

Toxoplasma gondii infection in wild birds in Poland

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Wild birds are an important reservoir of T*oxoplasma gondii*, however data concerning this issue in Poland are still limited. Assessment of *T. gondii* prevalence in wild birds and genetic characteristics of isolated parasites can improve the knowledge about their sources and ways of circulating in environment.

The aim of study was to assess the prevalence of *Toxoplasma* infection in selected species of wild birds in northern and central Poland using PCR and molecular characteristics of isolated parasites.

MATERIAL AND METHODS. Samples of tissues (brain, heart, liver, kidneys and lungs) from 96 wild birds: white storks (54), common buzzards (9), mute swans (7), common terns (4), carrion crows (3), mallard ducks (3), rock pigeons (3), great crested grebes (2), western jackdaws (2), hawks (2), great spotted woodpeckers (2), common crane (1), Eurasian magpie (1), common raven (1), European herring gull (1) and white-tailed eagle (1), were collected from wild birds rehabilitation centers in northern and central Poland. After homogenization and digestion (by pepsin) of tissue samples, DNA was isolated using QIAmp DNA Mini Kit (Qiagen) according to the manufacturer's instruction. DNA T. gondii was detected by amplification of 35-fold-repetitive B1 fragment gene in nested PCR (Grigg & Boothroyd, 2001) and in Real time PCR (Lin et al., 2000). To estimate the clonal type of detected parasite, for selected positive samples, multilocus PCR was performed using additional genetic markers according to the method described by Su et al. (2010). Amplicons were sequenced and analyzed using Geneious software and compared with the sequences deposited in NCBI database using Blast.

RESULTS. In total, among 202 tissue samples examined by nested and Real time PCR, T. gondii DNA was found in 11 samples (5.4%), including 8 positive results in nested PCR and 6 positive results in Real time PCR. *T. gondii* DNA was found in 5 samples of hearts, 3 brains, 1 kidney, 1 liver and 1 lungs. Summarized, DNA of *T. gondii* was detected in 8 of 96 examined wild birds (8,3%), including 3 common buzzards, 2 hawks, 1 white stork, 1 common raven and 1 common tern. Multilocus sequence typing of selected B1 positive samples using additional genetic markers, mostly found type II of *T. gondii* (3'SAG2, 5'SAG2, GRA6, BTUB markers), however type II/III (SAG1) and type I (APICO) were also detected.

SUMMARY. The results of study indicate quite frequent infection of *T. gondii* among examined wild birds (8.3%), especially among birds of prey (common buzzards and hawks). Obtained data can confirm the important role of wild birds as an intermediate hosts of *T. gondii* in sylvatic environment in Poland.