Whole Genome Sequencing of Human BK Polyomavirus Using Next-Generation Sequencing

Poster Number : 98

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Introduction

In immunocompromised patients, human BK polyomavirus (BKPyV) has been linked to two major complications in transplant recipients, polyomavirus associated nephropathy / polyomavirus associated haemorrhagic cystitis Genetic heterogeneity. The implications of BKPyV strains or viral polymorphisms on the evolution and intensity of viral physiopathology are poorly described.

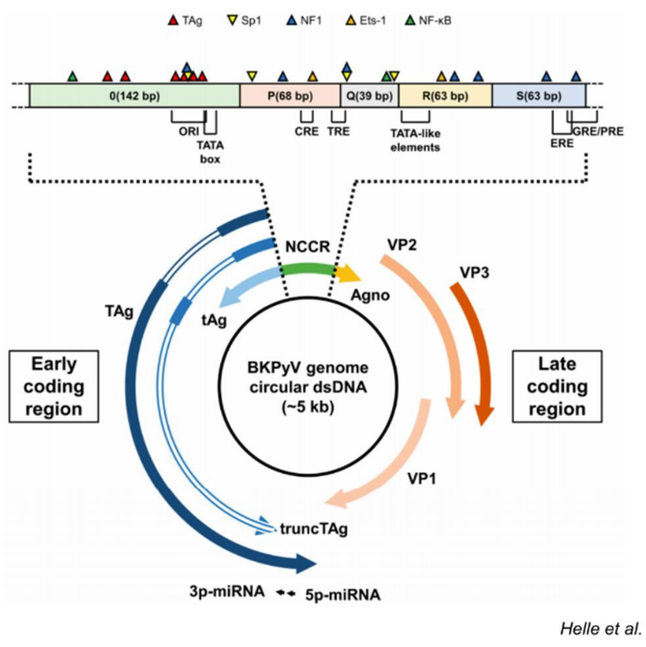

Fig 2. Whole-genome sequence of human BK polyomavirus (Helle et al. Viruses 2017)

Methods

The BKPyV whole genome (WG) was amplified using two set of primers and the libraries were generated using the DeepChek® NGS Library preparation V2. The resulting libraries were sequenced using the iSeq100 and the run was performed generating 2×151bp read length data. A consensus sequence of 20% was generated using the DeepChek® - WG BKv software.

Results

The median coverage per sample for the WGS of BKPyV was 23’000 reads. High analytical reproducibility and repeatability were evidenced by Percent Agreement being 100%. Duplicated samples in two different NGS runs were 100% homologous. Bkv Subtype Ia, IVc-2, Ib-2 and Ib-2 were found and 100% of concordance with Sanger sequencing was observed. NGS detected all the mutations found by Sanger sequencing and identified additional mutation.

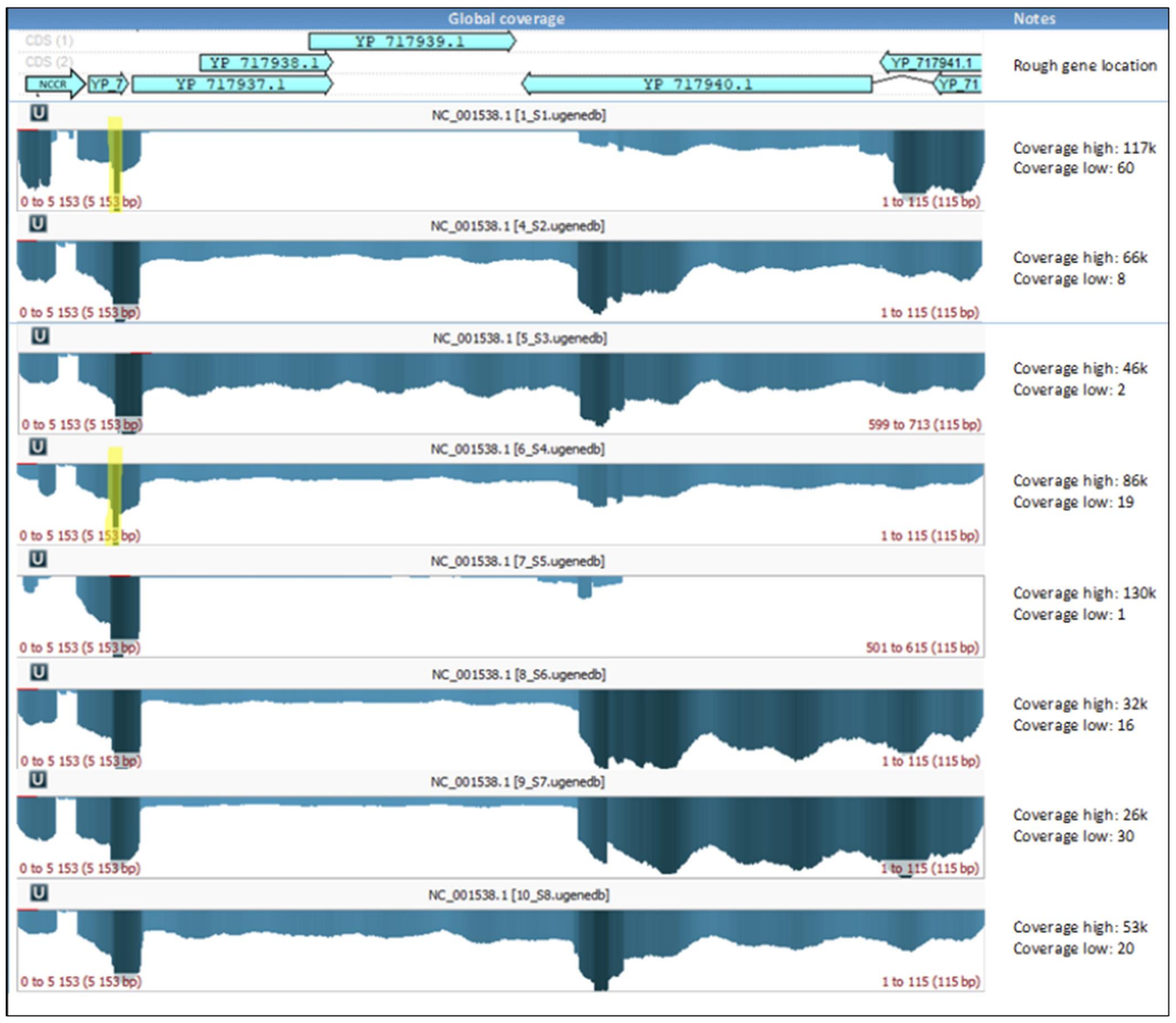

Fig 2. NGS coverage of the human BK polyomavirus (Whole-genome sequencing)

Table 1. Sanger versus NGS

Sample	Sanger Subtype	NGS Subtype
1_S1	Ia	Ia
4_S2	IVc-2	IVc-2
5_S3	IVc-2	IVc-2
6_S4	Ib-2	Ib-2
7_S5	Ib-2	Ib-2
8_S6	Ib-2	Ib-2
9_S7	Ib-1	Ib-1
10_S8	Ib-1	Ib-1

Discussion

This study is the first evaluation of the WG BKPyV using the iSeq100 combined with an easy software. The NGS should occupy a major place in virus surveillance and clinical care, thanks to its decreasing costs (due to COVID-19 pandemic) and ability to reveal resistant variants and study their impact; especially on detection of potential new clinically relevant mutations in the BKPyV genome.

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