Trends in Microbiology | **Microbe of the Month**

Orientia tsutsugamushi

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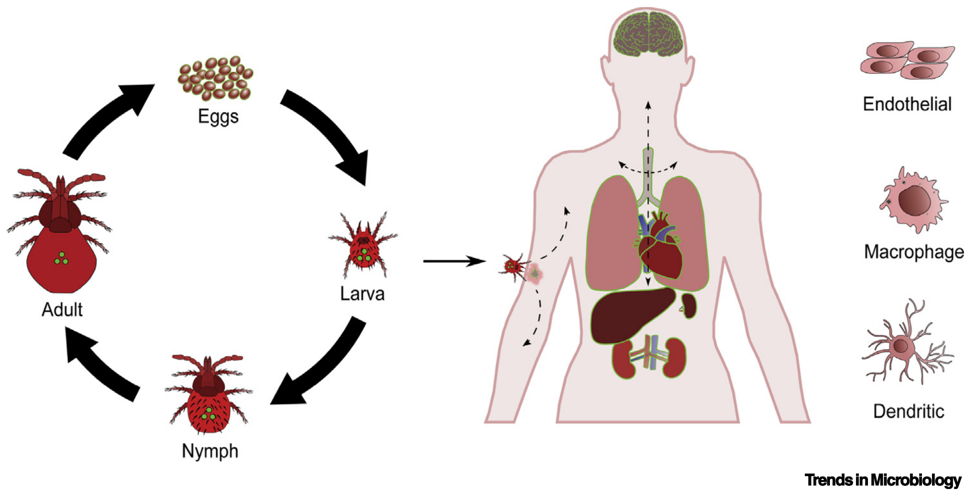
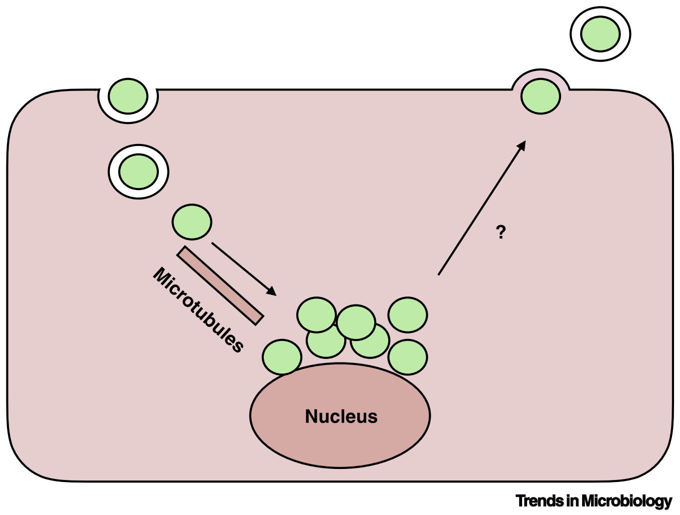


Orientia tsutsugamushi is an obligate intracellular bacterial pathogen that causes the mite-borne human disease scrub typhus, one of the most widespread and severe rickettsial infections. Symptoms typically begin 7–14 days after inoculation and include headache, fever, rash, myalgia, and a painless eschar at the site of the mite's bite. Untreated, the disease can escalate to cause multiple organ failure and death. Major challenges to disease control include slow and inaccurate diagnostic tests and low awareness amongst clinicians.

O. tsutsugamushi infects a range of host cell types including endothelial cells, monocytes/macrophages, and dendritic cells, and it replicates directly in the host cell cytoplasm. Aspects of its infection cycle and biology differentiate it from other genera in the family Rickettsiaceae; these include a microtubule-driven mode of motility, a budding mechanism of host cell exit, a minimal peptidoglycan-like cell wall, and a highly repetitive genome.



TAXONOMY AND CLASSIFICATION:
KINGDOM: Bacteria
PHYLUM: Proteobacteria
CLASS: Alphaproteobacteria
ORDER: Rickettsiales
FAMILY: Rickettsiaceae
GENUS: *Orientia*
SPECIES: *tsutsugamushi*
KEY STRAINS: Karp, Kato, Gilliam, Boryong, Ikeda, TA716, TA763, TA686, Kawasaki, Kuroki, Saitama, Shimokoshi
Gram-negative, pleomorphic rod-shaped bacterium

KEY FACTS:

An obligate intracellular bacterium that infects monocytes, macrophages, dendritic cells, and endothelial cells; it disseminates via blood and lymphatic systems.

O. tsutsugamushi lives in trombiculid mites.

A single circular chromosome of 1.93–2.47 Mb. No known plasmids. 2086–2709 predicted genes, with a core genome of 657 genes.

One of the most highly repetitive bacterial genomes known. Almost 50% of the genome is comprised of repetitive DNA elements.

No lipopolysaccharides (LPS). Minimal peptidoglycan-like structure in the cell wall.

The organism encodes multiple Ankyrin-repeat-containing effector proteins that interact with host cell pathways.

The outer membrane is dominated by highly abundant surface protein TSA56. This has variable domains that differ between strains. This protein is important in serological diagnostics and as a vaccine candidate.

The doubling time is approximately 8–9 h.

Currently, the organism is genetically intractable.

DISEASE FACTS:

Poor natural immunity; reinfections are common.

Historically confined to Asia-Pacific but recent reports of locally acquired cases in the Middle East and Latin America.

Estimated to infect at least one million people each year globally and likely the most common treatable cause of nonmalarial fever in the Asia-Pacific region.

Responsive to doxycycline (primary choice), azithromycin, rifampicin, and chloramphenicol.

Serology and molecular techniques are the main diagnostic approaches, but both have important limitations.

There is currently no preventative vaccine available.

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