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The distribution and host selection of the chigger mite *Leptotrombidium yongshengense* (Acari: Trombiculidae) in southwest China

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Chiggers (chigger mites) are the exclusive vector of *Orientia tsutsugamushi* (Ot), the causative agent of scrub typhus (tsutsugamushi disease). Although more than 3,000 chigger species have been recorded globally (Nielsen *et al*. 2021), only a few can effectively transmit Ot. Most effective vector species are from the genus *Leptotrombidium* of the family Trombiculidae (Paulraj *et al.* 2021; Balasubramanian *et al.* 2024), and *Leptotrombidium yongshengense* Yu and Yang, 1986 belongs to this genus. *Leptotrombidium yongshengense* was first named and described by Chinese scholars (Yu and Yang 1986), but little is known about this chigger species except the initial morphological description (Wang and Yu 1992; Stekolnikov 2013; Nielsen *et al.* 2021). Based on field surveys and taxonomic identification between 2001 and 2022, the present study retrospectively reports the distribution and host selection of *L. yongshengense* in the region for the first time.

The original data came from previous field surveys at 114 survey sites of southwest China (97° 21'–110 °11' E, 21° 08–33° 41' N) between 2001 and 2022. The 114 survey sites covered the five provincial regions of southwest China namely, Yunnan, Guizhou, Sichuan, Chongqing and Xizang (Tibet). Rodents and other sympatric small mammal hosts were routinely captured with mouse cages, and chiggers were collected from the body surface of the hosts (Li 1997; Guo *et al.* 2013). All the collected chiggers from each host were mounted onto glass slides with Hoyer's medium. After the process of drying, dehydration and transparency in an electric heat drying oven, all the chiggers were taxonomically identified to species under a microscope (Olympus, Tokyo, Japan) (Li 1997; Peng *et al.* 2015). Based on the taxonomic identification, *L. yongshengense* was selected as the subject of the present study. The constituent ratio (C_r), prevalence (P_M), mean abundance (*MA*) and mean intensity (*MI*) were calculated to reflect the infestation status of *L. yongshengense* on its hosts (Peng *et al.* 2018). The patchiness index (m^*/m) was used to measure the spatial distribution pattern of *L.*

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yongshengense among different individuals of the hosts (Lopez 2005), and the association coefficient (V) was used for the interspecific association between *L. yongshengense* and other main chigger species (Guo *et al.* 2006).

Leptotrombidium yongshengense was found at 26 out of 114 survey sites in the five provincial regions of southwest China from 2001 to 2022. A total of 7,028 *L. yongshengense* were identified from 379 rodents and other sympatric small mammal hosts at 26 positive sites, of which 56.85% of *L. yongshengense* were from Sichuan (constituent ratio C_r = 56.86%, 3996/7028), 33.45% from Yunnan (C_r = 33.45%, 2351/7028) and 9.69% from Guizhou (C_r = 9.69%, 681/7028). The 379 positive hosts, from which *L. yongshengense* were collected, belong to 29 species, 17 genera, 6 families and 4 orders (Fig. 1). Among the six families of hosts, the family Muridae and Sciuridae belong to the order Rodentia, the family Erinaceidae and Soricidae belong to the order Eulipotyphla, the family Tupaiidae belongs to the order Scandentia, and the family Ochotonidae belongs to the order Lagomorpha.

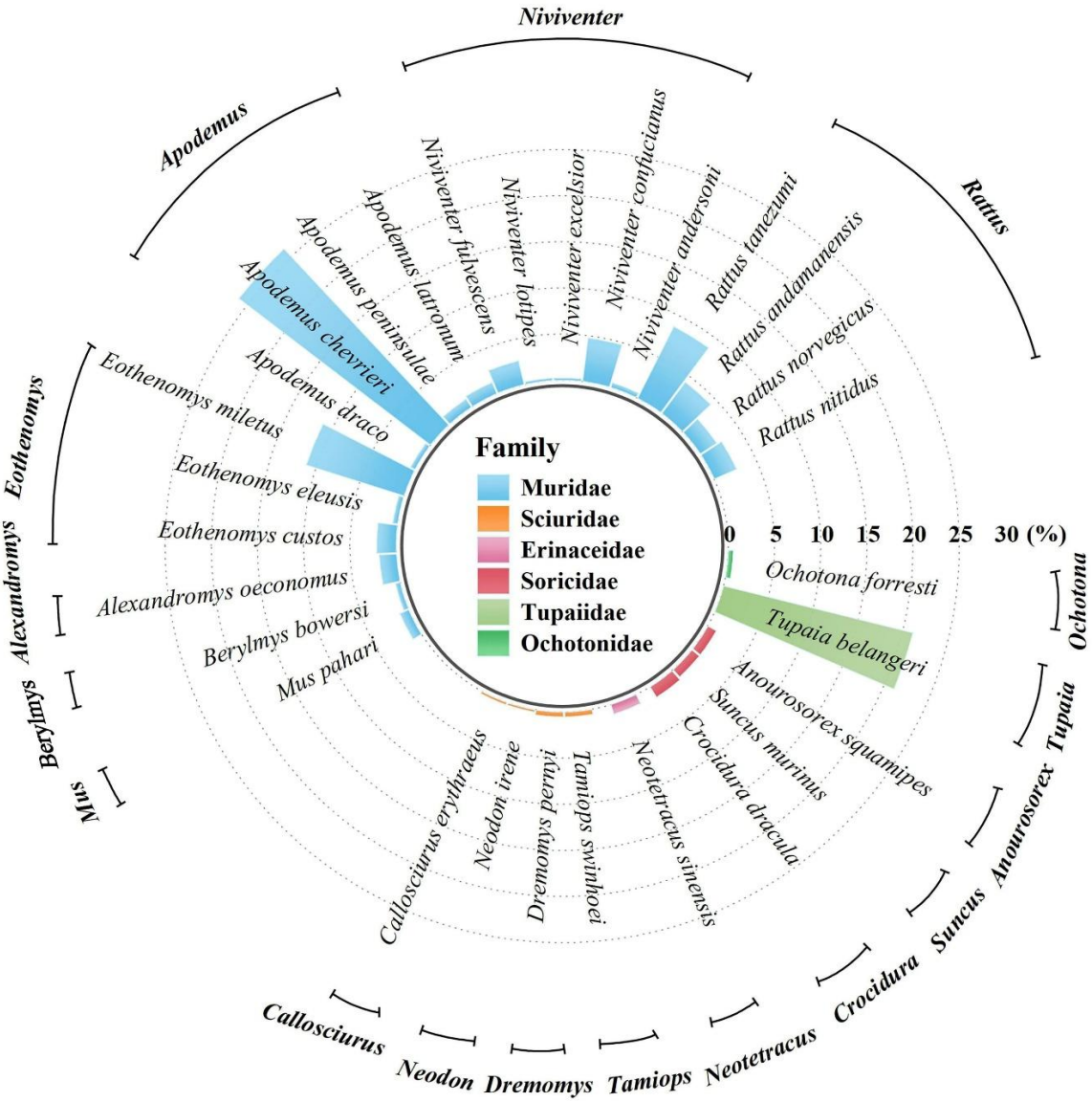

Figure 1. Visualization of the constituent ratio (C_r) of 7032 *Leptotrombidium yongshengense* mites on 379 hosts of different families, genera and species in southwest China (2001–2022).

In vertical distribution, *L. yongshengense* had relatively high C_r, P_M, *MA* and *MI* in high altitude gradients (1000–2000 m, 2000–3000 m, and > 3000 m) compared to the low altitude, under 1000 m ($P < 0.05$, Table 1). Most *L. yongshengense* came from the mountainous landscape ($C_r = 99.50\%$) with much higher infestation indices ($P_M = 2.59\%$, $MA = 0.49$ chiggers/per examined host, $MI = 18.90$ chiggers/per infested host) than those in the flatland landscape (Table 1, $P < 0.01$). All 7,028 *L. yongshengense* were from the outdoor habitat, and no *L. yongshengense* was found in the indoor habitat. The results reveal the fluctuation of *L. yongshengense* in different environments with environmental heterogeneity. *Leptotrombidium yongshengense* have a tendency to live in outdoors of mountainous areas with high altitudes.

Table 1. Geographical distribution of *Leptotrombidium yongshengense* along different environment gradients in southwest China (2001–2022).

Different environmental gradients		*L. yongshengense*		Infestation indices		
		No.	C_r (%)	P_M (%)	*MA*	*MI*
Altitudes (m)	< 1000	42	0.6	0.35	0.01	2.47
	1000–2000	3579	50.92	2.3	0.56	24.35
	2000–3000	2508	35.69	2.68	0.38	14.17
	> 3000	899	12.79	1.23	0.29	23.66
Landscape	Flatland	35	0.5	0.14	0.01	3.89
	Mountainous	6993	99.5	2.59	0.49	18.9

The majority of *L. yongshengense* were identified from *Apodemus chevrieri* ($C_r = 36.95\%$, 2597/7028), *Tupaia belangeri* ($C_r = 31.76\%$, 2232/7028) and *Alexandromys oeconomus* ($C_r = 11.23\%$, 789/7028), with the highest infestation indices on the vole *A. oeconomus* (Table 2, $P < 0.05$). The results suggest that *L. yongshengense* has an obvious host-preference, and *A. oeconomus* has a high susceptibility to the infestation of *L. yongshengense*. A previous report showed that *L. deliense*, belonging to the same genus with *L. yongshengense*, was mainly distributed in low altitude areas in southwest China, and its main host was the rat *Rattus tanezumi* (Lv *et al.* 2021). The above differences between *L. yongshengense* and *L. deliense* reflect the interspecific difference in geographical distribution and host selection.

Table 2. Infestation indices and patchiness index (*m*/m*) of *Leptotrombidium yongshengense* on three important species of small mammal hosts in southwest China (2001–2022).

Names of hosts	Constituent ratios and infestation indices of *L. yongshengense*					*m*/m*
	No.	C_r, %	P_M, %	*MA*	*MI*	
A. chevrieri	2597	36.95	4.14	1.09	26.23	168.26
T. belangeri	2232	31.76	28.88	8.06	27.90	11.13
A. oeconomus	789	11.23	58.33	65.75	112.71	2.89

The values of *m*/m* for *L. yongshengense* were higher than the border value (*m*/m* > 1) for determining the aggregated distribution (Table 2), indicating *L. yongshengense* is of aggregated distribution among different individuals of its hosts. The aggregated distribution pattern of *L.*

yongshengense is consistent with other chigger species (Yin *et al*. 2021), which is beneficial to the growth, development, reproduction and population expansion of chiggers and some other parasites (Nicácio *et al.* 2019). The association coefficient for *L. yongshengense* and *L. rusticum* was $V = 0.10$ ($\chi^2 = 216.47$, $P < 0.01$), and for *L. yongshengense* and *L. scutellare* was $V = 0.07$ ($\chi^2 = 104.79$, $P < 0.01$). Two association coefficients were very low (close to 0), indicating that these chigger species are almost independent of each other in host selection (Guo *et al.* 2006).

Most *L. yongshengense* were from adult hosts ($C_r = 97.20\%$, 6831/7028) with higher P_M, *MA*, and *MI* than those on juvenile hosts (Table 3, $P < 0.05$), indicating that *L. yongshengense* tends to parasitize adult hosts with age-bias in the selection of hosts. The large body surface area, frequent foraging and activities may make adult hosts easy to be invaded by chigger mites and other parasites (Kataranovski *et al.* 2011). More of *L. yongshengense* were found on male hosts; however, the differences of P_M, *MA* and *MI* between male and female hosts were of no statistical significance (Table 3, $P > 0.05$).

Table 3. Infestation indices of *Leptotrombidium yongshengense* on different ages and sexes of hosts in southwestern China (2001–2022).

Ages and sexes of hosts		Constituent ratios and infestation indices of *L. yongshengense*				
		No.	C_r (%)	P_M (%)	*MA*	*MI*
Ages	Adult	6831	97.20	2.51	0.49	19.35
	Juvenile	197	2.80	0.81	0.06	7.58
Sexes	Female	3343	47.57	2.11	0.41	19.44
	Male	3684	52.43	2.27	0.41	17.88

The present study indicates that *L. yongshengense* is a common species of chigger mites with a wide geographical distribution and large population in southwest China. The study has enriched the scientific information about *L. yongshengense* and the genus *Leptotrombidium*. Due to the lack of direct evidence to prove whether *L. yongshengense* can effectively transmit Ot, the epidemiological significance of its distribution in southwest China remains to be further studied.

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