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A comprehensive investigation of trombiculid mite larvae of chiggers

Siddiqi Nameera[#1], Mohd Naseem[#2], Surti Sehjad[3], Muzaffar Ahmed Farooqui[4], Irfan Ahmad[5], Nawaj Sharif[6]
[1] Department of Pharmaceutics, S.C.T's College of Pharmacy, Mitmita, Aurangabad, Maharashtra, India
[2] Department of Unani, Regional Research Institute of Unani Medicine, Aligarh, Uttar Pradesh, India
[3] Department of Pharmaceutical Analysis, School of Pharmacy,Parul University, Vadodara, Gujarat, India
[4] Department of Pharmaceutical Chemistry, Aurangabad Pharmacy College, Mitmita, Aurangabad, Maharashtra, India
[5] Department of Unani, Regional Research Institute of Unani Medicine, Mumbai, Maharashtra, India
[6] Department of Pharmaceutical Chemistry, Ali Allana College of Pharmacy, Akkalkuwa, Nandurbar, Maharashtra, India

Abstract
Chigger mites (Acari: Trombiculidae) are a specialised biological vector of scrub typhus, a zoonotic illness. They are also regarded as a valuable therapeutic arthropod vector. The disease-causing gram-negative bacterium Orientia tsutsugamushi is carried by chigger mite larvae and possesses a unique parasitism mechanism. The study intends to give a general overview of the range and prevalence of different species of vector mites worldwide, with a focus on India. Chigger mites are found all over the world as ectoparasites of a wide range of vertebrate hosts, including rats, cattle, aves, and occasionally invertebrates, after a number of study articles were reviewed. The zoonotic fever disease scrub typhus, which is caused by Orientia tsutsugamushi, is widespread in the Asia-Pacific region. The biology of trombiculids is undoubtedly hard, and their relatively restricted ability to self-disperse means that manipulating the microbiome or symbiotic trans-infections in chiggers may never be feasible on a large scale. To control scrub typhus and other viral diseases spread by these most mysterious of vectors, new repellents, insecticides, or even vaccines could be developed with the help of a deeper understanding of the chigger microbiome and lateral gene transfers from microorganisms in trombiculid genomes.

Keywords: Microbiome, scrub typhus, Orientia tsutsugamushi, chigger mite, zoonotic disease

Introduction

Orientia is the genus of bacteria that causes scrub typhus. The only known vectors of these intracellular bacterial infections are the larval stage of trombiculid mites (Acari: Trombiculidae), also referred to as chiggers. There are 700 hazardous species of mites known to exist worldwide, and 250 of those species are important for public health. While humans might become unintentional hosts, chiggers mostly parasitise wild vertebrate hosts such small mammals, reptiles, and birds. The more well-known genus Rickettsia, which contains the arthropod-borne diseases that cause endemic and epidemic typhus as well as spotted fevers, is closely linked to Orientia species. The zoonotic fever disease scrub typhus, which is caused by Orientia tsutsugamushi, is widespread in the Asia-Pacific region. Scrub typhus has a median fatality rate of 6% and can cause complications such as pneumonitis, myocarditis, and encephalitis if it is not identified and treated quickly. Due to the recognition of endemic scrub typhus outside of the Asia-Pacific region in the early 21st century, Candidatus Orientia chuto from the Middle East and East Africa [3-5] and Candidatus Orientia chiloensis from South America [6] have been identified. Molecular information from chigger and wildlife reservoirs, along with human serological surveys, suggest that Orientia is spreading to other regions of the world, particularly Africa, where there have been suspected human cases.

Chiggers are unique among human disease vectors for two main reasons. To begin with, they don't consume blood. Chiggers have an unusual way of eating in which, only after attaching to their host, they form a structure like straw called a stylostome through secreted chemicals. The stylostome is used to inject digestive enzymes into the skin, and the chigger consumes liquified cells and tissue fluid. Second, it is generally believed that chiggers only feed once before leaving their host to undergo three nymphal stages—the protonymph, deutonymph, and tritonymph—and eventually mature into adults. The post-larval stages are predators that live freely in soil and mostly consume the eggs of other arthropods.

Table 1: List of potential vertebrate microbial pathogens found in chiggers through focused surveys

Pathogen species	Chigger species	Microbial Taxa
Rickettsia spp.	Cheladonta costulata, Eutrombicula sp., Hirsutiella zachvatkini,L. peromysci, L. scutellare, N. autumnalis, Neotrombicula vulgaris,unidentified pooled chiggers	Bacteria (Alpha-proteobacteria)
Candidatus Rickettsia colombianensi	Eutrombicula tinami, B. sinnamaryi, Herpetacarus hertigi, Quadraseta trapezoides, and Trombewingia bakeri	
Candidatus Rickettsia leptotrombidium	L. scutellare	
Rickettsia felis	Blankaartia sinnamaryi, Eutrombicula sp., Leptotrombidium peromysci and L. scutellare	
Rickettsia sp. Cf15	Unidentified pooled chiggers	
Rickettsia helvetica	Hirsutiella zachvatkini and	
	Kepkatrombicula storkani	

Rickettsia sp. MB74-1	Unidentified pooled chiggers	
Rickettsia japonica	Unidentified pooled chiggers	
Rickettsia sp. TwKM03	L. deliense and unidentified pooled chiggers	
Rickettsia monacensis	Hirsutiella zachvatkini	
Rickettsia typhi	Eutrombicula sp., L. peromysci and unidentified pooled chiggers	
Rickettsia sp. TwKM02	L. deliense and unidentified pooled chiggers	
Hantaan orthohantavirus (Hantavirus)	Leptotrombidium scutellare	Virus (Bunyavirales)
B. garinii	Neotrombicula spp.	Bacteria (Spirochaetia)
B. valaisiana	Neotrombicula spp.	

Transmission of Viruses through Chiggers

In the Far East, which includes northeastern China, Korea, and eastern Russia, the hantaan orthohantavirus is the cause of Korean hemorrhagic fever. Hantaan orthohantavirus, like scrub typhus, is a zoonotic infection that persists in rodents without killing its natural host, which is mostly the striped field mouse, Apodemus agrarius. But unlike Orientia species, Hantaan orthohantavirus is thought to spread straight from rodent to human or vice versa, without the necessity for an arthropod vector, either by biting or inhaling aerosolised excreta. Supporting information was gathered from a Texas field site where RNA from a distinct hantavirus, known as Bache, was found in chiggers that were feeding on rodent hosts that were negative for the hantavirus. Additionally, a free-living trombiculid in the predatory stage of its life cycle was recovered from the soil. Epidemiological data supporting the laboratory and field investigations further suggest that the peak human transmission of Hantaan orthohantavirus in Qingdao, China, was predicted by meteorological conditions related to mite abundance (e.g., relative humidity) following the rodent reproductive season. Ultimately, a study conducted on South Korean soldiers revealed that the two best defences against contracting Korean hemorrhagic fever were sleeping in barracks rather than outside on the ground and using pesticides or repellant.

The last category of possible pathogens identified from chiggers is composed of Rickettsia species (Table 1). In fact, Rickettsia species may be more common than Orientia species in chiggers worldwide. Up to now, fed chiggers recovered from small mammals in Brazil, the USA, Slovakia, South Korea, Thailand, Vietnam, mainland China, and Taiwan have been found to have Rickettsia spp. DNA. In addition, chiggers in Brazil have been found to parasitise birds. Crucially, it has been shown that there may be vertical transmission of Rickettsia spp. DNA from questing L. scutellare in Japan, together with DNA from two other endosymbionts, Wolbachia and Rickettsiella. Chiggers contain a variety of rickettsial strains, the majority of which belong to the Transitional group, according to genetic investigations. This clade contains endosymbionts of ticks that have not been linked to human infections (e.g., Rickettsia hoogstraalii), as well as important pathogens like Rickettsia australis, an agent of Queensland tick typhus, and Rickettsia akari, an agent of rickettsialpox, which is transmitted by gamasid mites. Therefore, it is still unknown if the Rickettsia species seen in chiggers are vertebrate pathogens, arthropod-restricted symbionts, or a combination of the two. However, a Taiwanese study indicates that "Rickettsia sp. clone MB74-1" and "Rickettsia sp. TwKM02" show some specialisation towards chiggers, as they are rarely found in the rodent host or co-infesting ectoparasites like fleas and ticks. These strains may belong to the same species because molecular detection of them was accomplished with distinct gene targets. In South Korea, chiggers have been observed to contain sequences similar to these.

Numerous investigations of feeding chiggers have identified at least two more alpha-proteobacteria with pathogenic potential, Bartonella spp. and Rickettsia spp. (Table 1). In various genera of chiggers (Blankaartia, Leptotrombidium, and Schoengastia) obtained from rodents in both the northern and southern parts of Thailand, the DNA of Bartonella tamiae, the pathogen that causes human bartonellosis, was found. Moreover, chigger nucleotide sequences closely matched those of human clinical isolates; however, no additional research has been done to assess vertical transmission in unfed larvae or chigger-mediated transmission to naïve rats. Bartonella species have been found in combined chigger samples from the Mekong Delta region of Vietnam. Chiggers from Bartonella-infected rats had a higher rate of Bartonella infection than chiggers from uninfected rats; however, these results are difficult to interpret in the absence of research on the possible laboratory animal-to-chigger transmission of Bartonella spp.

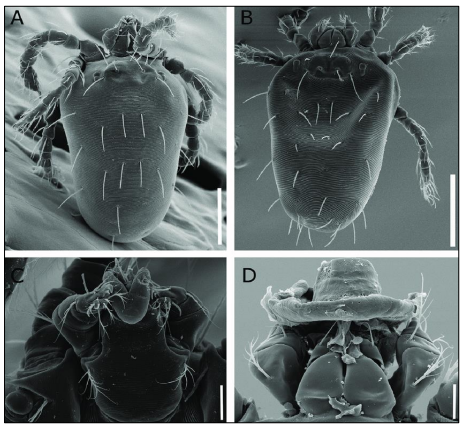

Fig 1: Chigger (Trombicula sp.)

Fig 2: Scan electron microscope images of chiggers

Conclusion

Within trombiculid mites, there are apparently a lot of opportunities for microbe–microbe interactions due to the quantity of vertically transmitted bacteria present in wild chigger populations, particularly in the reproductive organs. Studies to ascertain the impact of the chigger microbiome on vector competence and the population dynamics of Orientia in trombiculid populations are desperately needed, since heritable bacteria can compete during maternal transmission. The tick symbiont Rickettsia buchneri inhibits the growth of rickettsiae that are pathogenic to vertebrates, and Wolbachia blocks the spread of arboviruses in Aedes aegypti mosquitoes. These are two examples of other arthropod vector systems that provide precedents for potential microbiome-mediated pathogen transmission interference. The biology of trombiculids is undoubtedly hard, and their relatively restricted ability to self-disperse means that manipulating the microbiome or symbiotic transinfections in chiggers may never be feasible on a large scale. To control scrub typhus and other viral diseases spread by these most mysterious of vectors, new repellents, insecticides, or even vaccines could be developed with the help of a deeper understanding of the chigger microbiome and lateral gene transfers from microorganisms in trombiculid genomes.

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