Chapter – 1

Introduction
Health is defined as a state of complete physical, mental and social well-being and not merely the absence of disease. The Disease is a state of pathological disruption in structure and functions of human body organs. Diseases can be classified into Infectious and non-infectious diseases. Infectious diseases are caused by infection of Microorganisms. World Health Organisation (WHO) reported, of all infectious diseases, more than 17% of diseases are of Vectorborne diseases (VBD) and results in 1 million deaths annually. VBD are diseases that are transmitted to humans by the bite of living organisms called vectors. These vectors transmit infections between humans or from animals to humans. Blood sucking insects like mosquitoes, ticks, flies and fleas serve as vectors. Infected mosquitoes can cause Malaria, Dengue, Chikungunya (CHIK), Japanese encephalitis, Rift valley fever, Yellow fever and zika diseases. VBD are also called as Arthropod Born (ARBO) Viral diseases.

Among VBD, CHIKF was the neglected disease in Asia and other continents till 2005-06 due to sharing similar clinical manifestations of dengue and limited diagnostic facility. Vijayapura district, Karnataka state reported 80,000 clinically suspected cases annually during 2006-2008 outbreak and still a statistically significant number of cases are reported in current years. This study was conducted to find out the prevalence of CHIK in and around Vijayapura district. Clinically suspected CHIK cases should be confirmed by laboratory diagnosis. CHIK IgM ELISA test is the most widely used diagnostic tool for the diagnosis. False positive serology results are reported due to antigenic cross-reactivity of CHIK with other Alphavirus. (semliki forest antigen complex) To overcome this limitation molecular
confirmation was carried out. Real-time polymerase chain reaction (RTPCR) is the gold standard test for the diagnosis of CHIKF.

Three genotypes were observed in CHIKV, namely East Central South African (ECSA), West African and Asian. The nomenclature of genotype is based on its first isolation in the respective continent. Previously (before 2000) the genotypes were reported only from respective continent viz ECSA in east central and South Africa, West African in West Africa and Asian in Asia. Transcontinental movement of genotypes has been observed in last decade. ECSA genotype was responsible for 2005-06 outbreak in India and Indian ocean and currently Asian genotype is causing outbreaks in Europe and America. So the study was conducted to find out the genotype prevalent in the area.

Phylogenetic studies are important to trace the origin of the virus, follow the pattern of disease spreading, genetic relatedness of current strains with previous isolates as well as to discriminate between the strains among different geographical area. Hence we want to correlate strains from our study within themselves and between previously reported strains.

It was documented that a single point mutation in E1 gene E1A226V alters host range, host adaptability, virulence and infectivity of CHIKV and results in the large spread of disease and severe clinical manifestations. The observed mutations may alter the protein structure. So the study was conducted to find out the mutations in E1 gene to correlate infectivity, virulence and clinical manifestations.