

LIST OF FIGURES

FIGURE NO.	LEGEND	PAGE NO.
2.1	Chikungunya genome cassette (Galán-Huerta et al., 2015)	11
3.1	Genome of dengue virus (Vasilakis et al., 2011)	34
5.1	District map of Kerala showing area of sample collection from suspected cases of Chikungunya infection	79
5.2	Agarose gel image showing clinical samples positive for Chikungunya; amplification of 305bp in E2 gene of CHIKV on 1% agarose gel.	80
5.3	Clinical Symptoms of patients infected with Chikungunya	81
5.4	Age-wise distribution of suspected cases of Chikungunya in 2008 and 2009	82
5.5	Age-wise distribution of RT-PCR positive cases of Chikungunya in 2008 and 2009	83
5.6	RT-PCR positivity and duration of fever	84
5.7	Application of WHO 2009 dengue case classification on study subjects	85
5.8	Distribution of dengue positivity based on various serological assays	85
5.9	Profile of clinical symptoms in Dengue confirmed cases	86
5.10	Agarose gel electrophoresis showing standardized RT-PCR with dengue stock virus and the clinical sample	88
5.11	Image showing amplified DNA of CprM gene of dengue (511bp) on 1% Agarose gel	88
5.12	Standardization of CHIKV-DENV multiplex RT-PCR	91
5.13	Clinical samples showing dengue positives by multiplex RT-PCR for CHIKV and DENV	91
5.14	Clinical samples showing chikungunya positive by multiplex RT-PCR	92
5.15	Phylogenetic tree of CHIKV study isolates and 360 sequences derived from GenBank database generated using a maximum likelihood on the partial sequence of E2 gene sequence (305bp). Bootstrap analysis was performed	97

	with 1000 replicates to determine confidence values on the clades within trees. The S27 (AF369024) prototype strain and O'nyong nyong (out group) were used in the tree	
5.16	Distribution of CHIKV strains Clade I and Clade III based on phylogenetic analysis in Kerala and Chennai	98
5.17	Alignment of E2 nucleotide sequences of CHIKV along with Tanzania 1952 sequence and consensus sequences from GenBank database. Dots indicate a match with reference sequence. Unique nucleotide substitution highlighted with circle	99
5.18	Phylogenetic tree was generated using CHIKV isolates and with the consensus sequences of different years isolate derived from GenBank database generated using a maximum likelihood on the partial sequence of E2 gene sequence (305bp). Bootstrap analysis was performed with 1000 replicates	100
5.19	Graph represents quality estimation of E2 protien of CHIKV using SLAC method. X-axis represents codon positions; Y-axis represents normalized dN-dS value obtained by SLAC method	100
5.20	A. Complete E2 protein structure prediction using S27 prototype CHIKV strain boxed with sequenced region. Figure B. Sequenced region (transmembrane domain) of E2 gene from our study sample. Figure C. Super imposed image of sequenced region which indicates amino acid substituted region.	102
5.21	Cytokines (A-TNF- α , B-IL-6, C-IL8, D-IFN- γ , E-IL-10) of samples were determined (pg/ml) in CHIKV RT-PCR positive and CHIKV RT-PCR Negative sample	110
5.22	Cytokines (A-TNF- α , B-IL-6, C-IL8, D-IFN- γ , E-IL-10) of samples were determined (pg/ml) in DENV RT-PCR positive and DENV RT-PCR Negative sample	111
5.23	Cytokines (A-TNF- α , B-IL-6, C-IL8, D-IFN- γ , E-IL-10)	112

	of samples were determined (pg/ml) in Dengue Acute and Convalescent samples	
5.24	A-TNF- α , B-IL-6, C-IL8, D-IFN- γ , E-IL-10) of samples were determined (pg/ml in different dengue groups based on WHO2009 classification – Dengue fever, Dengue Warning Signs and Severe Dengue	113
5.25	Amplification curve obtained for DENV-1 positive samples and positive control	114
5.26	Amplification curve obtained for DENV-2 positive sample and positive control	114