

Abstract

In the third year of this project, the identification of chigger mites in Hualien County has finished. There are totally 2,565 chigger mites that have been identified. Four genera and 25 species were differential, including seven *Leptotrombidium* species: *L. deliense*, *L. imphalum*, *L. kawamurai*, *L. wugongense*, *L. lianghense*, *L. fuji*, and *Leptotrombidium* sp.; 15 *Walchia* species: *W. xishaensis*, *W. zangnanica*, *W. kritochaeta*, *W. parapacifica*, *W. jiangxiensis*, *W. neosinensis*, *W. acugastia*, *W. fragilis*, *W. turmalis*, *W. pacifica*, *W. huensis*, *Walchia* sp.1, *Walchia* sp.2, *Walchia* sp.3, *Walchia* sp.4; 2 *Gahrlepiea* species: *G. latiscutata*, *Gahrlepiea* sp.; and one species belong to new genus. *Leptotrombidium deliense*, 70.1% in total, was the most abundant species, following by *L. imphalum* (12.48%), *L. kawamurai* (4.52%), *Walchia* sp.3 (3.43%) and *Walchia* sp.1 (2.38%). According to the data of rickettsia harbored by chigger mites in Hualien County, it is very obviously that *Orientia tsutsugamushi* was detected in *Leptotrombidium* spp. sampling from August 2000 to June 2001, the average MIR was 7.17. Determining the serotypes of rickettsia with restriction enzyme *Hha*I and *Sfa*NI in the PCR product, most of the samples were like Karp and Gilliam, the number of both serotypes was nearly equal. The identification of chigger mites in Nantou County, due to little collection, only 199 chigger mites has been identified. Three genera and seven species were differential, including *L. deliense*, *L. kawamurai*, *L. fuji*, *L. lianghense*, *W. pacifica*, *W. huensis*; and one species belong to *Trombiculindus*. The abundant species were *W. pacifica* (56.3%) and *W. huensis* (30.25%). Owing to little information, we cannot evaluate vector species in Nantou County. To obtain ribosomal DNA fragment, from 18S to 28S, in chigger mites collected from Kinmen County, using primers designed from ITS region, and amplified 18S-ITS1 and ITS2-28S regions by nested-PCR, contig these regions to get full 18S to 28S DNA fragment. Phylogenetic tree of seven chigger mites collected from Kinmen County constructed based on base-sequence homologies of 18S-28S genes with *Cecidophyopsis alpina* (AJ297569) as outgroup, it showed that three *Leptotrombidium* species on same group, *Odontacarus*, *Ascoschoengastia* and *Helenicula* on another group, *Walchia* was on different branch. The sequence homology compared *L. scutellare*, *L. yui*, *Walchia chinensis*, *Odontacarus majesticus*, *Ascoschoengastia indica*, and *Helenicula* sp. to *L. deliense* were 88%, 90%, 62%, 68%, 55%, and 53%, respectively. Using PCR-RFLP, we have established the methods to identify chigger mite species and detect rickettsia in the same time.

Keywords : scrubs typhus ; chigger mite ; *Orientia tsutsugamushi* ; ribosomal DNA PCR ; Nested PCR