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A study of polyomavirus BK (BKV) variants from renal-transplant recipients

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Following the usually asymptomatic infection with polyomavirus BK (BKV), the virus remains latent in various organs including kidneys. Immunodeficiency may lead to viral reactivations—sometimes accompanied by disease. BKV-allograft nephropathy (BKVAN) is recognized as an important cause of allograft failure in renal-transplant recipients. The BKV genome contains a hypervariable non-coding control region (NCCR). DNA sequence variation in this region may influence on viral replication and enhance the pathogenic potential of BKV.

Using a real-time PCR assay we screened for BKV in urine-, plasma- and kidney samples from renal-transplant recipients with elevated S-creatinine. Furthermore, we sequenced the NCCR of viral strains from 7 and 4 patients with and without BKVAN, respectively. In urine from the majority of patients only BKV(WWT) NCCR was identified. However, one patient harboured at least 10 novel variants. Two patients demonstrated a variant almost identical to previously reported isolates from renal transplant recipients in USA and China. The majority of blood samples contained only low amounts of BKV DNA. In those successfully sequenced BKV(WWT) NCCR was detected. The most rearranged NCCR-variants were detected in kidney biopsies from patients with BKVAN.

We are currently studying the replication potential of new BKV NCCR variants using a cassette strategy combining NCCRs from clinical samples with a constant genomic backbone.