DISSERTATIONES
BIOLOGICAE
UNIVERSITATIS
TARTUENSIS
400

ANTS TULL

Domesticated and wild mammals as reservoirs for zoonotic helminth parasites in Estonia

DISSERTATIONES BIOLOGICAE UNIVERSITATIS TARTUENSIS
400

DISSERTATIONES BIOLOGICAE UNIVERSITATIS TARTUENSIS
400

ANTS TULL

Domesticated and wild mammals as reservoirs for zoonotic helminth parasites in Estonia

UNIVERSITY OF TARTU
Press
1632

Department of Zoology, Institute of Ecology and Earth Sciences,
Faculty of Science and Technology, University of Tartu, Estonia

Dissertation was accepted for the commencement of the degree of *Doctor philosophiae* in Zoology (animal parasitology) at the University of Tartu on June 6, 2022 by the Scientific Council of the Institute of Ecology and Earth Sciences University of Tartu.

Supervisors: Prof. Urmas Saarma, University of Tartu, Estonia

PhD Epp Moks, Veterinary and Food Laboratory, Estonia

Opponent: Dr. Smaragda Sotiraki, Veterinary Research Institute, Hellenic Agricultural Organisation- Demeter, Greece.

Commencement: Room 127, Liivi Street 2, Tartu, on 31 August 2022 at 9.15 a.m

Publication of this thesis is granted by the Institute of Ecology and Earth Sciences, University of Tartu

ISSN 1024-6479
ISBN 978-9949-03-965-4 (print)
ISBN 978-9949-03-966-1 (pdf)

University of Tartu Press
www.tyk.ee

CONTENTS

LIST OF ORIGINAL PUBLICATIONS

I. Tull, A., Moks, E., Laurimaa, L., Keis, M., & Süld, K. (2020). Endoparasite infection hotspots in Estonian urban areas. Journal of Helminthology, 94, E104. https://doi.org/10.1017/S0022149X19000920

II. Tull, A., Moks, E., & Saarma, U. (2021). Endoparasite prevalence and infection risk factors among cats in an animal shelter in Estonia. Folia Parasitologica, https://doi.org/10.14411/fp.2021.010

III. Tull, A., Valdmann, H., Rannap, R., Kaasiku, T., Tammeleht, E., & Saarma, U. (2022). Free-ranging rural dogs are highly infected with helminths, contaminating environment nine times more than urban dogs. Journal of Helminthology, 96, E19. https://doi.org/10.1017/S0022149X22000116

IV. Tull, A., Valdmann, H., Tammeleht, E., Kaasiku, T., Rannap, R., & Saarma, U. (2022). High overlap of zoonotic helminths between wild mammalian predators and rural dogs – a potential One Health concern? *Manuscript submitted.*

The author's contribution to the papers (* moderate contribution, ** high contribution, *** very high contribution)

	I	**II**	**III**	**IV**
Original idea	**	**	***	***
Study design	**	***	***	***
Data collection	***	***	**	**
Data analysis	***	***	***	***
Manuscript preparation	***	***	***	***

1. INTRODUCTION

Since the dawn of industrial revolution in the beginning of 18th century, human actions, and policies resulting in urbanization, industrialization and land-use change have consistently boosted the fragmentation and destruction of wildlife habitats. Thus, humans have altered ecosystems on a scale never seen before, which entails problems from high environmental pollution and biodiversity loss to outbreaks of infectious diseases (McMahon et al., 2018; Keys et al., 2019).

Approximately 60% (>800) of pathogens, originating from domesticated animals or wildlife cause human diseases called zoonoses (infectious diseases transmitted between animals and humans). Moreover, it has been estimated that nearly 43% of human infections caused by zoonotic pathogens originate from carnivore hosts (Cleaveland et al., 2001). An overview by Taylor et al. (2001) has identified 1415 species of infectious pathogenic organisms to humans, including 538 bacteria, 307 fungi, 287 helminths, 217 viruses and prions and 66 protozoa. Taken together, these pathogens have a high impact on human health, socio-economics, animals and ecosystems, making parasitic diseases of wildlife a rising One Health concern (Jenkins et al., 2015; Waindok et al., 2021; Casulli et al., 2022).

In 2004, the Wildlife Conservation Society (WCS) forged the term 'One World, One Health', partly in response to the understanding of wildlife as the likely cause of the global outbreak of severe acute respiratory syndrome (SARS) (Kruse et al., 2004). As one of the main focus has been on predicting and mitigating the emergence of zoonotic wildlife diseases, much more focus should be paid on preventing zoonotic diseases by taking into account opinions and warnings from scientists (Cheng et al., 2007). So, to mitigate the impacts of these zoonotic diseases to planetary health, the One Health approach is used, which main idea is that animal health, human health and environmental health are basically interlaced and mutually dependent of each other.

Parasites are globally present among wildlife populations, and the presence of parasites does not directly imply that wildlife is sick. In a naturally functioning ecosystem, parasites can serve as indicators of high biodiversity (Hudson et al., 2006). However, human degraded ecosystems enhance the overlap between domesticated carnivores (primarily dogs and cats) and wildlife species, facilitating transmission of many parasitic infectious diseases (Otranto et al., 2015).

The term helminth applies for parasitic worms, belonging to various taxons: Platyhelminthes (flukes, flat- and tapeworms); Nematoda (roundworms); Nematomorpha (Gordian worms) and Acanthocephala (thorny-headed worms), (Bowman, 2013). These taxa consist of large and diverse group of organisms, some of them are free-living, but most are parasitic, living in, or on most invertebrates as well as vertebrate animals (Bush et al., 2001).

Among these, soil transmitted helminths (STH) or geohelminths are a group of parasitic nematodes (e.g., the roundworm *Ascaris lumbricoides* – the largest intestinal nematode infecting humans and causing ascariasis) infecting both

humans as well as animals via ingestion of viable eggs or through contact with larvae. According to WHO (2022) approximately 1.5 billion people are infected with STHs worldwide, meaning that the main infection route goes by hand-to-mouth contact after exposure to contaminated environment. In general, geohelminths feed on host tissues, including blood, which causes iron and protein loss; hookworms (e.g. *Ancylostomatidae: U. stenocephala, Ancylostoma* spp.) result in chronic intestinal blood loss, causing anemia. Generally, parasitic worms decrease absorption of nutrients, competing for viable vitamins (e. g. vitamin A) in the intestine and reducing hosts` physical fitness (WHO, 2022).

Other zoonotic parasites, like biohelminths (e.g., the fox tapeworm *Echinococcus multilocularis* – the smallest tapeworm, also capable of infecting humans, causing a disease called alveolar echinococcosis, which is one of the most life-threatening helminthic infections in humans), have more complex life cycles, depending on intermediate (development of larval stages) and definitive hosts (sexual reproduction), but some of them may even grow larger in a reservoir/paratenic host or remain in a dormant stage (Bowman, 2013). As both domestic and wildlife animals can be affected with parasites because of their sympatric populations, potential parasite spillover from wild carnivores to domesticated animals and from the latter to humans may appear. Moreover, while dogs and cats serve as definitive hosts for zoonotic parasites, these zoonotic agents can be directly transmitted to humans via human-pet contact.

The population of Europe is approximately 750 000 000 humans, making nearly 10% of the global world population. It is known that nearly 110 million cats and 90 million dogs live in human households (40%) in Europe (FEDIAF, 2021), excluding stray cats and dogs, probably an additional few million individuals. Since most pet dogs are taken to outdoor activities by their owners or are free-ranging, their territories overlap with wild carnivores of which red foxes are the most abundant followed by raccoon dogs, wolves and golden jackals. The wild canid infection dynamic overlapping with domesticated carnivores is complex, depending mainly on their dietary habits and therefore of enzootic parasites (present at some stable rate in a population) in food objects (paratenic, intermediate or reservoir hosts). As each species occupies its own environmental niche, meaning the concrete spectrum of resources that can be utilized by a species, it very often overlaps with other species. It is therefore beneficial for parasites, as they can expand their own ecological niche which in turn suggests that ecologically plastic parasites maximize their geographical distribution, host diversity and abundance.

1.1. Zoonotic endoparasites of companion animals (dogs, cats)

1.1.1. Cat endoparasites of zoonotic importance

Nematoda

The feline roundworm *Toxocara cati* (syn. *mystax*) is a common cat endoparasite with a worldwide distribution that causes toxocariasis in humans that can cause rheumatic, visceral, neurologic, asthmatic problems and even blindness (Smith and Beaver, 1953; Schantz, 1994). Cat is the definitive host, in which the parasite lives in as adults within the lumen of the small intestine, and rodent, bird, earthworm, ant and soil invertebrate species act as paratenic hosts (Dubinsky, 1994; Despommier, 2003). It is an important zoonotic endoparasite not only because it infects young kittens but it causes human toxocariasis. The disease is associated with poverty, but other risk factors include sex, rural areas and exposure to pets. Ingestion of viable, embryonated eggs from contaminated sources (e.g. soil and earthworms etc.) will trigger the infection or the infection is acquired transplacentally via the female cat. The human acts as an aberrant (abnormal) host, in which after the larvae have hatched from eggs, they do not mature into adults, instead visceral larva migrans (VLM) wander through intestines or damage the eyes` optic nerve caused by ocular larva migrans (OLM) (Despommier, 2003). Moreover, the seropositive status has been associated with asthma and epilepsy, poor neurocognitive function and increased serum lead levels. Among humans, children are at highest risk becoming infected with *T. cati* by accidentally swallowing viable eggs (geophagia) during play in sandboxes or on playgrounds that have been contaminated by infected cats or attached eggs on the animal hair stick on the hand. Children from rural areas have had higher infection risk than children from the urban settlement (Dubinsky, 1994; Shokouhi and Abdi, 2018). Preventing infections with *T. cati* are possible to some extent, e.g. covering sandpits with panels, routine treatment of cats with ivermectin or mebendazole might prove enough effective if the guidance of ESCCAP (2020) is followed. According to studies by Talvik et al. (2006) and Kroten et al. (2016) sandboxes and parks in urban and suburban areas are contaminated with *Toxocara* sp. eggs, showing that free-roaming and stray cats distribute zoonotic *Toxocara* sp. eggs, whereas children are the main risk group for larval toxocariasis.

Protozoa

It is often challenging to determine protozoan endoparasite transmission routes from wild to domestic carnivores because they are described by complex networks within their ecosystems. Some of these endoparasites can be transmitted via contaminated soil or food (e.g., *Toxoplasma* sp.) and water (e.g., *Cryptosporidium* spp.), not to mention direct transmission from cats to humans.

Therefore, knowledge of such transmission cycles is essential to map the hazards which in turn lead to the implementation of possible control methods.

The obligate intracellular parasitic protozoan *Toxoplasma gondii* is another zoonotic ubiquitous endoparasite that can infect cats, humans, livestock (e. g. poultry, cattle and pigs) and a myriad of wildlife species, including marine mammals (Dubey and Jones, 2008; Jokelainen et al., 2015). It causes a disease called toxoplasmosis that is associated with neuropsychiatric and behavioural conditions (Milne et al., 2020). Felids are the key host species in the life cycle of *T. gondii* excreting resistant oocysts to the environment, following sporulation during which infective sporozoites evolve. After swallowing the sporulated oocysts by new intermediate host (e.g., human), sporozoites transform into invasive tachyzoites. Tachyzoites undergo asexual reproduction by penetrating all nucleated cells and replicating rapidly in an intracytoplasmic vacuole. The host cells are disrupted due to the following repeated intravacuolar replication and tachyzoites invade adjacent cells resulting in tissue destruction being thus responsible for the clinical symptoms of the disease. As a result of the immune response, the pathogenic process is terminating with the formation of tissue cysts containing slowly replicating bradyzoites which can persist in the intermediate host for a lifetime. Tissue cysts can be found in the brain, skeletal and cardiac muscles or in the retina that are the infective stages for intermediate and definitive hosts through predation.

Humans get the infection by ingesting (sporulated oocysts) tissue cysts from undercooked meat and/or consuming food or water contaminated with oocysts, or congenical or lactogenic transmission occurs from mother to fetus causing miscarriage or other complications (e.g. hydro- or microcephalus). It is also possible to ingest oocysts from the contaminated environment (e.g. soil), (Dubey and Jones, 2008). Small mammals, mainly rodents (e.g. *Rattus norvegicus*, *Apodemus agrarius*, *Mus musculus*) have been considered as the intermediate hosts of *T. gondii.* Even though it has been estimated by Dubey (1995) that most cats only shed oocysts for only one week in their life, the oocysts show extreme resistance against environmental conditions and may be viable in the soil up to one year but even more in the water environment (VanWormer et al., 2013). Several studies have found that *T. gondii* is highly endemic in Estonian wildlife, showing seroprevalence in nearly a quarter of moose (*Alces alces*) and wild boar (*Sus scrofa*) (Jokelainen et al., 2015; Remes et al., 2018). Even higher (60%) seroprevalence has been found in shelter cats (Must et al., 2015). The seroprevalence in the general human population was 55.8% but even higher in hunters (65%) (Lassen et al., 2016).

Cestoda

Cats are commonly definitive hosts for three tapeworms in Europe, although they can be infected with *Diphyllobothrium latum* (*syn. Dibothriocephalus latus*) and a few other non-typical species. Typical cat tapeworms are cosmopolitan

Hydatigera (syn. Taenia) taeniaeformes, Dipylidium caninum and *Mesocestoides* spp. (Bowman, 2013) but also *E. multilocularis* (Knapp et al., 2018; Karamon et al., 2019). The intermediate host of zoonotic *H. taeniaeformes* are mainly rodents (rats, mice and muskrats) in which the larvae mature in the liver (Smyth, 1994). One of the most widespread zoonotic tapeworm is *D. caninum* that has fleas and lice (*Pulex irritans, Ctenocephalides felis, C. canis, Trichodectes canis*) as its intermediate hosts, causing dipylidiasis in humans. In most cases, the disease is asymptomatic, albeit diarrhea, anorexia, rectal itching, abdominal colic and pain due to the emerging proglottids may appear (García-Agudo et al., 2014). Definitive hosts get the infection by accidentally ingesting fleas or louse. It has also a very active gravid proglottids, having the capability to frequently exit the anus and moving in the fur in the perianal region of an infected host. If the proglottids dry, the egg packets are released that resemble small rice grains, which will be consumed by fleas. Humans, especially children may become infected by ingesting fleas (Smyth, 1994; Bush et al., 2001). Studies in France and Poland have found *E. multilocularis* in cats that causes alveolar (multilocular) hydatid disease in humans resulting in a multicyst made up of proliferating vesicles that localizes in liver or lungs (Bristow et al., 2012; Knapp et al., 2018; Karamon et al., 2019.

1.1.2. The overall endoparasite prevalence in cats and risk factors

The overall endoparasite prevalence among cats has been found to range from 20.5% in Europe up to 83% in the United States (Kostopoulou et al., 2017; Wyrosdick et al., 2017). The most prevalent nematode helminths in most studies belong to zoonotic *T. cati* ranging from 8.3% up to 36.6% (Kostopoulou et al., 2017; Zottler et al., 2019). In rare cases, *Ancylostoma* spp. with zoonotic potential has been the most prevalent (27.6%) nematode in cats (Wyrosdick et al., 2017). The prevalence of tapeworms is much lower and is ranging between 0.8% up to 11.1% (Kostopoulou et al., 2017; Zottler et al., 2019). Generally, studies have found eggs from family Taeniidae, but some common tapeworm species have been determined at species level like zoonotic *Hydatigera taeniaeformis* and *Dipylidium caninum*; protozoan endoparasite infection prevalence diapason has been ranging from 0.2% up to 12.4%, including infrequently occurring zoonotic *T. gondii*/non-zoonotic *Hammondia hammondi* oocysts, but higher infection prevalences have been found with *Cystoisospora* spp. and zoonotic *Cryptosporidium* spp. and *Giardia* sp. (Mircean et al., 2010; Becker et al., 2012; Kostopoulou et al., 2017; Zottler et al., 2019). The abovementioned zoonotic endoparasites pose a serious threat to human health, especially to children often playing in contaminated areas (e.g. sandboxes, recreational areas) with endoparasite eggs/oocysts (Talvik et al., 2006; Schurer et al., 2013). The main risk factors for high infection predominance with endoparasites is considered straying, living in rural environment and juvenile age (Mircean et al., 2010;

Becker et al., 2012; Nijsse et al., 2016; Zottler et al., 2019). In addition, consumption of raw or undercooked meat, hunting and older age have been the key risk factors for *T. gondii* infection, and also originating from multi-cat households, catteries is a risk factor for *Giardia* sp. (Jokelainen et al., 2012; Deksne et al., 2013; Must et al., 2015; Blasco et al., 2017).

1.2. Dog endoparasites of zoonotic importance

Nematoda

Dogs serve as definitive host for zoonotic *Toxocara canis* – one of the most important gastrointestinal helminth in dogs that can affect also human health, causing toxocariasis in humans as described above in *T. cati*. The infection may occur when dogs ingests embryonated eggs from contaminated environment (soil, rodents, birds, earthworms etc.), or the disease is acquired in utero (e.g. transplacentally) or via milk (transmammary) from the infected female dog. *Toxocara* spp. eggs are unembryonated when passed in feces of dogs (and cats) into the environment. Under optimal conditions (25–30 ºC, relative humidity of 85–95%) the development into infective larval stage in the egg requires 9–15 days, but it could take time from three to six weeks up to several months, or even one year (Overgaauw, 1997). After ingestion of the eggs, eggs will hatch in the hosts` duodenum (within 2–4 h), then larvae penetrate the mucosal layer of the intestine. Later, when the intestinal wall is penetrated, the larvae invade lymph vessels, migrating to the mesenteric lymph nodes. The next route includes migration to the liver via the portal circulation in venous capillaries. After reaching the liver, most larvae will continue to migrate, exiting the liver via *vena cava*, passing the heart and arriving in the lung through pulmonary artery (Webster, 1958). Some of the larvae are trapped in capillaries and remain in the liver. From the lung alveoli, two different routes are possible, tracheal migration to develop into adult (larvae penetrate alveoli wall continuing their migration via bronchioles and trachea to the pharynx where they are swallowed and can mature into adult worms in the intestine) or a somatic migration during which larvae re-enter the circulatory system via alveoli, being distributed to the somatic tissue and remain arrested as an infected larva (Bowman, 2013). Depending on age, the likelihood of somatic migration progressively increases in older (one or two months old) dogs because of the acquired immunity, and larvae stay in arrested state in the tissues of kidneys, liver, central nervous system and skeletal muscles (Schnieder et al., 2011; Bowman et al., 2013). When paratenic hosts (mice, rats, rabbits, pigs, etc.) become infected with embryonated eggs, the infection occurs directly without tracheal migration, probably because the larvae have already migrated in the tissue of previous host, reaching a stage of maturity (Overgaauw, 1997; Bowman, 2013).

Protozoa

One of the cosmopolitan zoonotic protozoa species is *Giardia doudenalis* (syn. *G. intestinalis* and *G. lamblia*) that can infect gastrointestinal tract (causing giardiasis) of a multitude of mammalian host, including humans, especially children via contaminated food, water or soil. The groups of *Giardia* are discussed as assemblages according to molecular findings of which assemblage A is zoonotic for humans but C and D are host-specific for dogs (Claerebout et al., 2009; Bowman, 2013). Approximately, 7% of the world`s human population is infected with *Giardia* in their intestine (Bowman, 2013). The zoonotic disease is usually not life-threatening but it can become severe in young children and immunocompromised humans resulting in diarrhoea which may become chronic for months (Bush et al., 2001). *Giardia* spp. parasitize in the small intestine where trophozoites attach to the mucosal epithelial cells by their adhesive discs (suckers). Trophozoites are passed to the environment and form infective cysts, otherwise they do no persist in the environment and do not cause infections (Bowman, 2013).

Cestoda

There are 18 orders in the tapeworm class, of which two have zoonotic importance. Tapeworms of the order are mainly found in terrestrial animals and Diphyllobothriidae have aquatic stages as part of their transmission cycles (Bowman, 2013).

The Cyclophyllidae infect a myriad on animals, e.g. amphibian, reptile, bird and mammal species throughout the world. Most tapeworm species found in bird and mammals belong to this order. Similarly, most common tapeworm species found in humans or domesticated mammals belong also to this taxon. Some of the most hazardous tapeworms belong to the family Taeniidae that can grow up to 10 m (*Taenia saginata*) or only a couple of millimetres (*Echinococcus* spp.) but also cause serious harm to its host (e.g. human). Gravid taeniid proglottids or segments are shed by carnivorous definitive host via the anus containing tens of thousands of eggs in each gravid proglottid. The segments have the ability to move freely around on the surface of faecal samples, emptying themselves of their eggs and are dispersed by flies and other insects. On ingestion from the contaminated environment by a suitable intermediate host (generally prey to the definitive host), the oncosphere penetrates the gut wall of intestine and migrates further into the tissues (liver, skeletal or cardiac muscles) and develops into a cysticercus (bladderworm), which is infectious to the definitive host (Bush et al., 2001; Bowman, 2013). So, once the definitive host swallows the second larval stage within a intermediate host (e.g. rodent), the bladder is digested away and the scolex attaches itself in the mucosa of the small intestine where it begins to grow into an adult stage (Bowman, 2013).

Furthermore, the genus *Echinococcus* comprises mainly of two zoonotically important taxa, *E. multilocularis* and a taxonomically yet unresolved *E. granulosus*

sensu lato (*s.l.*) complex, that likely contains several species (Thompson, 2008; Saarma et al., 2009). The fox tapeworm *E. multilocularis* is mainly distributed in the northern hemisphere and uses foxes (red fox and arctic fox), but also other canids (wolves and dogs) as definitive hosts, when they have opportunities to prey on rodents, who act as intermediate host. The parasite causes alveolar echinococcosis in liver of rodents, such as voles and lemmings, as well as in humans. In the latter, cysts are typically sterile proliferating and infiltrating surrounding tissue, making surgical intervention very complicated. If not treated timely, the infected human can die (Smith, 1994; Bowman, 2013).

The larval stage of *E. granulosus s.l.* occurs in herbivorous mammals (sheep, swine, cattle, moose, kangaroos, caribou, etc.) who act as intermediate hosts. Human can be an aberrant intermediate host. Infection results in disease called cystic echinococcosis (CE). The adult worm develops in at least 11 species of canids such as dogs, wolves and jackals etc., who act as definitive hosts. Domestic ungulates (sheep, horses and swine) and dogs are a part of the anthropogenic cycle exposing *E. granulosus s.l.* to humans. The CE is starting after ingestion of a small (30–40 μm) egg that eventually can grow to a very large cyst(s) in humans and may become a lethal disease if not treated timely (Smith, 1994; Bush et al., 2001).

1.2.1. The overall endoparasite prevalence in dogs and risk factors

The overall prevalence of dog endoparasites is different in various European countries, depending mainly on origin of the dog (rural, urban, shelter). Generally, infection prevalence is significantly higher in rural regions rather than in urban areas (Fok et al., 2001; Dubna et al., 2007; Papajova et al., 2014). Furthermore, stray and shelter dogs have even higher infection prevalence with endoparasites (Kostopoulou et al., 2017; Regidor-Cerrillo et al., 2020). Tapeworms, having zoonotic potential, are more common in rural settlements than in urban environment, including Taeniidae and *Dipylidium caninum* (Dubna et al., 2007; Papajova et al., 2014). Among nematodes, *T. canis* has been the most prevalent zoonotic parasite in rural areas in Czech Republic and in Hungary (Fok et al., 2001; Dubna et al., 2007). However, higher prevalence of *T. canis* has been revealed in urban areas of Slovak Republic (Papajova et al., 2014). Spanish stray dogs and rural dogs in Portugal have had highest prevalence with zoonotic hookworms (Ancylostomatidea) (Cardoso et al., 2014; Regidor-Cerrillo et al., 2020). Due to the applied antigen test, shelter dogs in Greece had highest prevalence with potentially zoonotic *Giardia* spp., followed by potentially zoonotic *Cryptosporidium* spp. (Kostopoulou et al., 2017), but in most cases, the most prevalent protozoan is *Cystoisospora* spp.

1.3. Red fox, golden jackal and other predator endoparasites of zoonotic importance

The red fox, a highly adaptable (plastic) canid species, has habituated the urban as well as rural settlements in Europe, distributing a myriad of endoparasites that are brought near to humans and their pets (Deplazes et al., 2004; Laurimaa et al., 2015a). In Estonia, a total of 17 endoparasite taxa have been found in red foxes, including 10 of them with zoonotic potential (Laurimaa et al., 2016b). Another canid on the way to colonizing the northern hemisphere is the golden jackal. The species was reported in Estonia in 2013, having naturally migrated to Estonia from the Caucasian population (Rutkowski et al., 2015). It has been reported by Gherman and Mihalca (2017) that a total of 194 parasite species are distributed by golden jackals, a majority of them, including zoonotic (i.e. *Toxocara* spp., *Echinococcus* spp.), are shared with cats and dogs (Bružinskaitė-Schmidhalter et al., 2011; Citterio et al., 2021). In a previous study, Jõgisalu et al. (2019) have found in Estonia that the most prevalent endoparasites of jackals are *A. alata* and *U. stenocephala*, both having zoonotic potential. One of the most abundant and successful canid in Europe and beyond, aside from the red fox, is the raccoon dog, a common definitive host for many zoonotic helminths. Laurimaa et al. (2016a) described a minimum of 32 helminth species of which 19 are zoonotic in raccoon dogs.

On one end of the scale, among predators that harbour zoonotic helminths, dominate domesticated animals (primarily dog and cats) with their helminths, but on the other end of the scale, wildlife predators can be found with their diverse parasite communities, often with infection rates ranging from 90% up to 100%. Wildlife taxa (e.g. Carnivora, Artiodactyla) keep wildlife diseases endemic in natural ecosystems that often interlace with anthropogenic rural and urban environments.

Thus, the main aims of the present study were to:

1) Identify endoparasites with zoonotic potential in Estonian domesticated and wildlife animals, mainly in cats and dogs, but also in wildlife species (red fox, golden jackal), (**I**, **II**, **III**, **IV**);

2) Determine endoparasite transmission routes in the urban environment and factors impacting the cycle, (**I**, **II**);

3) Compare urban and rural endoparasite fauna among dogs and cats, (**I**, **II**, **III**);

4) Assess the effect of diet on the infection risk among mammalian predators, and to evaluate the overlap between helminth fauna of domesticated (dog) and wildlife canids (red fox, golden jackal), (**III**, **IV**).

2. MATERIAL AND METHODS

2.1. Methods used to study endoparasites of domesticated and wild mammals

2.1.1. Sample collection

In order to study the helminth burden of domesticated and wild carnivores, faecal samples of 657 urban dogs, 290 shelter cats, 84 rural dogs, 131 red foxes, 65 golden jackals, 19 pine martens, 5 American minks, 2 grey wolves, a rural cat and an otter were analysed (**I, II, III, IV**). Fieldworks for sampling were carried out during 2013–2019: (**I**) autumn 2013 till winter 2014, (**II**) August 2015 till October 2016 and (**III** and **IV**) April till June of 2019. The sample collection originated from various towns and rural areas. The urban dog samples (n = 657) were collected from smaller towns (Elva, n = 102; Kunda, n = 89 and Rakvere, n = 29) and larger towns (Pärnu, n = 37 and Tartu, n = 400), (**I**); whereas the rural dog samples (n = 84) originated from Western Estonia (Häädemeeste, n = 13; Hiiumaa, n = 3 and Matsalu National Park, n = 68) as well as did the wild mammal samples (Häädemeeste, n = 31; Hiiumaa, n = 15 and Matsalu National Park, n = 239), (**III, IV**). The sample data of **I** and **III** were summed up (n = 741) to compare findings among rural (n = 84) and urban (n = 657) dogs. Since shelter cat faecal samples were collected from Tartu Animal Shelter, these samples were further divided into rural (n = 160) and urban (n = 130) cats according to their original capture location (**II**).

The study design used only non-invasive methods meaning that none of the studied vertebrate (host) animals were handled or their welfare risked. Samples were held at –80°C for a minimum period of seven days to inactivate highly pathogenic zoonotic parasites, for example *Echinococcus* spp. and *Toxocara* spp. that are endemic in Estonia (Moks et al., 2006; 2008; Laurimaa et al., 2015a, b).

2.1.2. Parasite identification and prevalence

Prior to the analysis, samples were thawed, then concentration flotation technique was applied using sodium chloride [(NaCl, specific gravity = 1.2 g/cm^3 (**I–III**) or NaCl + glucose solution, specific gravity = 1.2–1.3 g/cm^3 (**IV**)], (Roepstorff and Nansen 1998). The glucose was added to further increase the detection rate of taeniid ova. All the helminth eggs and oocysts were counted up in the McMaster chamber per helminth taxa (at species, genus or family level), (**I–II**) or up to 100 per taxa in a sample to prevent large time consumption (**III–IV**), therefore, this is considered as relative intensity. The endoparasite prevalence was determined as the proportion of all eggs/oocysts of all eggs in scats. Endoparasite eggs and/or oocysts were determined based on their morphological characteristics (**I–IV**) or genetically (**III**) (Pavlásek and Ryan 2007; Bowman, 2013; Khatat et al., 2016; Dubey, 2018; Tokiwa et al., 2018; Greenwood, 2020).

Molecular methods were applied to distinguish between similar tapeworm (genus *Taeniidae*) and nematode eggs. For this, single eggs were pipetted on microslides into distilled water droplets and subsequently isolated with a pipette into 1.5 ml tubes for genetic analysis. Genomic DNA was extracted from the isolated eggs and a 506 bp (base pair) for Cestoda or 917 bp fragment for Nematoda of mtDNA COI gene were amplified as described in **II**.

2.1.3. Molecular identification of dogs

Scats of different canid species are sometimes difficult to distinguish and to avoid mixing the data of various species, a genetic analysis was conducted to identify predator species (III–IV). Genomic DNA was isolated from scats using the QIAamp Fast DNA Stool Mini Kit (Qiagen, Hilden, Germany) according to the manufacturer's protocol. A hypervariable fragment of the mitochondrial DNA (mtDNA) control region that enables to distinguish between wolves and dogs in Estonia, was polymerase chain reaction (PCR)-amplified and sequenced as described in Plumer et al. (2018) The same mtDNA fragment allows also distinguishing other canids (IV). In brief, a 351 base-pair (bp) fragment of the mtDNA control region was PCR-amplified using 0.25 pmol of primers Canis1F and Canis3R. The reaction mixture (20 µl in total), contained 2 µl of DNA, 4 µl of 5× Phusion HF buffer, 0.4 mM deoxynucleoside triphosphate (dNTP) and 0.2 µl Phusion HS II polymerase (Thermo Fisher Scientific, Waltham, USA). The following PCR cycling parameters were used: 30 s at 98 °C, then 10 cycles: 10 s at 98 °C, 30 s at 68 °C (with touchdown of –0.8 °C per cycle), 45 s at 72 °C; then 35 cycles: 10 s at 98 °C, 30 s at 60 °C, 45 s at 72 °C, and finally 2 min at 72 °C. PCR products were purified with 1 U of both FastAP and ExoI (Thermo Fisher Scientific). Purified PCR products were sent for sequencing to the core laboratory of the Institute of Genomics at the University of Tartu. Sequences of both DNA chains were aligned with CodonCode Aligner v.5.0.2 (CodonCode Corp.) to produce consensus sequences and corrected using BioEdit v.7.2.5 (Hall, 1999). The length of the final alignment was 245 bp and the dataset was further aligned with homologous wolf and dog sequences (Hindrikson et al., 2012; Plumer et al., 2018), red fox, and golden jackal (**III–IV**) sequences from Estonia.

2.1.4. Molecular identification of food objects

For the identification of birds, mammals, reptiles and fish, a 303 bp fragment of mtDNA cox1 gene was PCR-amplified with primers AVS2F and AVS3R as described in **III** and **IV**. PCR reactions were carried out in a total volume of 20 µl with 1x Phusion HF Buffer (Thermo Fisher Scientific), 0.2 mM dNTP, 0.25 µM of each primer and 0.4 U Phusion Hot Start II DNA Polymerase and 2 µl of purified DNA. The PCR mixture was initially denatured at 98 °C for 30 s, followed by 10 touchdown cycles for 10 s at 98 °C, 20 s at 60 °C (reducing the temperature 1 °C per cycle) and 30 s at 72 °C, followed by 30 cycles of 10 s at

98 °C, 20 s at 50 °C and 30 s at 72 °C. In case the PCR was negative due to highly degraded DNA, we performed a second analysis by PCR-amplifying a shorter, 183 bp fragment of mtDNA 12S rRNA gene, using primers Ave12F and Ave12R, described in Oja et al. (2017). PCR products were checked using 2% 1xTAE gel-electrophoresis and visualized under UV radiation using ethidium bromide.

PCR products were purified, sequenced and nucleotide BLAST (https://blast.ncbi.nlm.nih.gov/Blast.cgi) was used to identify various taxa, such as reptiles, fish and birds in **III** and **IV**.

2.1.5. Morphological analyses of food objects

The morphological analysis of food object is described in Valdmann & Saarma (2020). Shortly, faecal samples were processed according to standard laboratory procedures (Reynolds & Aebischer, 1991). Non-mammal remains (e.g., birds) recovered in predator scats were identified in comparison with reference materials. Mammal remains were identified by examining the cuticular pattern and the medulla of the hairs using reference manuals (Teerink, 1991; Toth, 2017) and hairs collected from hunted animals (**III**, **IV**).

2.1.6. Spatial analyses

The spatial analyses included descriptive maps created with the Free & Open Source QGIS (3.24). The aim was to visualize the geographical locations of predator scats and to measure the average distance between private houses and the collected scat samples (**III, IV**). Further, the buffer distance around faecal samples was considered as the average free-ranging or straying area of mammalian predators from detached houses. Another buffer was generated in **IV** by adding together the first buffer with the infected faecal samples layer situated inside the buffer zone to count detached houses in the potential hazard zone. The map layers originated from public WMS services (Land Board, 2022).

2.1.7. Statistical analyses

Proportions were compared in **II–IV** using Chi-squared tests of independence (PROC FREQ) to determine independent variables associated with overall (co)infection and single taxa (species, genus, family) prevalence. If one or more cells in the 2 X 2 contingency tables had expected values of less than 5, Fisher's exact test was used. The non-parametric Mann-Whitney U test was used to compare the mean parasite richness between three larger canid (red fox, golden jackal, dog) groups (**IV**). Chi-squared and non-parametric tests were performed using software of SAS Studio v9.04 (SAS Institute, Cary NC, 2021).

In general, all statistical models contained dependent (response) variables determined as (co)infection risk (0 – uninfected; 1 = infected) or infection intensity (the sum of counted ova/oocysts), (**I–IV**). The same aforementioned analogy

applied for a specific endoparasite taxa (species, genus, family) infection or intensity (**II–IV**). Various predictor variables were formed to identify factors impacting infection intensity and co(infections) with endoparasites. Generalized linear mixed models (**I**) or generalized linear models (package 'glmmTMB', Brooks et al., 2017 or 'logistf', Heinze & Ploner, 2018) with a binomial error distribution were used for evaluating overall and single endoparasite prevalence (**II–IV**). Models with a negative binomial error distribution were used for assessing the factors influencing endoparasite intensity (**I–IV**). Models were compared using the Akaikes' information criterion corrected for small samples (AICc) (Burnham & Anderson, 2004). Package "MuMIn" (Barton, 2019) was used for conducting model selection and model averaging. Only models with the highest Akaike weight *wi*(AIC), (ΔAICc<2) were described as the model with the highest Akaike weight provides a continuous measure of strength of evidence. It is especially important to assess the weight of evidence in favor of the best model when a binary decision is made and the other candidate models (with higher AIC values) are simply discarded (Wagenmakers et al., 2004). Furthermore, the weights (*wi*) of the same factors presented in one model set were summed for calculating the relative variable importance (RVI), (**I, III, IV**). All statistical modeling was performed in R (R Development Core Team, 2022).

To estimate the infection risk and intensity of urban dogs (**I**), the following independent variables: 'excrement size' (excrement were classified according to their diameter: <15 mm as 'small', 15–20 mm 'medium', >20 mm as 'large'), 'town size'(small towns – less than 20,000 inhabitants or large towns – more than 40,000 inhabitants), 'housing type' (detached individual houses or densely populated apartment-houses), 'season' (autumn, winter, spring, summer) and 'potential hazard zone' (sidewalk or potential hazard zones consisting of green areas and recreational zones near public playgrounds, schools or nurseries). The random variable included location (town).

To model the conjunction between (co)infection prevalence and intensity among shelter cats (**II**), a set of explanatory variables were included: age (young or adult), location (rural or urban) and the time spent in the animal shelter (1–14 days, ≥15 days), (see further details of variables in Table 1 in **II**). Furthermore, a distinct group of potentially directly transmittable zoonotic endoparasites was formed consisting of *T. gondii/H. hammondi*, *Cryptosporidium* spp., *Giardia* sp., *Cystoisospora* spp., *T. cati* and *E. aerophilus* (**II**, Online Resource 4).

Last but not least, the (co)infection prevalence and intensity among predators, mainly dogs, red foxes and golden jackals was analysed in Western Estonian rural areas (**III, IV**). The independent variable (food object) was divided into five categorical variables: rodent, game, bird, dog food and plant material. Aside from the food objects, urban dog (co)infection prevalence data (**I**) was compared to rural dog (co)infection prevalence (**II**) to compare infection risk of endoparasites in these areas.

To measure the overlap of helminths between various host species (dog, red fox and golden jackal), the Pianka's Index (Pianka, 1973) was calculated (0 – no overlap, 1 – total overlap), (**IV**).

3. RESULTS

3.1. Endoparasites of urban and rural animals and possible transmission patterns

3.1.1. General zoonotic endoparasite fauna

In rural areas (**III**, **IV**), out of the 315 genetically identified predator scat samples 84 belonged to dogs, 131 to red foxes, 65 to golden jackals, 19 to pine martens, 7 to raccoon dogs, 5 to American minks, 2 to grey wolves, 1 to a cat and 1 to an otter. Of these hosts six helminth taxa (Taeniidae*,* 265; *Eucoleus spp./Trichuris spp*., 158; *U. stenocephala,* 64; *T. canis*, 28; *T. leonina,* 4 and *T. cati,* 1) were determined with a total frequency of 520 helminth specimen.

In total, 657 and 84 faecal samples of urban and rural dog were analysed, respectively (**I; III**). Urban dog faecal samples included five endoparasite species or genera with an overall prevalence of nearly 10% (**I**; Table 1). The most abundant endoparasites among urban dogs were *U. stenocephala* (3.5%) and *Toxocara* spp. (3.4%). In comparison with urban dogs, the overall helminth prevalence differed nearly nine times between urban and rural dogs (9.8% and 87%, respectively), (I, III). However, the rural dog scat samples contained in total 116 helminth specimen: Taeniidae (65.5%), followed by *Trichuris* spp./*Eucoleus* spp. (15.5%), *U. stenocephala* (14.7%) and *T. canis* (4.3%), (**III**, Fig. 2). The general parasitological examination of shelter cats indicated that nearly half (47.6%; 138/290) were infected with endoparasites (**II**, Table 3). The highest prevalence rate was assessed for *T. cati* (36.6%), followed by *Cystoisospora* spp. (12.4%), Taeniidae (4.1%), *T. gondii/H. hammondi* (3.4%), *E. aerophilus* (2.1%), *Cryptosporidium* spp. (2.1%), *Ancylostoma* sp. (0.7%) and *Giardia* sp. (0.7%) (**II, Fig. 1**). Genetic analyses revealed two potentially zoonotic helminth species among shelter cats, namely *Ancylostoma tubaeforme* and *Hydatigera taeniaeformis*.

Among wild predators, 92.4% (121/131) of red fox environmental scat samples were infected with endoparasites. The most prevalent infection included *Eucoleus* spp./*Trichuris* spp. (80.2%; 105/131), followed by Taeniidae (76.3%; 100/131) and *U. stenocephala* (24/131, 18.3%) (**IV**, Table 1). The golden jackal scat samples had comparably high proportion of infected scats (90.8%; 59/65) with the red fox scats containing most frequently eggs of Taeniidae (87.7%; 57/65), followed by *U. stenocephala* (18/65; 27.7%) and *Eucoleus* spp./*Trichuris* spp. (21.5%; 14/65), (**IV**, Table 1). The niche overlap of helminth taxa revealed highest result for golden jackals and dog (0.99) and slightly lower results were found between red foxes and golden jackals (0.84) as well as between dogs and red foxes (0.84), (**IV**).

3.1.2. Rural and urban zoonotic endoparasite (co)infections among domesticated and wild animals

Considering the non-invasive coprological study methods applied (**I–IV**), it was not possible to detect all endoparasites. The main focus was on determining helminth (tape- and roundworm) parasite taxa at species, genus or at least family level. Thus, the detected species richness might be an underestimation of the real species abundance. In **III** and **IV** genetic methods were applied to determine helminth species but most likely due to high UV-radiation in spring season the ova were too degraded for DNA isolation compared to **II** where endoparasite eggs were isolated from fresh faecal material.

Coinfections in domesticated animals were significantly lower among urban cats ($\beta_{URBAN} = -1.3$; SE = 0.4; P = 0.0005) and dogs (P < 0.0001) than among rural cats and dogs, (**II, III**). Rural dogs (73/741; 9.9%) had significantly higher (P < 0.0001) (co)infection prevalence with biohelminths (Taeniidae), while urban dogs were significantly (co)infected with geohelminths (P < 0.0001), mainly with zoonotic *U. stenocephala* and with *Toxocara* spp. (P = 0.5), (**III**, Fig. 4). Moreover, rural dogs preying on rodents had significantly (3.7 times) higher odds to be coinfected than rural dogs who had not preyed on rodents ($\beta_{RODENT} = 1.3$; SE = 0.6; P = 0.02). The model also indicated a 63% of reduction in rural dogs' coinfection with helminths, if they consumed dog food ($\beta_{DOGFOOD} = -1.0$; SE = 0.6; P = 0.1), (**III**).

Furthermore, shelter cats had also significant difference in infection prevalence between rural and urban cats (P = 0.0006). Namely, over half of rural cats (56.7%; 91/160) were infected with endoparasites compared to the 1/3 of infected urban cats (36.2%; 47/130), (**II**, Table 3). In resemblance with dogs, urban cats had significantly lower endoparasite infection prevalence with Taeniidae ($\beta_{URBAN} = -2.1$; SE = 1.1, P = 0.04) but also with *T. cati* ($\beta_{URBAN} = -1.0$; SE = 0.3; P < 0.001) and overall helminths ($\beta_{URBAN} = -1.0$; SE = 0.3; P < 0.001) than rural cats (**II**, Table 2). Rural cats in quarantine up to 14 days had significantly higher endoparasite infection prevalence with directly transmittable zoonotic endoparasites than urban cats in quarantine ($\chi^2 = 5.5$; P = 0.01), (in **II** Online Resource 4).

Of the wild predators, the highest coinfection prevalence (80.2%) was found among red foxes being the most coinfected with Taeniidae and *Eucoleus* spp./ *Trichuris* spp. (62.9%) (**IV**; Table 2). The golden jackal had much lower coinfection prevalence (46.2%) of which the most prominent coinfection occurred between Taeniidae and *U. stenocephala* (36.7%). Furthermore, diet affects the coinfection prevalence with multiple helminths among predators, preying on rodents increased the risk of coinfection with multiple helminth taxa 2.5 times than not preying on rodents ($\beta_{RODENT} = 0.9$; SE = 0.3; P < 0.001), (**IV**).

3.1.3. Main infection models and main zoonotic endoparasite transmission patterns and dynamics among domesticated pets

Main infection prevalence models revealed lower infection with endoparasites among larger urban dogs (β_{Large} = –1.0, SE = 0.4) than among small dogs. Depending on the housing type, higher endoparasite prevalence was predicted in apartment-house districts ($\beta_{ApartmentHouse}$ = 0.9, SE = 0.3) than in private house regions. The infection gradient between large and small towns implied higher endoparasite infection prevalence ($\beta_{SmallTown}$ = 0.8; SE = 0.3) as well as intensity ($\beta_{SmallTown}$ = 1.5, SE = 0.8) towards smaller towns (**I**). However, while comparing urban areas with rural areas, higher endoparasite infection prevalence shifts from larger and smaller towns towards rural areas where helminth prevalence between urban and rural dogs differs approximately 9 times (**I, III**) reaching ~ 90% in rural areas (III, **IV**). Similar findings were acquired for zoonotic roundworms (*Toxocara* spp., *U. stenocephala* and *Capillaria* spp.) infections with one exception, meaning that urban dogs have higher infection prevalence in potential hazard zones than on streets ($\beta_{PotentialHazardZone}$ = 0.6; SE = 0.3). Also, spatial analyses confirmed for rural areas that at least 160 private houses were situated in the buffer zone of ≤ 578 m in which the average distance of an infected environmental scat to a private reached as far as 59 meters (**IV**). Analogous patterns apply for infection intensity models with endoparasites and roundworms. Infection intensity models imply for both groups (endoparasites and roundworms) higher infection intensity in apartment-house districts than near detached houses ($\beta_{ApartmentHouse}$ = 2.3; SE = 0.7). Large-sized dogs tend to have lesser intensity with both parasite groups than small-sized dogs (β_{Large} = –1.5; SE = 0.8). Different seasons have an important impact on the endoparasite infection dynamics, mainly the infection prevalence and intensity increased in spring and autumn but decreased in summer season compared to winter season (**IV**).

Age of shelter cats determined the infection risk and intensity with endoparasites. Juvenile cats had significantly higher infection prevalence with helminths (β_{YOUNG} = 0.5; SE = 0.3; P = 0.04) as well as 2.7 times higher infection intensity (β_{YOUNG} = 1.0; SE = 0.4; P = 0.02) and with zoonotic *T. cati* (β_{YOUNG} =0.7; SE = 0.3; P = 0.01) than adult cats. On the other hand, compared to adult cats, young ones had significantly lower infection prevalence with *T. gondii/H. hammondi* (β_{YOUNG} = –2.8; SE = 1.5; P = 0.003) (**II**, Table 2). In quarantine cats, some endoparasite [(*Cystoisospora* spp. ($\beta_{QUARANTINE}$ = –1.3; SE = 0.4; P = 0.001)] and with total protozoa ($\beta_{QUARANTINE}$ = –0.8; SE = 0.3; P = 0.01)] infection prevalence decreased, but the opposite effect applied for cats ready to be adopted. On the contrary, other endoparasites (*Cryptosporidium* spp. [($\beta_{QUARANTINE}$ = 2.3; SE = 1.5; P = 0.03) and with *E. aerophilus* ($\beta_{QUARANTINE}$ = 2.3; SE = 1.4; P = 0.03)] were more common in quarantine cats and less found among cats ready for adoption (see in **II** Table 2).

Diet preferences also shape the endoparasite fauna among rural predators. Indeed, preying on various intermediate, reservoir/paratenic hosts increases significantly infection risk with helminth taxa (**III**, **IV**). When predators preyed

on reptiles or rodents, the infection risk with *Eucoleus* spp./*Trichuris* spp. increased 5.5 ($\beta_{REPTILE} = 1.7$; SE = 0.7; $P < 0.01$) and 3 ($\beta_{RODENT} = 1.1$; SE = 0.3; $P < 0.0001$) times, respectively (**IV**). Among golden jackals, the infection prevalence ($\beta_{RODENT} = 2.6$; SE = 0.7; $P < 0.001$) and intensity ($\beta_{RODENT} = 4.1$; SE = 1.3; $P < 0.001$), ($\beta_{GAME} = 2.6$; SE = 1.2; $P = 0.03$) with helminths *Eucoleus* spp./ *Trichuris* spp. increased significantly, if preying on rodents or game. Notably, red foxes had up to 4 times higher odds to be infected with *T. canis*, if they feed on plant material ($\beta_{PLANT} = 1.4$; SE = 0.6; $P = 0.02$), (**IV**).

4. DISCUSSION

4.1. Endoparasites with zoonotic potential

Our results indicate clearly that domesticated animals, dogs and cats, as well as sympatric wildlife predators distribute endoparasites with zoonotic potential (**I–IV**). It has been shown that dogs can transmit over 60 zoonotic parasites infecting humans (Macpherson et al., 2013), originating from wildlife species like red foxes and golden jackals (Gherman and Mihalca, 2017). Over a third of examined shelter cats in the **II** study (36.6%) excreted parasitic stages of zoonotic *Toxocara cati* which is one of the most prevalent zoonotic gastrointestinal helminth worldwide (Gracenea et al., 2009; Becker et al., 2012; Loftin et al., 2019; Tull et al., 2021), (Table 1), causing toxocariasis in humans, mainly in young children (Despommier, 2003). Also, helminths that only in rare cases have infected humans such as *Hydatigera taeniaeformis, Ancylostoma tubaeforme* and *Eucoleus aerophilus* were found. It has been suspected, that their zoonotic potential is probably not well studied or known (Rossin et al., 2004; Altreuther et al., 2005; Lalošević et al., 2008), (Table 1). Genetic analysis confirmed the presence of *H. taeniaeformis* (**II**), which can cause severe illness in humans (Ekanayake et al., 1999), (Table 1). Formerly, Valdmann et al. (2004) have demonstrated infections with *H. taeniaeformis* (3%) in Estonian Eurasian lynx. The tapeworm *H. taeniaeformis* has a cosmopolitan distribution and it uses felines as definitive hosts. The findings of the **II** study imply that high infection rates of *T. cati, A. tubaeforme, E. aerophilus* and *H. taeniaeformis* in cats, originating from various areas, especially from rural areas, indicate coexisting sylvatic and synanthropic cycles, and imply a simple transmission route of zoonotic parasites between sympatric intermediate and definitive or reservoir hosts in the environment. Thus, domestic cats, rather than wild carnivores, could pose a greater risk for human's health because of their close contacts with people. The lack of accurate diagnostics or infrequent diagnosis of the aforementioned endoparasites may result in higher numbers of infected humans. Hence, health workers and officials need to consider the possibility that stray cats distribute zoonotic endoparasites that are a threat to human health.

Table 1. Main cat endoparasites in studies in Europe and in the US.

	Switzerland (Zottler et al., 2019)	Germany (Becker et al., 2012)	Romania (Mircean et al., 2010)	US (Wyrosdick et al., 2017)	Greece (Kostopoulou et al., 2017)	Estonia (Tull et al., 2021)
Method	scat+morphology+duplex PCR	scat+morphology+antigen	scat+morphology	scat+morphology	scat+morphology+antigen+PCR	scat+morphology+PCR
Sample size	n = 664	n = 837	n = 414	n = 76	n = 264	n = 290
Cat status	stray, shelter, owned	shelter	household	shelter	shelter, household	shelter, rural, urban
Cestoda						
Taenia-type*	11.1% (74/n)	2.0%			0.8%	2.4% (7/n)
*Hydatigera taeniaeformis**			2.7% (11/n)			1.7% (5/n)
*Dipylidium caninum**	0.6% (4/n)		0.2% (1/n)			
*Diphyllobothrium latum**	0.2% (1/n)					
Mesocestoides spp.*				1.3% (1/n)		
Nematoda						
*Toxocara cati**	18.5% (123/n)	27.1%	20.3% (84/n)	6.6% (5/n)	8.3%	36.6% (106/n)
Capillaria sp.	4.7% (31/n)	5.0%			4.2%	
*Eucoleus aerophilus**			3.1% (13/n)			2.1% (6/n)
*Ancylostoma tubaeforme**						0.3% (1/n)
Ancylostoma spp.*			10.1% (42/n)	27.6% (21/n)		0.3% (1/n)
Aelurostrongylus abstrusus	2.3% (15/n)	1.0%	5.6% (23/n)			

	Switzerland (Zottler et al., 2019)	Germany (Becker et al., 2012)	Romania (Mircean et al., 2010)	US (Wyrosdick et al., 2017)	Greece (Kostopoulou et al., 2017)	Estonia (Tull et al., 2021)
Hookworms*	1.1% (7/n)	1.1%			7.6%	
Strongyloides spp.*			3.4% (14/n)			
Aonchotheca putorii				1.3% (1/n)		
Spirometra sp.*				7.9% (6/n)		
Protozoa						
*Cryptosporidium spp.**				6.6% (5/n)	6.8%	2.1% (6/n)
*Giardia sp.**	0.8% (5/n)	0.7%; 6.8 (cysts vs antigen)	0.7% (3/n) D	3.9% (3/n)	9.5%	0.7% (2/n)
Cystoisospora sp./Isospora sp.	8.1% (54)	7.5%	5.3% (22/n) IF; 8.9% (37/n) IR	1.3% (1/n) CF; 13.2% (10/n) CR		12.4% (36/n)
Toxoplasma gondii/ Hammondia hammondi*	0.6% (4/n)	0.1%	1.2% (5/n)		0.4%	3.4% (10/n)
H. hammondi	0.5% (3/n)					
*Toxoplasma-type**	0.3% (2)					
*Sarcocystis sp**	0.2% (1)		1.0% (4/n)	1.3% (1/n)		
overall prevalence [e]	31.3% (208/n)	33.6% (281/n)	34.3% (142/n)	83.0%	20.5%	47.6% (138/n)

[*] – potentially zoonotic endoparasites; [e] – including all parasites in the study; [D] – *Giardia doudenalis*; [IF] – *Isospora felis*; [IR] – *Isospora rivolta*; [CF] – *Cystoisospora felis*; [CR] – *Cystoisospora rivolta*

Among dogs, the difference between rural and urban dog's endoparasite prevalence differed significantly, nearly 9 times (87.0% vs 9.8%, respectively; **III, IV**), (Table 2). In Estonia, stray dogs are uncommon, whereas free-ranging dogs are abundant in rural areas. In larger towns, dog owners are obliged to remove pet excrements from public areas, while it is uncommon to remove faecal scats in rural areas. Faecal material collected in public areas is, thus, a useful tool for determining environmental contamination with endoparasites, often with zoonotic potential. In **I** it was revealed that the most common zoonotic helminths in urban settlements are geohelminths, namely *U. stenocephala* and *Toxocara* spp. (Table 2), which was also demonstrated by Talvik et al. (2006) over a decade ago. In the study **III**, a very low prevalence of *T. canis* among rural dogs was found, although previous studies have shown that *T. canis* was one of the most prevalent helminth species in rural areas in Hungary and the Slovak Republic (Fok et al., 2001; Antolová et al., 2004; Papajova et al., 2014). The low prevalence of *T. canis* may be likely due to the high prevalence of taeniid species that have taken over or displaced *T. canis* in competition for nutrients in the intestine.

The most prevalent endoparasites among rural dog and cats were biohelminths of family Taeniidae, which consists of zoonotic tapeworms (e. g. *Echinococcus* spp., *Taenia* spp.), in lieu of geohelminths in urban areas **(II–IV**). It is known that most of the taeniid species that occur in dogs have zoonotic potential (e. g., *Dipylidium caninum*, *Dibothriocephalus latus*, *Taenia* spp. and *Echinococcus* spp.). In the case of rural cats, they had significantly higher infection with *T. cati* and Taeniidae than urban cats (Table 2). In study **III**, a higher prevalence of taeniids was revealed than in most other studies in Europe (Dubná et al., 2007; Soriano et al., 2010; Schurer et al., 2013; Papajová et al., 2014; Tull et al., 2020 and 2021), (Table 2). The high prevalence (65.5%) of taeniids may result from coastal effect where more opportunities are presented to prey on raw fish. Fish remnants or raw fish can be fed to rural dogs by humans or can be found in coastal areas during roaming. The occurrence of *D. latus* in grizzly and black bears and in wolves has been linked to seasonality when hosts' diet shifts to salmon (Frechette & Rau, 1978; Gau et al., 1999; Bryan et al., 2012).

Table 2. Potentially zoonotic endoparasites in dogs in European studies.

Parasite	Czech Republic (Dubna et al. 2007)		Portugal (Cardoso et al. 2013)	Slovak Republic (Papajova et al. 2014)		Hungary (Fok et al. 2001)		Spain (Regidor-Cerrillo et al. 2020)		Greece (Kostopoulou et al. 2017)			Estonia (Tull et al. 2020 and 2021)	
	rural	urban	rural	rural	urban	rural	urban	rural	stray	shelter	house-hold	shephard/ rural	rural	urban
Method	scat+ morphology		scat+ morpho-logy+ PCR	scat+ morphology		scat+ morphology		scat+ morphology+ PCR		scat+ morphology+ antigen+PCR			scat+ morphology	
Sample size	n = 540	n = 3780	n = 301	n = 70	n = 508	n = 206	n = 284	n = 131	n = 102	n = 278	n = 529	n = 72	n = 84	n = 657
Cestoda														
Taenia-type*	3.5%	1.0%	1.7%	11.4%	3.0%	2.4%	2.8%	3.0%				6.9%	65.5%	0.5%
*Dipylidium caninum**	1.3%	0.7%		0.0%	0.2%	1.0%	0.4%							
Spirometra sp.			0.3%											
Nematoda														
Toxocara spp.*	13.7%	6.2%	8.0%	12.9%	13.8%	30.1%	24.3%	6.1%	18.6%	12.2%	5.1%	8.3%	4.3%	3.4%
Toxascaris sp.	1.7%	0.9%		0.0%	4.1%	0.0%	2.1%	2.3%	13.7%	6.1%	0.9%	2.8%		
Trichuris sp.*	1.7%	1.1%	29.9%	0.0%	10.0% [TV]	23.3% [TV]	20.4% [TV]	31.3%	40.2%				15.5%[k]	
Trichuris spp./Eucoleus spp.*	0.6%				1.2%	12.9%							15.5%[k]	
Capillaria spp.*	0.6%	0.6%	0.7%	0.0%	1.2%	7.3%	0.0%			0.7% [f]	1.9% [f]	4.2% [f]		0.3%
Ancylostomatidae/ hookworm*			40.9%	8.6%	9.1%	13.1%	8.1%	29.7%	43.1%	9.7%	5.3%	33.3%		

Parasite	Czech Republic (Dubna et al. 2007)		Portugal (Cardoso et al. 2013)	Slovak Republic (Papajova et al. 2014)		Hungary (Fok et al. 2001)		Spain (Regidor-Cerrillo et al. 2020)		Greece (Kostopoulou et al. 2017)			Estonia (Tull et al. 2020 and 2021)	
Uncinaria sp.*	0.9%	0.4%											14.7%	3.5%
Ancylostoma sp.*	0.7%	0.4%												
Spirocerca	1.1%	0.2%												
Protozoa														
Cystoisospora spp./*Isospora* spp.	8.0%	2.4%	4.0%			3.4%	3.5%	3.8%	6.9%	7.6%	2.5%	8.3%		
Cryptosporidium spp.*	2.0%	1.4%						0.8%	5.9%	14.7%	1.9%	1.4%		2.1%
Sarcocystis sp.*	3.0%	0.6%												
*Neospora**/ *Hammondia*	1.3%	0.5%												
Giardia spp.*	2.2%	0.1%						2.3%	3.9%	54.3%	12.9%	4.2%		
*Coccidia**				0.0%	2.2%									2.1%
overall prevalence	41.7%	17.6%	58.8%	31.4%	29.7%	56.3%	50.7%	58.8%	72.5%	62.9%	23.8%	51.4%	87.0%	9.8%

** – zoonotic or potentially zoonotic parasites; f – family Capillariidae; TV – Trichuris vulpis; [k] – no differentiation in the study*

Over the recent years, toxocariasis has gained a lot of attention, while this disease was listed as one of the five most neglected parasitic infections according by the Centers for Disease Control and Prevention (CDC) in the United States. In Estonia, Remm & Remm (2014) demonstrated that dog owners have a significantly higher risk for infection with *Toxocara* spp. Last but not least, a study by Lassen et al. (2016) found higher *T. canis* seroprevalence in animal caretakers than in the general population. The epidemiology of *T. canis* is also largely affected by the age of the host. The highest infection rates with *T. canis* were found among puppies of four weeks old, but the infection decreased in older dogs (Barutzki & Schaper, 2013). The results in **I** stated smaller dogs to have more infections with endoparasites than larger dogs, which is in accordance with previous studies, where endoparasite transmission by puppies is described (Fontanarrosa et al., 2006; Barutzki & Schaper, 2011). However, small-sized dogs may also pose a serious hazard in towns by contaminating the environment with endoparasites as an infected dog with *T. canis* can shed 10 000 eggs in each gram of faecal material (Ahmad et al., 2011). In the last decade, small dogs have become increasingly popular pets in the US, and the situation appears similar in Estonia (Ferdman, 2015; Teng et al., 2016; Tull et al., 2020). Although it was not possible to differentiate between puppies and small dogs (**I**), the result is alarming, as both puppies and small dogs are highly attractive to children and probably have a higher degree of physical contact with humans (e.g. face licking, sharing bed with owner, petting etc.) than larger dogs. Elderly people may also prefer small dogs, as they are more affordable and easier to handle than medium- or large-sized dogs. Thus, it is likely that people underestimate the risk of disease transmission and zoonotic infections associated with small dogs (**I**).

In addition to helminths, in **I** and **II**, protozoan species were also determined with morphological methods. However, thawing of the samples could have had reduced the detection rate of oocysts. Additionally, the small dimensions of oocysts or intermittent stages could have impaired the detection rate of protozoan parasites by morphology (McGlade et al., 2003). As it was not possible to identify all endoparasite taxa at species level, it is likely that some cats and dogs had infections with zoonotic *Cryptosporidium parvum, Giardia duodenalis* assemblage A or *Cryptosporidium felis/canis* (Cacciò et al., 2002; Tzannes et al., 2008; Heyworth, 2016). Although the prevalence of *Giardia* sp., *Cryptosporidium* spp. and *Cystoisopora* spp. was not high, these parasites can rapidly spread during dogs walking on the same areas, as shown by Bugg et al. (1999) in Australia, where dogs only treated with anthelmintics targeting roundworms were infected by *Giardia* sp. Therefore, further studies are needed in order to determine protozoan infections at species level. Although, *Cystoisospora* spp. do not have zoonotic potential, they can cause gastrointestinal diseases in cats and dogs (Palmer et al., 2008). In future studies, it is crucial to distinguish between zoonotic parasite taxa at species level to estimate their composition in various hosts (dogs, cats and wildlife predators) and how predator-prey dynamics impact the distribution and infection routes of these zoonotic helminths.

4.2. Main zoonotic endoparasite transmission patterns and dynamics among domesticated pets

The infection gradient with endoparasites in shifting from large towns to smaller towns and from smaller towns to rural areas (**I**, **III, IV**). Despite of the above pattern, there have evolved evident continuous endoparasite transmission routes (infection hotspots) in towns as indicated by **I** and **II**. In towns, contamination with zoonotic parasites is concentrated in areas of high human density, in areas dominated by multi-stored apartment blocks and in potentially hazardous zones, including playgrounds, recreational areas near schools/nurseries, whereas adopted shelter cats can act as zoonotic disease distributers. The study **I** demonstrated that parasite infection prevalence is higher in smaller than in larger towns. There may be restricted availability of areas in smaller towns that are suitable for dog walking, and, conversely, easier access to rural trails. In addition, opportunistic mesocarnivores, like the red fox, raccoon dog, pine marten and badger (*Meles meles*), may occur more frequently in and around smaller towns, presenting a potential source of infection with zoonotic parasites (Deplazes et al., 2004; Bateman & Fleming, 2012). Moreover, the **II** and **III** study suggests that rural areas are in comparison with urban areas by far more contaminated with helminths and the infection risk among dogs is nine times higher in rural areas than in towns. Free-ranging rural dogs and cats preying on various reservoir, paratenic or intermediate hosts boost their infection risk with parasites, including zoonotic. Rural cats had more coinfections with multiple endoparasites than urban cats, which is related to their ability to roam freely, encountering more contacts with other feral or free-ranging cats, and thus facilitating parasite transmission between them. Rural areas also offer a wide variety of hosts to prey on. Further, rural dogs preying on rodents had higher coinfection risk with helminths than rural dogs consuming other food objects. In rural and suburban areas, rodents such as *Arvicola terrestris*, *Microtus arvalis*, *Myodes glareolus* and *Apodemus agrarius* can be paratenic or intermediate hosts for *E. multilocularis* and *Toxocara* spp. (Antolová et al., 2004; Reperant et al., 2009). Another serious problem displayed is access to raw meat and offal of domestic and wild animals in rural areas. It is known, for example, that dogs scavenging internal organs of wild game infected with *E. granulosus s.l.* can become a direct source of infection to humans and domestic animals (Baneth et al., 2016). What is more, contamination of pastures or coastal meadows with scats of infected wild carnivores, as implied in **IV**, also results in *E. granulosus s.l.* infection of domestic ruminants. The establishment of a pastoral cycle may then result from the feeding of uncooked offal from these domestic animals to dogs (Bowman, 2013). In Estonia *E. granulosus s.l.* has been found in dogs (Laurimaa et al., 2015b), grey wolves (Moks et al., 2006), but also in moose (*Alces alces*; Moks et al., 2008) and roe deer (C*apreolus capreolus*; Marcinkutė et al., 2015). It is therefore important to highlight the high possibility that rural dogs may be infected with zoonotic *E. granulosus s.l.*

A second infection route of zoonotic endoparasites includes shelter cats in quarantine and young kittens (<1 year), (**II**). So, in the **II** study, it was discovered that the composition of endoparasite species as well as infection trend was different for quarantine (1–14 days in shelter) and cats ready for adoption (≥15 days in the shelter). During the stay in the shelter, some parasites (*Cystoisospora* spp. and total protozoan species) flourished, meaning that their infection prevalence was significantly higher among cats ready for adoption but decreased among quarantine cats. The opposite effect applied to infection prevalence with *Cryptosporidium* spp. and *E. aerophilus*, namely these parasites were more common in quarantine cats than in the ready for adoption

group. Another seriously infected cat group included juvenile cats who had significantly higher endoparasite infection prevalence with zoonotic *T. cati* and nearly three times higher infection intensity with endoparasites than adult cats. The **II** study suggests that more attention should be paid to infection with protozoa and *T. cati* because infected cats may pose a threat not only to other shelter cats, but also to the shelter staff and new owners. Some shelter cats may experience stress-induced appetite loss and may not consume enough anthelmintics that is mixed with food, facilitating endoparasite spread in the shelter. Thus, animal shelters with high endoparasite prevalence and intensity should re-evaluate their parasite control procedures (Spain et al., 2001; Villeneuve et al., 2015; Blasco et al., 2017; Zottler et al., 2019), (Table 1). Faecal samples should be taken frequently from quarantine cats and measures undertaken for adequate isolation, environmental hygiene and, in indicated cases, treatment to prevent parasite spread (ESCCAP, 2018).

The potential hazard zones formulated in study **I** included recreational sites and green areas near schools and nurseries, functioning as infection hotspots. These are mainly sites where people tend to walk their dogs, resulting in higher environmental contamination and an increased amount of contacts between dogs as well as with overlapping wild canid scats. Thus, the infection cycle may be 'closed' in the apartment-house region. Poor excrement-removal practice also supports higher endoparasite prevalence in soil. The finding is important from an epidemiological perspective and is consistent with theoretical models, linking host density to the opportunity of a parasite to invade a population of hosts (Morand & Poulin, 1998). Dubná et al. (2007) also suggested that the occurrence of *Toxocara* eggs was high in public parks of urban areas because of the growing dog population and due to the relatively small dog walking areas. Moreover, the overlap between urbanized red foxes and dog scats can cause direct (zoonotic) endoparasite transmission, e.g. Gecchele et al. (2020) showed in UK that areas with higher greenspace ratios contained more red fox scats, and indeed, these scats were more likely infected with endoparasites, as well as had more parasite richness. Contradictory to the results of Talvik et al. (2006) who found more endoparasites near detached houses, in the study **I,** higher endoparasite prevalence and intensity dominated near apartment blocks. It is likely that dogs living in detached houses are kept in yards, with less access to streets, compared to dogs from apartments that are walked more widely by their owners at least once a day. As the density of humans and pets is probably highest in areas dominated by apartment blocks, it is also likely that endoparasites are also concentrated in the green areas surrounding apartment blocks.

4.3. Other endoparasites of mammalian predators and possible host-parasite link with diet

Scats collected during field work provide little background information about the investigated hosts. Previously, only excrement location has been used to identify risk factors for parasite transmission in different areas (Antolová et al., 2004; Dubná et al., 2007; Dado et al., 2012). However, if genetic methods are applied, much more information can be obtained about host species and their dietary habits as well as parasites (**III, IV**). In studies **III** and **IV** genetic methods were used to distinguish between various mammal predators, also their food objects were determined by genetic as well as morphological methods. The most abundant canids were according to genetic analyses the red fox, golden jackal and dog.

In **IV**, a very high endoparasite overlap between golden jackals and rural dogs (99%) was revealed. Moreover, all three canid species had very high infection prevalence, around or more than 90%. The environmental scat samples of red foxes, golden jackals and dogs were highly parasitized with Taeniidae, followed by *Eucoleus* spp./*Trichuris* spp., *U. stenocephala* and *T. canis* (Table 3 and Table 4). Furthermore, households, situated near to the infected environmental scats were mapped, and a total of 160 private houses (probably even more, since all living land areas cannot be found in the register) located on average up to 59 m from an infected scat. These findings are alarming due to the fact that rural dogs provide a direct transmission link of zoonotic helminths from sympatric wildlife predators to dogs and from dogs to humans, meaning that the sylvatic endoparasite cycle is deeply interlaced with synanthropic endoparasite cycle. Therefore, these findings are important from the aspect of One Health, providing viable evidence that rural areas are under continuous helminth contamination and relevant healthcare institutions should focus more on rural areas to diagnose helminth infections among companion animals (especially dogs) and in general human population. Otherwise, these diseases remain neglected, posing health risks for children.

Several infection prevalence models indicated, that among predators, preying on paratenic or intermediate hosts (rodents, reptiles) increases significantly the infection risk with helminths, mainly with *Eucoleus* spp./*Trichuris* spp. (**IV**). The latter are geohelminths and mammalian predators become infected by ingesting eggs of *E. aerophilus* or *T. vulpis* from the environment (attached to plants or distributed in water and soil), but infection may also occur when consuming invertebrates (earthworms), Norway rats (*Rattus norvegicus*) or reptiles (Rataj et al., 2011; Rothenburger et al., 2014; Traversa et al., 2014; Wolf et al., 2014). Similarly, in dogs (**III**), the infection intensity was higher among rural dogs preying on rodents and game. However, feeding dogs dog food, decreased the infection risk with helminths, especially with *Eucoleus* spp./*Trichuris* spp. In paper **IV**, a surprising relationship between consumed plant material and infection with *T. canis* among red foxes indicated that infection prevalence with *T. canis* increased when diet consisted of plants, referring to potential self-medicating behaviour as suggested also for raccoon dogs by Laurimaa et al. (2016a), or possible geohelminth infection route via plant material.

Table 3. Helminth infections in red foxes in European countries.

Parasites of red foxes	Italy (Citterio et al., 2021)	United Kingdom (Gecchele et al., 2020)	Slovak Republic (Miterpàkovà et al., 2009)	Lithuania (Bružinskaitė-Schmidhalter et al., 2011)	Denmark (Saeed et al., 2006)	Estonia (Laurimaa et al., 2016)	Estonia (Tull et al., 2022)
Method	scat+ multiplex PCR	scat+ morphology	scat+ morphology	intestines+ morphology+ PCR	intestines, organs+morpho-logy+PCR	intestines+ morphology+ PCR	scat+ morphology
Sample size	n = 2872	n = 224	n = 1198	n = 310	n = 1040	n = 111	n = 131
Cestoda							
Taenia-type		12.6% vs 4.7% (summer vs autumn)	12.2% (146/n)				76.3% (100/n)
Taenia crassiceps	35% (76/217)			26.4% (71/269)	0.2%		
Taenia polyacantha	26.2% (57/217)			61.7% (166/269)			
Echinococcus multilocularis	13.8% (30/217)			58.7% (158/269)	0.3%	31.5% (34/108)	
Taenia krabbei	0.9% (2/217)						
Taenia taeniaeformis	0.9% (2/217)			3.7% (10/269)	1.0%		
Dipylidium caninum	0.9% (2/217)		0.5% (5/n)				
Taenia serialis	0.5% (1/217)						
Mesocestoides litteratus	2.3 (5/217)						
Mesocestoides spp.	5.1 (5/217)		5.8% (70/n)	78.4% (211/269)	35.6%	77.8% (84/108)	
Taenia spp.	1.4 (3/217)				21.5%	70.4% (76/180)	
Hymenolepis diminuta			0.6% (7/n)				

Parasites of red foxes	Italy (Citterio et al., 2021)	United Kingdom (Gecchele et al., 2020)	Slovak Republic (Miterpàkovà et al., 2009)	Lithuania (Bružinskaitė-Schmidhalter et al., 2011)	Denmark (Saeed et al., 2006)	Estonia (Laurimaa et al., 2016)	Estonia (Tull et al., 2022)
Nematoda							
Toxocara canis		14.3% vs 13.1%	12.5% (150/n)	40.5% (109/269)	59.4%	29.6% (32/108)	13.7% (18/n)
Toxascaris leonina			42.9% (514/n)		0.6%	5.6% (6/108)	0.8% (1/n)
Trichuris spp./*Eucoleus* spp.							80.2% (105/n)
Capillaria spp.			22.4% (268/n)		80.5%[p]	91.5% (97/106)	
Eucoleus aerophilus		52.1% vs 32.7%		97.1% (101/104)	74.1%	87.6% (92/105)	
Trichuris vulpis			33.5% (401/n)		0.5%[d]		
Ancylostomatidae							
Uncinaria stenocephala		47.1% vs 42.0%	6.9% (83/n)	76.9% (207/269)	68.6%	84.3% (91/108)	18.3% (24/131)
Ancylostoma caninum			18.1% (217/n)		0.6%		
overall prevalence [e]	7.6%	83.9%	83.3%	NE	92.4%	93.8%	92.4%

NE – not estimated; [d] – *Trichuris vulpis*; [p] – *Capillaria plica*; [e] – including all parasites in the study

Table 4. Helminth infections in golden jackals in European countries and Iran.

Parasites of golden jackals	Bulgaria (Kirkova et al. 2011)	Serbia (Ćirović et al. 2015)	Serbia (Ilić et al. 2016)	Serbia (Lalošević et al. 2016)	Iran (Dalimi et al. 2006)	Iran (Meshgi et al. 2009)	Switzerland (Frey et al. 2022)	Hungary (Balog et al. 2021)	Estonia (Tull et al. 2022)
Method	intestines+ morphology	intestines+ morphology	intestines+ morphology	intestines+ morphology	intestines+ morphology	intestines, organs+ morphology	intestines+ morphology+ multiplex PCR	intestines+ morphology+ multiplex PCR	scat+ morphology
Sample size	n = 56	n = 447	n = 60	n = 28	n = 10	n = 79	n = 5	n = 173	n = 65
Cestoda									
Taenia-type									87.7% (57/n)
Echinococcus multilocularis				14.3% (4/n)			40% (2/n)	15.6% (27/n)	
Echinococcus granulosus	1.9%					8.9% (7/n)		1.7% (3/n)	
Taenia hydatigena		0.9%			10% (1/n)	2.5%–5% (2;4/n)			
Dipylidium caninum	3.8%	1.6%			20% (2/n)	10.1% (8/n)			
Mesocestoides litteratus		4.7%							
Mesocestoides spp.	34.6%	5.8%			70% (7/n)	15.2%–21.5% (12;17/n)			
Taenia spp.	23.0%								

Parasites of golden jackals	Bulgaria (Kirkova et al. 2011)	Serbia (Ćirović et al. 2015)	Serbia (Ilić et al. 2016)	Serbia (Lalošević et al. 2016)	Iran (Dalimi et al. 2006)	Iran (Meshgi et al. 2009)	Switzerland (Frey et al. 2022)	Hungary (Balog et al. 2021)	Estonia (Tull et al. 2022)
Nematoda									
Toxocara canis	7.7%	1.6%	23.3% (14/n)		10% (1/n)	5% (4/n)			4.6% (3/n)
Toxascaris leonina	5.8%				30% (3/n)				4.6% (3/n)
Trichuris spp./ *Eucoleus* spp.									21.5% (14/n)
Capillaria spp.	16.4%								
Trichuris vulpis	30.7%		11.7 (7/60)						
Ancylostomatidae			33.3% (20/n)						
Uncinaria stenocephala	84.6%					6.3% (5/n)			27.7% (18/n)
Ancylostoma caninum	11.5%	0.2%				2.5% (2/n)			
overall prevalence[e]	100%	10.3%	12.2%	14.3%	100%	33.3%	40%		90.8% (59/n)

[e] – including all parasites in the study

SUMMARY

Nowadays, the human-animal bond is beneficial for human physical and mental health as domesticated animals are raised (besides for food, work etc.) for companionship and therapy. However, companion animals (mostly dogs and cats) also pose potential hazards to our health as they are hosts for agents of zoonotic diseases, transmitted between animals and humans. In the light of zoonotic diseases, a worldwide concept of One Health has been established based on collaboration in all aspects of health care for humans, animals, and the environment. However, the importance of companion animals, such as cats and dogs, as disease distributers is often underestimated, whereas potential threats related to wild mammals is largely neglected. Therefore, to assess environmental contamination with zoonotic parasites and potential threats, it is necessary to understand the abundance and taxonomic composition of zoonotic parasites in pets and wild mammals in both urban and rural environments.

The aims of the study were to identify endoparasites with zoonotic potential in domesticated and wildlife animals in Estonia, mainly in cats and dogs, but also in wildlife species (red fox, golden jackal etc.), (**I**, **II**, **III**, **IV**). Furthermore, one of the goals was to determine endoparasite transmission routes in the urban environment and factors impacting the parasite cycles (**I**, **II**), and to compare urban and rural endoparasite fauna among dogs and cats (**I**, **II**, **III**). Last but not least, the effect of diet was assessed to evaluate the infection risk among mammalian predators, and to evaluate the overlap between helminth fauna of domesticated (dog) and wildlife canids such as the red fox and golden jackal (**III**, **IV**).

Our results indicate clearly that domesticated animals (dogs and cats) as well as sympatric wildlife predators distribute endoparasites with zoonotic potential (**I–IV**). Over a third of examined shelter cats (36.6%) excreted parasitic stages of zoonotic *Toxocara cati*. Moreover, among cats, helminths (*Hydatigera taeniaeformis*, *Ancylostoma tubaeforme* and *Eucoleus aerophilus*) with zoonotic potential were found. In dogs, it was revealed that the most common group of zoonotic helminths in urban settlements are geohelminths, namely *U. stenocephala* and *Toxocara* spp., both zoonotic (**I**, **II**). The comparison of helminth prevalence between rural and urban dogs and cats revealed alarming results (**I**, **II**, **III**). Namely, rural areas are in comparison with urban areas by far more contaminated with helminths, revealing a 9-fold difference between urban (~10%) and rural (~90%) dog`s endoparasite fauna. Territories of wildlife canids (red fox and golden jackal) often overlap with rural dogs, which poses a direct threat to human health. Our studies have shown that in addition to very high helminth prevalence, there is also a high overlap of helminth fauna between rural dogs, golden jackals and red foxes. All these predators were highly infected with zoonotic helminths of the family Taeniidae, but also with zoonotic roundworms. Moreover, the environmental scats, contaminated with endoparasite ova, were situated on average 60 m from nearest living lands, where, in total 160 households (private property) could be found, which places the infected scats to human's backyards (**IV**).

Over half of rural cats (56.7%) were infected with endoparasites compared to the 1/3 of infected urban cats (36.2%). Rural cats in quarantine (up to 14 days) had significantly higher endoparasite infection prevalence with directly transmittable zoonotic endoparasites than urban cats in quarantine. The most prevalent endoparasites among rural dogs and cats were biohelminths, rather than geohelminths in urban areas **(II, III**).

The general infection gradient of endoparasites is shifting from large towns towards smaller towns and from smaller towns to rural areas (**I**, **III, IV**). However, towns have

their own endoparasite transmission routes (infection hotspots), whereas the infection risk and prevalence are higher in smaller than in larger towns. So, the potential hazard zones formulated in **I** included recreational sites and green areas near schools and nurseries, functioning as important infection hotspots compared to streets. Apartment-house region had also higher endoparasite prevalence risk in lieu of the detached-house region, supporting a 'closed' infection cycle in the apartment-house region where the soil may have permanent geohelminth contamination throughout the year (**I**).

Another endoparasite transmission cycle is linked with cats and a shelter (**III**) where young (< 1 year) cats and cats ready for adoption (≥15 days in the shelter) had heavy endoparasite burdens with also zoonotic parasites. During the stay in the shelter, some endoparasites (*Cystoisospora* spp. and total protozoan species) flourished, meaning that their infection prevalence was significantly higher among cats ready for adoption but decreased among quarantine cats (1–14 days in shelter). The opposite effect applied to infection prevalence with *Cryptosporidium* spp. and *E. aerophilus*, namely these parasites were more common in quarantine cats than in the ready for adoption group. Juvenile cats had seriously higher endoparasite infection prevalence with zoonotic *T. cati* and nearly three times higher infection intensity with overall endoparasites than adult cats (**III**).

Since the parasite infection occurrence is closely related to predator-prey relations in food webs, the studied diet among predators enabled to distinguish relationships between parasites and consumed food objects (**III**, **IV**). In nature, prey objects (rodents, reptiles, birds, earthworms etc.) serve as intermediate, reservoir or paratenic hosts where parasites mature or stay dormant. We demonstrated that if rural dogs preyed on rodents and game, the infection rate increased. On the other hand, if people cared for their dogs and fed them dog food, there was a (63%) reduction of coinfection with helminths (**III**). For predators (red fox, golden jackals, dogs, raccoon dogs etc.), preying on rodents increased the coinfection rate with multiple endoparasites. Several infection prevalence models indicated among predators that preying on paratenic or intermediate hosts (rodents, reptiles) significantly increases the infection risk with helminths, mainly with *Eucoleus* spp./*Trichuris* spp. A surprising relationship between consumed plant material and infection with *T. canis* among red foxes indicated that infection prevalence with *T. canis* increased when diet consisted of plant material, referring to potential self-medicating behaviour or possible higher geohelminth infection via plant material (**IV**).

To conclude, domesticated companion animals such as dogs and cats can act as transmitters of zoonotic parasites capable of affecting human health, and are therefore of One Health concern. The overlap between free-ranging companion animals and wildlife predators ensures an enzootic parasite cycle in an anthropogenic landscape. Therefore, it is of utmost importance to highlight possible parasite transmission routes and species compositions in wild and domesticated animals. It is equally important to educate and counsel people by experts to minimize zoonotic disease transmissions. One of the main concluding messages of my PhD work is that a regular monitoring of zoonotic parasites among wildlife and domesticated animals should be implemented to reduce the burden of zoonotic diseases.

SUMMARY IN ESTONIAN

Kodu- ja metsloomadega levivad zoonootilised siseparasiidid Eestis

Inimese ja lemmiklooma vaheline suhe on muutunud tänapäeval väga oluliseks, pakkudes mitmeid hüvesid nii füüsilisele kui ka vaimsele tervisele, ent teisalt on koduloomad (nagu koerad ja kassid) mitmete zoonootiliste haiguste levitajad, võimaldades haiguste levikut loomadelt inimestele ja vastupidi. Zoonootiliste haiguspuhangute ärahoidmiseks on pandud alus *One Health* (Üks Tervis) kontseptsioonile (üks tervis, üks maailm), mis hõlmab interdistsiplinaarset koostööd kogu maailmas, sidudes ühtseks tervikuks inimese tervishoiu koos loomade ning keskkonnaga. Parasiitide edasikandumist loomade vahendusel inimesele on sageli alahinnatud, mistõttu on oluline uurida mets- ja lemmikloomade parasiteeritust, eriti zoonootiliste parasiitidega. Nakkusriski hindamine aitab vältida inimeste nakkumist, seda eriti väikelaste puhul, kes on oluliselt suurema nakkusriskiga kui täiskasvanud.

Töö eesmärkideks oli kindlaks teha Eestis lemmikloomade (koer, kass) ja kiskjatega (punarebane, harilik šaakal jt) levivad zoonootilised siseparasiidid (**I**, **II**, **III**, **IV**). Uurida, millised on linnakeskkonnas peamised siseparasiitide levikuteed ning millised tegurid seda mõjutavad (**I**, **II**); ühtlasi oli üheks eesmärgiks võrrelda kasside ja koerte nakatumist siseparasiitidega linna- ja maapiirkonnas (**I, II, III**). Samuti hinnati, kuidas kiskjaliste toitumine mõjutab nende nakkusriski siseparasiitidega ning võrreldi kodu (koer)- ja metsloomade (punarebane, harilik šaakal) parasitofauna kattuvust;(III, IV).

Uuringud kinnitavad üheselt, et nii Eesti lemmikloomad (koerad ja kassid) kui ka metsloomad (punarebane, harilik šaakal, jt.) on nakatunud zoonootiliste siseparasiitidega (**I–IV**). Varjupaiga kassidest olid enam kui kolmandik (36,6%) nakatunud zoonootilise nematoodi kassisolkmega (*Toxocara cati*). Samuti leiti varjupaiga kassidelt mitmeid teisi zoonootilisi helminte (nt *Hydatigera taeniaeformis*, *Ancylostoma tubaeforme* ja *Eucoleus aerophilus*), kes nakatavad inimesi, kuid kelle epidemioloogiast on seni vähe teada. Linnadest leiti koertelt enim geohelminte, kellest on zoonootilised untsinaaria (*Uncinaria stenocephala*) ja kutsikasolge (*Toxocara canis*) (**I**, **II**). Linna- ja maapiirkonna kasside ja koerte siseparasiitide uuringute tulemused näitasid kõrget nakatumise taset (**I**, **II**, **III**). Tuvastasin, et maapiirkonna koerad olid üheksa korda enam nakatunud helmintidega kui linnakoerad (vastavalt 90% ja 10%). Maapiirkondades elavate koerte kõrget nakkustaset soosivad arvatavasti ulukkiskjalised, kellest 90% olid nakatunud ning kelle territoorium kattub suuresti koduloomadega. Põhiliselt olid ulukkoerlased nakatunud zoonootiliste paeluslastega (*Taeniidae*), aga võrdlemisi sageli esines ka mitmeid teisi zoonootilisi helminte nagu nematoodid *Eucoleus spp./Trichuris spp*., untsinaariat (*U. stenocephala*) ja kutsikasolget (*T. canis*). Murettekitav on ka leid, et enamik nakkunud väljaheidetest asusid keskmiselt vaid 60 m kaugusel elamumaadest, kus paiknes vähemalt 160 majapidamist.

Üle poole maapiirkondades elavatest kassidest (56,7%) olid nakatunud siseparasiitidega, veidi vähem esines nakkust linnades elavatel kassidel (36,2%). Kusjuures maapiirkondade kassidel, kes olid varjupaigas karantiinis (kuni 14 päeva), esines märkimisväärselt rohkem otsesel teel edasikanduvaid zoonootilisi siseparasiite kui karantiinis linnapiirkonna kassidel. Nii maapiirkonna koertel kui -kassidel esines siseparasiitidest märksa enam biohelminte kui linnapiirkonna koertel ja -kassidel **(II, III**).

Töös leiti, et Eestis on välja kujunenud üldine siseparasiitide levimus, kus nakkusrisk on väikseim suurlinnades, seejärel järgnevad väikelinnad ning suurim nakkustase

on maapiirkondades (**I**, **III, IV**). Vaatamata linnade madalamale nakkustasemele, on siiski linnakeskkonnas välja kujunenud konkreetsed nakkusteed (nn nakkuse tulipunktid), kusjuures nakkusrisk on kõrgem väikelinnades kui suurlinnades. Mainitud tulipunktides puhke- ja rohealadel, millest osad paiknesid ka lasteaedade ja koolide läheduses esines oluliselt rohkem siseparasiitidega saastunud väljaheiteid kui rohealadel tänavaservades. Samuti oli nakkusrisk kõrgem paneelmajade ümbruskonnas, võrreldes eramajade piirkonnaga. Arvatavasti on tekkinud paneelmajade läheduses suletud nakkusring, kus pinnas on alaliselt nakkusvõimeliste geohelmintide munadega saastunud (**I**).

Veel üks oluline siseparasiitide levikuteekond on seotud varjupaiga kassidega, kus pea pooled kassid (ca 50%) on nakatunud vähemalt ühe parasiidiliigiga. Enim olid zoonootiliste siseparasiitidega nakatunud noored (< 1 a) ja koduootel kassid (olnud varjupaigas ≥15 päeva ehk läbinud karantiini perioodi). See tähendab, et varjupaigas veedetud aja jooksul suutsid mõned siseparasiidid plahvatuslikult vohama hakata (nt *Cystoisospora* spp.) võrrelduna karantiini kassidega (1–14 päeva karantiinis). Erandi moodustasid zoonootilised parasiidid algloom *Cryptosporidium* spp. ja ümaruss *Eucoleus aerophilus* – koduootel kassid olid vähem nakatunud kui karantiini kassid. Noortel kassidel esines oluliselt enam nakkust kassisolkmega ning nende nakkuse intensiivsus oli kolm korda suurem kui täiskasvanud kassidel (**III**).

Kuna parasiitide esinemine on tihedalt seotud toiduahelaga, st kiskja-saakloom suhtega, siis uuriti kiskluse ja söödud toiduobjektide seoseid parasiteeritusega (**III**, **IV**). Looduses võivad saakliigid (nt närilised, herbivoorid, roomajad, linnud, vihmaussid jne) olla parasiitidele kas vahe-, säilitus- või lisaperemeesteks, kelles parasiidid arenevad mittesuguliselt või püsivad aastaid mitteaktiivses staadiumis. Uuring näitas, et kui maapiirkondade koerad toitusid närilistest ja jahiulukitest, siis nakkusrisk suurenes, samas kui koertel, kes olid söönud koeratoitu, oli parasiidiliike vähem (**III**). Kiskjaliste (punarebane, harilik šaakal, koer, metsnugis jt) puhul selgus, et närilistest toitumine suurendas oluliselt enamate parasiidiliikidega nakatumist. Mitmed nakkuse mudelid näitasid, et kui kiskjalised toitusid vahe- või säilitusperemeestest (närilised, roomajad), siis tõusis nakatumine helmintidega (nt *Eucoleus* spp./*Trichuris* spp.). Üllataval kombel tuvastati uuringus seos punarebase taimedest toitumise ja parasiteerituse vahel. Nimelt leiti, et mida rohkem esines toidus taimset komponenti, seda enam oldi nakkunud kutsikasolkmega, mis viitab kas potentsiaalsele tervenemiskäitumisele seedekulglast siseparasiitide väljutamiseks (taimede abil) või hoopis suuremale võimalusele nakatuda geohelmintidega (**IV**).

Kokkuvõtteks saab öelda, et lemmikloomad (koerad-kassid) võivad olla paljude zoonooside levitajad ja võivad nakatada inimesi parasiitidega, kellest osad on eluohtlikud. Mets- ja koduloomade kattuvad areaalid inimtekkelises maastikus võimaldavad parasitaarsetel nakkushaigustel püsida mõlemas populatsioonis. Lisaks sellele, et on äärmiselt vajalik uurida võimalikke zoonooside levikuteid ning määrata kindlaks zoonooside tekitajad, on võrdväärselt oluline ka harida ja nõustada inimesi eriala ekspertide poolt, et vähendada zoonootilistesse haigustesse nakatumist. Võimalike nakkusriskide hindamiseks oleks vaja püsivalt seirata looduskeskkonnas levivaid ohtlikke zoonootilisi parasiite nii mets- kui koduloomadel.

REFERENCES

1. Ahmad, N., Maqbool, A., Saeed, K., Ashraf, K., and Qamar, M.F., 2011. Toxocariasis, its zoonotic importance and chemotherapy in dogs. The Journal of Animal and Plant Sciences 21(2), 142–145.
2. Altreuther, G., Borgsteede, F.H.M., Buch, J., Charles, S.D., Cruthers, L., Epe, C., Young, D.R., Krieger, K.J., 2005. Efficacy of a topically administered combination of emodepside and praziquantel against mature and immature *Ancylostoma tubaeforme* in domestic cats. Parasitology Research 97, S51–S57. https://doi.org/10.1007/s00436-005-1444-1
3. Antolová, D., Reiterová, K., Miterpáková, M., Stanko, M., Dubinský, P., 2004. Circulation of *Toxocara* spp. in suburban and rural ecosystems in the Slovak Republic. Veterinary Parasitology 126, 317–324. https://doi.org/10.1016/j.vetpar.2004.08.005
4. Balog, T., Nagy, G., Halász, T., Csányi, E., Zomborszky, Z., Csivincsik, Á., 2021. The occurrence of *Echinococcus* spp. in golden jackal (*Canis aureus*) in southwestern Hungary: Should we need to rethink its expansion? Parasitology International 80, 102214. https://doi.org/10.1016/j.parint.2020.102214
5. Baneth, G., Thamsborg, S.M., Otranto, D., Guillot, J., Blaga, R., Deplazes, P., Solano-Gallego, L., 2016. Major Parasitic Zoonoses Associated with Dogs and Cats in Europe. Journal of Comparative Pathology 155, S54–S74. https://doi.org/10.1016/j.jcpa.2015.10.179
6. Barton, K., 2019. Multi-Model Inference. R package version 1.43.6. Available at https://CRAN.R-project.org/package=MuMIn, (accessed 25 April 2021).
7. Barutzki, D., Schaper, R., 2013. Age-Dependant Prevalence of Endoparasites in Young Dogs and Cats up to One Year of Age. Parasitology Research 112, 119–131. https://doi.org/10.1007/s00436-013-3286-6
8. Barutzki, D., Schaper, R., 2011. Results of Parasitological Examinations of Faecal Samples from Cats and Dogs in Germany between 2003 and 2010. Parasitology Research 109, 45–60. https://doi.org/10.1007/s00436-011-2402-8
9. Bateman, P.W., Fleming, P.A., 2012. Big city life: carnivores in urban environments. Journal of Zoology 287, 1–23. https://doi.org/10.1111/j.1469-7998.2011.00887.x
10. Becker, A.-C., Rohen, M., Epe, C., Schnieder, T., 2012. Prevalence of endoparasites in stray and fostered dogs and cats in Northern Germany. Parasitology Research 111, 849–857. https://doi.org/10.1007/s00436-012-2909-7
11. Blasco, X., Salas, A., Manuelian, C.L., Torre, C. and Ortuño, A., 2017. Intestinal Parasitic Infection in Multi-Cat Shelters in Catalonia. ISR J. Vet. Med, 72, pp.16–21.
12. Bowman, D.D., 2013. Georgis' parasitology for veterinarians. 10th edn. St. Louis, Missouri, Elsevier.
13. Bristow, B.N., Lee, S., Shafir, S., Sorvillo, F., 2012. Human Echinococcosis Mortality in the United States, 1990–2007. PLoS Neglected Tropical Diseases 6, e1524. https://doi.org/10.1371/journal.pntd.0001524
14. Brooks, E.M,, Kristensen, K., Benthem, J.K., Magnusson, A., Berg, W.C,, Nielsen, A., Skaug, J.H., Maechler, M., and Bolker, M.B., 2017. glmmTMB balances speed and flexibility among packages for zero-inflated generalized linear mixed modeling. R Journal 9(2), 378–400.

15. Bružinskaitė-Schmidhalter, R., Šarkūnas, M., Malakauskas, A., Mathis, A., Torgerson, P.R., Deplazes, P., 2012. Helminths of red foxes (*Vulpes vulpes*) and raccoon dogs (*Nyctereutes procyonoides*) in Lithuania. Parasitology 139, 120–127. https://doi.org/10.1017/S0031182011001715
16. Bryan, H.M., Darimont, C.T., Hill, J.E., Paquet, P.C., Thompson, R.C.A., Wagner, B., and Smits, J.E.G., 2012. Seasonal and biogeographical patterns of gastrointestinal parasites in large carnivores: wolves in a coastal archipelago. Parasitology 139 (6), 781–790.
17. Bugg, R.J., Robertson, I.D., Elliot, A.D., Thompson, R.C.A., 1999. Gastro-intestinal Parasites of Urban Dogs in Perth, Western Australia. The Veterinary Journal 157, 295–301. https://doi.org/10.1053/tvjl.1998.0327
18. Burnham, K.P., and Anderson, D.R., 2004. Model selection and multimodel inference. New York, Springer, 515 pp.
19. Bush, A. O., 2001. Parasitism: The diversity and ecology of animal parasites. Cambridge University Press.
20. Cardoso, A.S., Costa, I.M.H., Figueiredo, C., Castro, A., Conceição, M.A.P., 2014. The occurrence of zoonotic parasites in rural dog populations from northern Portugal. Journal of Helminthology. 88, 203–209. https://doi.org/10.1017/S0022149X13000047
21. Caccio, S., 2002. Human Infection with *Cryptosporidium felis*: Case Report and Literature Review. Emerging Infectious Diseases 8, 85–86. https://doi.org/10.3201/eid0801.010269
22. Casulli, A., Massolo, A., Saarma, U., Umhang, G., Santolamazza, F., Santoro, A., 2022. Species and genotypes belonging to Echinococcus granulosus sensu lato complex causing human cystic echinococcosis in Europe (2000–2021): a systematic review. Parasites & Vectors 15, 109. https://doi.org/10.1186/s13071-022-05197-8
23. Cheng, V.C.C., Lau, S.K.P., Woo, P.C.Y., Yuen, K.Y., 2007. Severe Acute Respiratory Syndrome Coronavirus as an Agent of Emerging and Reemerging Infection. Clinical Microbiology Reviews 20, 660–694. https://doi.org/10.1128/CMR.00023-07
24. Ćirović, D., Pavlović, I., Penezić, A., Kulišić, Z., Selaković, S., 2015. Levels of infection of intestinal helminth species in the golden jackal *Canis aureus* from Serbia. Journal of Helminthology 89, 28–33. https://doi.org/10.1017/S0022149X13000552
25. Citterio, C.V., Obber, F., Trevisiol, K., Dellamaria, D., Celva, R., Bregoli, M., Ormelli, S., Sgubin, S., Bonato, P., Da Rold, G., Danesi, P., Ravagnan, S., Vendrami, S., Righetti, D., Agreiter, A., Asson, D., Cadamuro, A., Ianniello, M., Capelli, G., 2021. *Echinococcus multilocularis* and other cestodes in red foxes (*Vulpes vulpes*) of northeast Italy, 2012–2018. Parasites & Vectors 14, 29. https://doi.org/10.1186/s13071-020-04520-5
26. Claerebout, E., Casaert, S., Dalemans, A.-C., De Wilde, N., Levecke, B., Vercruysse, J., Geurden, T., 2009. *Giardia* and other intestinal parasites in different dog populations in Northern Belgium. Veterinary Parasitology 161, 41–46. https://doi.org/10.1016/j.vetpar.2008.11.024
27. Cleaveland, S., Laurenson, M.K., Taylor, L.H., 2001. Diseases of humans and their domestic mammals: pathogen characteristics, host range and the risk of emergence. Philosophical Transactions of the Royal Society of London. B 356, 991–999. https://doi.org/10.1098/rstb.2001.0889

28. Dado, D., Izquierdo, F., Vera, O., Montoya, A., Mateo, M., Fenoy, S., Galván, A.L., García, S., García, A., Aránguez, E., López, L., del Águila, C., Miró, G., 2012. Detection of Zoonotic Intestinal Parasites in Public Parks of Spain. Potential Epidemiological Role of Microsporidia: Detection of Zoonotic Intestinal Parasites in Public Parks. Zoonoses and Public Health 59, 23–28. https://doi.org/10.1111/j.1863-2378.2011.01411.x
29. Dalimi, A., Sattari, A., Motamedi, Gh., 2006. A study on intestinal helminthes of dogs, foxes and jackals in the western part of Iran. Veterinary Parasitology 142, 129–133. https://doi.org/10.1016/j.vetpar.2006.06.024
30. Deksne, G., Petrusēviča, A., Kirjušina, M., 2013. Seroprevalence and Factors Associated with *Toxoplasma gondii* Infection in Domestic Cats from Urban Areas in Latvia. Journal of Parasitology 99, 48–50. https://doi.org/10.1645/GE-3254.1
31. Deplazes, P., Hegglin, D., Gloor, S., Romig, T., 2004. Wilderness in the city: the urbanization of *Echinococcus multilocularis*. Trends in Parasitology 20, 77–84. https://doi.org/10.1016/j.pt.2003.11.011
32. Despommier, D., 2003. Toxocariasis: Clinical Aspects, Epidemiology, Medical Ecology, and Molecular Aspects. Clinical Microbiology Reviews 16, 265–272. https://doi.org/10.1128/CMR.16.2.265-272.2003
33. Dubey, J.P., 2018. A review of *Cystoisospora felis* and *C. rivolta*-induced coccidiosis in cats. Veterinary Parasitology 263, 34–48. https://doi.org/10.1016/j.vetpar.2018.09.016
34. Dubey, J., Jones, J., 2008. *Toxoplasma gondii* infection in humans and animals in the United States. International Journal for Parasitology 38, 1257–1278. https://doi.org/10.1016/j.ijpara.2008.03.007
35. Dubey, J.P., 1995. Duration of Immunity to Shedding of *Toxoplasma gondii* Oocysts by Cats. The Journal of Parasitology 81, 410. https://doi.org/10.2307/3283823
36. Dubinský, P., Havasiová-Reiterová, K., Peťko, B., Hovorka, I., Tomašovičová, O., 1995. Role of small mammals in the epidemiology of toxocariasis. Parasitology 110, 187–193. https://doi.org/10.1017/S0031182000063952
37. Dubná, S., Langrová, I., Nápravník, J., Jankovská, I., Vadlejch, J., Pekár, S., Fechtner, J., 2007. The prevalence of intestinal parasites in dogs from Prague, rural areas, and shelters of the Czech Republic. Veterinary Parasitology 145, 120–128. https://doi.org/10.1016/j.vetpar.2006.11.006
38. Ekanayake, S., Warnasuriya, N. D., Samarakoon, P. S., Abewickrama, H., Kuruppuarachchi, N. D., & Dissanaike, A. S., 1999. An unusual 'infection' of a child in Sri Lanka, with *Taenia taeniaeformis* of the cat. Annals of tropical medicine and parasitology, 93(8), 869–873. https://doi.org/10.1080/00034989957871
39. ESCCAP: Worm Control in Dogs and Cats. 2020. European Scientific Counsel Companion Animal Parasites. Sixth Edition. Malvern Hills Science Park, Malvern, 42 pp.
40. ESCCAP: Control of Intestinal Protozoa in Dogs and Cats. 2018. European Scientific Counsel Companion Animal Parasites. Second Edition. Malvern Hills Science Park, Malvern, 22 pp.
41. Estonian Land Board (2021) WMS services. Available at https://kaart.maaamet.ee/wms/alus? (accessed 14 May 2022).
42. Ferdman, A.R., 2015. Tiny dogs are taking over this country. The Washington Post, 26 February.

43. Fok, E., Szatmári, V., Busák, K., Rozgonyi, F., 2001. Epidemiology: Prevalence of intestinal parasites in dogs in some urban and rural areas of Hungary. Veterinary Quarterly 23, 96–98. https://doi.org/10.1080/01652176.2001.9695091
44. Fontanarrosa, M.F., Vezzani, D., Basabe, J., Eiras, D.F., 2006. An epidemiological study of gastrointestinal parasites of dogs from Southern Greater Buenos Aires (Argentina): Age, gender, breed, mixed infections, and seasonal and spatial patterns. Veterinary Parasitology 136, 283–295. https://doi.org/10.1016/j.vetpar.2005.11.012
45. Frechette, J-L., and Rau, M.E., 1978. Seasonal changes in the prevalence of ova of *Diphyllobothrium ursi* and *Baylisascaris transfuga* in the feces of the black bear (*Ursus americanus*). Journal of Wildlife Diseases 14(3), 342–344.
46. Frey, C.F., Basso, W.U., Zürcher-Giovannini, S., Marti, I., Borel, S., Guthruf, S., Gliga, D., Lundström-Stadelmann, B., Origgi, F.C., Ryser-Degiorgis, M.-P., 2022. The golden jackal (*Canis aureus*): A new host for *Echinococcus multilocularis* and *Trichinella britovi* in Switzerland. Schweizer Archiv fur Tierheilkunde 164, 71–78. https://doi.org/10.17236/sat00338
47. García-Agudo, L., García-Martos, P., Rodríguez-Iglesias, M., 2014. *Dipylidium caninum* infection in an infant: a rare case report and literature review. Asian Pacific Journal of Tropical Biomedicine 4, S565–S567. https://doi.org/10.12980/APJTB.4.2014APJTB-2014-0034
48. Gau, R.J., Kutz, S., and Elkin, B.T., 1999. Parasites in grizzly bears from the central Canadian Arctic. Journal of Wildlife Diseases 35(3), 618–621.
49. Gecchele, L.V., Pedersen, A.B. and Bell, M., 2020. Fine-scale variation within urban landscapes affects marking patterns and gastrointestinal parasite diversity in red foxes. Ecology and evolution, 10(24), pp.13796–13809.
50. Gherman, C.M., Mihalca, A.D., 2017. A synoptic overview of golden jackal parasites reveals high diversity of species. Parasites Vectors 10, 419. https://doi.org/10.1186/s13071-017-2329-8
51. Gracenea, M., Gómez, M., Torres, J., 2009. Prevalence of intestinal parasites in shelter dogs and cats in the metropolitan area of Barcelona (Spain). Acta Parasitologica 54. https://doi.org/10.2478/s11686-009-0005-7
52. Greenwood, J. S., 2011. Protozoan Parasites of Veterinary importance. https://cupdf.com/document/protozoan-parasites-of-veterinary-importance-image-handout-3-toxoplasma-.html?page=1 (visited May 24, 2022)
53. Deksne, G., Petrusēviča, A., Kirjušina, M., 2013. Seroprevalence and Factors Associated with *Toxoplasma gondii* Infection in Domestic Cats from Urban Areas in Latvia. Journal of Parasitology 99, 48–50. https://doi.org/10.1645/GE-3254.1
54. Dubná, S., Langrová, I., Nápravník, J., Jankovská, I., Vadlejch, J., Pekár, S., Fechtner, J., 2007. The prevalence of intestinal parasites in dogs from Prague, rural areas, and shelters of the Czech Republic. Veterinary Parasitology 145, 120–128. https://doi.org/10.1016/j.vetpar.2006.11.006
55. Hall, T. A., 1999. Bioedit: A user-friendly biological sequence alignment editor and analysis program for windows 95/98/NT. Nucleic Acids Symposium Series 41, 95–98.
56. Heinze, G., and Ploner, M., 2018. logistf: Firth's Bias-Reduced Logistic Regression. R package version 1.23. Available at https://CRAN.R-project.org/package=logistf, (accessed 10 October 2021).
57. Heyworth, M.F., 2016. *Giardia duodenalis* genetic assemblages and hosts. Parasite 23, 13. https://doi.org/10.1051/parasite/2016013

58. Hindrikson, M., Männil, P., Ozolins, J., Krzywinski, A., Saarma, U., 2012. Bucking the Trend in Wolf-Dog Hybridization: First Evidence from Europe of Hybridization between Female Dogs and Male Wolves. PLoS ONE 7, e46465. https://doi.org/10.1371/journal.pone.0046465
59. Hudson, P.J., Dobson, A.P., Lafferty, K.D., 2006. Is a healthy ecosystem one that is rich in parasites? Trends in Ecology & Evolution 21, 381–385. https://doi.org/10.1016/j.tree.2006.04.007
60. Jenkins, E.J., Simon, A., Bachand, N., Stephen, C., 2015. Wildlife parasites in a One Health world. Trends in Parasitology 31, 174–180. https://doi.org/10.1016/j.pt.2015.01.002
61. Jokelainen, P., Simola, O., Rantanen, E., Näreaho, A., Lohi, H., Sukura, A., 2012. Feline toxoplasmosis in Finland: cross-sectional epidemiological study and case series study. Journal of Veterinary Diagnostic Investigation 24, 1115–1124. https://doi.org/10.1177/1040638712461787
62. Jokelainen, P., Velström, K., Lassen, B., 2015. Seroprevalence of *Toxoplasma gondii* in free-ranging wild boars hunted for human consumption in Estonia. Acta Veterinaria Scandinavica 57, 42. https://doi.org/10.1186/s13028-015-0133-z
63. Karamon, J., Sroka, J., Dąbrowska, J., Bilska-Zając, E., Zdybel, J., Kochanowski, M., Różycki, M., Cencek, T., 2019. First report of *Echinococcus multilocularis* in cats in Poland: a monitoring study in cats and dogs from a rural area and animal shelter in a highly endemic region. Parasites & Vectors 12, 313. https://doi.org/10.1186/s13071-019-3573-x
64. Keys, P.W., Galaz, V., Dyer, M., Matthews, N., Folke, C., Nyström, M., Cornell, S.E., 2019. Anthropocene risk. Nature Sustainability 2, 667–673. https://doi.org/10.1038/s41893-019-0327-x
65. Elhamiani Khatat, S., Rosenberg, D., Benchekroun, G., Polack, B., 2016. Lungworm *Eucoleus aerophilus* (*Capillaria aerophila*) infection in a feline immunodeficiency virus-positive cat in France. Journal of Feline Medicine and Surgery Open Reports 2, 205511691665164. https://doi.org/10.1177/2055116916651649
66. Knapp, J., Giraudoux, P., Combes, B., Umhang, G., Boué, F., Said-Ali, Z., Aknouche, S., Garcia, C., Vacheyrou, M., Laboissière, A., Raton, V., Comte, S., Favier, S., Demerson, J.-M., Caillot, C., Millon, L., Raoul, F., 2018. Rural and urban distribution of wild and domestic carnivore stools in the context of *Echinococcus multilocularis* environmental exposure. International Journal for Parasitology 48, 937–946. https://doi.org/10.1016/j.ijpara.2018.05.007
67. Kostopoulou, D., Claerebout, E., Arvanitis, D., Ligda, P., Voutzourakis, N., Casaert, S., Sotiraki, S., 2017. Abundance, zoonotic potential and risk factors of intestinal parasitism amongst dog and cat populations: The scenario of Crete, Greece. Parasites & Vectors 10, 43. https://doi.org/10.1186/s13071-017-1989-8
68. Kroten, A., Toczylowski, K., Kiziewicz, B., Oldak, E., & Sulik, A., 2016. Environmental contamination with *Toxocara* eggs and seroprevalence of toxocariasis in children of northeastern Poland. Parasitology research, 115(1), 205–209. https://doi.org/10.1007/s00436-015-4736-0
69. Kruse, H., Kirkemo, A.-M., Handeland, K., 2004. Wildlife as Source of Zoonotic Infections. Emerging Infectious Diseases. 10, 2067–2072. https://doi.org/10.3201/eid1012.040707

70. Lalošević, D., Stanojev-Jovanović, D., Lalošević, V., Pozio, E., Klem, I., 2008. Pulmonary Capillariasis Miming Bronchial Carcinoma. The American Journal of Tropical Medicine and Hygiene 78, 14–16. https://doi.org/10.4269/ajtmh.2008.78.14
71. Lassen, B., Janson, M., Viltrop, A., Neare, K., Hütt, P., Golovljova, I., Tummeleht, L., Jokelainen, P., 2016. Serological Evidence of Exposure to Globally Relevant Zoonotic Parasites in the Estonian Population. PLoS ONE 11, e0164142. https://doi.org/10.1371/journal.pone.0164142
72. Laurimaa, L., Davison, J., Süld, K., Plumer, L., Oja, R., Moks, E., Keis, M., Hindrikson, M., Kinkar, L., Laurimäe, T., Abner, J., Remm, J., Anijalg, P., Saarma, U., 2015a. First report of highly pathogenic *Echinococcus granulosus* genotype G1 in dogs in a European urban environment. Parasites & Vectors 8, 182. https://doi.org/10.1186/s13071-015-0796-3
73. Laurimaa, L., Davison, J., Plumer, L., Süld, K., Oja, R., Moks, E., Keis, M., Hindrikson, M., Kinkar, L., Laurimäe, T., Abner, J., Remm, J., Anijalg, P., Saarma, U., 2015b. Noninvasive Detection of *Echinococcus multilocularis* Tapeworm in Urban Area, Estonia. Emerging Infectious Diseases. 21, 163–164. https://doi.org/10.3201/eid2101.140136
74. Loftin, C.M., Donnett, U.B., Schneider, L.G., Varela-Stokes, A.S., 2019. Prevalence of endoparasites in northern Mississippi shelter cats. Veterinary Parasitology: Regional Studies and Reports 18, 100322. https://doi.org/10.1016/j.vprsr.2019.100322
75. Macpherson, C.N.L., Meslin, F.-X., Wandeler, A.I. (Eds.), 2012. Dogs, zoonoses, and public health, 2nd ed. ed. CABI, Oxfordshire; Boston.
76. Marcinkutė, A., Šarkūnas, M., Moks, E., Saarma, U., Jokelainen, P., Bagrade, G., Laivacuma, S., Strupas, K., Sokolovas, V. and Deplazes, P., 2015. *Echinococcus* infections in the Baltic region. Veterinary Parasitology, 213(3–4), pp.121–131.131.
77. McMahon, B.J., Morand, S., Gray, J.S., 2018. Ecosystem change and zoonoses in the Anthropocene. Zoonoses Public Health 65, 755–765. https://doi.org/10.1111/zph.12489
78. McGlade, T.R., Robertson, I.D., Elliot, A.D., Read, C., Thompson, R.C.A., 2003. Gastrointestinal parasites of domestic cats in Perth, Western Australia. Veterinary Parasitology 117, 251–262. https://doi.org/10.1016/j.vetpar.2003.08.010
79. Milne, G., Webster, J.P., Walker, M., 2020. *Toxoplasma gondii*: An Underestimated Threat? Trends in Parasitology 36, 959–969. https://doi.org/10.1016/j.pt.2020.08.005
80. Mircean, V., Titilincu, A., Vasile, C., 2010. Prevalence of endoparasites in household cat (*Felis catus*) populations from Transylvania (Romania) and association with risk factors. Veterinary Parasitology 171, 163–166. https://doi.org/10.1016/j.vetpar.2010.03.005
81. Miterpáková, M., Hurníková, Z., Antolová, D., Dubinský, P., 2009. Endoparasites of red fox (Vulpes vulpes) in the Slovak Republic with the emphasis on zoonotic species Echinococcus multilocularis and *Trichinella* spp. Helminthologia 46, 73–79. https://doi.org/10.2478/s11687-009-0015-x
82. Moks, E., Jõgisalu, I., Valdmann, H., Saarma, U., 2008. First report of *Echinococcus granulosus* G8 in Eurasia and a reappraisal of the phylogenetic relationships of 'genotypes' G5-G10. Parasitology 135, 647–654. https://doi.org/10.1017/S0031182008004198

83. Moks, E., Jõgisalu, I., Saarma, U., Talvik, H., Järvis, T., Valdmann, H., 2006. Helminthologic survey of the wolf (*Canis lupus*) in Estonia, with an emphasis on Echinococcus granulosus. Journal of Wildlife Diseases 42, 359–365. https://doi.org/10.7589/0090-3558-42.2.359
84. Morand, S., Poulin, R., 1998. Density, body mass and parasite species richness of terrestrial mammals. Evolutionary Ecology 12, 717–727. https://doi.org/10.1023/A:1006537600093
85. Must, K., Lassen, B., Jokelainen, P., 2015. Seroprevalence of and Risk Factors for *Toxoplasma gondii* Infection in Cats in Estonia. Vector-Borne and Zoonotic Diseases 15, 597–601. https://doi.org/10.1089/vbz.2015.1809
86. Nijsse, R., Ploeger, H.W., Wagenaar, J.A., Mughini-Gras, L., 2016. Prevalence and risk factors for patent *Toxocara* infections in cats and cat owners' attitude towards deworming. Parasitology Research 115, 4519–4525. https://doi.org/10.1007/s00436-016-5242-8
87. Oja, R., Soe, E., Valdmann, H., Saarma, U., 2017. Non-invasive genetics outperforms morphological methods in faecal dietary analysis, revealing wild boar as a considerable conservation concern for ground-nesting birds. PLoS ONE 12, e0179463. https://doi.org/10.1371/journal.pone.0179463
88. Otranto, D., Cantacessi, C., Pfeffer, M., Dantas-Torres, F., Brianti, E., Deplazes, P., Genchi, C., Guberti, V., Capelli, G., 2015. The role of wild canids and felids in spreading parasites to dogs and cats in Europe. Veterinary Parasitology 213, 12–23. https://doi.org/10.1016/j.vetpar.2015.04.022
89. Overgaauw, P.A.M., Nederland, V., 1997. Aspects of *Toxocara* Epidemiology: Toxocarosis in Dogs and Cats. Critical Reviews in Microbiology 23, 233–251. https://doi.org/10.3109/10408419709115138
90. Palmer, C.S., Thompson, R.C.A., Traub, R.J., Rees, R., Robertson, I.D., 2008. National study of the gastrointestinal parasites of dogs and cats in Australia. Veterinary Parasitology 151, 181–190. https://doi.org/10.1016/j.vetpar.2007.10.015
91. Papajová, I., Pipiková, J., Papaj, J., Čižmár, A., 2014. Parasitic contamination of urban and rural environments in the Slovak Republic: dog's excrements as a source. Helminthologia 51, 273–280. https://doi.org/10.2478/s11687-014-0241-8
92. Pavlasek, I., Ryan, U., 2007. The first finding of a natural infection of *Cryptosporidium muris* in a cat. Veterinary Parasitology 144, 349–352. https://doi.org/10.1016/j.vetpar.2006.10.005
93. Pianka, E.R., 1973. The Structure of Lizard Communities. Annual Review of Ecology, Evolution, and Systematics 4, 53–74.
94. Plumer, L., Talvi, T., Männil, P., Saarma, U., 2018. Assessing the roles of wolves and dogs in livestock predation with suggestions for mitigating human–wildlife conflict and conservation of wolves. Conservation Genetics 19, 665–672. https://doi.org/10.1007/s10592-017-1045-4
95. QGIS Development Team (version 3.18), 2021. QGIS Geographic Information System. Open Source. Geospatial Foundation Project. Available at http://qgis.osgeo.org, (accessed 14 May 2022).
96. R Core Team, 2021. R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. URL https://www.R-project.org/.

97. Rataj, A.V., Lindtner-Knific, R., Vlahović, K., Mavri, U., Dovč, A., 2011. Parasites in pet reptiles. Acta Veterinaria Scandinavica 53, 33. https://doi.org/10.1186/1751-0147-53-33
98. Regidor-Cerrillo, J., Arranz-Solís, D., Moreno-Gonzalo, J., Pedraza-Díaz, S., Gomez-Bautista, M., Ortega-Mora, L.M., Collantes-Fernandez, E., 2020. Prevalence of intestinal parasite infections in stray and farm dogs from Spain. Revista Brasileira de Parasitologia Veterinária. 29, e014920. https://doi.org/10.1590/s1984-29612020063
99. Remes, N., Kärssin, A., Must, K., Tagel, M., Lassen, B., Jokelainen, P., 2018. *Toxoplasma gondii* seroprevalence in free-ranging moose (*Alces alces*) hunted for human consumption in Estonia: Indicator host species for environmental Toxoplasma gondii oocyst contamination. Veterinary Parasitology: Regional Studies and Reports 11, 6–11. https://doi.org/10.1016/j.vprsr.2017.11.001
100. Remm, M., and Remm, K., 2014. Studies on enterobiasis, toxoplasmosis and toxocariasis in Estonia. pp. 182–195 In Schærström A, Jørgensen SH, Kistemann T and Sivertun Å (Eds) Geography and Health: A Nordic Outlook. Stockholm, Sweden, The Swedish National Defence College.
101. Reperant, L.A., Hegglin, D., Tanner, I., Fischer, C., Deplazes, P., 2009. Rodents as shared indicators for zoonotic parasites of carnivores in urban environments. Parasitology 136, 329–337. https://doi.org/10.1017/S0031182008005428
102. Reynolds, J. C. and Aebischer, N.J., 1991. Comparison and quantification of carnivore diet by faecal analysis: a critique, with recommendations, based on a study of the fox *Vulpes vulpes*. Mammal Review 21(3), 97–122.
103. Roepstorff, A., Nansen, P., 1998. Epidemiology, diagnosis and control of helminth parasites of swine. Food and Agriculture Organization of the United Nations, Rome.
104. Rossin, A., Malizia, A.I., Denegri, G.M., 2004. The role of the subterranean rodent *Ctenomys talarum* (Rodentia: Octodontidae) in the life cycle of *Taenia taeniaeformis* (Cestoda: Taeniidae) in urban environments. Veterinary Parasitology 122, 27–33. https://doi.org/10.1016/j.vetpar.2004.03.001
105. Rothenburger, J.L., Himsworth, C.G., Lejeune, M., Treuting, P.M., Leighton, F.A., 2014. Lesions associated with *Eucoleus* sp. in the non-glandular stomach of wild urban rats (*Rattus norvegicus*). International Journal for Parasitology: Parasites and Wildlife 3, 95–101. https://doi.org/10.1016/j.ijppaw.2014.04.003
106. Rutkowski, R., Krofel, M., Giannatos, G., Ćirović, D., Männil, P., Volokh, A.M., Lanszki, J., Heltai, M., Szabó, L., Banea, O.C., Yavruyan, E., Hayrapetyan, V., Kopaliani, N., Miliou, A., Tryfonopoulos, G.A., Lymberakis, P., Penezić, A., Pakeltytė, G., Suchecka, E., Bogdanowicz, W., 2015. A European Concern? Genetic Structure and Expansion of Golden Jackals (*Canis aureus*) in Europe and the Caucasus. PLoS ONE 10, e0141236. https://doi.org/10.1371/journal.pone.0141236
107. Saeed, I., Maddox-Hyttel, C., Monrad, J., Kapel, C.M.O., 2006. Helminths of red foxes (*Vulpes vulpes*) in Denmark. Veterinary Parasitology 139, 168–179. https://doi.org/10.1016/j.vetpar.2006.02.015
108. Saarma, U., Jõgisalu, I., Moks, E., Varcasia, A., Lavikainen, A., Oksanen, A., Simsek, S., Andresiuk, V., Denegri, G., González, L.M., Ferrer, E., Gárate, T., Rinaldi, L., Maravilla, P., 2009. A novel phylogeny for the genus *Echinococcus*, based on nuclear data, challenges relationships based on mitochondrial evidence. Parasitology 136, 317–328. https://doi.org/10.1017/S0031182008005453
109. SAS Institute Inc. 2021, Version 9.04, Cary, NC.

110. Shokouhi, S., & Abdi, J., 2018. Seroprevalence of *Toxocara* in Children from Urban and Rural Areas of Ilam Province, West Iran. Osong public health and research perspectives, 9(3), 101–104. https://doi.org/10.24171/j.phrp.2018.9.3.03
111. Schlüter, D., Däubener, W., Schares, G., Groß, U., Pleyer, U., Lüder, C., 2014. Animals are key to human toxoplasmosis. International Journal of Medical Microbiology 304, 917–929. https://doi.org/10.1016/j.ijmm.2014.09.002
112. Schantz, P., M., 1994. Of worms, dogs, and human hosts: continuing challenges for veterinarians in prevention of human disease. Journal of the American Veterinary Medical Association, 204(7), 1023–1028.
113. Schnieder, T., Laabs, E.-M., Welz, C., 2011. Larval development of *Toxocara canis* in dogs. Veterinary Parasitology 175, 193–206. https://doi.org/10.1016/j.vetpar.2010.10.027
114. Schurer, J.M., Ndao, M., Skinner, S., Irvine, J., Elmore, S.A., Epp, T., Jenkins, E.J., 2013. Parasitic Zoonoses: One Health Surveillance in Northern Saskatchewan. PLoS Neglected Tropical Diseases 7, e2141. https://doi.org/10.1371/journal.pntd.0002141
115. Smith, M.H. and Beaver, P.C., 1953. Persistence and distribution of *Toxocara* larvae in the tissues of children and mice. Pediatrics, 12(5), pp. 491–497.
116. Smyth, J. D., and Derek Wakelin. 1994. Introduction to animal parasitology. Cambridge, Eng: Cambridge University Press.
117. Soriano, S.V., Pierangeli, N.B., Roccia, I., Bergagna, H.F.J., Lazzarini, L.E., Celescinco, A., Saiz, M.S., Kossman, A., Contreras, P.A., Arias, C., Basualdo, J.A., 2010. A wide diversity of zoonotic intestinal parasites infects urban and rural dogs in Neuquén, Patagonia, Argentina. Veterinary Parasitology 167, 81–85. https://doi.org/10.1016/j.vetpar.2009.09.048
118. Spain, C.V., Scarlett, J.M., Wade, S.E. and McDonough, P., 2001. Prevalence of enteric zoonotic agents in cats less than 1 year old in central New York State. Journal of Veterinary Internal Medicine, 15(1), pp.33–38.
119. Talvik, H., Moks, E., Mägi, E., Järvis, T., Miller, I., 2006. Distribution of Toxocara infection in the environment and in definitive and paratenic hosts in Estonia. Acta Veterinaria Hungarica 54, 399–406. https://doi.org/10.1556/avet.54.2006.3.10
120. Taylor, L.H., Latham, S.M., woolhouse, M.E.J., 2001. Risk factors for human disease emergence. Philosophical Transactions of the Royal Society of London. B 356, 983–989. https://doi.org/10.1098/rstb.2001.0888
121. Teng, K.T., McGreevy, P.D., Toribio, J.-A.L.M.L., Dhand, N.K., 2016. Trends in popularity of some morphological traits of purebred dogs in Australia. Canine Genetics Epidemiology 3, 2. https://doi.org/10.1186/s40575-016-0032-2
122. Teerink, B.J., 1991. Hair of west-European mammals: Atlas and identification key. 1st edn. Cambridge, Cambridge University Press.
123. The European Pet Food Industry (FEDIAF), 2021, Annual Report 2021. Available at https://www.fediaf.org/annual-report.html
124. Thompson, R.C.A., 2008. The taxonomy, phylogeny and transmission of *Echinococcus*. Experimental Parasitology 119, 439–446. https://doi.org/10.1016/j.exppara.2008.04.016
125. Tóth, M., 2017. Hair and Fur Atlas of Central European Mammals. Pars Ltd, Nagykovácsi, Hungary.
126. Tokiwa, T., Ohnuki, A., Kubota, R., Tamukai, K., Ike, K., 2018. Morphological and molecular characterization of *Cystoisospora* sp. from Asian small-clawed otters *Aonyx cinereus*. International Journal for Parasitology: Parasites and Wildlife 7, 268–273. https://doi.org/10.1016/j.ijppaw.2018.07.00

127. Traversa, D., Frangipane di Regalbono, A., Di Cesare, A., La Torre, F., Drake, J., Pietrobelli, M., 2014. Environmental contamination by canine geohelminths. Parasites & Vectors 7, 67. https://doi.org/10.1186/1756-3305-7-67
128. Tull, A., Moks, E., Laurimaa, L., Keis, M., & Süld, K. (2020). Endoparasite infection hotspots in Estonian urban areas. Journal of Helminthology, 94, E104. https://doi.org/10.1017/S0022149X19000920
129. Tull, A., Moks, E., & Saarma, U. (2021). Endoparasite prevalence and infection risk factors among cats in an animal shelter in Estonia. Folia Parasitologica, https://doi.org/10.14411/fp.2021.010
130. Tull, A., Valdmann, H., Rannap, R., Kaasiku, T., Tammeleht, E., & Saarma, U. (2022). Free-ranging rural dogs are highly infected with helminths, contaminating environment nine times more than urban dogs. Journal of Helminthology, 96, E19. https://doi.org/10.1017/S0022149X22000116
131. Tzannes, S., Batchelor, D.J., Graham, P.A., Pinchbeck, G.L., Wastling, J., German, A.J., 2008. Prevalence of *Cryptosporidium*, *Giardia* and *Isospora* species infections in pet cats with clinical signs of gastrointestinal disease. Journal of Feline Medicine and Surgery 10, 1–8. https://doi.org/10.1016/j.jfms.2007.05.006
132. Valdmann, H., and Saarma, U., 2020. Winter diet of wolf (*Canis lupus*) after the outbreak of African swine fever and under the severely reduced densities of wild boar (*Sus scrofa*). Hystrix, the Italian Journal of Mammalogy 31, 154–156.
133. Valdmann, H., Moks, E., Talvik, H., 2004. Helminth Fauna of Eurasian Lynx (*Lynx lynx*) in Estonia. Journal of Wildlife Diseases 40, 356–360. https://doi.org/10.7589/0090-3558-40.2.356
134. VanWormer, E., Fritz, H., Shapiro, K., Mazet, J.A.K., Conrad, P.A., 2013. Molecules to modeling: *Toxoplasma gondii* oocysts at the human–animal–environment interface. Comparative Immunology, Microbiology and Infectious Diseases 36, 217–231. https://doi.org/10.1016/j.cimid.2012.10.006
135. Villeneuve, A., Polley, L., Jenkins, E., Schurer, J., Gilleard, J., Kutz, S., Conboy, G., Benoit, D., Seewald, W., Gagné, F., 2015. Parasite prevalence in fecal samples from shelter dogs and cats across the Canadian provinces. Parasites & Vectors 8, 281. https://doi.org/10.1186/s13071-015-0870-x
136. Waindok, P., Raue, K., Grilo, M.L., Siebert, U., Strube, C., 2021. Predators in northern Germany are reservoirs for parasites of One Health concern. Parasitology Research 120, 4229–4239. https://doi.org/10.1007/s00436-021-07073-3
137. Webster, G.A., 1958. A Report on *Toxocara Canis*. Comparative Medicine 8.
138. Wolf, D., Vrhovec, M.G., Failing, K., Rossier, C., Hermosilla, C., Pantchev, N., 2014. Diagnosis of gastrointestinal parasites in reptiles: comparison of two coprological methods. Acta Veterinaria Scandinavica 56, 44. https://doi.org/10.1186/s13028-014-0044-4
139. World Health Organization, 2022. https://www.who.int/news-room/fact-sheets/detail/soil-transmitted-helminth-infections (page visited May 11th 2022).
140. Wyrosdick, H.M., Chapman, A., Martinez, J., Schaefer, J.J., 2017. Parasite prevalence survey in shelter cats in Citrus County, Florida. Veterinary Parasitology: Regional Studies and Reports 10, 20–24. https://doi.org/10.1016/j.vprsr.2017.07.002
141. Zottler, E.-M., Bieri, M., Basso, W., Schnyder, M., 2019. Intestinal parasites and lungworms in stray, shelter and privately owned cats of Switzerland. Parasitology International 69, 75–81. https://doi.org/10.1016/j.parint.2018.12.005

ACKNOWLEDGEMENTS

I would like to sincerely thank my supervisors, Epp and Urmas, who had the patience to teach me a lot and supported me on writing my thesis. I`d also offer my special gratitude to Harri who filled the void when Epp changed her workplace.

On this long journey I thank my parents and grandparent, Ebe-Liis, Aivo and Elbe, for their support. I also thank my wife, Tiina, for her encouragement, and who took care of little Tuuli Lauren, even in the holidays, so that I could focus on writing the thesis.

I would also thank my colleagues (Liina, Teivi, Egle, Maris) for their help and support and all other honor belongs to people and staff who have helped to collect scats for my work or gave any other suggestions and help in the study period.

Special gratitude goes also to the Tartu Animal Shelter for their helpful cooperation.

Last but not least, I`d thank my best friend Kaur for believing and couching me during the study period.

The work was supported by research funding from the Estonian Ministry of Education and Research: grant IUT20-32 (Evolutionary and contemporary processes in populations of mammals and their pathogens; 1.01.2014–31.12.2019); and grant PRG1209 (Studies of life-threatening *Echinococcus* parasites globally and in Estonia; 1.01.2021–31.12.2025).

PUBLICATIONS

CURRICULUM VITAE

Name	Ants Tull
Date of birth	31.05.1990
Address	University of Tartu, Oecologicum, Liivi 2–210
Phone	53 969 479
ORCID	0000-0002-6632-4791
E-mail	ants.tull@ut.ee

Education

2015–2022	University of Tartu, PhD Zoology and Hydrobiology
2013–2015	University of Tartu, Faculty of Science and Technology, Zoology and Hydrobiology, Master of Science
2009–2013	University of Tartu, Faculty of Science and Technology, Ecology and Biodiversity Conservation, Bachelor of Science
1997–2009	High school of Kunda

Institutions and positions

01.11.2021–28.08.2022
University of Tartu, Faculty of Science and Technology, Institute of Ecology and Earth Sciences, Junior Researcher (1,00)

Publications

Tull, A., Moks, E., Laurimaa, L., Keis, M., & Süld, K. (2020). Endoparasite infection hotspots in Estonian urban areas. Journal of Helminthology, 94, E104. https://doi.org/10.1017/S0022149X19000920

Tull, A., Moks, E., & Saarma, U. (2021). Endoparasite prevalence and infection risk factors among cats in an animal shelter in Estonia. Folia Parasitologica, https://doi.org/10.14411/fp.2021.010

Tull, A., Valdmann, H., Rannap, R., Kaasiku, T., Tammeleht, E., & Saarma, U. (2022). Free-ranging rural dogs are highly infected with helminths, contaminating environment nine times more than urban dogs. Journal of Helminthology, 96, E19. https://doi.org/10.1017/S0022149X22000116

Tull, A., Valdmann, H., Tammeleht, E., Kaasiku, T., Rannap, R., & Saarma, U. (2022). High overlap of zoonotic helminths between wild mammalian predators and rural dogs as a neglected health risk to humans. *Manuscript submitted.*

Honours & awards

2019 Dora Plus (short-term mobility) activity T1.1 grant to participate in the 9th congress of the Scandinavian-Baltic Society for Parasitology (SBSP) and the Annual Meeting of the European Veterinary Parasitology College (EVPC), Copenhagen, Denmark.

Conference presentations

Oral presentation „Endoparasite infection hotspots in Estonian urban areas“ in the 8th conference of the scandinavian- Baltic Society for Parasitology (SBSP) and the 16th Annual Meeting of the European Veterinary Parasitology College (EVPC), held in Copenhagen, Denmark, October 10–11, 2019.

Oral presentation „Endoparasite prevalence and infection risk factors among shelter cats in an animal shelter in Estonia“ in the 11th Baltic Theriological Conference, held in 25–27 January, 2021 (online).

Oral presentation “Endoparasite Infection Hotspots in Estonian Urban Areas” held in PhD Student Conference of the Departments of Botany and Zoology Estonia, Tartu in 17.01.2020.

Oral presentation „Free-ranging rural dogs are highly infected with helminths, contaminating environment nine times more than urban dogs“ in the PhD Student Conference of the Departments of Botany and Zoology held in the 6th of May in 2022, Estonia, Põlvamaa, Cantervilla castle.

Membership in organizations

2020–... A member of Estonian Theriological Society
2020–... A member of Estonian Naturalists´ Society
2014–... A member of Estonian Ornithological Society

ELULOOKIRJELDUS

Nimi: Ants Tull
Sünniaeg: 31.05.1990
Aadress: Tartu Ülikool Ökoloogikum Liivi 2–210
Mobiil 53 969 479
ORCID 0000-0002-6632-4791
E-aadress ants.tull@ut.ee

Haridus

2015–2022	Tartu Ülikool, Zooloogia ja hüdrobioloogia, PhD
2013–2015	Tartu Ülikool, Zooloogia ja hüdrobioloogia, magistrikraad
2009–2013	Tartu Ülikool, Ökoloogia ja maateaduste instituut, ökoloogia ja elustiku kaitse, bakalaureusekraad
1997–2009	Kuna Ühisgümnaasium

Teenistuskäik

01.11.2021–28.08.2022
Tartu Ülikool, ÖMI, zooloogia osakond, nooremteadur (1,00)

Teaduskirjandus

Tull, A., Moks, E., Laurimaa, L., Keis, M., & Süld, K. (2020). Endoparasite infection hotspots in Estonian urban areas. Journal of Helminthology, 94, E104. https://doi.org/10.1017/S0022149X19000920

Tull, A., Moks, E., & Saarma, U. (2021). Endoparasite prevalence and infection risk factors among cats in an animal shelter in Estonia. Folia Parasitologica, https://doi.org/10.14411/fp.2021.010

Tull, A., Valdmann, H., Rannap, R., Kaasiku, T., Tammeleht, E., & Saarma, U. (2022). Free-ranging rural dogs are highly infected with helminths, contaminating environment nine times more than urban dogs. Journal of Helminthology, 96, E19. https://doi.org/10.1017/S0022149X22000116

Tull, A., Valdmann, H., Tammeleht, E., Kaasiku, T., Rannap, R., & Saarma, U. (2022). High overlap of zoonotic helminths between wild mammalian predators and rural dogs as a neglected health risk to humans. *Manuscript submitted.*

Uurimistoetused ja stipendiumid

2019 DoRa Pluss (lühiajaline õpiränne) T1.1,et osaleda 8ndal Skandinaavia-Balti Parasitoloogia kongressil 10–11. oktoober, 2019, Kopenhaagen, Taani.

Konverentsiettekanded

Suuline ettekanne „Endoparasite infection hotspots in Estonian urban areas“ 8ndal Skandinaavia-Balti Parasitoloogia kongressil 10–11. oktoober, 2019, Kopenhaagen, Taani.

Suuline ettekanne „Endoparasite prevalence and infection risk factors among shelter cats in an animal shelter in Estonia“ 11ndal Balti Terioloogia Konverentsil, 25–27 jaanuar, 2021 (läbi veebi).

Suuline ettekanne “Endoparasite Infection Hotspots in Estonian Urban Areas” BO-ZO osakondade doktorantide konverents Tartus 17.01.2020.

Suuline ettekanne „Free-ranging rural dogs are highly infected with helminths, contaminating environment nine times more than urban dogs BO-ZO osakondade doktorantide konverents 6ndal mail 2022, Põlvamaa, Cantervilla lossis.

Membership in organizations

2020–... Eesti Terioloogia Seltsi liige
2020–... Eesti Loodusuurijate Seltsi liige
2014–... Eesti Ornitoloogiaühingu liige

DISSERTATIONES BIOLOGICAE UNIVERSITATIS TARTUENSIS

1. **Toivo Maimets**. Studies of human oncoprotein p53. Tartu, 1991, 96 p.
2. **Enn K. Seppet**. Thyroid state control over energy metabolism, ion transport and contractile functions in rat heart. Tartu, 1991, 135 p.
3. **Kristjan Zobel**. Epifüütsete makrosamblike väärtus õhu saastuse indikaatoritena Hamar-Dobani boreaalsetes mägimetsades. Tartu, 1992, 131 lk.
4. **Andres Mäe**. Conjugal mobilization of catabolic plasmids by transposable elements in helper plasmids. Tartu, 1992, 91 p.
5. **Maia Kivisaar**. Studies on phenol degradation genes of *Pseudomonas* sp. strain EST 1001. Tartu, 1992, 61 p.
6. **Allan Nurk**. Nucleotide sequences of phenol degradative genes from *Pseudomonas sp.* strain EST 1001 and their transcriptional activation in *Pseudomonas putida*. Tartu, 1992, 72 p.
7. **Ülo Tamm**. The genus *Populus* L. in Estonia: variation of the species biology and introduction. Tartu, 1993, 91 p.
8. **Jaanus Remme**. Studies on the peptidyltransferase centre of the *E.coli* ribosome. Tartu, 1993, 68 p.
9. **Ülo Langel**. Galanin and galanin antagonists. Tartu, 1993, 97 p.
10. **Arvo Käärd**. The development of an automatic online dynamic fluorescense-based pH-dependent fiber optic penicillin flowthrought biosensor for the control of the benzylpenicillin hydrolysis. Tartu, 1993, 117 p.
11. **Lilian Järvekülg**. Antigenic analysis and development of sensitive immunoassay for potato viruses. Tartu, 1993, 147 p.
12. **Jaak Palumets**. Analysis of phytomass partition in Norway spruce. Tartu, 1993, 47 p.
13. **Arne Sellin**. Variation in hydraulic architecture of *Picea abies* (L.) Karst. trees grown under different enviromental conditions. Tartu, 1994, 119 p.
13. **Mati Reeben**. Regulation of light neurofilament gene expression. Tartu, 1994, 108 p.
14. **Urmas Tartes**. Respiration rhytms in insects. Tartu, 1995, 109 p.
15. **Ülo Puurand**. The complete nucleotide sequence and infections *in vitro* transcripts from cloned cDNA of a potato A potyvirus. Tartu, 1995, 96 p.
16. **Peeter Hõrak**. Pathways of selection in avian reproduction: a functional framework and its application in the population study of the great tit (*Parus major*). Tartu, 1995, 118 p.
17. **Erkki Truve**. Studies on specific and broad spectrum virus resistance in transgenic plants. Tartu, 1996, 158 p.
18. **Illar Pata**. Cloning and characterization of human and mouse ribosomal protein S6-encoding genes. Tartu, 1996, 60 p.
19. **Ülo Niinemets**. Importance of structural features of leaves and canopy in determining species shade-tolerance in temperature deciduous woody taxa. Tartu, 1996, 150 p.

20. **Ants Kurg**. Bovine leukemia virus: molecular studies on the packaging region and DNA diagnostics in cattle. Tartu, 1996, 104 p.
21. **Ene Ustav**. E2 as the modulator of the BPV1 DNA replication. Tartu, 1996, 100 p.
22. **Aksel Soosaar**. Role of helix-loop-helix and nuclear hormone receptor transcription factors in neurogenesis. Tartu, 1996, 109 p.
23. **Maido Remm**. Human papillomavirus type 18: replication, transformation and gene expression. Tartu, 1997, 117 p.
24. **Tiiu Kull**. Population dynamics in *Cypripedium calceolus* L. Tartu, 1997, 124 p.
25. **Kalle Olli**. Evolutionary life-strategies of autotrophic planktonic microorganisms in the Baltic Sea. Tartu, 1997, 180 p.
26. **Meelis Pärtel**. Species diversity and community dynamics in calcareous grassland communities in Western Estonia. Tartu, 1997, 124 p.
27. **Malle Leht**. The Genus *Potentilla* L. in Estonia, Latvia and Lithuania: distribution, morphology and taxonomy. Tartu, 1997, 186 p.
28. **Tanel Tenson**. Ribosomes, peptides and antibiotic resistance. Tartu, 1997, 80 p.
29. **Arvo Tuvikene**. Assessment of inland water pollution using biomarker responses in fish *in vivo* and *in vitro*. Tartu, 1997, 160 p.
30. **Urmas Saarma**. Tuning ribosomal elongation cycle by mutagenesis of 23S rRNA. Tartu, 1997, 134 p.
31. **Henn Ojaveer**. Composition and dynamics of fish stocks in the gulf of Riga ecosystem. Tartu, 1997, 138 p.
32. **Lembi Lõugas**. Post-glacial development of vertebrate fauna in Estonian water bodies. Tartu, 1997, 138 p.
33. **Margus Pooga**. Cell penetrating peptide, transportan, and its predecessors, galanin-based chimeric peptides. Tartu, 1998, 110 p.
34. **Andres Saag**. Evolutionary relationships in some cetrarioid genera (Lichenized Ascomycota). Tartu, 1998, 196 p.
35. **Aivar Liiv**. Ribosomal large subunit assembly *in vivo*. Tartu, 1998, 158 p.
36. **Tatjana Oja**. Isoenzyme diversity and phylogenetic affinities among the eurasian annual bromes (*Bromus* L., Poaceae). Tartu, 1998, 92 p.
37. **Mari Moora**. The influence of arbuscular mycorrhizal (AM) symbiosis on the competition and coexistence of calcareous grassland plant species. Tartu, 1998, 78 p.
38. **Olavi Kurina**. Fungus gnats in Estonia (*Diptera: Bolitophilidae, Keroplatidae, Macroceridae, Ditomyiidae, Diadocidiidae, Mycetophilidae*). Tartu, 1998, 200 p.
39. **Andrus Tasa**. Biological leaching of shales: black shale and oil shale. Tartu, 1998, 98 p.
40. **Arnold Kristjuhan**. Studies on transcriptional activator properties of tumor suppressor protein p53. Tartu, 1998, 86 p.
41. **Sulev Ingerpuu**. Characterization of some human myeloid cell surface and nuclear differentiation antigens. Tartu, 1998, 163 p.

42. **Veljo Kisand**. Responses of planktonic bacteria to the abiotic and biotic factors in the shallow lake Võrtsjärv. Tartu, 1998, 118 p.
43. **Kadri Põldmaa**. Studies in the systematics of hypomyces and allied genera (Hypocreales, Ascomycota). Tartu, 1998, 178 p.
44. **Markus Vetemaa**. Reproduction parameters of fish as indicators in environmental monitoring. Tartu, 1998, 117 p.
45. **Heli Talvik**. Prepatent periods and species composition of different *Oesophagostomum* spp. populations in Estonia and Denmark. Tartu, 1998, 104 p.
46. **Katrin Heinsoo**. Cuticular and stomatal antechamber conductance to water vapour diffusion in *Picea abies* (L.) karst. Tartu, 1999, 133 p.
47. **Tarmo Annilo**. Studies on mammalian ribosomal protein S7. Tartu, 1998, 77 p.
48. **Indrek Ots**. Health state indicies of reproducing great tits (*Parus major*): sources of variation and connections with life-history traits. Tartu, 1999, 117 p.
49. **Juan Jose Cantero**. Plant community diversity and habitat relationships in central Argentina grasslands. Tartu, 1999, 161 p.
50. **Rein Kalamees**. Seed bank, seed rain and community regeneration in Estonian calcareous grasslands. Tartu, 1999, 107 p.
51. **Sulev Kõks**. Cholecystokinin (CCK) – induced anxiety in rats: influence of environmental stimuli and involvement of endopioid mechanisms and serotonin. Tartu, 1999, 123 p.
52. **Ebe Sild**. Impact of increasing concentrations of O_3 and CO_2 on wheat, clover and pasture. Tartu, 1999, 123 p.
53. **Ljudmilla Timofejeva**. Electron microscopical analysis of the synaptonemal complex formation in cereals. Tartu, 1999, 99 p.
54. **Andres Valkna**. Interactions of galanin receptor with ligands and G-proteins: studies with synthetic peptides. Tartu, 1999, 103 p.
55. **Taavi Virro**. Life cycles of planktonic rotifers in lake Peipsi. Tartu, 1999, 101 p.
56. **Ana Rebane**. Mammalian ribosomal protein S3a genes and intron-encoded small nucleolar RNAs U73 and U82. Tartu, 1999, 85 p.
57. **Tiina Tamm**. Cocksfoot mottle virus: the genome organisation and translational strategies. Tartu, 2000, 101 p.
58. **Reet Kurg**. Structure-function relationship of the bovine papilloma virus E2 protein. Tartu, 2000, 89 p.
59. **Toomas Kivisild**. The origins of Southern and Western Eurasian populations: an mtDNA study. Tartu, 2000, 121 p.
60. **Niilo Kaldalu**. Studies of the TOL plasmid transcription factor XylS. Tartu, 2000, 88 p.
61. **Dina Lepik**. Modulation of viral DNA replication by tumor suppressor protein p53. Tartu, 2000, 106 p.
62. **Kai Vellak**. Influence of different factors on the diversity of the bryophyte vegetation in forest and wooded meadow communities. Tartu, 2000, 122 p.

63. **Jonne Kotta**. Impact of eutrophication and biological invasionas on the structure and functions of benthic macrofauna. Tartu, 2000, 160 p.
64. **Georg Martin**. Phytobenthic communities of the Gulf of Riga and the inner sea the West-Estonian archipelago. Tartu, 2000, 139 p.
65. **Silvia Sepp**. Morphological and genetical variation of *Alchemilla L.* in Estonia. Tartu, 2000. 124 p.
66. **Jaan Liira**. On the determinants of structure and diversity in herbaceous plant communities. Tartu, 2000, 96 p.
67. **Priit Zingel**. The role of planktonic ciliates in lake ecosystems. Tartu, 2001, 111 p.
68. **Tiit Teder**. Direct and indirect effects in Host-parasitoid interactions: ecological and evolutionary consequences. Tartu, 2001, 122 p.
69. **Hannes Kollist**. Leaf apoplastic ascorbate as ozone scavenger and its transport across the plasma membrane. Tartu, 2001, 80 p.
70. **Reet Marits**. Role of two-component regulator system PehR-PehS and extracellular protease PrtW in virulence of *Erwinia Carotovora* subsp. *Carotovora*. Tartu, 2001, 112 p.
71. **Vallo Tilgar**. Effect of calcium supplementation on reproductive performance of the pied flycatcher *Ficedula hypoleuca* and the great tit *Parus major,* breeding in Nothern temperate forests. Tartu, 2002, 126 p.
72. **Rita Hõrak**. Regulation of transposition of transposon Tn*4652* in *Pseudomonas putida*. Tartu, 2002, 108 p.
73. **Liina Eek-Piirsoo**. The effect of fertilization, mowing and additional illumination on the structure of a species-rich grassland community. Tartu, 2002, 74 p.
74. **Krõõt Aasamaa**. Shoot hydraulic conductance and stomatal conductance of six temperate deciduous tree species. Tartu, 2002, 110 p.
75. **Nele Ingerpuu**. Bryophyte diversity and vascular plants. Tartu, 2002, 112 p.
76. **Neeme Tõnisson**. Mutation detection by primer extension on oligonucleotide microarrays. Tartu, 2002, 124 p.
77. **Margus Pensa**. Variation in needle retention of Scots pine in relation to leaf morphology, nitrogen conservation and tree age. Tartu, 2003, 110 p.
78. **Asko Lõhmus**. Habitat preferences and quality for birds of prey: from principles to applications. Tartu, 2003, 168 p.
79. **Viljar Jaks**. p53 – a switch in cellular circuit. Tartu, 2003, 160 p.
80. **Jaana Männik**. Characterization and genetic studies of four ATP-binding cassette (ABC) transporters. Tartu, 2003, 140 p.
81. **Marek Sammul**. Competition and coexistence of clonal plants in relation to productivity. Tartu, 2003, 159 p
82. **Ivar Ilves**. Virus-cell interactions in the replication cycle of bovine papillomavirus type 1. Tartu, 2003, 89 p.
83. **Andres Männik**. Design and characterization of a novel vector system based on the stable replicator of bovine papillomavirus type 1. Tartu, 2003, 109 p.

84. **Ivika Ostonen**. Fine root structure, dynamics and proportion in net primary production of Norway spruce forest ecosystem in relation to site conditions. Tartu, 2003, 158 p.
85. **Gudrun Veldre**. Somatic status of 12–15-year-old Tartu schoolchildren. Tartu, 2003, 199 p.
86. **Ülo Väli**. The greater spotted eagle *Aquila clanga* and the lesser spotted eagle *A. pomarina*: taxonomy, phylogeography and ecology. Tartu, 2004, 159 p.
87. **Aare Abroi**. The determinants for the native activities of the bovine papillomavirus type 1 E2 protein are separable. Tartu, 2004, 135 p.
88. **Tiina Kahre**. Cystic fibrosis in Estonia. Tartu, 2004, 116 p.
89. **Helen Orav-Kotta**. Habitat choice and feeding activity of benthic suspension feeders and mesograzers in the northern Baltic Sea. Tartu, 2004, 117 p.
90. **Maarja Öpik**. Diversity of arbuscular mycorrhizal fungi in the roots of perennial plants and their effect on plant performance. Tartu, 2004, 175 p.
91. **Kadri Tali**. Species structure of *Neotinea ustulata*. Tartu, 2004, 109 p.
92. **Kristiina Tambets**. Towards the understanding of post-glacial spread of human mitochondrial DNA haplogroups in Europe and beyond: a phylogeographic approach. Tartu, 2004, 163 p.
93. **Arvi Jõers**. Regulation of p53-dependent transcription. Tartu, 2004, 103 p.
94. **Lilian Kadaja**. Studies on modulation of the activity of tumor suppressor protein p53. Tartu, 2004, 103 p.
95. **Jaak Truu**. Oil shale industry wastewater: impact on river microbial community and possibilities for bioremediation. Tartu, 2004, 128 p.
96. **Maire Peters**. Natural horizontal transfer of the *pheBA* operon. Tartu, 2004, 105 p.
97. **Ülo Maiväli**. Studies on the structure-function relationship of the bacterial ribosome. Tartu, 2004, 130 p.
98. **Merit Otsus**. Plant community regeneration and species diversity in dry calcareous grasslands. Tartu, 2004, 103 p.
99. **Mikk Heidemaa**. Systematic studies on sawflies of the genera *Dolerus, Empria,* and *Caliroa* (Hymenoptera: Tenthredinidae). Tartu, 2004, 167 p.
100. **Ilmar Tõnno**. The impact of nitrogen and phosphorus concentration and N/P ratio on cyanobacterial dominance and N_2 fixation in some Estonian lakes. Tartu, 2004, 111 p.
101. **Lauri Saks**. Immune function, parasites, and carotenoid-based ornaments in greenfinches. Tartu, 2004, 144 p.
102. **Siiri Rootsi**. Human Y-chromosomal variation in European populations. Tartu, 2004, 142 p.
103. **Eve Vedler**. Structure of the 2,4-dichloro-phenoxyacetic acid-degradative plasmid pEST4011. Tartu, 2005. 106 p.
104. **Andres Tover**. Regulation of transcription of the phenol degradation *pheBA* operon in *Pseudomonas putida*. Tartu, 2005, 126 p.
105. **Helen Udras**. Hexose kinases and glucose transport in the yeast *Hansenula polymorpha*. Tartu, 2005, 100 p.

106. **Ave Suija**. Lichens and lichenicolous fungi in Estonia: diversity, distribution patterns, taxonomy. Tartu, 2005, 162 p.
107. **Piret Lõhmus**. Forest lichens and their substrata in Estonia. Tartu, 2005, 162 p.
108. **Inga Lips**. Abiotic factors controlling the cyanobacterial bloom occurrence in the Gulf of Finland. Tartu, 2005, 156 p.
109. **Krista Kaasik**. Circadian clock genes in mammalian clockwork, metabolism and behaviour. Tartu, 2005, 121 p.
110. **Juhan Javoiš**. The effects of experience on host acceptance in ovipositing moths. Tartu, 2005, 112 p.
111. **Tiina Sedman**. Characterization of the yeast *Saccharomyces cerevisiae* mitochondrial DNA helicase Hmi1. Tartu, 2005, 103 p.
112. **Ruth Aguraiuja**. Hawaiian endemic fern lineage *Diellia* (Aspleniaceae): distribution, population structure and ecology. Tartu, 2005, 112 p.
113. **Riho Teras**. Regulation of transcription from the fusion promoters generated by transposition of Tn*4652* into the upstream region of *pheBA* operon in *Pseudomonas putida*. Tartu, 2005, 106 p.
114. **Mait Metspalu**. Through the course of prehistory in India: tracing the mtDNA trail. Tartu, 2005, 138 p.
115. **Elin Lõhmussaar**. The comparative patterns of linkage disequilibrium in European populations and its implication for genetic association studies. Tartu, 2006, 124 p.
116. **Priit Kupper**. Hydraulic and environmental limitations to leaf water relations in trees with respect to canopy position. Tartu, 2006, 126 p.
117. **Heili Ilves**. Stress-induced transposition of Tn*4652* in *Pseudomonas Putida.* Tartu, 2006, 120 p.
118. **Silja Kuusk**. Biochemical properties of Hmi1p, a DNA helicase from *Saccharomyces cerevisiae* mitochondria. Tartu, 2006, 126 p.
119. **Kersti Püssa**. Forest edges on medium resolution landsat thematic mapper satellite images. Tartu, 2006, 90 p.
120. **Lea Tummeleht**. Physiological condition and immune function in great tits (*Parus major* l.): Sources of variation and trade-offs in relation to growth. Tartu, 2006, 94 p.
121. **Toomas Esperk**. Larval instar as a key element of insect growth schedules. Tartu, 2006, 186 p.
122. **Harri Valdmann**. Lynx (*Lynx lynx*) and wolf (*Canis lupus*) in the Baltic region: Diets, helminth parasites and genetic variation. Tartu, 2006. 102 p.
123. **Priit Jõers**. Studies of the mitochondrial helicase Hmi1p in *Candida albicans* and *Saccharomyces cerevisia*. Tartu, 2006. 113 p.
124. **Kersti Lilleväli**. Gata3 and Gata2 in inner ear development. Tartu, 2007, 123 p.
125. **Kai Rünk**. Comparative ecology of three fern species: *Dryopteris carthusiana* (Vill.) H.P. Fuchs, *D. expansa* (C. Presl) Fraser-Jenkins & Jermy and *D. dilatata* (Hoffm.) A. Gray (Dryopteridaceae). Tartu, 2007, 143 p.

126. **Aveliina Helm**. Formation and persistence of dry grassland diversity: role of human history and landscape structure. Tartu, 2007, 89 p.
127. **Leho Tedersoo**. Ectomycorrhizal fungi: diversity and community structure in Estonia, Seychelles and Australia. Tartu, 2007, 233 p.
128. **Marko Mägi**. The habitat-related variation of reproductive performance of great tits in a deciduous-coniferous forest mosaic: looking for causes and consequences. Tartu, 2007, 135 p.
129. **Valeria Lulla**. Replication strategies and applications of Semliki Forest virus. Tartu, 2007, 109 p.
130. **Ülle Reier**. Estonian threatened vascular plant species: causes of rarity and conservation. Tartu, 2007, 79 p.
131. **Inga Jüriado**. Diversity of lichen species in Estonia: influence of regional and local factors. Tartu, 2007, 171 p.
132. **Tatjana Krama**. Mobbing behaviour in birds: costs and reciprocity based cooperation. Tartu, 2007, 112 p.
133. **Signe Saumaa**. The role of DNA mismatch repair and oxidative DNA damage defense systems in avoidance of stationary phase mutations in *Pseudomonas putida.* Tartu, 2007, 172 p.
134. **Reedik Mägi**. The linkage disequilibrium and the selection of genetic markers for association studies in european populations. Tartu, 2007, 96 p.
135. **Priit Kilgas**. Blood parameters as indicators of physiological condition and skeletal development in great tits (*Parus major*): natural variation and application in the reproductive ecology of birds. Tartu, 2007, 129 p.
136. **Anu Albert**. The role of water salinity in structuring eastern Baltic coastal fish communities. Tartu, 2007, 95 p.
137. **Kärt Padari**. Protein transduction mechanisms of transportans. Tartu, 2008, 128 p.
138. **Siiri-Lii Sandre**. Selective forces on larval colouration in a moth. Tartu, 2008, 125 p.
139. **Ülle Jõgar**. Conservation and restoration of semi-natural floodplain meadows and their rare plant species. Tartu, 2008, 99 p.
140. **Lauri Laanisto**. Macroecological approach in vegetation science: generality of ecological relationships at the global scale. Tartu, 2008, 133 p.
141. **Reidar Andreson**. Methods and software for predicting PCR failure rate in large genomes. Tartu, 2008, 105 p.
142. **Birgot Paavel**. Bio-optical properties of turbid lakes. Tartu, 2008, 175 p.
143. **Kaire Torn**. Distribution and ecology of charophytes in the Baltic Sea. Tartu, 2008, 98 p.
144. **Vladimir Vimberg**. Peptide mediated macrolide resistance. Tartu, 2008, 190 p.
145. **Daima Örd**. Studies on the stress-inducible pseudokinase TRB3, a novel inhibitor of transcription factor ATF4. Tartu, 2008, 108 p.
146. **Lauri Saag**. Taxonomic and ecologic problems in the genus *Lepraria* (*Stereocaulaceae*, lichenised *Ascomycota*). Tartu, 2008, 175 p.

147. **Ulvi Karu**. Antioxidant protection, carotenoids and coccidians in greenfinches – assessment of the costs of immune activation and mechanisms of parasite resistance in a passerine with carotenoid-based ornaments. Tartu, 2008, 124 p.
148. **Jaanus Remm**. Tree-cavities in forests: density, characteristics and occupancy by animals. Tartu, 2008, 128 p.
149. **Epp Moks**. Tapeworm parasites *Echinococcus multilocularis* and *E. granulosus* in Estonia: phylogenetic relationships and occurrence in wild carnivores and ungulates. Tartu, 2008, 82 p.
150. **Eve Eensalu**. Acclimation of stomatal structure and function in tree canopy: effect of light and CO_2 concentration. Tartu, 2008, 108 p.
151. **Janne Pullat**. Design, functionlization and application of an *in situ* synthesized oligonucleotide microarray. Tartu, 2008, 108 p.
152. **Marta Putrinš**. Responses of *Pseudomonas putida* to phenol-induced metabolic and stress signals. Tartu, 2008, 142 p.
153. **Marina Semtšenko**. Plant root behaviour: responses to neighbours and physical obstructions. Tartu, 2008, 106 p.
154. **Marge Starast**. Influence of cultivation techniques on productivity and fruit quality of some *Vaccinium* and *Rubus* taxa. Tartu, 2008, 154 p.
155. **Age Tats**. Sequence motifs influencing the efficiency of translation. Tartu, 2009, 104 p.
156. **Radi Tegova**. The role of specialized DNA polymerases in mutagenesis in *Pseudomonas putida.* Tartu, 2009, 124 p.
157. **Tsipe Aavik**. Plant species richness, composition and functional trait pattern in agricultural landscapes – the role of land use intensity and landscape structure. Tartu, 2009, 112 p.
158. **Kaja Kiiver**. Semliki forest virus based vectors and cell lines for studying the replication and interactions of alphaviruses and hepaciviruses. Tartu, 2009, 104 p.
159. **Meelis Kadaja**. Papillomavirus Replication Machinery Induces Genomic Instability in its Host Cell. Tartu, 2009, 126 p.
160. **Pille Hallast**. Human and chimpanzee Luteinizing hormone/Chorionic Gonadotropin beta (*LHB/CGB*) gene clusters: diversity and divergence of young duplicated genes. Tartu, 2009, 168 p.
161. **Ain Vellak**. Spatial and temporal aspects of plant species conservation. Tartu, 2009, 86 p.
162. **Triinu Remmel**. Body size evolution in insects with different colouration strategies: the role of predation risk. Tartu, 2009, 168 p.
163. **Jaana Salujõe**. Zooplankton as the indicator of ecological quality and fish predation in lake ecosystems. Tartu, 2009, 129 p.
164. **Ele Vahtmäe**. Mapping benthic habitat with remote sensing in optically complex coastal environments. Tartu, 2009, 109 p.
165. **Liisa Metsamaa**. Model-based assessment to improve the use of remote sensing in recognition and quantitative mapping of cyanobacteria. Tartu, 2009, 114 p.

166. **Pille Säälik**. The role of endocytosis in the protein transduction by cell-penetrating peptides. Tartu, 2009, 155 p.
167. **Lauri Peil**. Ribosome assembly factors in *Escherichia coli*. Tartu, 2009, 147 p.
168. **Lea Hallik**. Generality and specificity in light harvesting, carbon gain capacity and shade tolerance among plant functional groups. Tartu, 2009, 99 p.
169. **Mariliis Tark**. Mutagenic potential of DNA damage repair and tolerance mechanisms under starvation stress. Tartu, 2009, 191 p.
170. **Riinu Rannap**. Impacts of habitat loss and restoration on amphibian populations. Tartu, 2009, 117 p.
171. **Maarja Adojaan**. Molecular variation of HIV-1 and the use of this knowledge in vaccine development. Tartu, 2009, 95 p.
172. **Signe Altmäe**. Genomics and transcriptomics of human induced ovarian folliculogenesis. Tartu, 2010, 179 p.
173. **Triin Suvi**. Mycorrhizal fungi of native and introduced trees in the Seychelles Islands. Tartu, 2010, 107 p.
174. **Velda Lauringson**. Role of suspension feeding in a brackish-water coastal sea. Tartu, 2010, 123 p.
175. **Eero Talts**. Photosynthetic cyclic electron transport – measurement and variably proton-coupled mechanism. Tartu, 2010, 121 p.
176. **Mari Nelis**. Genetic structure of the Estonian population and genetic distance from other populations of European descent. Tartu, 2010, 97 p.
177. **Kaarel Krjutškov**. Arrayed Primer Extension-2 as a multiplex PCR-based method for nucleic acid variation analysis: method and applications. Tartu, 2010, 129 p.
178. **Egle Köster**. Morphological and genetical variation within species complexes: *Anthyllis vulneraria* s. l. and *Alchemilla vulgaris* (coll.). Tartu, 2010, 101 p.
179. **Erki Õunap**. Systematic studies on the subfamily Sterrhinae (Lepidoptera: Geometridae). Tartu, 2010, 111 p.
180. **Merike Jõesaar**. Diversity of key catabolic genes at degradation of phenol and *p*-cresol in pseudomonads. Tartu, 2010, 125 p.
181. **Kristjan Herkül**. Effects of physical disturbance and habitat-modifying species on sediment properties and benthic communities in the northern Baltic Sea. Tartu, 2010, 123 p.
182. **Arto Pulk**. Studies on bacterial ribosomes by chemical modification approaches. Tartu, 2010, 161 p.
183. **Maria Põllupüü**. Ecological relations of cladocerans in a brackish-water ecosystem. Tartu, 2010, 126 p.
184. **Toomas Silla**. Study of the segregation mechanism of the Bovine Papillomavirus Type 1. Tartu, 2010, 188 p.
185. **Gyaneshwer Chaubey**. The demographic history of India: A perspective based on genetic evidence. Tartu, 2010, 184 p.

186. **Katrin Kepp**. Genes involved in cardiovascular traits: detection of genetic variation in Estonian and Czech populations. Tartu, 2010, 164 p.
187. **Virve Sõber**. The role of biotic interactions in plant reproductive performance. Tartu, 2010, 92 p.
188. **Kersti Kangro**. The response of phytoplankton community to the changes in nutrient loading. Tartu, 2010, 144 p.
189. **Joachim M. Gerhold**. Replication and Recombination of mitochondrial DNA in Yeast. Tartu, 2010, 120 p.
190. **Helen Tammert**. Ecological role of physiological and phylogenetic diversity in aquatic bacterial communities. Tartu, 2010, 140 p.
191. **Elle Rajandu**. Factors determining plant and lichen species diversity and composition in Estonian *Calamagrostis* and *Hepatica* site type forests. Tartu, 2010, 123 p.
192. **Paula Ann Kivistik**. ColR-ColS signalling system and transposition of Tn*4652* in the adaptation of *Pseudomonas putida*. Tartu, 2010, 118 p.
193. **Siim Sõber**. Blood pressure genetics: from candidate genes to genome-wide association studies. Tartu, 2011, 120 p.
194. **Kalle Kipper**. Studies on the role of helix 69 of 23S rRNA in the factor-dependent stages of translation initiation, elongation, and termination. Tartu, 2011, 178 p.
195. **Triinu Siibak**. Effect of antibiotics on ribosome assembly is indirect. Tartu, 2011, 134 p.
196. **Tambet Tõnissoo**. Identification and molecular analysis of the role of guanine nucleotide exchange factor RIC-8 in mouse development and neural function. Tartu, 2011, 110 p.
197. **Helin Räägel**. Multiple faces of cell-penetrating peptides – their intracellular trafficking, stability and endosomal escape during protein transduction. Tartu, 2011, 161 p.
198. **Andres Jaanus**. Phytoplankton in Estonian coastal waters – variability, trends and response to environmental pressures. Tartu, 2011, 157 p.
199. **Tiit Nikopensius**. Genetic predisposition to nonsyndromic orofacial clefts. Tartu, 2011, 152 p.
200. **Signe Värv**. Studies on the mechanisms of RNA polymerase II-dependent transcription elongation. Tartu, 2011, 108 p.
201. **Kristjan Välk**. Gene expression profiling and genome-wide association studies of non-small cell lung cancer. Tartu, 2011, 98 p.
202. **Arno Põllumäe**. Spatio-temporal patterns of native and invasive zooplankton species under changing climate and eutrophication conditions. Tartu, 2011, 153 p.
203. **Egle Tammeleht**. Brown bear (*Ursus arctos*) population structure, demographic processes and variations in diet in northern Eurasia. Tartu, 2011, 143 p.
205. **Teele Jairus**. Species composition and host preference among ectomycorrhizal fungi in Australian and African ecosystems. Tartu, 2011, 106 p.

206. **Kessy Abarenkov**. PlutoF – cloud database and computing services supporting biological research. Tartu, 2011, 125 p.
207. **Marina Grigorova**. Fine-scale genetic variation of follicle-stimulating hormone beta-subunit coding gene (*FSHB*) and its association with reproductive health. Tartu, 2011, 184 p.
208. **Anu Tiitsaar**. The effects of predation risk and habitat history on butterfly communities. Tartu, 2011, 97 p.
209. **Elin Sild**. Oxidative defences in immunoecological context: validation and application of assays for nitric oxide production and oxidative burst in a wild passerine. Tartu, 2011, 105 p.
210. **Irja Saar**. The taxonomy and phylogeny of the genera *Cystoderma* and *Cystodermella* (Agaricales, Fungi). Tartu, 2012, 167 p.
211. **Pauli Saag**. Natural variation in plumage bacterial assemblages in two wild breeding passerines. Tartu, 2012, 113 p.
212. **Aleksei Lulla**. Alphaviral nonstructural protease and its polyprotein substrate: arrangements for the perfect marriage. Tartu, 2012, 143 p.
213. **Mari Järve**. Different genetic perspectives on human history in Europe and the Caucasus: the stories told by uniparental and autosomal markers. Tartu, 2012, 119 p.
214. **Ott Scheler**. The application of tmRNA as a marker molecule in bacterial diagnostics using microarray and biosensor technology. Tartu, 2012, 93 p.
215. **Anna Balikova**. Studies on the functions of tumor-associated mucin-like leukosialin (CD43) in human cancer cells. Tartu, 2012, 129 p.
216. **Triinu Kõressaar**. Improvement of PCR primer design for detection of prokaryotic species. Tartu, 2012, 83 p.
217. **Tuul Sepp**. Hematological health state indices of greenfinches: sources of individual variation and responses to immune system manipulation. Tartu, 2012, 117 p.
218. **Rya Ero**. Modifier view of the bacterial ribosome. Tartu, 2012, 146 p.
219. **Mohammad Bahram**. Biogeography of ectomycorrhizal fungi across different spatial scales. Tartu, 2012, 165 p.
220. **Annely Lorents**. Overcoming the plasma membrane barrier: uptake of amphipathic cell-penetrating peptides induces influx of calcium ions and downstream responses. Tartu, 2012, 113 p.
221. **Katrin Männik**. Exploring the genomics of cognitive impairment: whole-genome SNP genotyping experience in Estonian patients and general population. Tartu, 2012, 171 p.
222. **Marko Prous**. Taxonomy and phylogeny of the sawfly genus *Empria* (Hymenoptera, Tenthredinidae). Tartu, 2012, 192 p.
223. **Triinu Visnapuu**. Levansucrases encoded in the genome of *Pseudomonas syringae* pv. tomato DC3000: heterologous expression, biochemical characterization, mutational analysis and spectrum of polymerization products. Tartu, 2012, 160 p.
224. **Nele Tamberg**. Studies on Semliki Forest virus replication and pathogenesis. Tartu, 2012, 109 p.

225. **Tõnu Esko**. Novel applications of SNP array data in the analysis of the genetic structure of Europeans and in genetic association studies. Tartu, 2012, 149 p.
226. **Timo Arula**. Ecology of early life-history stages of herring *Clupea harengus membras* in the northeastern Baltic Sea. Tartu, 2012, 143 p.
227. **Inga Hiiesalu**. Belowground plant diversity and coexistence patterns in grassland ecosystems. Tartu, 2012, 130 p.
228. **Kadri Koorem**. The influence of abiotic and biotic factors on small-scale plant community patterns and regeneration in boreonemoral forest. Tartu, 2012, 114 p.
229. **Liis Andresen**. Regulation of virulence in plant-pathogenic pectobacteria. Tartu, 2012, 122 p.
230. **Kaupo Kohv**. The direct and indirect effects of management on boreal forest structure and field layer vegetation. Tartu, 2012, 124 p.
231. **Mart Jüssi**. Living on an edge: landlocked seals in changing climate. Tartu, 2012, 114 p.
232. **Riina Klais**. Phytoplankton trends in the Baltic Sea. Tartu, 2012, 136 p.
233. **Rauno Veeroja**. Effects of winter weather, population density and timing of reproduction on life-history traits and population dynamics of moose (*Alces alces*) in Estonia. Tartu, 2012, 92 p.
234. **Marju Keis**. Brown bear (*Ursus arctos*) phylogeography in northern Eurasia. Tartu, 2013, 142 p.
235. **Sergei Põlme**. Biogeography and ecology of *alnus*- associated ectomycorrhizal fungi – from regional to global scale. Tartu, 2013, 90 p.
236. **Liis Uusküla**. Placental gene expression in normal and complicated pregnancy. Tartu, 2013, 173 p.
237. **Marko Lõoke**. Studies on DNA replication initiation in *Saccharomyces cerevisiae*. Tartu, 2013, 112 p.
238. **Anne Aan**. Light- and nitrogen-use and biomass allocation along productivity gradients in multilayer plant communities. Tartu, 2013, 127 p.
239. **Heidi Tamm**. Comprehending phylogenetic diversity – case studies in three groups of ascomycetes. Tartu, 2013, 136 p.
240. **Liina Kangur**. High-Pressure Spectroscopy Study of Chromophore-Binding Hydrogen Bonds in Light-Harvesting Complexes of Photosynthetic Bacteria. Tartu, 2013, 150 p.
241. **Margus Leppik**. Substrate specificity of the multisite specific pseudouridine synthase RluD. Tartu, 2013, 111 p.
242. **Lauris Kaplinski**. The application of oligonucleotide hybridization model for PCR and microarray optimization. Tartu, 2013, 103 p.
243. **Merli Pärnoja**. Patterns of macrophyte distribution and productivity in coastal ecosystems: effect of abiotic and biotic forcing. Tartu, 2013, 155 p.
244. **Tõnu Margus**. Distribution and phylogeny of the bacterial translational GTPases and the Mqsr/YgiT regulatory system. Tartu, 2013, 126 p.
245. **Pille Mänd**. Light use capacity and carbon and nitrogen budget of plants: remote assessment and physiological determinants. Tartu, 2013, 128 p.

246. **Mario Plaas**. Animal model of Wolfram Syndrome in mice: behavioural, biochemical and psychopharmacological characterization. Tartu, 2013, 144 p.
247. **Georgi Hudjašov**. Maps of mitochondrial DNA, Y-chromosome and tyrosinase variation in Eurasian and Oceanian populations. Tartu, 2013, 115 p.
248. **Mari Lepik**. Plasticity to light in herbaceous plants and its importance for community structure and diversity. Tartu, 2013, 102 p.
249. **Ede Leppik**. Diversity of lichens in semi-natural habitats of Estonia. Tartu, 2013, 151 p.
250. **Ülle Saks**. Arbuscular mycorrhizal fungal diversity patterns in boreonemoral forest ecosystems. Tartu, 2013, 151 p.
251. **Eneli Oitmaa**. Development of arrayed primer extension microarray assays for molecular diagnostic applications. Tartu, 2013, 147 p.
252. **Jekaterina Jutkina**. The horizontal gene pool for aromatics degradation: bacterial catabolic plasmids of the Baltic Sea aquatic system. Tartu, 2013, 121 p.
253. **Helen Vellau**. Reaction norms for size and age at maturity in insects: rules and exceptions. Tartu, 2014, 132 p.
254. **Randel Kreitsberg**. Using biomarkers in assessment of environmental contamination in fish – new perspectives. Tartu, 2014, 107 p.
255. **Krista Takkis**. Changes in plant species richness and population performance in response to habitat loss and fragmentation.Tartu, 2014, 141 p.
256. **Liina Nagirnaja**. Global and fine-scale genetic determinants of recurrent pregnancy loss. Tartu, 2014, 211 p.
257. **Triin Triisberg**. Factors influencing the re-vegetation of abandoned extracted peatlands in Estonia. Tartu, 2014, 133 p.
258. **Villu Soon**. A phylogenetic revision of the *Chrysis ignita* species group (Hymenoptera: Chrysididae) with emphasis on the northern European fauna. Tartu, 2014, 211 p.
259. **Andrei Nikonov**. RNA-Dependent RNA Polymerase Activity as a Basis for the Detection of Positive-Strand RNA Viruses by Vertebrate Host Cells. Tartu, 2014, 207 p.
260. **Eele Õunapuu-Pikas**. Spatio-temporal variability of leaf hydraulic conductance in woody plants: ecophysiological consequences. Tartu, 2014, 135 p.
261. **Marju Männiste**. Physiological ecology of greenfinches: information content of feathers in relation to immune function and behavior. Tartu, 2014, 121 p.
262. **Katre Kets**. Effects of elevated concentrations of CO_2 and O_3 on leaf photosynthetic parameters in *Populus tremuloides*: diurnal, seasonal and interannual patterns. Tartu, 2014, 115 p.
263. **Külli Lokko**. Seasonal and spatial variability of zoopsammon communities in relation to environmental parameters. Tartu, 2014, 129 p.
264. **Olga Žilina**. Chromosomal microarray analysis as diagnostic tool: Estonian experience. Tartu, 2014, 152 p.

265. **Kertu Lõhmus**. Colonisation ecology of forest-dwelling vascular plants and the conservation value of rural manor parks. Tartu, 2014, 111 p.
266. **Anu Aun**. Mitochondria as integral modulators of cellular signaling. Tartu, 2014, 167 p.
267. **Chandana Basu Mallick**. Genetics of adaptive traits and gender-specific demographic processes in South Asian populations. Tartu, 2014, 160 p.
268. **Riin Tamme**. The relationship between small-scale environmental heterogeneity and plant species diversity. Tartu, 2014, 130 p.
269. **Liina Remm**. Impacts of forest drainage on biodiversity and habitat quality: implications for sustainable management and conservation. Tartu, 2015, 126 p.
270. **Tiina Talve**. Genetic diversity and taxonomy within the genus *Rhinanthus.* Tartu, 2015, 106 p.
271. **Mehis Rohtla**. Otolith sclerochronological studies on migrations, spawning habitat preferences and age of freshwater fishes inhabiting the Baltic Sea. Tartu, 2015, 137 p.
272. **Alexey Reshchikov**. The world fauna of the genus *Lathrolestes* (Hymenoptera, Ichneumonidae). Tartu, 2015, 247 p.
273. **Martin Pook**. Studies on artificial and extracellular matrix protein-rich surfaces as regulators of cell growth and differentiation. Tartu, 2015, 142 p.
274. **Mai Kukumägi**. Factors affecting soil respiration and its components in silver birch and Norway spruce stands. Tartu, 2015, 155 p.
275. **Helen Karu**. Development of ecosystems under human activity in the North-East Estonian industrial region: forests on post-mining sites and bogs. Tartu, 2015, 152 p.
276. **Hedi Peterson**. Exploiting high-throughput data for establishing relationships between genes. Tartu, 2015, 186 p.
277. **Priit Adler**. Analysis and visualisation of large scale microarray data, Tartu, 2015, 126 p.
278. **Aigar Niglas**. Effects of environmental factors on gas exchange in deciduous trees: focus on photosynthetic water-use efficiency. Tartu, 2015, 152 p.
279. **Silja Laht**. Classification and identification of conopeptides using profile hidden Markov models and position-specific scoring matrices. Tartu, 2015, 100 p.
280. **Martin Kesler**. Biological characteristics and restoration of Atlantic salmon *Salmo salar* populations in the Rivers of Northern Estonia. Tartu, 2015, 97 p.
281. **Pratyush Kumar Das**. Biochemical perspective on alphaviral nonstructural protein 2: a tale from multiple domains to enzymatic profiling. Tartu, 2015, 205 p
282. **Priit Palta**. Computational methods for DNA copy number detection. Tartu, 2015, 130 p.
283. **Julia Sidorenko**. Combating DNA damage and maintenance of genome integrity in pseudomonads. Tartu, 2015, 174 p.

284. **Anastasiia Kovtun-Kante**. Charophytes of Estonian inland and coastal waters: distribution and environmental preferences. Tartu, 2015, 97 p.
285. **Ly Lindman**. The ecology of protected butterfly species in Estonia. Tartu, 2015, 171 p.
286. **Jaanis Lodjak**. Association of Insulin-like Growth Factor I and Corticosterone with Nestling Growth and Fledging Success in Wild Passerines. Tartu, 2016, 113 p.
287. **Ann Kraut**. Conservation of Wood-Inhabiting Biodiversity – Semi-Natural Forests as an Opportunity. Tartu, 2016, 141 p.
288. **Tiit Örd**. Functions and regulation of the mammalian pseudokinase TRIB3. Tartu, 2016, 182. p.
289. **Kairi Käiro**. Biological Quality According to Macroinvertebrates in Streams of Estonia (Baltic Ecoregion of Europe): Effects of Human-induced Hydromorphological Changes. Tartu, 2016, 126 p.
290. **Leidi Laurimaa**. *Echinococcus multilocularis* and other zoonotic parasites in Estonian canids. Tartu, 2016, 144 p.
291. **Helerin Margus**. Characterization of cell-penetrating peptide/nucleic acid nanocomplexes and their cell-entry mechanisms. Tartu, 2016, 173 p.
292. **Kadri Runnel**. Fungal targets and tools for forest conservation. Tartu, 2016, 157 p.
293. **Urmo Võsa**. MicroRNAs in disease and health: aberrant regulation in lung cancer and association with genomic variation. Tartu, 2016, 163 p.
294. **Kristina Mäemets-Allas**. Studies on cell growth promoting AKT signaling pathway – a promising anti-cancer drug target. Tartu, 2016, 146 p.
295. **Janeli Viil**. Studies on cellular and molecular mechanisms that drive normal and regenerative processes in the liver and pathological processes in Dupuytren's contracture. Tartu, 2016, 175 p.
296. **Ene Kook**. Genetic diversity and evolution of *Pulmonaria angustifolia* L. and *Myosotis laxa sensu lato* (Boraginaceae). Tartu, 2016, 106 p.
297. **Kadri Peil**. RNA polymerase II-dependent transcription elongation in *Saccharomyces cerevisiae*. Tartu, 2016, 113 p.
298. **Katrin Ruisu**. The role of RIC8A in mouse development and its function in cell-matrix adhesion and actin cytoskeletal organisation. Tartu, 2016, 129 p.
299. **Janely Pae**. Translocation of cell-penetrating peptides across biological membranes and interactions with plasma membrane constituents. Tartu, 2016, 126 p.
300. **Argo Ronk**. Plant diversity patterns across Europe: observed and dark diversity. Tartu, 2016, 153 p.
301. **Kristiina Mark**. Diversification and species delimitation of lichenized fungi in selected groups of the family Parmeliaceae (Ascomycota). Tartu, 2016, 181 p.
302. **Jaak-Albert Metsoja**. Vegetation dynamics in floodplain meadows: influence of mowing and sediment application. Tartu, 2016, 140 p.

303. **Hedvig Tamman**. The GraTA toxin-antitoxin system of *Pseudomonas putida*: regulation and role in stress tolerance. Tartu, 2016, 154 p.
304. **Kadri Pärtel**. Application of ultrastructural and molecular data in the taxonomy of helotialean fungi. Tartu, 2016, 183 p.
305. **Maris Hindrikson**. Grey wolf (*Canis lupus*) populations in Estonia and Europe: genetic diversity, population structure and -processes, and hybridization between wolves and dogs. Tartu, 2016, 121 p.
306. **Polina Degtjarenko**. Impacts of alkaline dust pollution on biodiversity of plants and lichens: from communities to genetic diversity. Tartu, 2016, 126 p.
307. **Liina Pajusalu**. The effect of CO_2 enrichment on net photosynthesis of macrophytes in a brackish water environment. Tartu, 2016, 126 p.
308. **Stoyan Tankov**. Random walks in the stringent response. Tartu, 2016, 94 p.
309. **Liis Leitsalu**. Communicating genomic research results to population-based biobank participants. Tartu, 2016, 158 p.
310. **Richard Meitern**. Redox physiology of wild birds: validation and application of techniques for detecting oxidative stress. Tartu, 2016, 134 p.
311. **Kaie Lokk**. Comparative genome-wide DNA methylation studies of healthy human tissues and non-small cell lung cancer tissue. Tartu, 2016, 127 p.
312. **Mihhail Kurašin**. Processivity of cellulases and chitinases. Tartu, 2017, 132 p.
313. **Carmen Tali**. Scavenger receptors as a target for nucleic acid delivery with peptide vectors. Tartu, 2017, 155 p.
314. **Katarina Oganjan**. Distribution, feeding and habitat of benthic suspension feeders in a shallow coastal sea. Tartu, 2017, 132 p.
315. **Taavi Paal**. Immigration limitation of forest plants into wooded landscape corridors. Tartu, 2017, 145 p.
316. **Kadri Õunap**. The Williams-Beuren syndrome chromosome region protein WBSCR22 is a ribosome biogenesis factor. Tartu, 2017, 135 p.
317. **Riin Tamm**. In-depth analysis of factors affecting variability in thiopurine methyltransferase activity. Tartu, 2017, 170 p.
318. **Keiu Kask**. The role of RIC8A in the development and regulation of mouse nervous system. Tartu, 2017, 184 p.
319. **Tiia Möller**. Mapping and modelling of the spatial distribution of benthic macrovegetation in the NE Baltic Sea with a special focus on the eelgrass *Zostera marina* Linnaeus, 1753. Tartu, 2017, 162 p.
320. **Silva Kasela**. Genetic regulation of gene expression: detection of tissue- and cell type-specific effects. Tartu, 2017, 150 p.
321. **Karmen Süld**. Food habits, parasites and space use of the raccoon dog *Nyctereutes procyonoides*: the role of an alien species as a predator and vector of zoonotic diseases in Estonia. Tartu, 2017, p.
322. **Ragne Oja**. Consequences of supplementary feeding of wild boar – concern for ground-nesting birds and endoparasite infection. Tartu, 2017, 141 p.
323. **Riin Kont**. The acquisition of cellulose chain by a processive cellobiohydrolase. Tartu, 2017, 117 p.

324. **Liis Kasari**. Plant diversity of semi-natural grasslands: drivers, current status and conservation challenges. Tartu, 2017, 141 p.
325. **Sirgi Saar**. Belowground interactions: the roles of plant genetic relatedness, root exudation and soil legacies. Tartu, 2017, 113 p.
326. **Sten Anslan**. Molecular identification of Collembola and their fungal associates. Tartu, 2017, 125 p.
327. **Imre Taal**. Causes of variation in littoral fish communities of the Eastern Baltic Sea: from community structure to individual life histories. Tartu, 2017, 118 p.
328. **Jürgen Jalak**. Dissecting the Mechanism of Enzymatic Degradation of Cellulose Using Low Molecular Weight Model Substrates. Tartu, 2017, 137 p.
329. **Kairi Kiik**. Reproduction and behaviour of the endangered European mink (*Mustela lutreola*) in captivity. Tartu, 2018, 112 p.
330. **Ivan Kuprijanov**. Habitat use and trophic interactions of native and invasive predatory macroinvertebrates in the northern Baltic Sea. Tartu, 2018, 117 p.
331. **Hendrik Meister**. Evolutionary ecology of insect growth: from geographic patterns to biochemical trade-offs. Tartu, 2018, 147 p.
332. **Ilja Gaidutšik**. Irc3 is a mitochondrial branch migration enzyme in *Saccharomyces cerevisiae*. Tartu, 2018, 161 p.
333. **Lena Neuenkamp**. The dynamics of plant and arbuscular mycorrhizal fungal communities in grasslands under changing land use. Tartu, 2018, 241 p.
334. **Laura Kasak**. Genome structural variation modulating the placenta and pregnancy maintenance. Tartu, 2018, 181 p.
335. **Kersti Riibak**. Importance of dispersal limitation in determining dark diversity of plants across spatial scales. Tartu, 2018, 133 p.
336. **Liina Saar**. Dynamics of grassland plant diversity in changing landscapes. Tartu, 2018, 206 p.
337. **Hanna Ainelo**. Fis regulates *Pseudomonas putida* biofilm formation by controlling the expression of *lapA*. Tartu, 2018, 143 p.
338. **Natalia Pervjakova**. Genomic imprinting in complex traits. Tartu, 2018, 176 p.
339. **Andrio Lahesaare**. The role of global regulator Fis in regulating the expression of *lapF* and the hydrophobicity of soil bacterium *Pseudomonas putida*. Tartu, 2018, 124 p.
340. **Märt Roosaare**. *K*-mer based methods for the identification of bacteria and plasmids. Tartu, 2018, 117 p.
341. **Maria Abakumova**. The relationship between competitive behaviour and the frequency and identity of neighbours in temperate grassland plants. Tartu, 2018, 104 p.
342. **Margus Vilbas**. Biotic interactions affecting habitat use of myrmecophilous butterflies in Northern Europe. Tartu, 2018, 142 p.

343. **Liina Kinkar**. Global patterns of genetic diversity and phylogeography of *Echinococcus granulosus* sensu stricto – a tapeworm species of significant public health concern. Tartu, 2018, 147 p.
344. **Teivi Laurimäe**. Taxonomy and genetic diversity of zoonotic tapeworms in the species complex of *Echinococcus granulosus* sensu lato. Tartu, 2018, 143 p.
345. **Tatjana Jatsenko**. Role of translesion DNA polymerases in mutagenesis and DNA damage tolerance in Pseudomonads. Tartu, 2018, 216 p.
346. **Katrin Viigand**. Utilization of α-glucosidic sugars by *Ogataea* (*Hansenula*) *polymorpha.* Tartu, 2018, 148 p.
347. **Andres Ainelo**. Physiological effects of the *Pseudomonas putida* toxin grat. Tartu, 2018, 146 p.
348. **Killu Timm**. Effects of two genes (DRD4 and SERT) on great tit (*Parus major*) behaviour and reproductive traits. Tartu, 2018, 117 p.
349. **Petr Kohout**. Ecology of ericoid mycorrhizal fungi. Tartu, 2018, 184 p.
350. **Gristin Rohula-Okunev**. Effects of endogenous and environmental factors on night-time water flux in deciduous woody tree species. Tartu, 2018, 184 p.
351. **Jane Oja**. Temporal and spatial patterns of orchid mycorrhizal fungi in forest and grassland ecosystems. Tartu, 2018, 102 p.
352. **Janek Urvik**. Multidimensionality of aging in a long-lived seabird. Tartu, 2018, 135 p.
353. **Lisanna Schmidt**. Phenotypic and genetic differentiation in the hybridizing species pair *Carex flava* and *C. viridula* in geographically different regions. Tartu, 2018, 133 p.
354. **Monika Karmin**. Perspectives from human Y chromosome – phylogeny, population dynamics and founder events. Tartu, 2018, 168 p.
355. **Maris Alver**. Value of genomics for atherosclerotic cardiovascular disease risk prediction. Tartu, 2019, 148 p.
356. **Lehti Saag**. The prehistory of Estonia from a genetic perspective: new insights from ancient DNA. Tartu, 2019, 171 p.
357. **Mari-Liis Viljur**. Local and landscape effects on butterfly assemblages in managed forests. Tartu, 2019, 115 p.
358. **Ivan Kisly**. The pleiotropic functions of ribosomal proteins eL19 and eL24 in the budding yeast ribosome. Tartu, 2019, 170 p.
359. **Mikk Puustusmaa**. On the origin of papillomavirus proteins. Tartu, 2019, 152 p.
360. **Anneliis Peterson**. Benthic biodiversity in the north-eastern Baltic Sea: mapping methods, spatial patterns, and relations to environmental gradients. Tartu, 2019, 159 p.
361. **Erwan Pennarun**. Meandering along the mtDNA phylogeny; causerie and digression about what it can tell us about human migrations. Tartu, 2019, 162 p.

362. **Karin Ernits**. Levansucrase Lsc3 and endo-levanase BT1760: characterization and application for the synthesis of novel prebiotics. Tartu, 2019, 217 p.
363. **Sille Holm**. Comparative ecology of geometrid moths: in search of contrasts between a temperate and a tropical forest. Tartu, 2019, 135 p.
364. **Anne-Mai Ilumäe**. Genetic history of the Uralic-speaking peoples as seen through the paternal haplogroup N and autosomal variation of northern Eurasians. Tartu, 2019, 172 p.
365. **Anu Lepik**. Plant competitive behaviour: relationships with functional traits and soil processes. Tartu, 2019, 152 p.
366. **Kunter Tätte**. Towards an integrated view of escape decisions in birds under variable levels of predation risk. Tartu, 2020, 172 p.
367. **Kaarin Parts**. The impact of climate change on fine roots and root-associated microbial communities in birch and spruce forests. Tartu, 2020, 143 p.
368. **Viktorija Kukuškina**. Understanding the mechanisms of endometrial receptivity through integration of 'omics' data layers. Tartu, 2020, 169 p.
369. **Martti Vasar**. Developing a bioinformatics pipeline gDAT to analyse arbuscular mycorrhizal fungal communities using sequence data from different marker regions. Tartu, 2020, 193 p.
370. **Ott Kangur**. Nocturnal water relations and predawn water potential disequilibrium in temperate deciduous tree species. Tartu, 2020, 126 p.
371. **Helen Post**. Overview of the phylogeny and phylogeography of the Y-chromosomal haplogroup N in northern Eurasia and case studies of two linguistically exceptional populations of Europe – Hungarians and Kalmyks. Tartu, 2020, 143 p.
372. **Kristi Krebs**. Exploring the genetics of adverse events in pharmacotherapy using Biobanks and Electronic Health Records. Tartu, 2020, 151 p.
373. **Kärt Ukkivi**. Mutagenic effect of transcription and transcription-coupled repair factors in *Pseudomonas putida.* Tartu, 2020, 154 p.
374. **Elin Soomets**. Focal species in wetland restoration. Tartu, 2020, 137 p.
375. **Kadi Tilk**. Signals and responses of ColRS two-component system in *Pseudomonas putida.* Tartu, 2020, 133 p.
376. **Indrek Teino**. Studies on aryl hydrocarbon receptor in the mouse granulosa cell model. Tartu, 2020, 139 p.
377. **Maarja Vaikre**. The impact of forest drainage on macroinvertebrates and amphibians in small waterbodies and opportunities for cost-effective mitigation. Tartu, 2020, 132 p.
378. **Siim-Kaarel Sepp**. Soil eukaryotic community responses to land use and host identity. Tartu, 2020, 222 p.
379. **Eveli Otsing**. Tree species effects on fungal richness and community structure. Tartu, 2020, 152 p.
380. **Mari Pent**. Bacterial communities associated with fungal fruitbodies. Tartu, 2020, 144 p.

381. **Einar Kärgenberg**. Movement patterns of lithophilous migratory fish in free-flowing and fragmented rivers. Tartu, 2020, 167 p.
382. **Antti Matvere**. The studies on aryl hydrocarbon receptor in murine granulosa cells and human embryonic stem cells. Tartu, 2021, 163 p.
383. **Jhonny Capichoni Massante**. Phylogenetic structure of plant communities along environmental gradients: a macroecological and evolutionary approach. Tartu, 2021, 144 p.
384. **Ajai Kumar Pathak.** Delineating genetic ancestries of people of the Indus Valley, Parsis, Indian Jews and Tharu tribe. Tartu, 2021, 197 p.
385. **Tanel Vahter.** Arbuscular mycorrhizal fungal biodiversity for sustainable agroecosystems. Tartu, 2021, 191 p.
386. **Burak Yelmen.** Characterization of ancient Eurasian influences within modern human genomes. Tartu, 2021, 134 p.
387. **Linda Ongaro.** A genomic portrait of American populations. Tartu, 2021, 182 p.
388. **Kairi Raime.** The identification of plant DNA in metagenomic samples. Tartu, 2021, 108 p.
389. **Heli Einberg.** Non-linear and non-stationary relationships in the pelagic ecosystem of the Gulf of Riga (Baltic Sea). Tartu, 2021, 119 p.
390. **Mickaël Mathieu Pihain.** The evolutionary effect of phylogenetic neighbourhoods of trees on their resistance to herbivores and climatic stress. Tartu, 2022, 145 p.
391. **Annika Joy Meitern.** Impact of potassium ion content of xylem sap and of light conditions on the hydraulic properties of trees. Tartu, 2022, 132 p.
392. **Elise Joonas.** Evaluation of metal contaminant hazard on microalgae with environmentally relevant testing strategies. Tartu, 2022, 118 p.
393. **Kreete Lüll.** Investigating the relationships between human microbiome, host factors and female health. Tartu, 2022, 141 p.
394. **Triin Kaasiku.** A wader perspective to Boreal Baltic coastal grasslands: from habitat availability to breeding site selection and nest survival. Tartu, 2022, 141 p.
395. **Meeli Alber.** Impact of elevated atmospheric humidity on the structure of the water transport pathway in deciduous trees. Tartu, 2022, 170 p.
396. **Ludovica Molinaro.** Ancestry deconvolution of Estonian, European and Worldwide genomic layers: a human population genomics excavation. Tartu, 2022, 138 p.
397. **Tina Saupe.** The genetic history of the Mediterranean before the common era: a focus on the Italian Peninsula. Tartu, 2022, 165 p.
398. **Mari-Ann Lind.** Internal constraints on energy processing and their consequences: an integrative study of behaviour, ornaments and digestive health in greenfinches. Tartu, 2022, 137 p.
399. **Markus Valge.** Testing the predictions of life history theory on anthropometric data. Tartu, 2022, 171 p.