


WikiJournal Preprints/Orientia tsutsugamushi, the agent of scrub typhus



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Author: Kholhring Lalchhandama , *et al.*

Orientia tsutsugamushi is a mite-borne bacterium belonging to the family Rickettsiaceae and is responsible for the disease scrub typhus in humans. It is an obligate intracellular parasite of Trombiculid mites, in which natural transmission is maintained from female to its eggs (transovarial transmission) and from the eggs to adults (transtadial transmission). With a genome of only 2.4– 2.7 Mb, it has the most repeated DNA sequences among bacteria. It is transmitted by mite larvae (chiggers) to humans and rodents through accidental bite. Naosuke Hayashi first described it in 1920, giving the name *Theileria tsutsugamushi*, but was renamed to *Orientia tsutsugamushi* in 1995, owing to its unique properties. Unlike other Gram-negative bacteria, its cell wall lacks lipophosphoglycan and peptidoglycan. It instead has a unique 56kDa type-specific antigen (TSA56), which renders the bacterium to exist in many strains (sub-types) such as Karp, Gilliam, Kato, Shimokoshi, Kuroki, and Kawasaki. Primarily indicated by undifferentiated febrile illnesses, the infection can be complicated and often fatal. Diagnosis is This article is an unpublished pre-print undergoing public peer review organised by the *WikiJournal of Medicine*.

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25 **Author info:**

26 Department of Zoology, PUC Campus, Mizoram University, Aizawl 796001, India

27 chhandama@gmail.com


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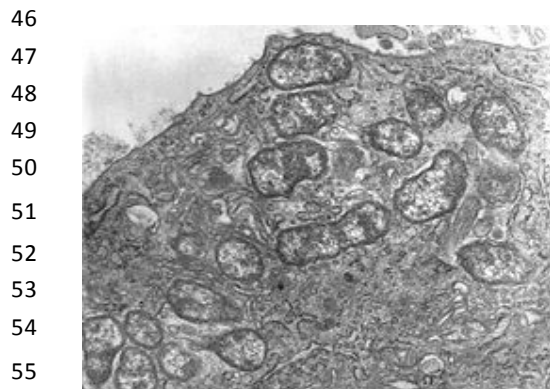
31 difficult and requires laborious techniques
32 such as Weil–Felix test, rapid
33 immunochromatographic test,
34 immunofluorescence assays, ELISA, or PCR.
35 Eschar, if present on the skin, is a good
36 indicator. One million infections are
37 estimated to occur annually in the
38 endemic region called Tsutsugamushi
39 Triangle, which covers the Russian Far East
40 in the north, Japan in the east, northern
41 Australia in the south, and Afghanistan in
42 the west.

43 Antibiotics such as azithromycin and doxycycline are the main prescription drugs. There is no
44 working vaccine.

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Keywords: *Orientia tsutsugamushi*, scrub typhus, *Leptotrombidium*, febrile illness, vaccine, immunity

45 **Biology**



O. tsutsugamushi belongs to Gram-negative bacteria and is a permanent (obligate) parasite in mites. Within a single host cell, *O. tsutsugamushi* rapidly divides into many individuals as shown in Figure 1. A unicellular organism, it is rod shaped and measures 0.5 to 0.8 μm wide and 1.2 to 3.0 μm long. Due to similarity, it was initially categorised in the genus *Rickettsia*, but later assigned a separate genus, *Orientia*,^[1] which it shares (so far) only with *Candidatus Orientia chuto*.^[2] It is larger and broader, but shorter than other rickettsial bacteria. During reproduction, it divides (by binary fission) into two daughter cells by the process of budding. While undergoing budding, it accumulates on the host cell surface unlike other bacteria. One complete budding takes 9 to 18 hours.^[3]

56 **Figure 1** | A transmission electron micrograph
57 of a mesothelial cell of a mouse containing
58 numerous *O. tsutsugamushi*. [CDC, CC-BY 3.0](#)

59 The bacterium is enclosed by a cell wall on the outside and cell membrane on the
 60 inside (Figure 2). The cell covering take up stains such as Giemsa and Gimenez
 61 stains. Although its cell wall has a classic bacterial double layer, its outer leaflet is
 62 much thicker than the inner one, which is just the opposite in *Rickettsia*
 63 species.^[4] A capsule layer that forms a spherical halo in other bacteria is missing.
 64 The cell wall is soft and tender due to the absence of peptidoglycan, which is
 65 otherwise characteristic of the rigid cell walls of other bacteria. Classic bacterial
 66 lipophosphoglycans such as muramic acid, glucosamine, hydroxy fatty acids,
 67 heptose, and 2-keto-3-deoxyoctonic acid are also absent in the cell wall. Due to
 68 the absence of peptidoglycan, the bacterium is naturally resistant to all β -lactam
 69 antibiotics (such as penicillin), to which *Rickettsia* species are normally sensitive
 70 to.^[5] Its genome totally lacks the genes for lipophosphoglycan synthesis, but does
 71 contain those for peptidoglycan. In fact, peptidoglycan is synthesised in very small
 72 quantity that can hardly be detected and plays minor or no role in the cell wall.
 73 There are unique genes such as *PBP1*, *alr*, *dapF*, and *murl*, which are not known
 74 in other bacteria.^[6] The cell membrane is also chemically different in its
 75 protein composition, and this difference gives rise to strain variations within
 76 the species itself.^[7] The cytoplasm is clear and shows distinct DNA and
 77 ribosomes.

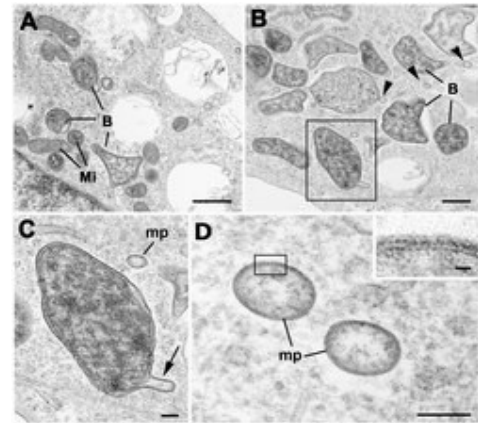
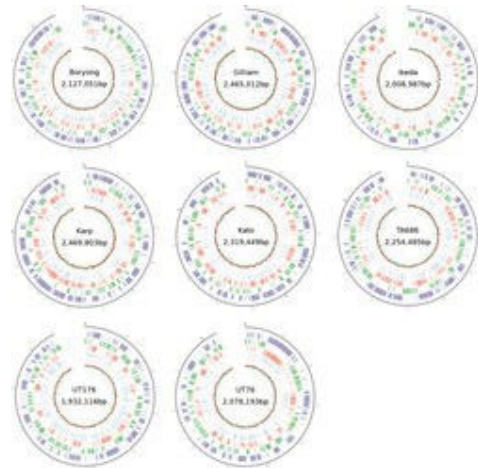


Figure 2 | *O. tsutsugamushi* in human (U937) cells. B = the bacteria; mp = microparticles formed by the outer cell wall leaflet.
 Paris et al., 2012 CC-BY 3.0

78 The bacterium is highly virulent such that its isolation and cell culture are done
 79 only in a laboratory with biosafety level 3 facility. Unlike other bacteria which can
 80 easily grow on different culture media, it can be grown only in the yolk sacs of
 81 developing chicken embryos and in cultured cell lines such as HeLa, BHK, Vero,
 82 and L929 cell lines.^[8] In contrast to *Rickettsia* species which reside in the nucleus
 83 of the host cell, it mostly grow within the cytoplasm of the host cell.^[9]
 84 Genetically, it differs from other *Rickettsia* by only 9%.^[10] Even though
 85 adaptation to obligate intracellular parasitism among bacteria generally results
 86 in reduced genome, it has a genome size of about 2.0–2.7 Mb depending on the
 87 strains (Figure 3), which is comparatively larger than those of other rickettsiales
 88 – two times larger than that of *Rickettsia prowazekii*,^[11] the most well-known
 89 member. The entire genome is distributed in a single chromosome. Whole
 90 genome sequences are available only



91 for Ikeda and Boryong strains, both from the Republic of Korea. The genome of **Figure 3 |** Genomes of *O. tsutsugamushi* Ikeda
 92 strain is 2,008,987 base pairs (bp) long, and contains 1,967 protein-coding strains. genes.^[12] The Boryong strain is larger with
 93 2,127,051 bp and 2,179 protein-coding

Batty et al., 2017 CC-BY 3.0 genes.^[13]

94
 95 Genome comparison shows only 657 core genes among the different strains.^[14]
 96 With about 42–47% of repetitive sequences, *O. tsutsugamushi* has the most highly repeated bacterial genome sequenced so far.^[15]
 97 The repeated DNA sequence includes short repetitive sequences, transposable elements (including insertion sequence elements,
 98 miniature inverted-repeat transposable elements, a Group II intron), and a greatly amplified integrative and conjugative element
 99 (ICE) called the rickettsial amplified genetic element (RAGE).^[13] RAGE is also found in other rickettsial bacteria. In *O.*
 100 *tsutsugamushi*, however, RAGE contains a number of genes including *tra* genes typical of type IV secretion systems and gene for
 101 ankyrin repeat–containing protein. Ankyrin repeat–containing proteins are secreted through a type I secretion system into the
 102 host cell. The precise role of type IV secretion system in *O. tsutsugamushi* is not known. It may be involved in horizontal gene
 103 transfer between the different strains.^[16]

Life cycle and transmission

104 *O. tsutsugamushi* is naturally transmitted in the mite population belonging to the genus
105 *Leptotrombidium*. It can be transmitted by a female to its eggs through the process called
106 transovarial transmission, and from the eggs to larvae and adults through the process of
107 transtadial transmission. Thus, the bacterial life cycle is maintained entirely in mites. Infection to rodents and humans is an
108 accidental transmission from the bite of mite larvae, and not required for reproduction or survival of the bacterium. In fact, in
109 rodents and humans the transmission is stopped, and the bacterium meets a dead end.^[7]

110 In rodent and human infections, *Leptotrombidium deliense* is the most universal vector of *O. tsutsugamushi*. *L. pallidum*, *L. fletcheri*
111 and *L. scutellare* are also carriers in many countries. In addition, *L. akamushi* is an endemic carrier in Japan, *L. chiangraiensis* and
112 *L. imphalum* in Thailand, *L. gaohuensis* in China, and *L. arenicola* in Malaysia and Indonesia.^[17] In parts of India, a different mite
113 species, *Schoengastiella ligula* is also a major vector.^[18] The third-stage larvae, commonly referred to as chiggers (Figure 4), are
114 the only ectoparasitic stage feeding on the body fluids of rodents and other opportunistic mammals. Thus, they are the only stage
115 in the life of mites that cause infection. Wild rats of the genus *Rattus* are the principal natural hosts of the chiggers.^[19] Chiggers
116 feed only once on a mammalian host. The feeding usually takes 2 to 4 days. In contrast to most parasites, they do not feed on
117 blood, but instead on the body fluid through the hair follicles or skin pores. They possess a special feeding apparatus called
118 stylostome on their heads. Their saliva can dissolve the host tissue around the feeding site, so that they ingest the liquefied tissue.
119 *O. tsutsugamushi* is present in the salivary glands of mites and is released into the host tissue during this feeding.^[20]

Cellular invasion

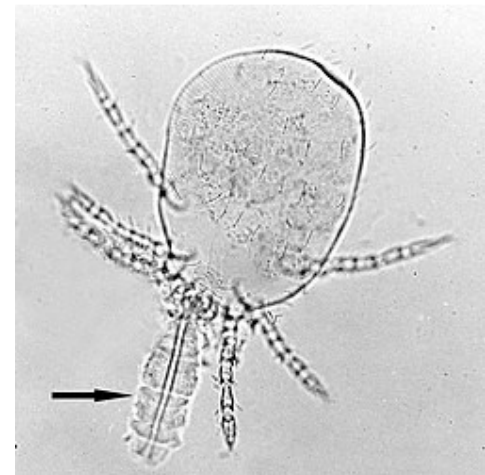


Figure 4 | Chigger with its feeding apparatus, the stylostome (arrowhead).

Walker, 2012 CC-BY 3.0

121 *O. tsutsugamushi* initially attacks the myelocyte (young white blood cells) in the
122 area of inoculation, and then the endothelial cells lining the vasculature. The
123 process of cellular invasion is shown in Figure 5. In the blood circulation, it targets
124 professional phagocytes (cell eaters white blood cells) such as dendritic cells and
125 macrophages in all organs as the secondary targets. The parasite first attaches
126 itself to the target cells using surface proteoglycans present on the host cell and
127 bacterial surface proteins such as TSP56 (TSA56) and surface cell antigens (ScaA
128 and ScaC).^{[21][22]} These proteins interact with the host fibronectin to induce
phagocytosis (the process of swallowing the bacterium). The ability to actually
enter the host cell depends on integrin-mediated signaling and reorganisation of
actin cytoskeleton.^[23]

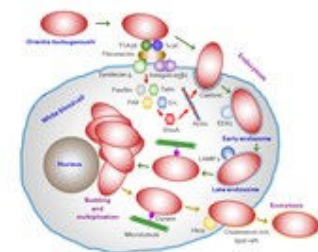


Figure 5 | Mechanism of cell invasion by *O. tsutsugamushi*.

Chhandama, 2018 CC-BY 3.0

129 *O. tsutsugamushi* has a special adaptation for surviving in the host cell by evading
130 the host immune reaction. Once it interacts with the host cells, it causes the host cell membrane to form a transportation bubble
131 called a clathrin-coated vesicle by which it gets transported in the cytoplasm. Inside the cytoplasm, it makes an exit from the
132 vesicle (now known as an endosome) before it is destroyed (in the process of cell-eating called autophagy) by the lysosomes.^[24]
133 It then moves towards the nucleus, specifically at the perinuclear region, where it starts to grow and multiply. Unlike other closely

134 related bacteria which use actin-mediated processes for movement in the cytoplasm (called intracellular trafficking or transport),
135 *O. tsutsugamushi* is unusual in using microtubule-mediated processes similar to those employed by viruses such as adenoviruses
136 and herpes simplex viruses. Further, the escape (exocytosis) from an infected host cell is also unusual. It forms another vesicle
137 using the host cell membrane, gives rise to a small bud, and releases itself from the host cell surface while still enclosed in the
138 vesicle. The membrane-bound bacterium is formed by interaction between cholesterol-rich lipid rafts as well as HtrA, a 47-kDa
139 protein on the bacterial surface.^[25] However, the process of budding and importance of the membrane-bound bacterium are not
140 yet understood.

141 Strains

142 *O. tsutsugamushi* is a diverse species of bacteria. Ida A. Bengtson of the United States Public Health Services was the first to note
143 the existence of different strains using antigen-antibody interaction (complement fixation test) in 1944.^[26] He observed that
144 different strains had varying degree of virulence, and that the blood sera having different strains could cross react. By 1946, he
145 established that there were three principal strains (serotypes), namely Karp (from New Guinea), Gilliam (from India) and Seerangay
146 (from British Malaya).^[27] Akira Shishido discovered Kato strain, in addition to Gilliam and Karp, in Japan in 1958.^[28] Since then six
147 basic antigenic strains are recognised, namely Gilliam, Karp, Kato, Shimokoshi, Kawasaki, and Kuroki. Karp is the most abundant
148 strain accounting for about 50% of all infections.^[17] But in Korea, the major strain is Boryong.^[29] So far, more than 30 different
149 strains have been established in humans.^[15] The number is much higher if the strains in rodents and mites are taken into account.
150 For example, a study in Japan in 1994 reported 32 strains, 14 from human patients, 12 from wild rodents, and 6 from trombiculid
151 mites. The different strains exert different levels of virulence, and the most virulent is KN-3, which is predominant among wild
152 rodents.^[30] Another study in 1996 reported 40 strains.^[31] Genetic methods have revealed even greater complexity than had been
153 previously described (for example, Gilliam is further divided into Gilliam and JG types). Due to immunological differences of the
154 serotypes, simultaneous and repeated infection with different strains is possible.^{[32][33]}

155 Antigenic variation

156 *O. tsutsugamushi* has four major surface-membrane proteins (antigens) having molecular weights 22 kDa, 47 kDa, 56 kDa and 110
157 kDa. A 56-kDa type specific antigen (TSA56) is the most important because it is not produced by any other bacteria, and is
158 responsible for making the genetic diversity in different strains.^[34] It accounts for about 10–15% of the total cell proteins. The
159 22kDa, 47-kDa or 110-kDa antigens are not normally detected by sophisticated diagnostic tests. But clinical tests easily detect the
160 TSA56, making it the main target in diagnosis.^[35] The protein assists the adhesion and entry of the bacterium into host cells, as
161 well as evasion of the host's immune reaction. It varies in size from 516 to 540 amino acid residues between different strains, and
162 its gene is about 1,550 base pairs long. It contains four hypervariable regions, indicating that it synthesise many antigenically
163 different protein but of the same kind.^[31] There are also 11-kDa and 60-kDa proteins inside the bacterium which are very similar
164 to GroES and GroEL of the bacterium *Escherichia coli*, but not that of *Rickettsia* species.^[36] GroES and GroEL are heat shock
165 proteins belonging to the family of molecular chaperones in bacteria. DNA analysis have shown that the *GroES* and *GroEL* genes
166 are indeed present in
167 *O. tsutsugamushi* with slight variation in different strain and they produce the 11-kDa and 60-kDa proteins.^[37]

168 Disease

169
170 *O. tsutsugamushi* causes a complex and dangerous infection known as scrub typhus. Infection starts when chiggers bite on the
171 skin during their feeding. The bacteria are deposited at the site of feeding (inoculation) where they multiply. They cause
172 progressive tissue damage (necrosis). Necrosis progresses to inflammation of the blood vessels called vasculitis. This in turn causes
173 inflammation of the lymph nodes, called lymphadenopathy. Within a few days, vasculitis extends to various organs including liver,
174 brain, kidney, meninges and the lung.^[38] The disease is responsible for nearly a quarter of all the febrile (high fever) illness in
175 endemic areas. Mortality in severe case or due to improper treatment or misdiagnosis may be as high as 30-70%.^[39] About 6% of

176 infected people die untreated, and 1.4% of the patients die even with medical treatment. Moreover, death rate can be as high as
177 13% where medical treatment is not properly handled.^[40] In cases of misdiagnosis and failure of treatment, systemic
178 complications rapidly develop including acute respiratory distress syndrome, acute kidney failure, encephalitis, gastrointestinal
179 bleeding, hepatitis, meningitis, myocarditis, pancreatitis, pneumonia, septic shock, subacute thyroiditis, and multi-organ
180 dysfunctions.^[41] Harmful symptoms involving multiple organ failure and neurological impairment are difficult to treat, and can be
181 lifelong debilitation or directly fatal.^[41] The central nervous system is often affected and result in various complications including
182 cerebellitis, cranial nerve palsies, meningoencephalitis, plexopathy, transverse myelitis, neuroleptic malignant syndrome, and
183 Guillan-Barré syndrome.^[42] Death rates due to complications can be up to 14% in brain infections, and 24% with multiple organ
184 failure.^[40] It is the major cause of acute encephalitis syndrome in India, where viral infection Japanese encephalitis has been
185 regarded as the main factor.^[43]

186 Epidemiology

187 The World Health Organization in 1999 stated that:

188 “Scrub typhus is probably one of the most underdiagnosed
189 and underreported febrile illnesses requiring hospitalization
190 in the region. The absence of definitive signs and symptoms
191 combined with a general dependence upon serological tests
192 make the differentiation of scrub typhus from other common
193 febrile

diseases such as murine typhus, typhoid fever ” and
leptospirosis quite difficult.”^[44]

Scrub typhus is historically endemic to the Asia-Pacific region covering the
194 Russian Far East and Korea in the north to northern Australia in the south and
195 Afghanistan in the west, including islands of the western Pacific Oceans such as
196 Japan, Taiwan, Philippines, Papua New Guinea, Indonesia, Sri Lanka, and the Indian Subcontinent. This geographic region is
197 popularly called the Tsutsugamushi Triangle as shown in Figure 6.^[38] However, it has spread to Africa, Europe and South
198 America.^[45] One billion people are estimated to be at risk of infection at any moment and an average of one million cases occur
199 every year in the Tsutsugamushi Triangle. In the absence of proper medical care, the case fatality rate can go beyond 30% to as
200 high as 70% in some areas.^[20] The burden of scrub typhus in rural areas of Asia is huge, accounting for up to 20% of febrile sickness
201 in hospital, and seroprevalence (positive infection on blood test) over 50% of the population.^[46] More than one-fifth of the
202 population carry the bacterial antibodies, i.e. they had been infected, in endemic areas. South Korea has the highest level incidence
203 (with its highest of 59.7 infection out of 100,000 people in 2013), followed by Japan, Thailand, and China at top of the list.^[40]

204 Treatment

205 *O. tsutsugamushi* infection can be treated with antibiotics such as azithromycin, chloramphenicol, doxycycline, rifampicin,
206 roxithromycin, and tetracyclin. Doxycycline is the most commonly used and is considered as the drug of choice because of its high
207 efficacy and quick action. But in pregnant women and babies it is contraindicated, and azithromycin is the drug of choice. In
208 Southeast Asia, where doxycycline and chloramphenicol resistance have been experienced, azithromycin is recommended for all
209 patients.^[47] A randomized controlled trial and systematic review showed that azithromycin is the safest medication.^{[48][49]}

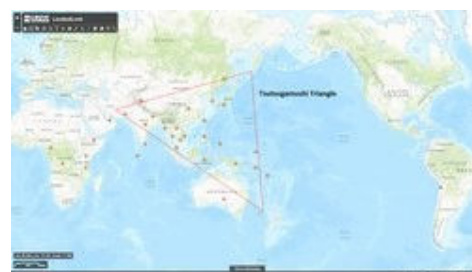


Figure 6 | Map showing the Tsutsugamushi Triangle.

Xu *et al.*, 2017 CC-BY 3.0

210 **Diagnosis**

211 **Symptom**

212 The main symptom of *O. tsutsugamushi* infection is high (febrile) fever; however,
213 the symptom is not unique and is similar to a group of acute undifferentiated
214 fever, which includes those of malaria, leptospirosis, typhoid, murine typhus,
215 chikungunya, and dengue fever.^{[50][51]} This makes precise clinical diagnosis
216 difficult, which often leads to misdiagnosis. The initial indications are fever with
217 chills, associated with headache, muscle pain (myalgia), sweating and vomiting.
218 The appearance of symptoms (the incubation period) takes between 6 and 21
219 days.^[38] A simple visual diagnosis is the presence of an inflamed scar-like scab
220 called eschar, which is regarded as "the most useful diagnostic clue in patients
221 with acute febrile illness". Eschar is formed on the skin where an infected mite
222 bit, usually seen in the armpit, groin or any abdominal area (Figure 7). In rare
223 cases, it can be seen on the cheek, ear lobe and dorsum of the feet.^[52] But the
224 problem is

that eschar is not always present. At the highest record, only 55% of scrub typhus
patients had eschar during an outbreak in south India.^[53] Also that eschar is not
specific to scrub typhus, as other rickettsial diseases such as Rocky Mountain
spotted fever,^[54] Brazilian spotted fever,^[55] and Indian tick typhus.^{[56][57]} Using
225 DNA analysis by advanced polymerase chain reaction, different rickettsial infection
226 can be identified from eschars.^{[58][59]}



Figure 6 | Eschar due to *O. tsutsugamushi* infection on the shoulder (a, b) of a woman and on the penis (c, d) of a man.

Le Viet *et al.*, 2017 [CC-BY 3.0](#)

228 **Blood test**

229 *O. tsutsugamushi* is most often detected from blood serum using Weil–Felix test. Weil–Felix test is the simplest and most rapid
230 test, but it is not sensitive or specific as it detects any kind of rickettsial infection. More sensitive tests such as rapid
231 immunochromatographic test (RICT), immunofluorescence assays (IFA), ELISA, and DNA analysis using polymerase chain reaction
232 (PCR) are used.^{[19][8]} IFA is regarded as the gold standard test, as it gives reliable result. However, it is expensive and not specific
233 for different rickettsial bacteria.^[60] ELISA and PCR can detect *O. tsutsugamushi*-specific proteins such as the TSA56 and GroEL so
234 that they are highly specific and sensitive.^[61] On the other hand, they are highly sophisticated and expensive techniques.

235 **Vaccine**

236 No licensed *O. tsutsugamushi* vaccines are currently available. The first vaccines were developed in the late 1940s, but failed in
237 clinical trials.^{[62][63]} Considered an ideal target, the unique TSA56 itself is highly variable in its chemical composition in different
238 strains. An effective vaccine for one strain is not useful for another. An ideal vaccine should give protection to all the strains present
239 locally. This complexity makes it difficult to produce a usable vaccine.^[64] A vaccine targeting the 47-kDa outer membrane protein
240 (OMP) is a promising candidate with experimental success in mice against Boryong strain.^[65] Combined targeting of TSA56 and
241 ScaA is also a good candidate for mixed-strain infection.^[22]

242 **Immunity**

243
244 There is no complete immunity to *O. tsutsugamushi* infection. Enormous antigenic variation among *O. tsutsugamushi* strains
245 makes the immune system unable to fully recognise them. An infected individual may develop a short-term immunity but that

246 disappears after a few month, and immunity to one strain does not confer immunity to another.^[64] An immunisation experiment
247 was done in 1950 in which 16 volunteers still developed the infection after 11–25 months of primary infection.^[66] It is now known
248 that the longevity of immunity depends on the strains of the bacterium. When reinfection occurs with the same strain as the
249 previous infection, there can be immunity for 5–6 years in monkeys.^[67] But in humans, immunity declines after one year, and
250 disappears within two years.^[68]

251 History

252
253 The earliest record of *O. tsutsugamushi* infection was in the 3rd century (313 C.E.) in China.^[69] Japanese were also familiar with
254 the link between the infection and mites for centuries. They gave several names such as *shima-mushi*, *akamushi* (red mite) or
255 *kedani* (hairy mite) disease of northern Japan, and most popularly as *tsutsugamushi* (from *tsutsuga* meaning fever or harm or
256 illness, and *mushi* meaning bug or insect). Japanese physician Hakuju Hashimoto gave the first medical account from Niigata
257 Prefecture in 1810. He recorded the prevalence of infection along the banks of the upper tributaries of Shinano River.^[70] The first
258 report to the Western world was made by Theobald Adrian Palm, a physician of the Edinburgh Medical Missionary Society at
259 Niigata in 1878. Describing his first-hand experience, Palm wrote:

260 “ Last summer [i.e. 1877], I had the opportunity of observing a disease which, so far as I know, is
261 peculiar to Japan, and has not yet been, described. It occurs, moreover, in certain well-marked
262 districts, and at a particular season of the year, so that the opportunities of investigating it do not
263 often occur. It is known here as the *shima-mushi*, or island-insect disease, and is so-named from the

264 belief that it is caused by the bite or sting of some insect peculiar to certain islands in the river
265 known as Shinagawa, which empties itself into the sea at Niigata.^[71]”

266 The aetiology of the disease was never apparent. In 1908, a mite theory of the transmission of tsutsugamushi disease was
267 postulated by Taichi Kitashima and Mikinosuke Miyajima.^[72] In 1915, a British zoologist Stanley Hirst suggested that the larvae of
268 mite *Microtrombidium akamushi* (later renamed *Leptotrombidium akamushi*) which he found on the ears of field mice could carry
269 and transmit the infection.^[73] In 1917, Mataro Nagayo and colleagues gave the first complete description of the developmental
270 stages such as egg, nymph, larva, and adult of the mite; and also asserted that only the larvae bites mammals, and are thus the
271 only carriers of the parasites.^[74] But then the actual infectious agent was not known, and it was generally attributed to either a
272 virus or a protozoan.^[75]

273 The causative pathogen was first identified by Naosuke Hayashi in 1920. Confident that the organism was a protozoan, Hayashi
274 concluded, stating, "I have reached the conclusion that the virus of the disease is the species of *Piroplasma* [protozoan] in
275 question... I consider the organism in Tsutsugamushi disease as a hitherto undescribed species, and at the suggestion of Dr. Henry
276 B. Ward designate it as *Theileria tsutsugamushi*."^[76] Discovering the similarities with the bacterium *R. prowazekii*, Mataro Nagayo
277 and colleagues gave a new classification with the name *Rickettsia orientalis* in 1930.^{[77][78]} (*R. prowazekii* is a causative bacterium
278 of epidemic typhus first discovered by American physicians Howard Taylor Ricketts and Russell M. Wilder in 1910; and described
279 by a

280 Brazilian physician Henrique da Rocha Lima in 1916.^[79])

281 The taxonomic confusion worsened. In 1931, Norio Ogata gave the name *Rickettsia tsutsugamushi*,^[80] while Rinya Kawamūra and
282 Yoso Imagawa independently introduced the name *Rickettsia akamushi*.^[81] Kawamūra and Imagawa discovered that the bacteria
283 are stored in the salivary glands of mites, and that mites feed on body (lymph) fluid, thereby establishing the fact that mites
284 transmit the parasites during feeding.^[82]

285 For more than 60 years there was no consensus on the choice of name – both *R. orientalis* and *R. tsutsugamushi* were equally
286 used. Akira Tamura and colleagues reported in 1991 the structural differences of the bacterium from *Rickettsia* species that

287 warranted separate genus, and proposed the name *Orientia tsutsugamushi*.^[9] Finally in 1995, they made a new classification
288 based on the morphological and biochemical properties, formally creating the new name *O. tsutsugamushi*.^[1]

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