

## Genetic Diversity Of *Orientia Tsutsugamushi* Causing Human Scrub Typhus In Upper Regions Of Thailand During 2004-2007

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Scrub typhus caused by gram negative obligate intracellular bacterium, *Orientia tsutsugamushi*, is a widely endemic disease in Asian Pacific regions, including Thailand. The disease is clinically difficult to diagnose and can be lethal if left without appropriated treatment. To develop a sensitive and specific diagnostic tool as well as an effective vaccine for *O. tsutsugamushi* strains circulating in Thailand, it is necessary to understand their genetic diversity and phylogenetic relationship. Utilizing PCR, we have screened 607 febrile patients' blood collected from upper regions of Thailand during 2004-2007. Fragment of *O. tsutsugamushi* specific gene encoding major protein antigen, 56 kDa was detected in 51 cases (8.4%). Amplified fragments spanning over 3 major variable regions of 56 kDa gene have been sequenced and analyzed. Resulting 56 kDa phylogenetic tree demonstrated that detected *O. tsutsugamushi* clustered into 10 clusters. Four clustered with previous reported groups, Gilliam, Kato, TA 716 and LA1, whereas six could probably form new diverse groups. No Karp-like strain was found. The group of *O. tsutsugamushi* will make a choice of reputative strains of each assemblage that would be used as a model of Thai strains for focusing on development of specific and sensitive diagnosed tool and following by vaccine development next.

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