCR assays were used to assess the presence of BKV and JC virus (JCV) genomes. BKV-positive tissue specimens were found in 32.1 and 22.1 % of PCA and BPH patients, respectively; in PCA group the number of positive BKV specimens/patients was significantly higher than in BPH group (3.06 vs. 1.73, p = 0.02). JCV genome was found in the biopsies collected from 28.1 and 24.2 % of PCA and BPH patients, respectively, with no significant difference in the rate of JCV specimens/patients between PCA and BPH groups. Our results support the putative causal association between BKV genome and PCA. Further studies are required to demonstrate the direct pathogenetic role of BKV in the PCA occurrence and progression in order to clear the tempting way of vaccine prophylaxis.

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