

Chapter 6

Summary and Conclusion

- ❖ The present study mainly comprised of two groups. One group containing individuals with healthy immune system and the other one containing individuals with suppressed immune system.
- ❖ For detection, NCCR region of the viral genome was amplified using specific primers. An incidence rate of JCPyV in the immunocompromised group of people was higher compared to the group consisting of non-immunocompromised individuals.
- ❖ Prevalence of JCPyV in tribes of this region was also studied. The incidence rate of JCPyV was lower in tribes of this region compared to the tribal population from other parts of the world.
- ❖ Frequency of JCPyV detection was found to be higher in males compared to the females in the tribal population of this region which is in accordance with other studies.
- ❖ Viral DNA load was quantified by real time PCR using SYBR green dye. Viral load was comparatively higher in this region than most of the studies done in other regions.
- ❖ A wide range of viral load was found in the samples. The mean viral load in urine was higher compared to the mean viral load present in blood.
- ❖ Nutritional deficiency might be the reason for immunodeficient conditions which in turn enhances susceptibility towards infections and might be reason for the presence of high viral load in healthy individuals of this region.
- ❖ Partial NCCR, VP1 and T-antigen sequences were deposited in GenBank for accession number.
- ❖ All the endemic NCCR sequences have an archetype-type of NCCR architecture with few mutations and deletions in the sequence.
- ❖ The NCCR sequences of isolates from Oraon and Munda tribes and the isolates from pregnant women group were almost identical. Upon comparison they were found to be mostly similar to the Tibetan strain LH3 type NCCR sequence.
- ❖ The NCCR architecture from Rabha isolates was almost identical to the archetype strain CY (98% similarity).

- ❖ A 10-nucleotide deletion in Block B and a two-nucleotide deletion in Block F were observed in some of the isolates of this region.
- ❖ The di-nucleotide deletion was found within the p53 binding site of endemic JCPyV strains from the Oraon/Munda group as well as in the NCCR sequences of pregnant women but the deletion was not present in NCCR sequences of Rabha tribal group.
- ❖ VP1 sequence and T-antigen comparison revealed that the endemic JCPyV isolates from the Rabha tribes have maximum similarity with the Type 1B which is mostly prevalent in Europe. And the isolates from Oraon and Munda tribes were almost identical to the Type 2D, the Indian subtype mostly prevalent in Asians and South Asians.