Original Research Article

<https://doi.org/10.20546/ijcmas.2021.1002.342>

Analysis of Mosquito Vector and Disease Spread through them in Kannur District, Kerala, India

Seema Gupta*, Bhramacharini Sheela, K. Smera, R. Niveditha, S. Soparnika,
P. K. Kartika, A. Ashwariya, S. Arundhati, K. Abhiram and P. Rithika

Amrita Vidyalayam, Punnol, Thalasshery, Kerala, India

**Corresponding author*

A B S T R A C T

Keywords

Mosquito, Tick,
Lice, Housefly,
Sandfly

Article Info

Accepted:
22 January 2021
Available Online:
10 February 2021

Mosquito born diseases are most devastating among the people around the world. It has been decades where medical professionals and researchers are trying to find a remedy to stop the pathogenicity and mortality due to these vector born diseases (VBD). In the present survey and study from Thalassery region of Kannur district of Kerala reveals three types of diseases spread by vector mosquito. The study also suggests the most infected regions with patients reporting with these diseases. Also, emphasis is to trace the seasons of infection along with the age group and gender being affected more. Along with this the varieties of mosquito available at various regions are trapped and morphologically analyzed to understand the diversity of these vectors.

Introduction

It has been a century wherein humans are trying to unfold the mystery of vector born diseases. Among various carriers of disease causing pathogens, insects plays major role. Among various diseases caused in humans, 17 % infections are through vectors (Ben Nelson S, *et al.*, 2017). Insects including mosquito, tick, lice, housefly, sandfly, etc. are some of the major vectors to spread fatal diseases in humans and other mammals. As vector born diseases is a major problem around world,

World health organisation (WHO) brought this issue into focus during world health day of 2014 (Geneva- World Health Organization, 2014). Among the present insect pest, mosquitoes spread many diseases such as dengue, malaria, yellow fever, lymphatic filariasis, chikungunya, etc., in people of India and other parts of world. They are one of the most dangerous vector as they have very adaptable lifecycle which enables tolerance for insecticides. Due to failure in controlling these dreadful vector and recurrence of fatal diseases upto million people die including

more of children (Caraballo *et al.*, 2014). At certain point Chikungunya was nearly disappeared from India, but it re-emerged from 2005 (Mourya *et al.*, 2001). Thus, the present study enables us to screen the mosquito species and disease caused by them in Kannur district of Kerala. As the climate and more of water bodies provides a favourable condition for these vectors to grow and transmit the disease causing pathogen in humans.

Materials and methods

Site of survey

The study through survey is conducted at various regions of Thalassery, Kannur, Kerala. This region lies 11°45'2.24"N 75°29'13.28"E, with total area of 23.96 km² and nearly 92,558 of population count. Thalassery lies 11m above sea level and has significant rainfall most months. The average annual temperature in Thalassery is 27.3 °C | 81.2 °F. The annual rainfall is 3512 mm.

Data collection

The information regarding mosquito born diseases was obtained by survey from various governmental and private hospitals at Thalassery. Cumulative data for 4 years which includes 2017 to 2020 records is considered and analyzed to understand the pathogenicity and types of vectors involved.

Result and Discussion

Mosquito surveillance

Samples of mosquito is collected and studies from various regions of Thalassery including Balathil, Edelpedika, Nambyapedika, Peringathur and Vadiyapedika. Collection is done during evening hours by trapping the insect through mosquito net and then was placed in an air tight container for few hours.

The dead insect is used to spread and photography through mobile (VivoV19, Vivo V9, I Phone 8 and Redmi note 6 pro) for documenting and further study of the same. The samples of mosquito is identified online through publications and research articles by morphological analysis (Pictorial keys for the identification of mosquitoes, Diptera: Culicidae associated with Dengue Virus Transmission, 2004; keys to the medically important mosquito species). The different types of mosquito traced in the localities are *Culex pipiens*, *Aedes aegypti*, *Culex quinquefasciatus* and *Anopheles stephensi*. Among which mosquitoes from *Culex* family were observed more in population (Figure 1).

Pathogenicity of mosquito born diseases

The data for mosquito born diseases are collected from year 2017 till 2020 through survey from various regions including governmental and non-governmental sources.

According to this pathogenicity of various vector borne diseases specifically involving mosquito are studied for most occurring disease along with age and gender based ratio of infection. Malignant tertian malaria (MT Malaria) caused by *P. falciparum* and Benign tertian malaria (BT Malaria) caused by *P. vivax* are the two prominent types of malaria identified in the individuals of Thalassery region.

Similar work has been done by P.G Shute in year 1946 on latency and long-term relapses in Benign Tertian malaria. Along with these two types of malaria, people are also detected with Dengue in large scale. The data in the table 1 and graph 1 reflects the pathogenicity of Flavivirus causing dengue more drastic than patients with malaria. Gender and age wise records states more infection diagnosed in female than in male patients.

Table.1 Data for various types of diseases caused by mosquito vector during year 2017-2020

Sr.no.	Type of Infection	Year per infected individual			
		2017	2018	2019	2020
1.	MT Malaria (<i>P.falciparum</i>)	44	58	61	59
2.	BT Malaria (<i>P.vivax</i>)	36	21	27	23
3.	Dengue	357	213	425	310
4.	Total patients	437	323	545	429

Table.2 Comparative data for various vector born diseases in an individual with age group and gender specification

Sr. No.	Study area		Yearly data for mosquito vector born pathogenicity											
			MT Malaria (<i>P.falciparum</i>)				BT Malaria (<i>P.vivax</i>)				Dengue (Flavivirus)			
			2017	2018	2019	2020	2017	2018	2019	2020	2017	2018	2019	2020
1.	Infected individuals		44	58	61	59	36	21	27	23	357	213	425	310
2.	Gender	Male	21	26	25	31	19	08	11	16	113	98	215	84
		Female	23	32	36	28	17	13	16	07	244	115	210	226
3.	Age group	Children	04	06	13	10	05	09	04	05	23	19	27	19
		Adults	22	33	39	32	19	08	15	10	293	158	330	179
		Aged	18	19	09	17	12	04	08	08	41	36	68	112

Graph.1 Representation of data for disease caused due to mosquito vector during 2017-2020

Fig.1 Different types of mosquito vectors traced from regions of Thalassery.

Culex pipiens

Aedes aegypti

Culex quinquefasciatus

Anopheles stephensi

Also, malaria and dengue infections are more in adults followed by old aged people and children. M. Emmanuel Bhaskar in 2010 through his studies on dengue haemorrhagic fever among adults from Chennai, south India have also observed that adults are more infected than children and old aged people. According to the reporting date of the patients, it is evident that pathogenicity of malarial parasite is more during march to may month of the year (Table 2). Whereas, Dengu is observed more into individuals during January – February month and later from June to November month. This may be due to the life cycle of the vector species of mosquito carrying these pathogens. Among the various

area of study from Thalassery, few region such as Panniyanoor, Poiloor, Ponniyam, Champad and Panoor shows more number of patients reporting with dengue and malaria and least number of patients are reported from Mahe.

Acknowledgement

The authors of this research paper extends gratitude towards Mata Amritanandamayi for her support and blessings for this research during this pandemic period. Also first author is thankful to Dr. Babu Ramachandran (MD Medicine) chairman of Tely hospital, Thalassery, for providing enormous help and

guidance for yearly data collection of patients with mosquito born diseases. First author also thanks and appreciate the efforts of co-authors and students of Amrita vidyalayam, Punnol, Thalassery.

References

- Ben Nelson S., G Ashok V., Nazer M., Manibalan S. (2017). Knowledge regarding mosquito borne diseases & control measures practiced among a rural population in a southern district of Tamil Nadu, South India. *Public Health Rev Int J Public Health Res.*;4(1):9-12.
- Caraballo H, King K, 2014. Emergency department management of mosquito-borne illness- malaria, dengue, and West Nile virus. *Emerg Med Pract.* 2014 May; 16(5)1-23; quiz 23-4.
- Keys to the medically important mosquito species. Zoogeographic Region. <http://www.wrbu.org/mqID/keysMQZoogeo.html>
- Leopoldo M. Rueda, 2004. Pictorial keys for the identification of mosquitoes (Diptera: Culicidae) associated with Dengue Virus Transmission. *Zootaxa* 589: 1–60 (2004) ISSN 1175-5326.
- M. Emmanuel Bhaskar, Swathy Moorthy, N. Senthil Kumar, and Preetam Arthur, 2010. Dengue haemorrhagic fever among adults – An observational study in Chennai, south India. *Indian J Med Res.*2010 Dec; 132(6): 738–740.
- Mourya, D. T., Thakare, J. P., Gokhale, M. D., Powers, A. M., Hundekar, S.L., Jayku-mar, P.C., Bondre, V.P., Souche, Y.S. and Padbidri, V.S, 2001. Isolation of Chikungunya Virus from *Aedes aegypti* Mosquitoes Collected in the Town of Yawat, Pune District, Maharashtra State, India. *Acta Virology*,45, 305-309.
- P.G Shute, 1946. Latency and long-term relapses in Benign Tertian malaria. *Transactions of The Royal Society of Tropical Medicine and Hygiene*, Volume 40, Issue 2, October 1946, Pages 189–200, [https://doi.org/10.1016/0035-9203\(46\)90056-9](https://doi.org/10.1016/0035-9203(46)90056-9).
- World Health Organization. A global brief on vector-borne diseases. Geneva- World Health Organization. 2014;54.

How to cite this article:

Seema Gupta, Bhramacharini Sheela, K. Smera, R. Niveditha, S. Soparnika, P. K. Kartika, A. Ashwariya, S. Arundhati, K. Abhiram and Rithika, P. 2021. Analysis of Mosquito Vector and Disease Spread through them in Kannur District, Kerala, India. *Int.J.Curr.Microbiol.App.Sci*. 10(02): 3128-3132. doi: <https://doi.org/10.20546/ijcmas.2021.1002.342>