Genetic Variation of Orientia Tsutsugamushi in a New Epidemic Area of Northern China.

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INTRODUCTION: Scrub typhus is a traditional tropical rickettsiosis. However, it emerged and rapidly spread in temperate zone since 1986, with epidemic season mainly in autumn and winter. Shandong province is a newly developed epidemic area of scrub typhus in northern China. The study aimed to investigate the prevalence of Orientia tsutsugamushi (O. tsutsugamushi) infection, and explore their genetic relationship in the area.

METHODS: During September 2010 to March 2012, we collected acute phase blood and eschars specimens from scrub typhus patients, and captured rodents every season. We amplified and sequenced the 56 kDa type-specific antigen gene of O. tsutsugamushi from the blood samples, spleen of the rodents, and chiggers parasitizing on the rodents, and designated them to genotypes according to sequence analysis.

RESULTS: A total of 826 rodents were captured. The rate of positivity for O. tsutsugamushi in Mus musculus and Rattus norvegicus was 3.6% and 1.7%, respectively. Natural infection of O. tsutsugamushi was found in Leptotrombidium taishanicum, L. linhuaikon-genese, L. intermedium, L. scutellare, L. palpale, the minimum positive rates of which were 5.9%, 3.2%, 1.2%, 0.8%, 0.8%, and 2.2%, respectively. Phylogenetic analysis identified four genogroups of O. tsutsugamushi prevalent in the study area, which were Kawasaki-related, Fuji-related, Shimokoshi-related and a new genogroup. Shimokoshi-like genotype was first detected from L. palpale. O. tsutsugamushi sequences from rodents and chiggers had homologies ranging from 69.6% to 100% with those infecting humans.

CONCLUSIONS: Genotypic diversity of O. tsutsugamushi was revealed in Shandong, with Kawasaki-related genotypes as the predominant types. High nucleotide homologies were identified among the O. tsutsugamushi sequences from scrub typhus patients, rodents, and chiggers. Assiduous surveillance of genetic variation of O. tsutsugamushi in hosts and identification of their pathogenic potentials are essential for the improvement of diagnostic capacity, vaccine development and assessment of epidemiological importance.