

## Gastrointestinal Helminth Fauna of the Lesser Japanese Mole (*Mogera imaizumii*) in Kanagawa Prefecture, Japan, and Analyses on Infection Status of Two Parasitic Nematode Species of the Host

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### 神奈川県産アズマモグラ (*Mogera imaizumii*) の消化管内寄生蠕虫相と線虫2種の感染状況の分析

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**ABSTRACT.** Sixty-two lesser Japanese moles (*Mogera imaizumii*) were captured on the Shonan Campus of Nihon University in Fujisawa City, Kanagawa Prefecture, from May 2002 to April 2004, and their gastrointestinal helminth fauna was surveyed. One species of cestodes, *Hymenolepis mogerae*, and 4 species of nematodes, *Ascarops mogera*, *Protospirura pseudomuris*, *Parastrongyloides winchesi* and *Tricholinstowia talpae*, were obtained. This is the first report on the helminth fauna of moles in Kanto District. Parasitism by 2 dominant nematode species, *A. mogera* and *T. talpae* showed intensive overdispersion with negative binomial distribution pattern. The factors, which affected the positive-negative infection status and abundance of the 2 dominant species were detected using a generalized linear model. In *A. mogera*, the main effect of host maturity was significant for the positive-negative infection status, whereas the main effect of host age and an interactive effect of host age and body weight were significant for the abundance in each optimal model. In *T. talpae*, the main effect of season of capture was only significant for both the positive-negative infection status and the abundance in each optimal model. These results were explained with some ecological features of the host animals, such as solitary habit and use of latrines, and the life cycle characteristics of helminths, such as use of intermediate hosts.

Key words : gastrointestinal helminth community, generalized linear model, insectivore, lesser Japanese mole, *Mogera imaizumii*

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### INTRODUCTION

The lesser Japanese mole (*Mogera imaizumii*) is a small fossorial mammal inhabiting many regions in eastern Japan [1-3]. Its gastrointestinal helminth fauna has been previously described [4-8]. However, these faunal reports are limited to information on taxonomy and distribution, based on limited numbers of samples from single or multiple localities. To clarify

the ecological aspects of gastrointestinal helminth infection of this host species, it is necessary to analyze community structure of the helminths of the host sample collected from a single locality during various seasons.

In this study, the authors obtained 62 individuals of this host species as well as multiple helminth samples belonging to 5 species. Their prevalence and abundance were analyzed using several statistical techniques to determine the ecological

features of the helminths and the hosts. The results are reported below.

## MATERIALS AND METHODS

All 62 lesser Japanese moles used in this study were captured from the Shonan Campus of Nihon University in Fujisawa City, Kanagawa Prefecture, from May 2002 to April 2004, using the Nishi-type cylindrical traps [9, 10]. The alimentary tracts of all 62 moles were removed from their carcasses, fixed in 10% formalin, stored in 70% ethanol, and dissected under binocular microscope. The collected platyhelminths were softened in 10% acetic acid, flattened on glass slides, and stained with acetocarmine. Detected nematodes were re-fixed in 10% formalin and cleared in lacto-phenol or in 5% glycerin-ethanol. These helminths were observed microscopically and identified up to the species level, as described in the literatures above [4-8] and those on related host species [11-13].

For analysis of helminth infection status, the prevalence, intensity, and abundance of all helminth species were recorded, and the k-values of the negative binomial distribution pattern [14] were calculated for the dominant species. Mann – Whitney's U tests were used for comparison of abundance of each combination of host age, sex, sexual maturity, and captive season groups on all helminth species detected. Furthermore, a generalized linear model (GZLM) was used for the detection of significant factors for the positive-negative infection status and abundance of dominant parasitic nematode species (*Ascarops moger*a and *Tricholinstowia talpae*, see Table 1), based on the PASW Statistics 18 software [15] with Akaike's Information Criterion (AIC), which was used to detect the optimal model. We used the following as candidate factors for GZLM analyses of *A. moger*a: maturity (observed microscopic sections of the testes and ovaries) [16], age (based on wearing pattern of upper molar row) [17, 18], body weight and sex of host individuals, locality (3 parts of the Campus), season of capture (reproductive: February – April; dispersal: May; stable: June – December; based on general ecology of the lesser Japanese mole [2, 3, 10, 19] and its reproductive

schedule in the Kanto District [16-18, 20, 21]), and positive-negative infection status of *T. talpae*. These candidate factors, except for the positive-negative infection status of *T. talpae*, were used for the GZLM analysis on *T. talpae*, as well as positive-negative infection status of *A. moger*a. The abundance data of the 2 nematode species was log-transformed, and the positive-negative infection status data was transformed using the logit function within a binomial distribution for the GZLM analyses. Unfortunately, data on maturity, age and/or body weight was lacking for 13, 26, and 3 of the moles, respectively. All statistical tests were conducted using the maximum possible number of moles with necessary data combinations (33 – 62 moles) on GZLM analyses.

## RESULTS

One species of cestodes, *Hymenolepis moger*ae (Cyclophyllidea: Hymenolepididae), and 4 species of nematodes, *Ascarops moger*a (Spirurida: Spirocercidae), *Protospirura pseudomuris* (Spirurida: Spiruridae), *Parastrongyloides winchesi* (Rhabditida: Strongyloididae), and *Tricholinstowia talpae* (Strongylida: Heligmonellidae), were sampled from the moles. Infection sites, prevalence, mean intensity, and abundance of the helminths are shown in Table 1. *A. moger*a and *T. talpae* were dominant, with high values of prevalence and abundance as compared with the other 3 helminth species. The variance of abundance of these 2 species was much larger than their mean, suggesting that these 2 species exhibited overdispersion, with a negative binomial distribution pattern. K-values of the negative binomial distribution pattern could also be calculated for only these 2 species (*A. moger*a: 0.265; *T. talpae*: 0.106), revealing that *T. talpae* showed a higher degree of negative binomial distribution than *A. moger*a.

Among the comparison of abundance of all combinations of host age, sex, sexual maturity and season groups, significant difference was detected between mature and immature host groups on abundance of *A. moger*a. ( $z = -1.77$ ,  $P < 0.05$ ), on which mean  $\pm$  SE were  $0.57 \pm 0.36$  and  $2.37 \pm 0.64$  in immature and mature host groups, respectively.

**Table 1** Prevalence, mean intensity, and abundance of the gastrointestinal helminths of lesser Japanese moles (*Mogera imaizumii*) from Kanagawa Prefecture, Japan

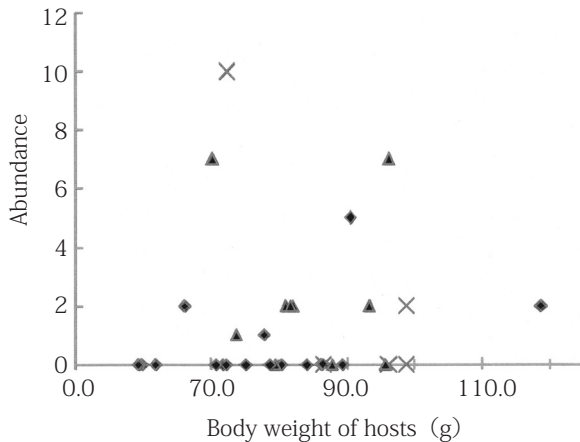
Helminths (infection sites <sup>1</sup> )	Prevalence <sup>2</sup>	Intensity <sup>3</sup>	Abundance <sup>4</sup>
Cestodes			
<i>Hymenolepis moger</i> ae (UI)	3 (4.8)	1.00 $\pm$ 0.00 (1, 1, 1)	0.05 $\pm$ 0.03 (0.05, 0.97)
Nematodes			
<i>Ascarops moger</i> a(S, UI)	27 (43.5)	4.67 $\pm$ 0.83 (1 – 16)	2.03 $\pm$ 0.46 (13.28, 6.53)
<i>Protospirura pseudomuris</i> (S)	1 ( 1.6)	1.00 $\pm$ 0.00 (1)	0.02 $\pm$ 0.02 ( 0.02, 1.00)
<i>Parastrongyloides winchesi</i> (S)	4 ( 6.5)	0.25 $\pm$ 0.25 (1 – 2)	0.08 $\pm$ 0.01 ( 0.11, 1.34)
<i>Tricholinstowia talpae</i> (UI)	16 (25.8)	6.44 $\pm$ 4.02 (1 – 66)	1.66 $\pm$ 1.07 (71.64, 43.12)

<sup>1</sup>S : stomach, UI : upper intestine, <sup>2</sup>number of positive hosts (%), <sup>3</sup>mean  $\pm$  SE (min – max, or numbers of all cases), <sup>4</sup>mean  $\pm$  SE (variance, variance/mean)

**Table 2** Results of analyses (optimal models) of the positive-negative infection status and abundance of 2 parasitic nematode species *Ascarops mogera* and *Tricholinstowia talpae* obtained from lesser Japanese moles (*Mogera imaizumii*) from Kanagawa Prefecture, Japan, using a generalized linear model

Parasites	Objective variants	AIC *	Adopted effects	P
<i>A. mogera</i>	Positive-negative infection	45.8	Maturity of hosts (M)	0.048 **
			M × <i>T. talpae</i> infection	0.280
	Abundance	106.1	Age of hosts	0.020 ***
			Body weight of hosts (BW)	0.364
<i>T. talpae</i>	Positive-negative infection	40.9	Maturity of hosts	0.672
			Season of capture	0.019 **
	Abundance	117.2	<i>A. mogera</i> infection	0.123
			Maturity of hosts	0.134
			Captive season	0.000 ***

(\* Akaike's Information Criterion; \*\* 0.01 < P < 0.05, \*\*\* P < 0.01)



**Fig. 1** Relationship between the abundance of *Ascarops mogera* from lesser Japanese moles (*Mogera imaizumii*) with regard to 2 host individual factors (age and body weight; square: 0-yr-old; triangle: 1-yr-old; cross: 2-yr-old or older)

The results of the analyses using the GZLM are shown in Table 2. In *A. mogera*, the main effect of host maturity was significant for predicting the positive-negative infection status, while the main effect of host age and interactive effect of host age and body weight were significant for the abundance in the respective optimal models with least AICs. The prevalence of *A. mogera* was 21.4% and 51.4% in immature and mature host individuals, respectively. Mean  $\pm$  SE of abundance of this nematode species in each host age were  $0.69 \pm 0.29$  in 0-year-old hosts,  $1.47 \pm 0.53$  in 1-year-old hosts, and  $2.40 \pm 1.73$  in 2-year-old or older hosts. These abundance values were slightly higher in the older moles. Relationships between the abundance of this nematode and 2 significant factors (age and

body weight of the host) are shown in Figure 1. The abundance was not related to the host body weight in the younger moles (0- and 1-year-old), but in older moles (2-year-old or older), it was apparently higher in the heavier individuals.

In *T. talpae*, only the main effect of season was significant for both the positive-negative infection status and abundance in both optimal models (Table 2). The prevalence, abundance, and intensity of this nematode species in each season are shown in Table 3. All of these 3 values are highest in the reproductive season of the hosts.

## DISCUSSION

The parasitic helminth fauna of Japanese moles was not yet reported in Kanto District; this study is the first to report the fauna in this district. There have been multiple reports on the helminth faunas in the host and related species, *Mogera wogura*, *M. tokudae* and *M. etigo*, in both Tokoku and Chubu Districts, which are located to the north and west of Kanto District, respectively [4-8, 11-13]. The present fauna was similar with those of these host species in the 2 districts. Therefore, we could biogeographically connect them.

Both dominant nematode species *A. mogera* and *T. talpae* exhibited an overdispersion distribution pattern with low k-values, i.e., a high degree of overdispersion in which most host individuals harbor none or few parasites while only few host individuals have a high parasite load. K-values have been calculated in many host-parasite relationships, such as the feral cat (*Felis catus*) [22], red grouse (*Lagopus lagopus scotica*) [23], anole lizards (*Anolis* spp.) [24] and 15 cases of microtine rodents (*Clethrionomys* spp. and *Microtus* spp.) [25]. In these examples, the values varied from 0.293 to  $\geq 10$  or converge into infinity, except for the helminths parasitizing the microtine rodents (11 cases), which showed k-values of 0.003 – 0.108 [25]. Compared to these values, the present values (*A. mogera*:

**Table 3** Prevalence, abundance, and intensity of *Tricholinstowia talpae* obtained from lesser Japanese moles (*Mogera imaizumii*) captured during various seasons in Kanagawa Prefecture, Japan

Seasons	Numbers of hosts		Prevalence (%)	Abundance *	Intensity *
	Total	Positive			
Reproductive (Feb.-April)	22	10	45.5	4.09 ± 2.9	9.00 ± 6.40
Dispersal (May)	8	1	12.5	0.25 ± 0.23	2.00
Stable (June – Dec.)	32	5	15.6	0.34 ± 0.16	2.20 ± 0.52
Summer (June – Oct.)	20	2	10.0	0.30 ± 0.21	3.00 ± 0.71
Autumn-winter (Sept. – Dec.)	12	3	25.0	0.42 ± 0.25	1.67 ± 0.54

\* Mean ± SE

0.265; *T. talpae*: 0.106) are extremely low. The intensive overdispersion of these 2 nematode species may be attributed to the ecological features of the host. Moles are typical solitary animals with strong territoriality, and so, home range overlaps are small, and direct contact among individuals is rare, except for their reproductive season [26-30]. This feature may decrease the chances of parasite transmission between host individuals. Conversely, moles use latrines constructed near their nests for excretion of feces [31-38], thus increasing their chances of parasite reinfection. Yokohata and Sagara [8] have reported a case of irregularly high intensity (>200 worms) of *T. talpae* observed in a captured Japanese mountain mole (*Euroscaptor mizura*), which was reared in a small cage (57 × 39 cm, 37 cm in depth) with natural forest litter. They attributed this high intensity to reinfection due to the rearing conditions. The lower chance of transmission between host individuals and higher chance of reinfection would increase the degree of overdispersion of some parasites.

The GZLM analyses showed that relatively few main and/or interactive effects were significant to *A. mogera* and *T. talpae* infection. All of the 4 significant factors—maturity, age and body weight of hosts, and season (highest in the reproductive season of hosts)—are related to the reproductive activity of the hosts. In the European species of moles, the home range size of males increases remarkably in the mating season [28, 30] and the activity of the female moles increases during lactating periods [28]. The increasing activity of moles in their reproductive season may also occur in the lesser Japanese moles, and it may contribute to increasing the opportunity of parasite infection. This phenomenon is more distinctive considering less opportunity of parasite transmission among the solitary host individuals out of their reproductive season, as mentioned above.

Interestingly, the significant factors were different between *A. mogera* and *T. talpae*. The contribution of season of capture was distinctive in *T. talpae* infection, but this was not the case for *A. mogera* infection. In *T. talpae* infection, only the season of capture was a significant factor for both the positive-negative infection status and abundance. This nematode species adopts a direct life cycle, and its larvae directly infect the moles from the environment, while *A. mogera* adopts an indirect

life cycle. A major intermediate host for the genus *Ascarops* is the scarabaeid beetle (e.g. Varma et al, [39]), which is an important part of the diet of Japanese moles [10, 19]. Kamoda et al. [21] showed that the lesser Japanese moles in Kanto District frequently eat scarabaeids throughout the year. In the case of possible reinfection of *T. talpae* mentioned above [8], the Japanese mountain mole was reared in a cage from October 9 to December 3, 1987. Most of the *T. talpae* detected from this host individual were immature. This means the period necessary for re-infection of *T. talpae* is about 2 months or less. This short minimum period for the life cycle further underscores the contribution of the season. Furthermore, both major significant factors in the *A. mogera* infection, namely, maturity and age of host, change irreversibly along their life stages. This suggests that *A. mogera* has a longer life cycle period and/or longer longevity than *T. talpae* and accumulated infection occurs throughout the life span of the moles.

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## 要 約

2002年5月から2004年4月にかけて、神奈川県藤沢市の日本大学湘南キャンパスで62頭のアズマモグラ (*Mogera imaizumii*) を捕獲し、消化管内寄生蠕虫相を調査した。条虫類1種、*Hymenolepis mogerae*、線虫類4種、*Ascarops mogera*、*Protospirura pseudomuris*、*Parastrongyloides winchesi*、*Tricholinstowia talpae* が得られ、関東地方のモグラ類の寄生蠕虫相の初報告となった。これらの優占的な線虫類2種、すなわち *A. mogera* および *T. talpae* は、負の二項分布を伴う顕著な集中分布を示した。これらの優占的な2種の感染の有無および感染虫体数に影響する因子を、一般化線形モデルで検出した。*A. mogera* では、最適なモデルにおいて、宿主の成熟の主効果が

感染の有無に、宿主の齢の主効果および宿主の齢と体重の交互作用効果が寄生虫体数に対して有意に影響していた。*T. talpae*では、最適なモデルにおいて、捕獲季節の主効果のみが、感染の有無と寄生虫体数に影響していた。これらの結果は、単独性や便所の使用のような宿主の社会・行動学的特性や、中間宿主の有無のような蠕虫の生活環上の特性によって説明された。

**キーワード：**アズマモグラ、一般化線形モデル、消化管内寄生蠕虫群集、食虫類、*Mogera imaizumii*

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