

Determination of the prevalence of *Fascioloides magna* (BASSI 1875) and other digenetic trematodes in *Galba truncatula* (O.F. MÜLLER 1774) in the area of Orth/Danube (Lower Austria)

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Digenetic trematodes comprise numerous species of great medical and veterinary importance. These parasites have complicated life cycles with multiple successive hosts. The introduced large American liver fluke *Fascioloides magna* was recorded in free-living red deer and roe deer in the wetlands of the Danube, east of Vienna since 2000. The aim of this study was to determine the current infection rate of the intermediate snail host *Galba truncatula* with *F. magna* and other digenetic trematodes in the area. A monitoring of *G. truncatula* from three locations near Orth/Danube was conducted during 2008. Single collections were taken from three locations from the opposed southern Danube banks (=other locations). A total of 3.871 *G. truncatula* were collected, measured and examined under the microscope for the presence of digenetic trematodes. Every tenth microscopically parasite-free snail was chosen as a random sample. Altogether 68 random samples and 30 microscopically detected isolated trematode stages were tested molecular biologically by PCR and sequencing. Two primer pairs were developed to enable both the detection of trematodes in general and the specific detection of *F. magna* in *G. truncatula*. In addition, a specific primer pair was chosen from literature for the detection of the common liver fluke *F. hepatica*, which is also a pathogen of humans.

Overall, 96 trematode infections (prevalence 2,48%) were detected in the 3.871 examined *G. truncatula*. Trematodes of Paramphistomoidea (prevalence 1,91%), Echinostomatoidea (0,46%) Strigeida (0,10%) and Plagiorchiida (0,05%) were found besides Fascioloidea. *F. magna* was found with an overall prevalence of 0,26% (n = 3.871), whereby the highest prevalence was found at the southern locations (0,47%, n = 427), but also at two northern locations (0,20%, n = 1.975 and 0,30%, n = 1.347). The common liver fluke *F. hepatica*, was found once in a snail collected at Orth. The infection peak of *F. magna* was in July (1,15%).

The comparison of microscopic and molecular biologic methods confirmed former studies, in which DNA-based methods have shown a higher sensitivity. It was possible to differentiate morphological similar trematode species by molecular genetic methods.

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Digitale Literatur/Digital Literature

Zeitschrift/Journal: [Berichte des Institutes für Geologie und Paläontologie der Karl-Franzens-Universität Graz](#)

Jahr/Year: 2010

Band/Volume: [15](#)

Autor(en)/Author(s): Haider M., Liesinger K.

Artikel/Article: [Determination of the prevalence of Fascioloides magna \(BASSI 1875\) and other digenetic trematodes in Galba truncatula \(O.F. MÜLLER 1774\) in the area of Orth/Danube \(Lower Austria\). 17](#)