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Intestinal helminth communities in the green lizard, *Lacerta viridis*, from Bulgaria

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Abstract

A data set comprising individual host/parasite lists from 100 *Lacerta viridis* (Reptilia: Lacertidae) belonging to four isolated populations in Bulgaria was studied. A total of seven helminth species was recovered (*Leptophallus nigrovenosus, Plagiorchis molini, Oswaldocruzia filiformis, Spauligodon extenuatus, Skrjabinelazia hoffmanni, Physaloptera clausa* and *Mesocestoides* sp.). *Lacerta viridis* is a new host record for the first five of these species. Communities of intestinal helminths of *L. viridis* consist of a few species which resulted in a low species richness, abundance and diversity of infracommunities, which exhibit substantial homogeneity among the four samples. A similar pattern of dominance of two nematode species leading to a relatively high community similarity at both infra- and component community levels was observed. While intestinal helminth communities in lizards from 'marginal' habitats were dominated by the host generalist, *O. filiformis*, those in hosts from 'typical' habitats were dominated by the lizard specialist *S. extenuatus*. The results indicate that the characteristics of the host's habitat are important in determining the composition rather than structure of intestinal helminth communities in *L. viridis*.

Introduction

The green lizard, *Lacerta viridis* Laurenti, 1768 (Reptilia: Lacertidae), is a southern European species that also occurs in central Europe and Asia Minor. Although its subspecies populations have the widest distribution in Europe among the members of the green lizard group (Arnold & Burton, 1978) very little is known about the parasites that affect wild European populations of *L. viridis* (Moravec, 1963; Sharpilo, 1976) in contrast to other species of the group (see Sharpilo, 1961; Moravec, 1963; Roca *et al.*, 1986; Lewin, 1992).

This paper reports on helminth parasites recovered in samples of four populations of *L. viridis* using a data set that has become available from Bulgaria, with a special reference to the composition and structure of the intestinal parasite communities in this host.

Materials and methods

The data set comprises the individual host/parasite lists of a total of 100 *L. viridis* belonging to four isolated

populations that were sampled at three localities in southwestern Bulgaria (Bachevo, Golak and Petrich) and one locality along the Black Sea coast (near Burgas). Some of the characteristics of the habitats where the lizards were collected are presented in table 1. Although the first two localities (Bachevo and Golak) are topographically quite close (only 5 km apart) we assume that there is no contact between the two lizard populations because they are separated by a small river and a road.

Hosts were examined for parasites using standard techniques and worms were preserved in 70% alcohol. Platyhelminths were stained with iron-acetocarmine (Georgiev *et al.*, 1986) and mounted in Canada balsam. Nematodes were cleared in lactophenol and studied as temporary mounts. All parasites were identified and the numbers of individuals of each species of each helminth infracommunity were recorded. Voucher material is deposited in the collection of the Central Laboratory of General Ecology, Bulgarian Academy of Sciences.

Ecological terms are used after Bush *et al.* (1997). Prevalences of 10% (see Bush *et al.*, 1990) and 30% were adopted as the lowest limits in identifying the component

V. Biserkov and A. Kostadinova

Table 1. Data for each of the four localities where *Lacerta viridis* were collected and for the prevalence (P%) and mean abundance (MA ± SD) of helminths found in each sample.

Locality	Bachevo		Golak		Petrich		Burgas	
Altitude (m)	700–800		700–800		150		100	
Isotherm (January; July)	−2°C; 16°C		−2°C; 16°C		1°C; 24°C		2°C; 23°C	
Habitat type	mesic		xeric		mesic		xeric	
Water bodies	small streams		none		irrigation canal		none	
Vegetation	grassland with predominantly deciduous trees		coniferous forest edges		meadow		meadow	
Sample size	40		26		18		16	
Helminth species	P%	MA	P%	MA	P%	MA	P%	MA
Cestodes								
1. *Mesocestoides* sp. (l)*	12.5	13.5 ± 8.2	15.4	27.1 ± 19.8				
Trematodes								
2. *Leptophallus nigrovenosus* (Bellingham, 1844)					11.1	0.6 ± 0.4		
3. *Plagiorchis molini* Lent et Freitas, 1940 (S)**	35.0	2.6 ± 0.9			16.7	0.2 ± 0.1		
Nematodes								
4. *Oswaldocruzia filiformis* (Goeze, 1782) (G)**	7.5	0.2 ± 0.2	15.4	0.9 ± 0.8	55.6	2.1 ± 0.7	43.8	1.5 ± 0.7
5. *Physaloptera clausa* (Rudolphi, 1819) (l)	2.5	0.1 ± 0.1	3.8	0.5 ± 0.5			12.5	0.3 ± 0.2
6. *Spauligodon extenuatus* (Rudolphi, 1819) (S)	35.0	6.2 ± 2.3	26.9	2.2 ± 1.1			6.3	0.3 ± 0.3
7. *Skrjabinelazia hoffmanni* Li, 1934 (S)	10.0	0.4 ± 0.4						

*l, larval helminths; **S, lizard specialist; ***G, generalist species.

and common species, respectively, within each sample. The following measures of community structure were calculated using infracommunity data: the mean number of helminth species and worms; the mean Brillouin's diversity index (HB, values calculated using natural logarithms); and the mean Berger-Parker dominance index (d).

Similarity was measured using Sorensen's binary coefficient for qualitative data and percent similarity index for quantitative data (Krebs, 1989). The within-community similarities were calculated using all possible comparisons while across-community similarities were based on three samples of ten randomly selected pairs of infracommunities. All similarity and diversity measures were calculated using the program BIODIV (Baev & Penev, 1993). Where possible, standard non-parametric tests (Spearman rank correlation, Kruskal-Wallis and Mann-Whitney tests) were applied (Sokal & Rohlf, 1981).

Results

Helminth species recovered

The species composition, prevalence and mean abundance of each helminth species in the four lizard populations are presented in table 1. A total of seven species of helminth was found to parasitize the green lizards. These included the larval cestode *Mesocestoides* sp., the trematodes *Leptophallus nigrovenosus* (Bellingham, 1844) and *Plagiorchis molini* Lent & Freitas, 1940, and the nematodes *Oswaldocruzia filiformis* (Goeze, 1782), *Spauligodon extenuatus* (Rudolphi, 1819), *Skrjabinelazia hoffmanni* Li, 1934 and larval *Physaloptera clausa* (Rudolphi, 1819). Of these, three species (*P. molini*, *S. extenuatus* and *S. hoffmanni*) can be regarded as obligatory parasites of

Lacertidae (see Sharpilo, 1976; Barker, 1987; Sharpilo & Iskova, 1989). *Lacerta viridis* is a new host record for the adult worms of all five species recovered during the study (see table 1).

The four lizard samples differed both in the number and the prevalence/abundance patterns of parasite species. The total number of species varied between 3 and 6 and the prevalence of individual species ranged from 2.5% to 55.6% (table 1). Three species of helminth exhibited a high prevalence in at least one of the populations. These were the nematodes *O. filiformis* (present in all four samples) and *S. extenuatus* (present in three of the four samples), and the digenean *P. molini* (present in two of the four samples). However, with the exception of larval *Mesocestoides* sp. recovered in two of the localities, the mean abundance of helminths was very low among the four samples ranging from 0.1 to 6.2 worms/host examined.

Structure of the intestinal helminth communities

The parameters of the intestinal helminth communities in the four green lizard populations are presented in table 2. Sixty-nine of the 100 *L. viridis* in the data set were infected with 1–3 species of helminths with a range of 1–76 worms. However, the proportion of the sample with no or one helminth species in all localities was notably high (range 0.83–0.96).

The distribution of species among the lizards followed a Poisson series which suggests a random pattern of infection in all four localities (Chi-Square 4.418, 1.221, 1.399 and 1.866; dF = 2, 1, 1 and 1 for samples from Bachevo, Golak, Petrich and Burgas, respectively; $P > 0.05$) while worms showed aggregated distributions (variance/mean ratio 29.6, 12.9, 5.9 and 4.1, respectively). The medians of both distributions among the four

Table 2. Characteristics of the intestinal helminth communities in *Lacerta viridis* from Bulgaria.

Locality Sample size	Bachevo 40	Golak 26	Petrich 18	Burgas 16
Total no. of species	5	3	3	3
No. of component species	3	2	3	2
Identity of common species*	*Pm, Se*	–	*Of*	*Of*
Max. no. of species/host	3	2	2	2
Mean no. of species/host ± SD	0.90 ± 0.74	0.46 ± 0.58	0.83 ± 0.71	0.63 ± 0.62
Max. no. of worms/host	76	27	15	10
Mean no. of worms/host ± SD	9.53 ± 16.8	3.58 ± 6.8	2.83 ± 4.1	2.06 ± 2.9
Mean Brillouin's index (HB) ± SD	0.074 ± 0.18	0.017 ± 0.09	0.081 ± 0.19	0.027 ± 0.11
Mean HB infected hosts only ± SD	0.105 ± 0.20	0.041 ± 0.13	0.122 ± 0.23	0.048 ± 0.14
Max. HB	0.72	0.45	0.57	0.45
Mean Berger-Parker index (d) ± SD	0.936 ± 0.14	0.970 ± 0.10	0.888 ± 0.20	0.968 ± 0.10
Min. d	0.53	0.67	0.50	0.71
Proportion of sample with 0 or 1 helminth species	0.83	0.96	0.83	0.94

Pm, Plagiorchis molini; Se, Spauligodon extenuatus; Of, Oswaldocruzia filiformis; HB and d, values calculated from natural logarithms.

populations studied were not essentially different (species, Kruskal-Wallis H = 6.83, $P = 0.078$; individuals, H = 6.19, $P = 0.103$). The only significant differences were observed between the samples from Bachevo and Golak (species, Mann–Whitney U = 351, $P = 0.027$, medians 1 and 0; individuals, U = 362.5, $P = 0.039$; medians 3 and 0, respectively).

At the component level, there were no perceptible differences in the parasite species richness between the four samples. The number of component species identified within the four component communities was very low (range 2–3; mean 2.5) and only three species (*P. molini, O. filiformis* and *S. extenuatus*) were common in some of them. Of these, the two nematode species numerically dominated the component communities although the pattern differed between localities. The lizard specialist *S. extenuatus* accounted for 64.8% and 61.3% of all helminths in the samples from Bachevo and Golak, respectively, while *O. filiformis* accounted for 72.5% and 72.7% of all helminths in the communities from Petrich and Burgas, respectively.

Infracommunities of intestinal helminths in *L. viridis* were depauperate. The mean species richness varied from 0.46 to 0.90 species/host and the mean infracommunity abundance ranged from 2.06 to 9.53 parasites/host (see table 2). Infracommunity diversity was notably low in all samples (range 0.017–0.081) and was positively correlated with species richness (Spearman's rho = 0.800, $P < 0.05$). The diversity remained low even when values were calculated using data for infected hosts only (range 0.041–0.122) due to the high dominance of a single parasite species (mean Berger-Parker index ranging between 0.888 and 0.97 among localities). Although every helminth species recovered dominated at least one community (summed data), the majority of the infracommunities were dominated by the two nematode species identified as common, and the pattern was similar to that revealed at the component level. *Spauligodon extenuatus* dominated 46% and 60% of the infracommunities in which it occurred (Bachevo and Golak), and *O. filiformis* dominated 75% and 66.7% at Petrich and Burgas, respectively.

Samples from two of the localities (Golak and Burgas)

seemed to exhibit the lowest complexity and diversity due to the higher proportion of hosts harbouring either a single or no parasite species. However, the distributions of the diversity and dominance among individual lizards did not differ significantly when the four samples were compared (diversity, Kruskal-Wallis H = 3.586, $P = 0.31$; dominance, H = 3.161, $P = 0.367$) and this is consistent with the distributional patterns of species and individual helminths presented above. There was no significant correlation between the sample size and the measures of infracommunity structure and diversity with the exception of the mean number of worms/host (Spearman's rho = 1.000, $P < 0.05$). This parameter, however, did not show any significant association with the infracommunity richness, diversity, dominance or the proportion of the sample with 0 and 1 species. Therefore, we assume that differences in the sample size did not bias the overall data on community structure and diversity in the system studied.

Similarity of intestinal helminth communities

Similarity values between helminth communities in *L. viridis* are presented in table 3. Although the species composition differed to a degree between localities, qualitative similarities between the four component communities were rather high due to the small number of species present (Sorensen's coefficient exceeding 0.5 in 4 out of 6 pair-wise comparisons, data not shown). The quantitative similarities among the samples (ranging from 0.080 to 0.725) exhibited differences which can be accounted for by the relatively high population densities of two nematode species, *S. extenuatus* and *O. filiformis*. The four samples fell into two groups with high similarity levels: (i) communities from Petrich and Burgas (0.725) numerically dominated by *O. filiformis*; and (ii) communities from Bachevo and Golak dominated by *S. extenuatus* (see table 3).

Whereas a much higher variability existed in the within-community percent similarity, values for which ranged between the extremes in all four samples (all possible comparisons), the mean similarity values for each sample were relatively high (see table 3). The highest

Table 3. Similarity values (percent similarity index) between helminth communities in *Lacerta viridis*.

	Bachevo	Golak	Petrich	Burgas
Bachevo	0.412 ± 0.02	0.647	0.080	0.186
Golak	0.266 ± 0.04	0.385 ± 0.07	0.258	0.531
Petrich	0.146 ± 0.03	0.238 ± 0.04	0.539 ± 0.05	0.725
Burgas	0.104 ± 0.03	0.290 ± 0.04	0.494 ± 0.05	0.492 ± 0.08

Values above the diagonal represent similarities between the component communities. Values on the diagonal are within-community similarities (mean ± s.e. for all possible comparisons between infracommunities), those below the diagonal represent across-community similarities (mean ± s.e. based on three samples of ten randomly selected pairs of infracommunities).

levels observed in two of the localities, Petrich (mean 0.539, median 0.500) and Burgas (mean 0.492, median 0.492), were due to the distribution of *O. filiformis* (a common species in both component communities) among individual lizards. Overall, within-community similarities were higher than across-community similarities which showed the highest levels (mean 0.495, median 0.444) between samples from Petrich and Burgas.

Discussion

A comparison of our faunistic data with the list of helminth species reported from *L. viridis* in the former Soviet Union (see Sharpilo, 1976 and references therein) emphasizes the peculiar characteristics of the Bulgarian data set comprising primarily intestinal helminths for which green lizards act as final hosts. Sixty-six per cent of the species in Sharpilo's list are larval helminths (vs. 28.6% in our species list) and 41.7% are recovered from the gastrointestinal tract (vs. 85.7% in our list). These differences could reflect the location of the lizard populations studied by Sharpilo (1976) at the periphery of the distributional range of the host species. The new host records for five species reported here add to the knowledge of helminths parasitizing *L. viridis* in Europe.

Communities of intestinal helminths in the four green lizard populations studied in Bulgaria exhibited features that place them among the most depauperate helminth communities. They consist of a restricted number of species, either characteristic for non-reptile vertebrate hosts or with low colonization abilities, which is reflected in the very high proportion of uninfected lizards and those hosts harbouring only one parasite species; the presence of few component and common species and the notably low infracommunity richness, abundance and diversity. Statistical tests showed a considerable homogeneity of the intestinal helminth infracommunities in the four lizard samples with respect to their structure parameters.

Although it is difficult to reveal patterns in such species-poor communities, two features of our data-set indicate that habitat characteristics are most important in setting the simple structure of this host–parasite system. Evidently, the presence of trematode species only in the samples from Bachevo and Petrich is related to the presence of permanent water bodies in these localities

which are necessary for the development of the digeneans. This, coupled with the increased humidity enhancing the survival and transmission of the helminths with direct life cycles, has led to somewhat higher levels of infracommunity richness and diversity of intestinal helminth communities of lizards from the two localities.

Our results also showed similar patterns of dominance of the two nematode species (*O. filiformis* and *S. extenuatus*) leading to a relatively high community similarity at both infra- and component community levels. Surprisingly, the most similar communities were sampled at the most distant localities (Petrich and Burgas) and this was due to the numerical dominance of *O. filiformis*, a generalist species parasitizing a wide range of amphibian and reptile hosts (Barker, 1987), while the communities sampled from the other two localities were dominated by the lizard specialist *S. extenuatus*. Considering the biology, ecology and distribution of *L. viridis* the two groups of lizard habitats detected can be described as 'typical' (Bachevo and Golak) and 'marginal' (Petrich and Burgas). Our results have shown that while intestinal helminth communities in lizards from 'marginal' habitats were dominated by a host generalist, those in hosts from 'typical' habitats were dominated by a host specialist. This indicates that helminth communities in *L. viridis* are affected by local environmental conditions rather than by geographical location. In a study on similar depauperate communities but in a substantially different system (*Anolis* lizards from seven islands in the Caribbean), Dobson *et al.* (1992) suggested that differences between habitats are as significant as differences between islands in determining parasite burdens in lizards.

This is the first data set on a reptile parasite community from the Palaearctic that allows comparisons of the community structure measures to those of various reptile hosts (but dominated by taxa studied in North America) evaluated by Aho (1990). Although slight variations in infracommunity richness was detected among the four samples of *L. viridis*, the values are within the range and close to the means revealed for Reptilia and Lacertilia (0.84 and 0.63, respectively, see Aho, 1990). The mean abundance of parasite communities in green lizards from Bulgaria, however, is considerably lower (range 2.06–9.53 vs. 59.67 and 38.21, respectively, see Aho, 1990). Therefore, our results tend to support the conclusion of Aho (1990) that parasite infracommunities in reptiles are isolationist and non-interactive.

Acknowledgements

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