Chapter – 7
Summary and Conclusion
7.1. Summary and Conclusion

7.1.1. The purpose of the study was to carry out the epidemiological surveillance in and around Vijayapura district and to find out the prevalence of CHIK disease, genotype responsible for, mutations present in E1 gene and their effect on protein structure, infectivity, virulence and host adaptability to *Aedes albopictus* mosquitoes.

7.1.2. A total of 500 blood samples from fever and arthralgia of 5 to 8 days were collected and tested for CHIK IgM antibodies by SD CHIK IgM ELISA kit.

7.1.3. Out of 500 samples 33 were positive for CHIK IgM antibodies.

7.1.4. 33 Sero-positive samples were selected for molecular confirmation and RTPCR was performed by using Amplisure ® CHIK RTPCR kit.

7.1.5. 31 out of 33 samples were positive for CHIK RNA.

7.1.6. The prevalence rate of CHIK was 6.2% in and around the Vijayapura district.

7.1.7. Statistical analysis concluded that there was no significant difference between suspected and confirmed cases with respect to year, sex, age and taluk.

7.1.8. E1 partial gene sequencing was performed for 9 RTPCR positive samples.

7.1.9. Phylogenetic analysis study revealed that the current strains belongs to ECSA genotype and which may evolved from Re-union island strains.
7.1.10. Three amino acid mutations E1K211E, E1M269V and E1D284E were consistently present and E1A226V mutation was absent in current strains.

7.1.11. The observed mutations didn’t affect the CHIK viral protein structure.

7.1.12. From the findings, we conclude that the current strains circulating in Vijayapura district may be less infective, less virulent and less adaptable to *Aedes albopictus* mosquitoes than Re-union island strains.
7.2. Limitations of the Study:

7.2.1. RTPCR was only performed to Sero-positive cases, which was the limitation of the study. CHIK IgM antibodies starts appearing 5 days after onset of illness and CHIK RNA can be detected till 8 days after onset of illness. So samples were collected between 5 to 8 days after onset of illness. So that samples should be positive for both CHIK IgM antibodies and CHIK RNA.

7.2.2. Genetic characterization was carried out only for 9 samples, due to low viral load we couldn’t get sequences from remaining samples.
7.3. Future Directions:

7.3.1. Future research is required to find out the mutations in whole genome.

7.3.2. Future studies to be carried out to check the effect of these mutations on viral characteristics.

7.3.3. Future research is required to find out the reasons for the mysterious behaviour of dramatic outbreaks, periods of prolonged absence, factors triggering outbreaks and replacement of Asian strains by ECSA strains.