Ophionyssus saurarum (Acari, Mesostigmata) infecting Lacerta agilis (Reptilia, Lacertidae)

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Material: one female
Free-living species, rare in Poland. It was found in moss, under bark and in nests of rodents. First record from mammals in Poland.
Family Hirstionyssidae Murray, 1877
5. Ixodes hexagonus Leach, 1815
Material: 7 larvae
In Poland, this species mainly was found in southern part of the country. It is the first record from the Lubuskie province. Among hosts are mentioned: Erinaceus sp., Mustela putorius (Linnaeus, 1758), M. nivalis (Linnaeus, 1758), Meles meles (Linnaeus, 1758), Castor fiber (Linnaeus, 1758), Clethrionomys glareolus (Schreber, 1780), Mus musculus (Linnaeus, 1758) C. familiaris and Ovis aries (Linnaeus, 1758) [10].

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References

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Ophionyssus saurarum (Acari, Mesostigmata) infecting Lacerta agilis (Reptilia, Lacertidae)

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ABSTRACT
Thirty specimens of sand lizard, Lacerta agilis, were analyzed and Ophionyssus saurarum was found on three of them. These parasitic mites were located in the ear opening of the host. The only lizard specimens which were infested were those that inhabit areas degraded by human activity.

Key words: mites, Acari, Mesostigmata, Ophionyssus, Lacerta.

Introduction
Given the difficulties in conducting direct observations of lizards and specific difficulties concerning their capture, the information on external parasites found on these reptiles is sporadic. Thus far, species such as Dermacentor (Dermacentor) reticulatus (Fabricius, 1794), Haemaphysalis (Haemaphysalis) concinna Koch, 1844, Ixodes (Exoplaqiger) trianguliceps Birula, 895, Ixodes (Ixodes) ricinus (L., 1758) and Ophionyssus saurarum (Oudemans, 1901) were most frequently reported [1–7].

Most parasitic mites found on lizards belong to the order Ixodida and only Ophionyssus saurarum belongs to the order Mesostigmata in terms of taxonomy. Due to its small size, as females reach approximately the length of 650 mm and the fact that it parasitizes in ear and nose openings this species is relatively rarely reported. Ophionyssus saurarum is one of the mites which are connected with a host in the way that can be defined as strictly absolute. This means that they are connected on the group of hosts which are taxonomically related, in this case only on lizards [6]. Ophionyssus saurarum is the vector of diseases of the lizards’ alimentary canal epithelium and blood cells, which is caused, among others, by coccidia Schellachia bolvarti Reichenschow, 1919 [5]. Owing to this each investigation of this species is also practical, as Lacerta agilis is the species protected by law in the majority of European countries.

Material and methods
The aim of this study was to determine the degree to which the Lacerta agilis lizard is infected with the parasitic mite Ophionyssus saurarum, depending on the host’s habitat. Moreover, attention was drawn to the place where the parasite was located on the host (nose and ear openings, eyes and the cloaca).

The material was collected between 2 May and 10 September 2007. Mites were collected by means of small cotton pads and then they were kept in 70% ethyl alcohol. The next stage of the laboratory investigation was to make microscopic preparations in the Hoyer fluid.

The investigation works were conducted in four research areas located in the vicinity of Poznan (52°26′N 16°51′E), in the vicinity of Chełmiec (50°47′N 16°13′E), in Stare Bogaczwicze (50°50′N 16°11′E) and in Iezy Mountain (50°53′N 15°18′E). The areas were selected in such a way as to represent habitats of the natural character and habitats largely transformed due to the anthropogenic pressure.
Results

Thirty specimens of the sand lizard Lacerta agilis were captured and analyzed and Ophionyssus saurarum was found on three of them. The mites were found in ear openings of two males and one female of Lacerta agilis. One mite was reported in two sand lizards in each ear and in one sand lizard there was one specimen in one ear. All Ophionyssus saurarum specimens were females and they were reported on sand lizards captured on degraded areas, which were greatly influenced by human activity.

According to Bregatova [2] adults of Ophionyssus saurarum are found in ear openings of Lacertidae, whereas protonymphs and deutonymphs are found in the area around the eye or the cloaca. Regrettably, it was impossible to confirm it definitely as the nymph forms were not reported, despite the analysis of both the eye and cloaca areas.

The low percentage of the Ophionyssus saurarum parasites in sand lizards, which was 10% in the present study, may indicate that this parasite poses little threat to these lizards.

References


Zwierzęce rezerwury inwazyjnych dla człowieka gatunków mikrosopyidiów

Animal reservoirs of human virulent microsporidian species

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Praca doktorska wykonana w Katedrze i Zakładzie Biologii i Parazytologii Lekarskiej Uniwersytetu Medycznego im. Karola Marcinkowskiego w Poznaniu i obronnna 3.06.2008 r.

Promotor: Prof. dr hab. Anna C. Majewska
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ABSTRACT. The main objective of the present study was to determined the occurrence of Encephalitozoon intestinalis, E. hellem, E. cuniculi, and Enterocytozoon bieneusi in Poland in animal faecal using the FISH (Fluorescent In Situ Hybridization) and multiplex FISH techniques. Additional objectives included: (1) identification of animal hosts of microsporidia that are infectious to humans amongst free-ranging, captive, livestock and domestic animals; (2) a molecular analysis of randomly selected parasite isolates and determination of their zoonotic potential; (3) evaluation of the role of animals in the dissemination of microsporidia spores in the environment, and an estimation of the potential risk of infection for other animals and humans. A total of 1340 faecal samples collected from 178 species of animals were examined using conventional staining (chromotrope-2R and calcofluor white M2R staining) and molecular techniques (FISH and multiplex FISH techniques). Microsporidian spores were detected in 33 faecal samples (2.5%) obtained from 17 animal species. Microsporidia were demonstrated more often in birds (6.1%) than in mammals (0.7%); the difference was statistically significant (p<0.00001). In addition, the prevalence of microsporidian infections in waterfowl was significantly higher than the prevalence of microsporidian infections in other animals (p<0.03). Animal reservoirs of human virulent microsporidia were disclosed in six of 38 sites where faecal samples were taken from animals. Three species of human virulent microsporidia were identified in animals. Spores of E. hellem were found in 25 faecal samples (1.9%) taken from 12 bird species (6 zoo bird species, 4 free-ranging bird species, 2 livestock bird species). Spores of E. intestinalis were identified in five faecal samples (0.4%) taken from two livestock bird species and two zoo mammal species. In turn, E. bieneusi spores were detected only in three faecal samples (0.2%) taken from three zoo mammal species. It was demonstrated that the new hosts of E. hellem are the following bird species: mallard duck (Anas platyrhynchos), grey leg goose (Anser anser), mute swan (Cygnus olor), black-necked swan (Cygnus melancoryphus), black swan (Cygnus atratus), coscoroba swan (Coscoroba coscoroba), black-crowned crane (Balearica pavonina), nicobar pigeon (Caloenas nicobarica) and carrion crow (Corvus corone). In addition, E. hellem was found for the first time in birds from the Anseriformes and Gruiformes orders. Whereas E. intestinalis was disclosed for the first time in the domestic goose (Anser anser f. domestica), red tailed lemur (Varecia variegata rubra) and the ring-tailed lemur (Lemur catta), while the black lemur (Eulemur macaco flavicans), mongoose lemur (Eulemur mongoz) and the Visayan warty pig (Sus cebifrons negrinus) were first found to carry E. bieneusi. The mammal species that were found to carry E. bieneusi and E. intestinalis are included in The IUCN Red List of Threatened Species. The results of the present study are significant from an epidemiological point of view. The wild, livestock and zoo animals that were found to carry microsporidia live in different conditions, and thus their role as animal reservoirs for these dangerous pathogens varies. Waterfowl birds may be the main source of contamination of surface waters with E. hellem spores and the protection of surface waters is virtually impossible. Moreover, isolates of E. hellem from mute swans have SSU rRNA sequences identical to E. hellem genotype reported 10 years ago in HIV-positive patient in USA (GenBank Accession no. L19070). This result indicate that E. hellem from mute swans can be a potential source of...