DISSERTATIONES
BIOLOGICAE
UNIVERSITATIS
TARTUENSIS
442

IRYNA YATSIUK

Evolution, species delimitation and diversity in myxomycetes: *Arcyria* and allied genera

DISSERTATIONES BIOLOGICAE UNIVERSITATIS TARTUENSIS

442

DISSERTATIONES BIOLOGICAE UNIVERSITATIS TARTUENSIS

442

IRYNA YATSIUK

Evolution, species delimitation and diversity in myxomycetes: *Arcyria* and allied genera

UNIVERSITY OF TARTU
Press

Department of Botany, 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 Botany and Mycology at the University of Tartu on August 29th, 2024 by the Scientific Council of the Institute of Ecology and Earth Sciences, University of Tartu.

Supervisors:	Prof. Urmas Kõljalg, University of Tartu, Estonia Prof. Leontyev Dmytro, Kharkiv National Pedagodical University, Ukraine
Opponent:	Associate professor Ivan García-Cunchillos, University of Warsaw, Poland
Commencement:	Oecologicum (J. Liivi 2, Tartu), room 127, on 21th of October 2024 at 10.15 a.m.

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

ISSN 1024-6479 (print)
ISBN 978-9916-27-671-6 (print)
ISSN 2806-2140 (pdf)
ISBN 978-9916-27-672-3 (pdf)

University of Tartu Press
www.tyk.ee

CONTENTS

LIST OF ORIGINAL PUBLICATIONS

I **Yatsiuk**, I., Leontyev, D., Schnittler, M., Ehlers, T., Mikryukov V., Kõljalg U., 2024. *Arcyria* and allied genera: taxonomic backbone and characters evolution. *FUSE*, accepted.

II **Yatsiuk**, I., Leontyev, D., López-Villalba, Á., Schnittler, M., Kõljalg, U., 2023. A new nivicolous species of *Lamproderma* (Myxomycetes) from lowland and mountainous regions of Europe. *Nova Hedwigia* 116, 105–136. https://doi.org/10.1127/nova_hedwigia/2023/0807

III Leontyev, D., **Yatsiuk**, I., 2024. Dataset of barcoded Reticulariaceae: ten years of DNA sequencing. *Biodiversity Data Journal* 12, e115630. https://doi.org/10.3897/BDJ.12.e115630

IV **Yatsiuk**, I., Leshchenko Yu., Viunnyk V., Leontyev, D., 2024. The comprehensive checklist of myxomycetes of Ukraine based on extended occurrence and reference datasets. *Biodiversity data journal*, 12: e120891. https://doi.org/10.3897/BDJ.12.e120891

V **Yatsiuk**, I., Kastanje, V., Adamonyte, G., 2020. A comprehensive checklist of Estonian myxomycetes. *Karstenia* 58, 239–247. https://doi.org/10.29203/ka.2020.497

Papers are cited throughout the thesis with the corresponding Roman numerals.

The author's contribution to the publications is shown below (* minor contribution; ** moderate contribution; *** major contribution/leading role).

	I	**II**	**III**	**IV**	**V**
Idea and study design	***	***	*	**	**
Fieldwork or other data sampling	***	***	–	**	**
Labwork and microscopy	***	***	–	–	***
Data management, analysis, visualisation	***	***	***	***	**
Manuscript writing	***	***	*	***	***

ABBREVIATIONS

16S, mitSSU	Mitochondrial ribosomal small subunit rDNA
18S, SSU	Nuclear ribosomal small subunit rDNA
BI	Bayesian Inference
bp	base pairs
DNA	Deoxyribonucleic acid
EF1–α	Translation elongation factor 1-alpha
FAIR (data, principles)	Findable, Accessible, Interoperable, Reusable
fam. nov.	new family
GBIF	Global Biodiversity Information Facility, www.gbif.org
gen. nov.	new genus
ITS	Internal transcribed spacer
LM	Light microscopy
ML	Maximum Likelihood
OTU	operational taxonomic unit
PCR	Polymerase chain reaction
rDNA	Nuclear ribosomal DNA (SSU, ITS, LSU)
SEM	Scanning electron microscopy
s. l.	sensu lato (Lat.), in a wide sense
s. str.	sensu stricto (Lat.), in a strict sense
sp. nov.	new species

INTRODUCTION

Myxomycetes, or Myxogastria, comprise approximately 1,050 species of macroscopic eukaryotes within the kingdom Amoebozoa (Adl et al., 2019). Unlike their amoeboid counterparts, myxomycetes have complex life cycle, which includes an amoeboid stage, a multinucleate mobile plasmodium, and the development of spore-bearing fruiting bodies (Fig. 1). In their amoeboid stage, myxomycetes are found in diverse substrates such as soil, decaying wood, living tree bark, leaf litter, and other plant debris. By some estimates based on transcriptome analyses, myxomycetes account for up to 50% of the biomass and 25% of the ribotypes among soil protozoans, playing crucial role as regulators of bacterial, algal, and protistean populations in terrestrial ecosystems (Urich et al., 2008). Many species of beetles, slugs and nematodes in their turn feed on myxomycetes obligately or accidentally (Keller and Everhart, 2010).

Despite their substantial ecological functions, myxomycetes have been systematically underrepresented in taxonomical and ecological research, including environmental DNA studies (Adl et al., 2014; Shchepin et al., 2019). The scarcity of taxonomical attention can be attributed to ongoing taxonomical impediment (Ebach et al., 2011). Since myxomycetes are not large charismatic organisms and due to their lack of direct economic importance, myxomycetes rarely attract significant research funding. However, the inadequate presence of myxomycetes in environmental DNA studies may be due to the enormous genetic variability, accumulated in this early-divergent group and difficult to discover with standard sets of primers, as well as because of the incompleteness of annotated reference libraries (Gao et al., 2019). This brings us back to the necessity of understanding (1) phylogenetic relations, (2) species boundaries, (3) developing of robust practices of species delimitation, description, and communication in myxomycetes.

Consequently, the first part of this thesis addresses phylogeny, evolution, and species delimitation practices in chosen groups of myxomycetes (**I**, **II**).

In the paper **I** I focus on the genus *Arcyria*, a large genus of the order Trichiales (García-Cunchillos et al., 2022), subclass *Lucisporomycetidae* or the "bright-spored" myxomycetes (Fig. 1). From the other genera it is traditionally distinguished by the combination of characters: sporocarpic, stalked fruiting bodies, early evanescent peridium leaving a basal cup, and hollow, typically branched in a net-like manner and ornamented with complex patterns capillitium (Fig. 2).

Arcyria includes 265 published species and infraspecific taxa, 55 of them are accepted according to the authoritative nomenclature database (Lado, 2005). The majority of them require revision, being taxonomic synonyms, taxa based on scarce descriptions or relying on doubtful morphological differences.

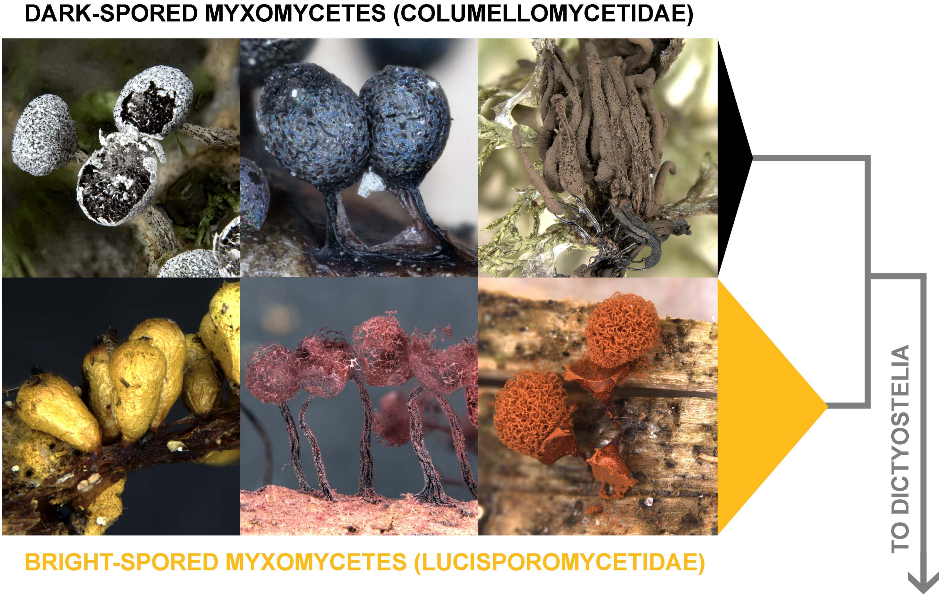

Figure 1. Representatives of dark-spored vs. bright-spored myxomycetes (left) and a simplified myxomycete phylogeny (right, tree sources: Kang et al., 2017; Leontyev et al., 2019b).

Originally, *Arcyria* and several other genera were described in a "tribus" (Rostafinski, 1875) that later was validly published as the family *Arcyriaceae* (Cooke, 1877). Since then, there has been debate about taxonomic position of *Arcyria*. Some authors recognized the family *Arcyriaceae*, although the scope of the family varied depending on chosen sets of characteristics (Lister and Lister, 1911; Macbride, 1922; Nannenga-Bremekamp, 1982). Others argued for lumping *Arcyria* and allied genera and placing them in the family *Trichiaceae* (Martin and Alexopoulos, 1969).

The first phylogenetic studies of bright-spored myxomycetes revealed that most genera of *Trichiales* were polyphyletic, but found *Arcyria* and *Arcyodes* to form a monophyletic group (Fiore-Donno et al., 2013). However, the latest published phylogeny (García-Cunchillos et al., 2022), that included wider sampling of *Arcyria* species, recovered an additional *Arcyria* clade emerging as sister to *Hemitrichia* Rostaf. However, no morphological characteristics were identified to differentiate two branches of *Arcyria*, and the sampling of taxa was still limited. Therefore, no taxonomic decisions have been made regarding the genus and the family (García-Cunchillos *et al.* 2022).

To sum up, although general outlines of the classification of bright-spored myxomycetes are emerging, robust phylogeny with comprehensive sampling, particularly in *Arcyria* is yet to be constructed, and new combinations of traits are to be discovered.

Figure 2. Morphological characters used for delimitation and identification of *Arcyria* s. l. and some representatives of the genus (right). Modified figure from the paper **I**.

Moving from a deep phylogeny to the species level, it has been shown that barcoding and metabarcoding are powerful tools that bring benefits to taxonomical, ecological, and conservational studies. In species delimitation, the concept of barcoding gap is used, i.e. barcode sequences of the same species must be more similar to each other, than to any of the sequences of other species. In eDNA studies, barcoding is used to distribute sequences into proxy units (OTUs) by applying universal sequence similarity thresholds across sequences from environmental samples (Collins and Cruickshank, 2013). Both applications found their place in myxomycetology during last decades, with first part of 18S rRNA gene comprising ca 550 bp as the barcoding marker (Clissmann et al., 2015; Leontyev et al., 2015; Schnittler et al., 2017; Shchepin et al., 2019). However, in view of the unique biology and immense genetic diversity of the group, both must be employed with caution. For example, the study based on short fragment of 18S as barcoding marker for dark-spored myxomycetes by Dahl et al. (2018) indicated the absence of a universal barcoding gap, suggesting that a single sequence similarity threshold might not suffice for accurate OTU-picking from environmental samples. Therefore, more research is needed to determine the best barcoding markers for both main groups of myxomycetes, their sequence lengths, and the optimal similarity thresholds. It is also important to test if UNITE Taxon Hypotheses paradigm is applicable to the myxomycetes (Kõljalg et al., 2020, 2013) e. g. if other than ITS DNA barcoding genes can be used to calculate Species Hypotheses and mapped against morphological characters. Paper **II** deals with a genus *Lamproderma*, a comparatively lately radiated, species-rich genus of *Columellomycetidae* (Fig 1). Taxonomically, in the paper **II** I describe one species new for science, but what is more important, in this publication I address the application of the barcoding gap in myxomycetes.

In the yet unpublished part of this research I further studied the barcoding gap in bright-spored myxomycetes (conference abstract Yatsiuk, 2023) and applied automatized species delimitation methods (ASAP, STACEY) to our sequenced and morphologically examined specimens of *Arcyria* in order to disentangle species complexes revealed in the paper **I**.

It is widely recognized that morphospecies in myxomycetes often differ from genetic species. Rather by rule than by exception, closer analyses of morphospecies of myxomycetes reveal multiple genetic units, often understood as cryptic species or biospecies (García-Martín et al., 2023; Leontyev et al., 2023a; Ronikier et al., 2022; Shchepin et al., 2017, 2022). Thus, there is the problem of integration of morphospecies-based data obtained in the past with an increasing influx of sequence-based data. In this light, as much as it is important to move forward developing species delimitation methods and detecting species from environment, it is equally vital to gather and systematize the information accumulated in previous studies. To effectively integrate the data across different species concepts and make more informed decisions about biodiversity management (Fišer et al., 2018), it is essential that data coming from different sources are published in FAIR (Findable, Accessible, Interoperable, Reusable) way (Wilkinson et al., 2016). This principle is wholly applicable to species inventories (Reyserhove et al., 2020). Therefore, a part of this thesis summarizes the effort in collecting and publishing primary data about species diversity of myxomycetes, specifically papers **III, IV, V** that demonstrate how the data obtained from various sources, may be reported according to FAIR principles.

Aims for the present thesis were:

1. To establish a reliable taxonomical backbone for *Arcyria* and allied genera within the bright-spored myxomycetes (**I**)
2. To reconstruct the evolutionary pathway of morphological characters and evaluate their application in taxonomy of bright-spored myxomycetes (**I**). Specifically for this aim the following hypotheses were tested:
   (i) a stalked sporocarp evolved independently in *Arcyriaceae*, *Hemitrichiaceae* and *Trichiaceae*
   (ii) an abundant, net-like capillitium attached to the cup or to the stalk evolved independently in *Arcyriaceae* and *Hemitrichiaceae*
   (iii) yellow pigments are plesiomorphic for *Arcyriaceae*, *Hemitrichiaceae*, and *Trichiaceae*, but red pigments evolved multiple times independently.
3. To assess the barcoding gap applicability in myxomycetes (**II**)
4. To investigate molecular vs. morphological species relationships in the genus *Arcyria* using exploratory and validaton species delimitation techniques (unpublished but part of the results is shown in pages 15–16 and Fig. 6)
5. To consolidate different types of data about the species diversity in myxomycetes and establish good practices in reporting species, whether as taxonomic novelties or in biodiversity studies (**III, IV, V**)

MATERIALS AND METHODS

Morphological studies

In total, over 500 specimens of *Arcyria* spp. previously attributed to 34 morphospecies, and 71 specimens of *Lamproderma* spp. previously attributed to 14 morphospecies were studied morphologically (Fig. 3). The specimens were either collected in the field by the authors of paper **I** and **II** or obtained from herbaria of the University of Tartu, Estonia (TUF), Estonian University of Life Sciences (TAAM), University of Alcala, Spain (AH), the University of Helsinki, Finland (H), the National Herbarium of Victoria, Australia (F), the Herbarium of the University of Greifswald, Germany (GFW, sc), University of Turku, Finland (TFU), V.N. Karazin Kharkiv National University, Ukraine (CWU), Geneva Botanical Gardens and Conservatory (G), Western Australian Herbarium (PERTH), the private collections of M. Meyer, France (MM), Teresa Van der Heul, Australia (TVDH), Anastasia Kochergina, Stanislav Sarzhevskyi, Yuliia Leshchenko, Petra Eimann, Bernard Woerly or Tyson Ehlers (Canada).

Specimens were visually studied, measured and photographed under a stereoscope or transmission microscope equipped with a camera. Slides for the light microscopy (LM) were mounted either in tap water, or Cotton Blue in lactic acid. Scanning electron microscopy (SEM) was performed on specimens spurred with platinum or gold ions. Details on equipment are provided in papers **I** and **II**.

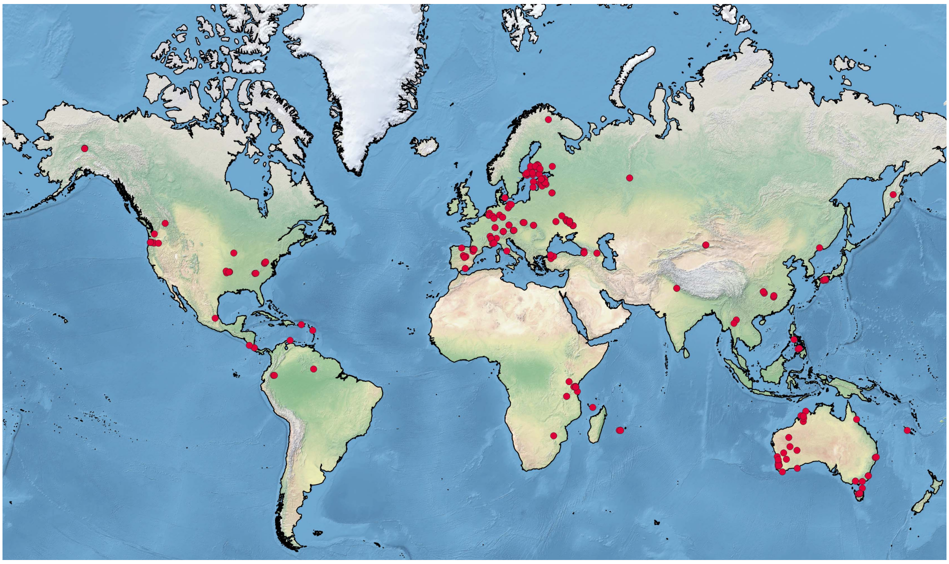

Figure 3. Map of collection localities of specimens studied for papers **I** and **II**.

Molecular and phylogenetic analyses

Genomic DNA was extracted from mature air-dried sporocarps without noticeable fungal contamination as described in detail in papers **II** and **I**. PCR was carried out using published or *de novo* designed sets of primers (**I, II**). Gene regions sequenced for the studies were partial 18S (ca 500–650 bp), partial or in separate cases full EF1–α (partial ca 700–850 bp, full ca 1150 bp), ITS (1000–2000 bp, for the paper **II**) and SSU–ITS–LSU region (paper **I**). Most of the sequences were obtained by Sanger method; SSU–ITS–LSU region was read by PacBio method, details are given in respective papers.

In total, 438 partial 18S, 300 EF1–α, 13 ITS and 21 SSU–ITS–LSU sequences were obtained *de novo*. Alignment of sequences was performed with different algorithms of MAFFT (Katoh et al., 2019), MACSE (Ranwez et al., 2018) or Bali-Phy (Suchard and Redelings, 2006), and manually adjusted. Phylogenetic analyses and tree reconstructions were carried out using Bayesian (Ronquist et al., 2012) and maximum likelihood: RaxML (Kozlov et al., 2019), and IQ-Tree (Nguyen et al., 2015) approaches. Phylogenetic trees were plotted in *ggtree* (Yu et al., 2017) or iTOL (Letunic and Bork, 2021).

Barcoding gap between morphospecies of *Lamproderma* in the paper **II** and in conference abstract (Yatsiuk, 2023) was calculated based on pairwise sequence distances using functions of R package *ape* (Paradis and Schliep, 2019). Optimal sequence similarity threshold in datasets of dark-spored and bright-spored myxomycetes was searched by minimizing the cumulative error (wrong lumping + wrong splitting), using functions of the package *spider* (Brown et al., 2012). Species delimitation for the genera *Arcyria* and *Heterotrichia* was performed with ASAP (Puillandre et al., 2021) as exploratory tool and STACEY (Jones, 2017) as more robust method.

Ancestral state reconstruction

Morphological traits specific to *Arcyria* s. l. such as fruiting body habit; capillitium attachment to the cup; capillitium, spore and cup ornamentation were plotted on the phylogenetic tree (**I**, Fig. 1).

The character evolution inference (**I**) was performed for characters suitable for mapping across the order Trichiales (fuiting body type, capillitium arrangements, colouration, see Fig. 1). The reconstruction of morphological character states was performed by stochastic character mapping (Bollback, 2006) using R package *phytools* 1.5-1 (Revell, 2012).

R environment (R Core Team, 2022) was used for analyses and producing most graphs in all papers.

Data acquisition and management (papers III–V)

The selected literature sources encompassed only scientific literature, including monographs, peer-reviewed journal articles, conference abstracts, annual reports of protected areas, PhD and Master's theses. Included herbarium specimens have either been identified or verified by professional myxomycetologists.

The paper **V** summarizes all available published data (24 sources) on myxomycetes of Estonia until 2020 and additionally includes revised unpublished material kept in herbaria TAAM, EAA, TUF (Pärtel et al., 2021a, 2021b). The occurrences were taxonomically assessed according to (Lado, 2005) and presented in classic checklist format "binomial+reference" (Fig. 4).

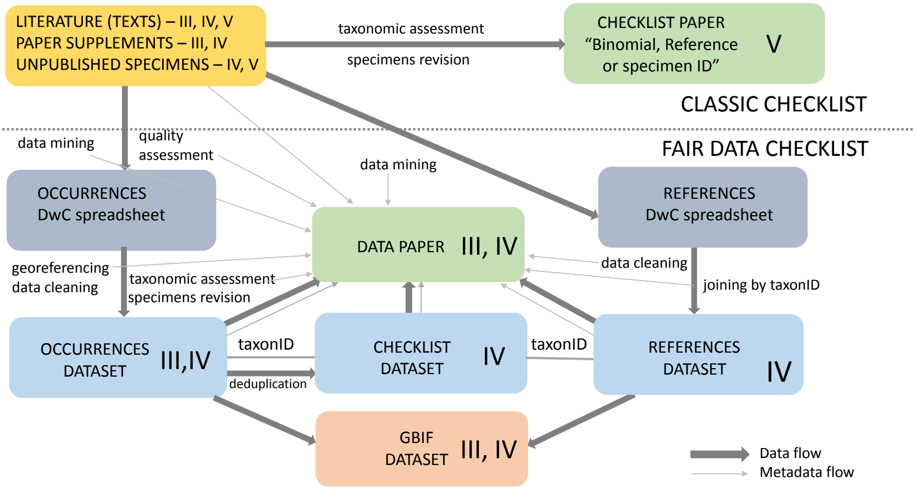

Figure 4. Schemes of data flow in the case of a classic checklist (**V**) and data papers **III** and **IV**.

The paper **III** encompasses collection data about myxomycete specimens, identified and barcoded within the project on critical revision of genera of Reticulariaceae in 2012–2022 (Leontyev et al., 2023a, 2015, 2019a). The paper **IV** summarizes all available published data (91 sources) on myxomycetes of Ukraine until 2023 with a minor supplement of unpublished specimens from the CWP herbarium. Occurrences in the papers **III** and **IV**, and also references in the paper **IV** were extracted into comma-separated spreadsheets containing columns named according to the Darwin Core standard (Wieczorek et al., 2012), followed by taxonomic assessment, georeferencing, and data cleaning procedures. After that the checklist (**IV**) was created automatically by extracting unique values from the scientificName column of the occurrence dataset (Fig. 4). Spreadsheets were checked and cleaned with Openrefine v. 3.2 (Ham, 2013). Taxa names were checked for misspelling by matching against the GBIF Species Matching tool (https://www.gbif.org/tools/species-lookup).

Data deposition, storage and publishing

DOI-cited datasets, containing specimens, alignments and sequences for the papers **I, II,** and **V** are available on PlutoF platform (https://plutof.ut.ee, Abarenkov et al., 2010). Links to the datasets: dx.doi.org/10.15156/BIO/807448, dx.doi.org/10.15156/BIO/2483934, dx.doi.org/10.15156/BIO/2483896, dx.doi.org/10.15156/BIO/2483892, dx.doi.org/10.15156/BIO/2959328, dx.doi.org/10.15156/BIO/2959329, dx.doi.org/10.15156/BIO/2959325.

Produced images of specimens and measurements of microstructures are available via PlutoF under CC BY 4.0 license. Datasets and original data for the papers **III** and **IV** are deposited in GBIF (https://www.gbif.org/) and Zenodo (https://www.zenodo.org/) platforms. New names and combinations were deposited in MycoBank (Robert et al., 2013).

RESULTS

Deep phylogeny of the genus *Arcyria*

Phylogenies inferred from 18S-EF1–α-mitSSU datasets demonstrate that the morphological genus *Arcyria* belongs to two evolutionary distant clades (A1 and A2 in Fig. 5), confirming the conclusion of García-Cunchillos *et al.* (2022) about the polyphyly of the genus. For taxonomic purposes we consider the robustly supported clade A1 as the family *Arcyriaceae* s. str., with one genus *Arcyria* s. str. The clade includes three subclades A1a, A1b and A1c that partially correspond to a visible morphological trait – colouration of spore masses.

The clade A2, although being partially supported by some methods of branch assessment in some of our phylogenies (**I**), was consistently recovered in the previous studies as well (Fiore-Donno et al., 2013; García-Cunchillos et al., 2022). Therefore, we classified the branch A2 + *Hemitrichia* as *Hemitrichiaceae* fam. nov., and re-erected the genus *Heterotrichia* Massee for the clade A2.

One taxon, showing a unique morphology is reconstructed as a sister to *Arcyriaceae* and described as a new genus *Spiromyxa* gen. nov. *incertae sedis* with one new species *S. slocanensis*.

Character evolution and taxonomic value of morphological traits in *Arcyria*

Our analysis demonstrated that neither of traits traditionally used to delimit the genus *Arcyria* s. l., such as evanescent peridium, capillitum arrangement and ornamentation, spore ornamentation is consistent with the phylogeny, being instead scattered across the branches of *Arcyriaceae* s. str. and *Hemitrichiaceae fam. nov* (see Fig. 2 and pictograms on Fig. 5). Noticeably, in both families the cup ornamentation on the inner side was often similar to the ornamentation of capillitium.

Importantly, the colouration of spore masses in the fresh condition appeared to be partially consistent with the phylogeny. Among three subclades of *Arcyriaceae* s. str. (A1a, A1b and A1c on the Fig. 5) one contains species with spore mass coloured in shades of red (A1a, hereinafter also as “red *Arcyria*”), and the rest two mostly contain species with pale spore mass (A1b, A1c). Species of *Hemitrichiaceae* fam. nov. are predominantly yellow, but can have red colouration as well.

The character evolution analysis did not provide conclusive results about the origin of stalks in Trichiales. However, there is some evidence that the last common ancestor of *Arcyriaceae, Hemitrichiaceae* and *Trichiaceae* was stalked; the stalk filled with spore-like bodies perpetuates in *Arcyriaceae* and *Hemitrichiaceae*, but is lost in the common ancestor of *Trichiaceae* and evolves within this family *de novo* as the stalk filled with refuse matter. The capillitium at the same ancestral node was reconstructed as elastic net attached to the stalk, and spore colouration as yellow (**I**).

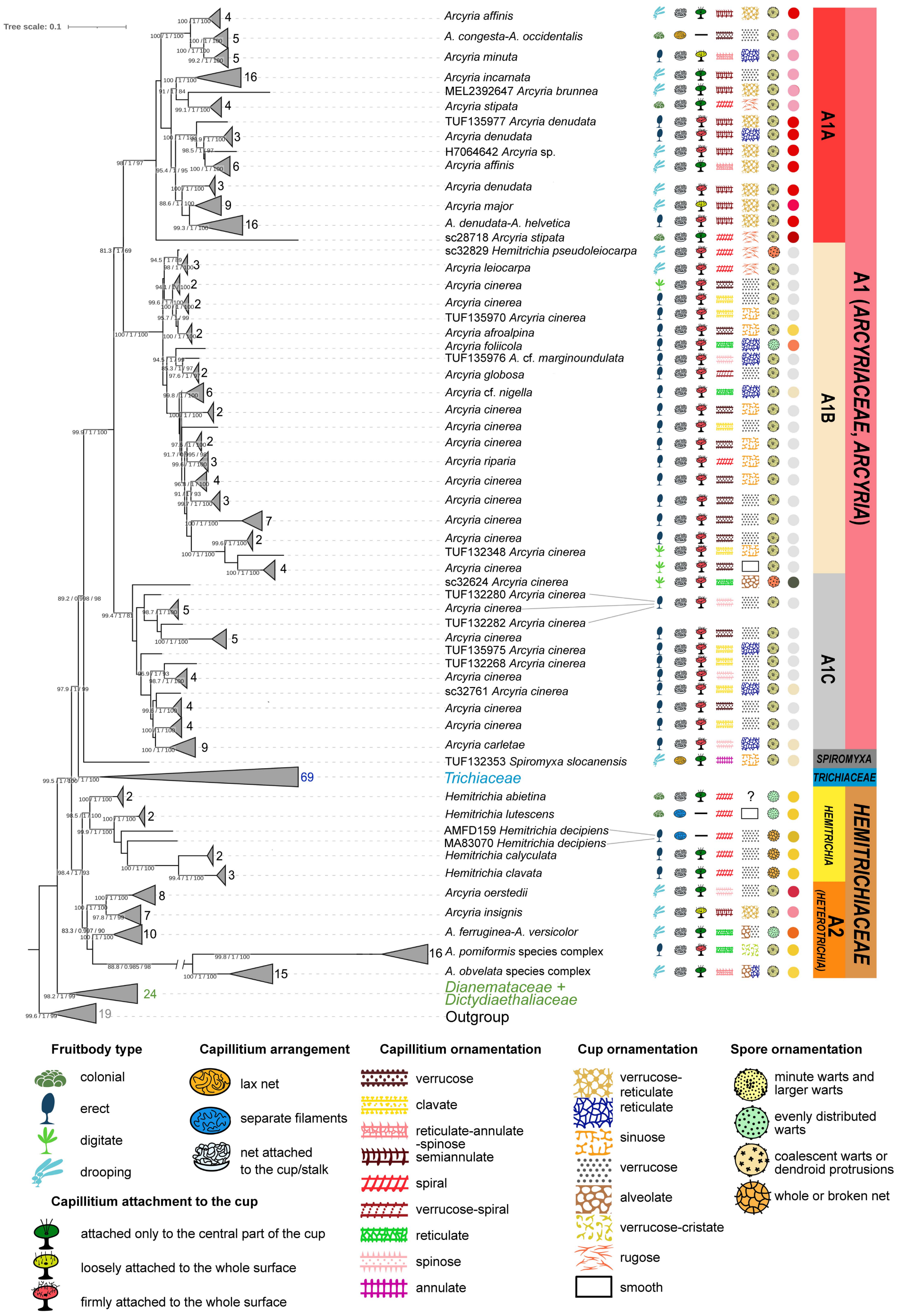

Figure 5. Phylogeny of *Trichiales* with the focus on the genus *Arcyria* (**I**), tree topology inferred from IQ-Tree analysis of the concatenated 18S–EF1–α–16S dataset. Numbers at nodes indicate SH-aLRT, aBayes and UFBoot support values. The length of triangles and numerals near collapsed branches indicate the number of specimens. The branches were collapsed if they formed a monophyletic clade and possessed the same combinations of traits according to the chosen classification (pictograms on the right). Pictograms denote the morphological traits (Fig 2), colored circles denote colouration.

Species complexes and species delimitation in myxomycetes

Based on the phylogeny of Trichiales with the focus on *Arcyria* we found that the majority of morphospecies of *Arcyria* including most common ones represents either species complexes, e. g. *A. obvelata* and *A. pomiformis*, or para- or polyphyletic taxa, with the extreme case of *A. cinerea* scattered over at least 23 branches, but as well *A. affinis, A. denudata,* and *A. stipata* (**I**, Fig. 5). Fifteen branches on three-gene tree are represented by singletons. Similarly, we found four lineages within a morphospecies *Lamproderma pulchellum* (**II**).

Different automated species delimitation approaches resulted in competing partition schemes that in some cases corresponded to species hypotheses relying on morphology, including 13 new provisional species names and excluding singletons, but in other cases were morphologically indistinguishable clusters (Fig. 6), hypothetically corresponding to complexes of cryptic species.

Distance-based, single-gene method ASAP applied to the 18S alignments suggested 49 partitions for red *Arcyria* (clade A1a, Fig. 5), and 23 partitions for *Heterotrichia* gen. nov. The same method based on EF1–α gene suggested 25 partitions for red *Arcyria* and 22 for *Heterotrichia*. The tree-based method that relies on the multispecies coalescent model (STACEY) suggested 37 or 31 partitions with ca. equal probability for red *Arcyria* (Fig. 6), and 24 for *Heterotrichia* (not shown here). Morphological examination allowed us to distinguish 17 species hypotheses in red *Arcyria* and 18 in *Heterotrichia,* excluding singletons. Thus, i. in all cases the number of morphological species hypotheses was lower than the number of units proposed by the automated species delimitation methods; ii. the automated methods were quite consistent in *Heterotrichia*, but highly inconsistent between each other and the used genes in red *Arcyria*.

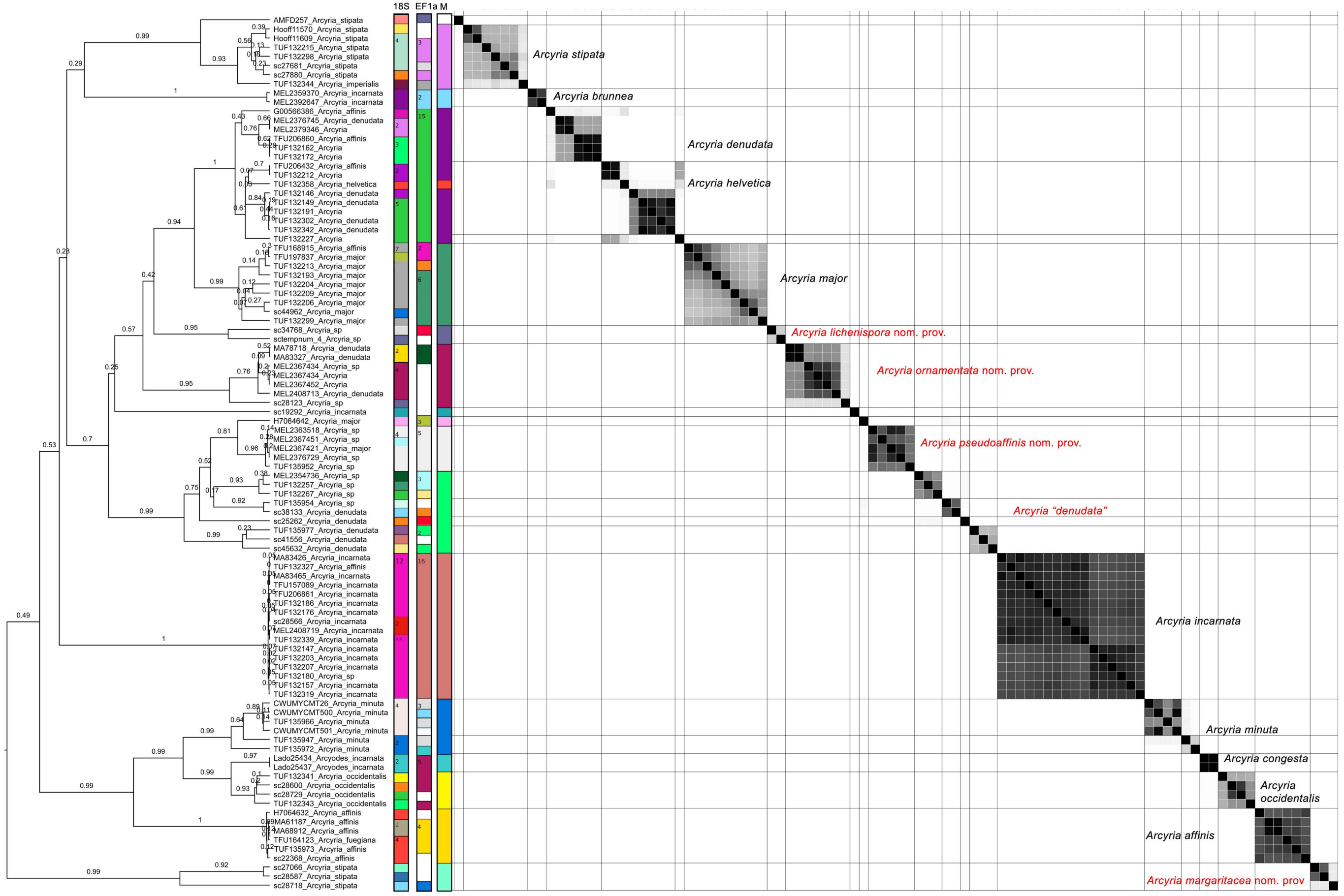

Figure 6. Results of species delimitation for red *Arcyria* (clade A1a) based on different genes and methods (ASAP, STACEY, morphology). Black squares denote probabilities of sequences to belong to the same species from STACEY analysis. Names of new provisional species are written in red, existing species names are in black. Three colored stacks near the tree denote competiting partition schemes: 18S (ASAP); EF1–α (ASAP); morphospecies.

Barcoding gap in myxomycetes

Most of the morphospecies of *Lamproderma* appeared to be separated from the nearest species by the local barcoding gap (**II**, results based on 18S marker are shown on Fig. 7, EF1–α not shown). Intraspecific pairwise distances calculated for 18S lied in a range 0–12.8%; EF1–α gene was more conservative (0–4%). In the analysed portion of *Arcyria* and *Heterotrichia* sequence data the local barcoding gap for both markers was also revealed in most cases (Yatsiuk, 2023). However, the distribution of intraspecific distances in both groups partly overlapped with the distribution of interspecific distances thus demonstrating no clear-cut groupwise threshold (**II**).

The analysis of 18S datasets of bright-spored vs. dark-spored myxomycetes showed that mean intra- and interspecific distances in the bright-spored clade were significantly higher than in the dark-spored clade.

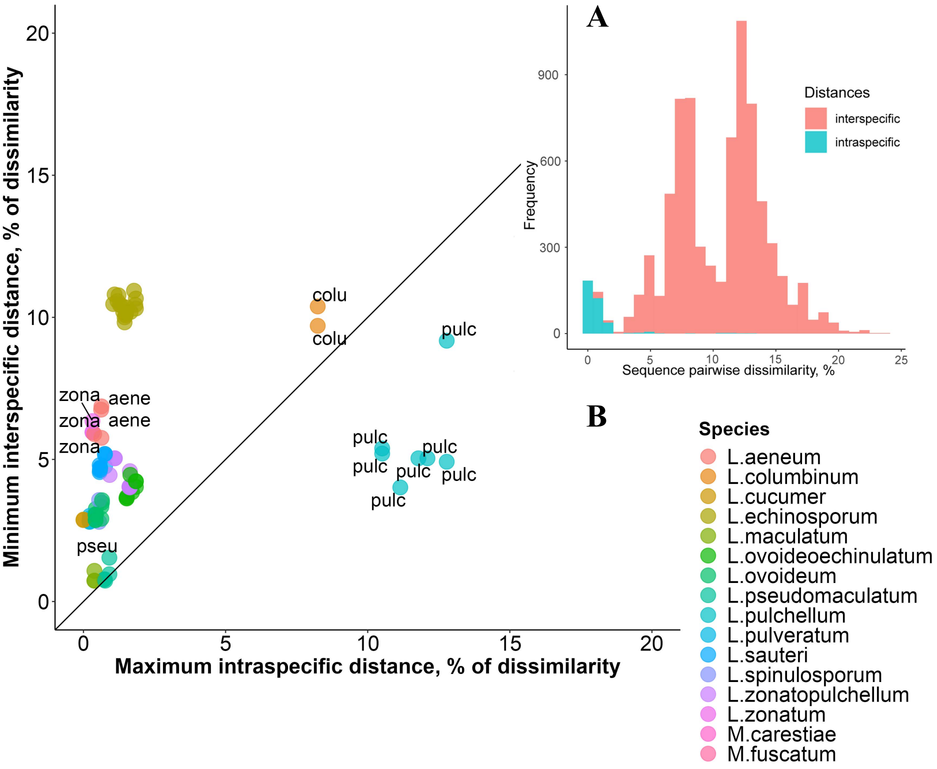

Figure 7. A – Histogram of inter- and intraspecific pairwise distances calculated for 18S alignment for species of *Lamproderma* and *Meriderma* from paper **II** (supplement 2). B – Maximal intraspecific distances vs with minimal inter-specific distances. Points lying above the black line belong to species that show a local barcode gap and can be identified via the chosen marker.

Despite the presence of a local barcoding gap in most morphospecies within both evolutionary branches of myxomycetes, two types of exceptions were noted, where the maximal intraspecific distance surpassed the minimal interspecific distance. The first type of exception was loose clusters of ribotypes exhibiting high intra- and high interspecific distances, which may represent either exremenly divergent species or the complexes of cryptic species, e. g. *L. pulchellum* (Fig. 7). The second exception involved closely related, but morphologically distinct species (both intra- and interspecific distances low). Examples of this were *Lamproderma maculatum–L. pseudomaculatum* (**II**) and *Heterotrichia ferruginea–H. versicolor* that differed from each other only by few species-specific substitutions (Yatsiuk, 2023).

The search for the optimal OTU-picking threshold revealed that the optimal range for dark-spored myxomycetes was 0.6–1.8 %, but in the bright-spored clade it was broader: 1.7–8.5%. Minimal cumulative errors were high in both groups and never reached zero.

Reporting the species diversity in myxomycetes

In papers **III**–**V** we present datasets that report species diversity of myxomycetes accordingly in Estonia, Ukraine, and barcoded specimens of Reticulariaceae worldwide.

The paper **V** encompasses 150 species representing 39 genera. The paper **IV** presents three datasets, Occurrences, Checklist and References published on GBIF. The datasets, including 5036 georeferenced occurrences, 339 taxa and 91 literature sources are formatted in DarwinCore terms and linked between each other through the taxonID field. Seventy-one of the used literature sources are uploaded to Zenodo repositorium in open access.

The paper **III** describes the occurrence dataset of 523 barcoded myxomycete specimens, gathered from five continents, published on GBIF, including 36 types. The dataset encompasses 43 distinct species and one subspecies of myxomycetes, including rare, endemic, and recently described taxa.

DISCUSSION

Taxonomy of myxomycetes has historically somewhat lagged compared to the state of the art in fungal taxonomy. However, works of the recent decades greatly improved the situation by developing more reliable phylogenetic frameworks for major groups (Fiore-Donno et al., 2013, 2012; García-Cunchillos et al., 2022; García-Martín et al., 2023; Leontyev et al., 2019b), and disentangling several species complexes (Dagamac et al., 2017; Feng and Schnittler, 2015; Janik et al., 2021; Leontyev et al., 2023a, 2015, 2019a; Shchepin et al., 2017, 2022).

Nonetheless, myxomycetes are taxonomically challenging due to their unique biology. In contrast to multicellular organisms, myxomycetes are scarce in features, which are mostly linked to their fruiting bodies. Fruiting bodies develop from plasmodia rapidly, therefore the environmental conditions during this period greatly influence the phenotype (Schnittler and Mitchell, 2000). Additionally, with the influx of sequence data it becomes evident that traits, earlier considered indicative for supraspecific taxa, instead evolved through complex pathways, including convergent evolution and reductive evolution (García-Cunchillos et al., 2021; Leontyev et al., 2019b).

This was clearly the case in my primary group of interest (**I**), polyphyletic *Arcyria* s. l. (Fiore-Donno et al., 2013; García-Cunchillos et al., 2022). Neither of the morphological traits such as habitus, stalk, capillitium, cup, that are traditionally used to delimit the genus or its subgenera were consistent with its phylogeny. However, I observed phylogenetically coherent patterns in colouration of spores *en massee,* a trait, previously given minor attention in *Arcyria* s. l. Given that, I proposed moderate adjustments to the system of *Trichiales* as an attempt to harmonize it, compromising between upholding the principle of monophyly, accurately reflecting the evolutionary pathways, and facilitating phenotypical recognition.

The ancestral character state reconstruction showed that the ancestor of three families, *Arcyriaceae* s. str., *Hemitrichiaceae* fam. nov. and *Trichiaceae* s. str., might have had a secondary stalk filled with spore-like bodies, secondary net-like capillitium, and yellowish spore colouration. These traits mostly persisted in *Hemitrichiaceae* and are partially present in *Arcyriaceae* (**I**), but have undergone drastic changes in *Trichiaceae*, including multiple instances of stalk loss and capillitium transformation (García-Cunchillos et al., 2022, 2021).

After clarifying the higher-level phylogeny of *Arcyria*, I advanced to a fine-level examination of species complexes in this group. However, as not uncommonly happens, this work progressed slower than planned. Consequently, to avoid publishing nomina nuda, I choose not to list yet formally unpublished species names in this thesis. Instead, I will further discuss key conclusions derived from our analyses, presented in papers **I**, **II** as well as the conference abstracts (Yatsiuk, 2023, Yatsiuk and Leontyev, 2023).

Both distance-based and tree-based automated species delimitation methods expectedly revealed the landscape of much finer hypothetical taxonomic units than morphology alone, supporting earlier findings of (Feng and Schnittler, 2017). Of 34 morphospecies studied only one, *A. oerstedii*, showed no considerable intraspecific variation and had no morphological "twins" elsewhere on the tree. Other than that, morphospecies were either polyphyletic or splitted onto several well-defined lineages or/and composed of sequences connected by long branches, in addition to high proportion of singleton sequences (**I**).

The existence of such multiple cryptic lineages, anywhere from three to 60 per morphospecies was convincingly demonstrated in previous single-species populational genetic studies (Dagamac et al., 2017; Feng and Schnittler, 2015; Janik et al., 2021; Leontyev et al., 2023a; Shchepin et al., 2017, 2022). Our study, being medium scale in terms of specimens per taxa sampling (average ca. 11 representatives per morphospecies), clearly demonstrates how widespread this phenomenon is across a wide range of taxa. It reveales a substantial amount of cryptic diversity to be described in *Arcyriaceae* and *Hemitricihaceae* and confirms the suggestion of Shchepin et al. (2022) that the actual number of species in myxomycetes may be several times higher than described.

The cryptic diversity in myxomycetes is usually explained by the existence of multiple, reproductively isolated biospecies that often co-occur on one research plot, but as well possess pronounced biogeographic structure worldwide (Janik et al., 2021; Leontyev et al., 2023a). To explain this phenomenon, the combination of sympatric and allopatric speciation has been suggested (Dagamac et al., 2017; Janik et al., 2020; Shchepin et al., 2022). However, since sequence-based methods alone usually do not strictly differentiate between the populational structure and established, reproductively isolated species (Carstens et al., 2013; Sukumaran and Knowles, 2017), other lines of evidence are being searched for. In some studies, thorough examination allowed to discover new traits that fully or partially distinguish biospecies (Dagamac et al., 2017; Janik et al., 2021; Leontyev et al., 2023b). However, other studies have not found such traits (Shchepin et al., 2022, 2017). In the research discussed here (**I**, **II**), I encountered both morphologically discernible and indiscernible lineages, even with the application of SEM. It should be mentioned, that regardless of whether these lineages are considered biospecies, cryptic species or other kinds of evolutionary units, there is still no community consensus about how to communicate them (Schnittler et. al. 2024).

As mentioned earlier, the revolution in species definitions in myxomycetes poses another challenge: bridging the biodiversity data accumulated in the past with current species inventories. The first stage of this process involves gathering previously reported data on species diversity and publishing them according to FAIR principles. Adopting these principles for species inventories is a significant departure from traditional approach (Reyserhove et al., 2020). Initially, I used the traditional approach in the paper **V**, but later changed the mindset towards "data fairness". Consequently, papers **III** and **IV** present data that are accompanied with rich metadata, employ persistent identifiers and are published not only in the journal itself but also in searchable resources GBIF and Zenodo (**Findable**); data are available for humans and machines from open data repositories (**Accessible**);

structured according to international data standard DwC (**Interoperable**) and are published under permissive Creative Commons licenses (**Reusable**).

Where this work should proceed?

Firstly, this work will be only considered complete when the identified species complexes within *Arcyria* and *Heterotrichia* are formally described.

More broadly, future myxomycete studies should include combining the multigene datasets from recent and upcoming myxomycete studies to create the reliable phylogeny of the whole group. The evolution of morphological traits should be traced accordingly, and taxonomy on supraspecific ranks harmonized. Equally important is to establish an annotated sequence database focused on myxomycetes barcode markers and helping to unequivocally communicate cryptic species. These goals would require a dedicated collaborative effort.

CONCLUSIONS

This thesis summarizes a series of studies on taxonomy, distribution, and genetic diversity of myxomycetes, with a particular focus on the genus *Arcyria* s. l. The main results and conclusions of this thesis are the following:

- The paper **I** provided a robust taxonomic backbone for *Arcyria* and allied genera with wide geographical and taxonomical sampling. This work has led to the emendment of the family *Arcyriaceae* s. str., establishment of a new family *Hemitrichiaceae*, a new genus *Spiromyxa*, and resurrection of the genus *Heterotrichia*.
- Practically all traits, traditionally used to delimit supraspecific taxa in *Arcyriaceae* appeared to be homoplastic or symplesiomorphic. However, colouration of the spore mass was identified to be more congruent with reconstructed trees; thus, it was used in delimitation of abovementioned genera and families.
- Most morphospecies of *Arcyria* sampled across the world and sequenced for the first time in this study appeared to be either species complexes, para- or polyphyletic entities (**I**). Similarly, at least four lineages were found that may represent cryptic species within a morphospecies *Lamproderma pulchellum* (**II**).
- Preliminary species delimitation analyses in *Arcyriaceae* s. str. demonstrated a tendency to oversplitting and high incongruence between used genes and methods of automated species delimitation as compared to morphology. However, in *Hemitrichiaceae* the delimitation schemes were much more congruent.
- Myxomycetes generally show a presence of a local barcoding gap between morphospecies, at least in thoroughly revised groups. However, there are exceptions representing i. morphologically indistinct lineages (cryptic species) and ii. morphologically distinct closely related species, where barcoding markers are very conservative. There is no universal OTU-picking threshold even at the genus level, presumably due to the difference in coalescent depth between species (**II**)
- The adherence to FAIR data principles is crucial for enhancing the reproducibility and utility of biodiversity data. Papers **III–V** demonstrate the evolution of views on importance of FAIR data publishing, and represent a pioneering effort in myxomycete studies.

REFERENCES

Abarenkov, K., Tedersoo, L., Nilsson, R.H., Vellak, K., Saar, I., Veldre, V., Parmasto, E., Prous, M., Aan, A., Ots, M., Kurina, O., Ostonen, I., Jõgeva, J., Halapuu, S., Põldmaa, K., Toots, M., Truu, J., Larsson, K.-H., Kõljalg, U., 2010. PlutoF—a web based workbench for ecological and taxonomic research, with an online implementation for fungal ITS sequences. *Evol. Bioinform. Online* 6, 189–196. https://doi.org/10.4137/EBO.S6271

Adl, S., Habura, A., Eglit, Y., 2014. Amplification primers of SSU rDNA for soil protists. *Soil Biol. Biochem.* 20, 1–16. https://doi.org/10.1016/j.soilbio.2013.10.024

Adl, S.M., Bass, D., Lane, C.E., Lukeš, J., Schoch, C.L., Smirnov, A., Agatha, S., Berney, C., Brown, M.W., Burki, F., Cárdenas, P., Čepička, I., Chistyakova, L., Campo, J. del, Dunthorn, M., Edvardsen, B., Eglit, Y., Guillou, L., Hampl, V., Heiss, A.A., Hoppenrath, M., James, T.Y., Karnkowska, A., Karpov, S., Kim, E., Kolisko, M., Kudryavtsev, A., Lahr, D.J.G., Lara, E., Gall, L.L., Lynn, D.H., Mann, D.G., Massana, R., Mitchell, E.A.D., Morrow, C., Park, J.S., Pawlowski, J.W., Powell, M.J., Richter, D.J., Rueckert, S., Shadwick, L., Shimano, S., Spiegel, F.W., Torruella, G., Youssef, N., Zlatogursky, V., Zhang, Q., 2019. Revisions to the classification, nomenclature, and diversity of Eukaryotes. *J. Eukar. Microbiol.* 66, 4–119. https://doi.org/10.1111/jeu.12691

Bollback, J.P., 2006. SIMMAP: Stochastic character mapping of discrete traits on phylogenies. *BMC Bioinformatics* 7, 88. https://doi.org/10.1186/1471-2105-7-88

Brown, S.D.J., Collins, R.A., Boyer, S., Lefort, M.-C., Malumbres-Olarte, J., Vink, C.J., Cruickshank, R.H., 2012. Spider: an R package for the analysis of species identity and evolution, with particular reference to DNA barcoding. *Mol. Ecol. Resour.* 12, 562–565. https://doi.org/10.1111/j.1755-0998.2011.03108.x

Carstens, B.C., Pelletier, T.A., Reid, N.M., Satler, J.D., 2013. How to fail at species delimitation. *Mol. Ecol.* 22, 4369–4383. https://doi.org/10.1111/mec.12413

Clissmann, F., Fiore-Donno, A.M., Hoppe, B., Krüger, D., Kahl, T., Unterseher, M., Schnittler, M., 2015. First insight into dead wood protistan diversity: a molecular sampling of bright-spored Myxomycetes (Amoebozoa, slime-moulds) in decaying beech logs. *FEMS Microbiol. Ecol.* 91. https://doi.org/10.1093/femsec/fiv050

Collins, R.A., Cruickshank, R.H., 2013. The seven deadly sins of DNA barcoding. *Mol. Ecol. Resour.* 13, 969–975. https://doi.org/10.1111/1755-0998.12046

Cooke, M.C., 1877. Contributions to Mycologia Britannica: The Myxomycetes of Great Britain. Williams and Norgate.

Dagamac, N.H.A., Rojas, C., Novozhilov, Y.K., Moreno, G.H., Schlueter, R., Schnittler, M., 2017. Speciation in progress? A phylogeographic study among populations of *Hemitrichia serpula* (Myxomycetes). *PLOS ONE* 12, e0174825. https://doi.org/10.1371/journal.pone.0174825

Dahl, M.B., Shchepin, O., Schunk, C., Menzel, A., Novozhilov, Y.K., Schnittler, M., 2018. A four year survey reveals a coherent pattern between occurrence of fruit bodies and soil amoebae populations for nivicolous myxomycetes. *Sci. Rep.* 8, 11662. https://doi.org/10.1038/s41598-018-30131-3

Ebach, M.C., Valdecasas, A.G., Wheeler, Q.D., 2011. Impediments to taxonomy and users of taxonomy: accessibility and impact evaluation. *Cladistics* 27, 550–557. https://doi.org/10.1111/j.1096-0031.2011.00348.x

Feng, Y., Schnittler, M., 2017. Molecular or morphological species? Myxomycete diversity in a deciduous forest in northeastern Germany. *Nova Hedwigia* 104, 359–380. https://doi.org/info:doi/10.1127/nova_hedwigia/2016/0326

Feng, Y., Schnittler, M., 2015. Sex or no sex? Group I introns and independent marker genes reveal the existence of three sexual but reproductively isolated biospecies in *Trichia varia* (Myxomycetes). *Org. Divers. Evol.* 15. https://doi.org/10.1007/s13127-015-0230-x

Fiore-Donno, A.M., Clissmann, F., Meyer, M., Schnittler, M., Cavalier-Smith, T., 2013. Two-gene phylogeny of bright-spored myxomycetes (slime moulds, superorder Lucisporidia). *PLOS ONE* 8, e62586. https://doi.org/10.1371/journal.pone.0062586

Fiore-Donno, A.M., Kamono, A., Meyer, M., Schnittler, M., Fukui, M., Cavalier-Smith, T., 2012. 18S rDNA phylogeny of *Lamproderma* and allied genera (Stemonitales, Myxomycetes, Amoebozoa). *PLOS ONE* 7, e35359. https://doi.org/10.1371/journal.pone.0035359

Fišer, C., Robinson, C.T., Malard, F., 2018. Cryptic species as a window into the paradigm shift of the species concept. *Mol. Ecol.* 27, 613–635. https://doi.org/10.1111/mec.14486

Gao, Y., Zhang, X., He, G., Shchepin, O.N., Yan, S., Chen, S., 2019. Influence of forest type on dark-spored myxomycete community in subtropical forest soil, China. *Soil Biol. Biochem.* 138, 107606. https://doi.org/10.1016/j.soilbio.2019.107606

García-Cunchillos, I., Estébanez, B., Lado, C., 2021. New approach to the ultrastructure of the capillitium in the order Trichiales (Myxomycetes, Amoebozoa) and its phylogenetic implications. *Protist* 172, 125805. https://doi.org/10.1016/j.protis.2021.125805

García-Cunchillos, I., Zamora, J.C., Ryberg, M., Lado, C., 2022. Phylogeny and evolution of morphological structures in a highly diverse lineage of fruiting-body-forming amoebae, order Trichiales (Myxomycetes, Amoebozoa). *Mol. Phylogenet. Evol.* 177, 107609. https://doi.org/10.1016/j.ympev.2022.107609

García-Martín, J.M., Zamora, J.C., Lado, C., 2023. Multigene phylogeny of the order Physarales (Myxomycetes, Amoebozoa): shedding light on the dark-spored clade. *Persoonia* 51, 89–124. https://doi.org/10.3767/persoonia.2023.51.02

Ham, K., 2013. OpenRefine (version 2.5). http://openrefine.org. Free, open-source tool for cleaning and transforming data. *J. Med. Libr. Assoc.* 101, 233–234. https://doi.org/10.3163/1536-5050.101.3.020

Janik, P., Lado, C., Ronikier, A., 2020. Range-wide phylogeography of a nivicolous protist *Didymium nivicola* Meyl. (Myxomycetes, Amoebozoa): striking contrasts between the Northern and the Southern hemisphere. *Protist* 171, 125771. https://doi.org/10.1016/j.protis.2020.125771

Janik, P., Szczepaniak, M., Lado, C., Ronikier, A., 2021. *Didymium pseudonivicola*: A new myxomycete from the austral Andes emerges from broad-scale morphological and molecular analyses of *D. nivicola* collections. *Mycologia* 113, 1327–1342. https://doi.org/10.1080/00275514.2021.1961068

Jones, G., 2017. Algorithmic improvements to species delimitation and phylogeny estimation under the multispecies coalescent. *J. Math. Biol.* 74, 447–467. https://doi.org/10.1007/s00285-016-1034-0

Kang, S., Tice, A.K., Spiegel, F.W., Silberman, J.D., Pánek, T., Čepička, I., Kostka, M., Kosakyan, A., Alcântara, D.M.C., Roger, A.J., Shadwick, L.L., Smirnov, A., Kudryavtsev, A., Lahr, D.J.G., Brown, M.W., 2017. Between a pod and a hard test: the deep evolution of amoebae. *Mol. Biol. Evol.* 34, 2258–2270. https://doi.org/10.1093/molbev/msx162

Katoh, K., Rozewicki, J., Yamada, K.D., 2019. MAFFT online service: multiple sequence alignment, interactive sequence choice and visualization. *Brief. Bioinform.* 20, 1160–1166. https://doi.org/10.1093/bib/bbx108

Keller, H.W., Everhart, S., 2010. Importance of myxomycetes in biological research and teaching. University of Nebraska – Lincoln, Department of Plant Pathology: Faculty Publications.

Kõljalg, U., Nilsson, H.R., Schigel, D., Tedersoo, L., Larsson, K.-H., May, T.W., Taylor, A.F.S., Jeppesen, T.S., Frøslev, T.G., Lindahl, B.D., Põldmaa, K., Saar, I., Suija, A., Savchenko, A., Yatsiuk, I., Adojaan, K., Ivanov, F., Piirmann, T., Pöhönen, R., Zirk, A., Abarenkov, K., 2020. The taxon hypothesis paradigm – on the unambiguous detection and communication of taxa. *Microorganisms* 8. https://doi.org/10.3390/microorganisms8121910

Kõljalg, U., Nilsson, R.H., Abarenkov, K., Tedersoo, L., Taylor, A.F.S., Bahram, M., Bates, S.T., Bruns, T.D., Bengtsson-Palme, J., Callaghan, T.M., Douglas, B., Drenkhan, T., Eberhardt, U., Dueñas, M., Grebenc, T., Griffith, G.W., Hartmann, M., Kirk, P.M., Kohout, P., Larsson, E., Lindahl, B.D., Lücking, R., Martín, M.P., Matheny, P.B., Nguyen, N.H., Niskanen, T., Oja, J., Peay, K.G., Peintner, U., Peterson, M., Põldmaa, K., Saag, L., Saar, I., Schüßler, A., Scott, J.A., Senés, C., Smith, M.E., Suija, A., Taylor, D.L., Telleria, M.T., Weiss, M., Larsson, K.-H., 2013. Towards a unified paradigm for sequence-based identification of fungi. *Mol. Ecol.* 22, 5271–5277. https://doi.org/10.1111/mec.12481

Kozlov, A.M., Darriba, D., Flouri, T., Morel, B., Stamatakis, A., 2019. RAxML-NG: a fast, scalable and user-friendly tool for maximum likelihood phylogenetic inference. *Bioinformatics* 35, 4453–4455. https://doi.org/10.1093/bioinformatics/btz305

Lado, C., 2005–2023. An on line nomenclatural information system of Eumycetozoa. URL http://www.nomen.eumycetozoa.com (accessed 7.11.2023).

Leontyev, D., Buttgereit, M., Kochergina, A., Shchepin, O., Schnittler, M., 2023a. Two independent genetic markers support separation of the myxomycete *Lycogala epidendrum* into numerous biological species. *Mycologia* 115, 32–43. https://doi.org/10.1080/00275514.2022.2133526

Leontyev, D., Ishchenko, Y., Schnittler, M., 2023b. Fifteen new species from the myxomycete genus *Lycogala*. *Mycologia* 115, 524–560. https://doi.org/10.1080/00275514.2023.2199109

Leontyev, D.V., Schnittler, M., Stephenson, S.L., 2015. A critical revision of the *Tubifera ferruginosa* complex. *Mycologia* 107, 959–985. http://dx.doi.org/10.3852/14-271

Leontyev, D.V., Schnittler, M., Stephenson, S.L., Novozhilov, Y.K., 2019a. Systematic revision of the *Tubifera casparyi–T. dictyoderma* complex: Resurrection of the genus *Siphoptychium* and introduction of the new genus *Thecotubifera*. *Mycologia* 111, 981–997. https://doi.org/10.1080/00275514.2019.1660842

Leontyev, D.V., Schnittler, M., Stephenson, S.L., Novozhilov, Y.K., Shchepin, O.N., 2019b. Towards a phylogenetic classification of the Myxomycetes. *Phytotaxa* 399, 209–238. https://doi.org/10.11646/phytotaxa.399.3.5

Letunic, I., Bork, P., 2021. Interactive Tree Of Life (iTOL) v5: an online tool for phylogenetic tree display and annotation. *Nucl. Ac. Res.* 49, W293–W296. https://doi.org/10.1093/nar/gkab301

Lister, A., Lister, G., 1911. A monograph of the Mycetozoa: a descriptive catalogue of the species in the Herbarium of the British Museum, 2nd ed. / rev. by Gulielma Lister. ed. Trustees of the British Museum, London. https://doi.org/10.5962/bhl.title.21191

Macbride, T.H., 1922. The North American slime-moulds; a descriptive list of all species of myxomycetes hitherto reported from the continent of North America, with notes on some extralimital species, New and rev. ed. ed. Macmillan Co, New York. https://doi.org/10.5962/bhl.title.33432

Martin, G.W., Alexopoulos, C.J., 1969. Slime molds: the Myxomycetes. University of Iowa Press, Iowa City.

Nannenga-Bremekamp, N.E., 1982. Notes on Myxomycetes. XXI. The use of polarized light as an aid in the taxonomy of the Trichiales. *Proc. Kon. Ned. Akad. Wetensch., Ser. C* 85, 541–562.

Nguyen, L.-T., Schmidt, H.A., von Haeseler, A., Minh, B.Q., 2015. IQ-TREE: A fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies. *Mol. Biol. Evol.* 32, 268–274. https://doi.org/10.1093/molbev/msu300

Paradis, E., Schliep, K., 2019. ape 5.0: an environment for modern phylogenetics and evolutionary analyses in R. *Bioinformatics* 35, 526–528. https://doi.org/10.1093/bioinformatics/bty633

Pärtel, K., Suija, A., Yatsiuk, I., 2021a. The Estonian mycological collections of Heinrich August Dietrich (1820–1897). *Acta Balt. Hist. Phil. Sci.* 9, 48–78. https://doi.org/10.11590/abhps.2021.2.03

Pärtel, K., Suija, A., Yatsiuk, I., 2021b. The mycological collection of G. C. Girgensohn from the middle of the 19th century. *Folia Cryptog. Estonica* 58. https://doi.org/10.12697/fce.2021.58.14

Puillandre, N., Brouillet, S., Achaz, G., 2021. ASAP: assemble species by automatic partitioning. *Mol. Ecol. Resour.* 21, 609–620. https://doi.org/10.1111/1755-0998.13281

R Core Team, 2022. R: A language and environment for statistical computing.

Ranwez, V., Douzery, E.J.P., Cambon, C., Chantret, N., Delsuc, F., 2018. MACSE v2: toolkit for the alignment of coding sequences accounting for frameshifts and stop codons. *Mol. Biol. Evol.* 35, 2582–2584. https://doi.org/10.1093/molbev/msy159

Revell, L.J., 2012. phytools: An R package for phylogenetic comparative biology (and other things). *Methods Ecol. Evol.* 3, 217–223. https://doi.org/10.1111/j.2041-210X.2011.00169.x

Reyserhove, L., Desmet, P., Oldoni, D., Adriaens, T., Strubbe, D., Davis, A.J.S., Vanderhoeven, S., Verloove, F., Groom, Q., 2020. A checklist recipe: making species data open and FAIR. *Database*, baaa084. https://doi.org/10.1093/database/baaa084

Robert, V., Vu, D., Amor, A.B.H., van de Wiele, N., Brouwer, C., Jabas, B., Szoke, S., Dridi, A., Triki, M., Daoud, S. ben, Chouchen, O., Vaas, L., de Cock, A., Stalpers, J.A., Stalpers, D., Verkley, G.J.M., Groenewald, M., dos Santos, F.B., Stegehuis, G., Li, W., Wu, L., Zhang, R., Ma, J., Zhou, M., Gorjón, S.P., Eurwilaichitr, L., Ingsriswang, S., Hansen, K., Schoch, C., Robbertse, B., Irinyi, L., Meyer, W., Cardinali, G., Hawksworth, D.L., Taylor, J.W., Crous, P.W., 2013. MycoBank gearing up for new horizons. *IMA Fungus* 4, 371–379. https://doi.org/10.5598/imafungus.2013.04.02.16

Ronikier, A., Janik, P., de Haan, M., Kuhnt, A., Zankowicz, M., 2022. Importance of type specimen study for understanding genus boundaries-taxonomic clarifications in *Lepidoderma* based on integrative taxonomy approach leading to resurrection of the old genus *Polyschismium*. *Mycologia* 114, 1008–1031. https://doi.org/10.1080/00275514.2022.2109914

Ronquist, F., Teslenko, M., van der Mark, P., Ayres, D.L., Darling, A., Höhna, S., Larget, B., Liu, L., Suchard, M.A., Huelsenbeck, J.P., 2012. MrBayes 3.2: efficient bayesian phylogenetic inference and model choice across a large model space. *Syst. Biol.* 61, 539–542. https://doi.org/10.1093/sysbio/sys029

Rostafinski, J.T., 1875. Sluzowce (Mycetozoa); Nakadem Biblioteki Kórnickiej, Paryz : https://doi.org/10.5962/bhl.title.63836

Schnittler, M., Mitchell, D.W., 2000. Species diversity in Myxomycetes based on the morphological species concept – a critical examination. *Stapfia* 73, 55–62.

Schnittler, M., Shchepin, O.N., Dagamac, N.H.A., Borg Dahl, M., Novozhilov, Y.K., 2017. Barcoding myxomycetes with molecular markers: challenges and opportunities. *Nova Hedwigia* 104, 323–341. https://doi.org/10.1127/nova_hedwigia/2017/0397

Schnittler, M., Leontyev D., Yatsiuk I., Ronikier A. Species descriptions in myxomycetes – can we settle on rules for good taxonomic practice? *IMA Fungus* (submitted)

Shchepin, O., Novozhilov, Y., Schnittler, M., 2017. Disentangling the taxonomic structure of the *Lepidoderma chailletii–carestianum* species complex (Myxogastria, Amoebozoa): genetic and morphological aspects. *Protistology* 10, 117–129. https://doi.org/10.21685/1680-0826-2016-10-4-1

Shchepin, O., Novozhilov, Y., Woyzichovski, J., Bog, M., Prikhodko, I., Fedorova, N., Gmoshinskiy, V., Borg Dahl, M., Dagamac, N.H.A., Yajima, Y., Schnittler, M., 2022. Genetic structure of the protist *Physarum albescens* (Amoebozoa) revealed by multiple markers and genotyping by sequencing. *Mol. Ecol.* 31, 372–390. https://doi.org/10.1111/mec.16239

Shchepin, O.N., Schnittler, M., Erastova, D.A., Prikhodko, I.S., Borg Dahl, M., Azarov, D.V., Chernyaeva, E.N., Novozhilov, Y.K., 2019. Community of dark-spored myxomycetes in ground litter and soil of taiga forest (Nizhne-Svirskiy Reserve, Russia) revealed by DNA metabarcoding. *Fun. Ecol.* 39, 80–93. https://doi.org/10.1016/j.funeco.2018.11.006

Suchard, M.A., Redelings, B.D., 2006. BAli-Phy: simultaneous Bayesian inference of alignment and phylogeny. *Bioinformatics* 22, 2047–2048. https://doi.org/10.1093/bioinformatics/btl175

Sukumaran, J., Knowles, L.L., 2017. Multispecies coalescent delimits structure, not species. *PNAS* 114, 1607–1612. https://doi.org/10.1073/pnas.1607921114

Wieczorek, J., Bloom, D., Guralnick, R., Blum, S., Döring, M., Giovanni, R., Robertson, T., Vieglais, D., 2012. Darwin Core: an evolving community-developed biodiversity data standard. *PLOS ONE* 7, e29715. https://doi.org/10.1371/journal.pone.0029715

Wilkinson, M.D., Dumontier, M., Aalbersberg, Ij.J., Appleton, G., Axton, M., Baak, A., Blomberg, N., Boiten, J.-W., da Silva Santos, L.B., Bourne, P.E., Bouwman, J., Brookes, A.J., Clark, T., Crosas, M., Dillo, I., Dumon, O., Edmunds, S., Evelo, C.T., Finkers, R., Gonzalez-Beltran, A., Gray, A.J.G., Groth, P., Goble, C., Grethe, J.S., Heringa, J., ’t Hoen, P.A.C., Hooft, R., Kuhn, T., Kok, R., Kok, J., Lusher, S.J., Martone, M.E., Mons, A., Packer, A.L., Persson, B., Rocca-Serra, P., Roos, M., van Schaik, R., Sansone, S.-A., Schultes, E., Sengstag, T., Slater, T., Strawn, G., Swertz, M.A., Thompson, M., van der Lei, J., van Mulligen, E., Velterop, J., Waagmeester, A., Wittenburg, P., Wolstencroft, K., Zhao, J., Mons, B., 2016. The FAIR Guiding Principles for scientific data management and stewardship. *Sci. Data* 3, 160018. https://doi.org/10.1038/sdata.2016.18

Yatsiuk, I., Leontyev, D. *Arcyria* and allied genera: taxonomic backbone, diversity and characters evolution. In: Abstract book. Proceedings of the 11th International Congress on the Systematics and Ecology of Myxomycetes, 28–31 August 2023. Tartu: University of Tartu. https://doi.org/10.5281/zenodo.8252604, P. 43

Yatsiuk, I**.** Barcoding in species delimitation and otu-picking for dark-spored vs. bright-spored myxomycetes. . In: Abstract book. Proceedings of the 11th International Congress on the Systematics and Ecology of Myxomycetes, 28–31 August 2023. Tartu: University of Tartu. https://doi.org/10.5281/zenodo.8252604, P. 44

Yu, G., Smith, D.K., Zhu, H., Guan, Y., Lam, T.T.-Y., 2017. ggtree: an r package for visualization and annotation of phylogenetic trees with their covariates and other associated data. *Methods Ecol. Evol.* 8, 28–36. https://doi.org/10.1111/2041-210X.12628

SUMMARY

Myxomycetes, or Myxogastria, comprise approximately 1,050 species within the kingdom Amoebozoa. Myxomycetes have complex life cycle, which includes an amoeboid stage, a multinucleate mobile plasmodium, and spore-bearing sporocarps. In their amoeboid stage, myxomycetes inhabit diverse substrates such as soil, bark of living trees, decaying wood, leaf litter, and other plant debris. There they feed on bacteria, algae and protists, and themselves are the source of food to beetles, slugs and nematodes, thus playing an important role in terrestrial ecosystems.

Despite their substantial ecological functions, myxomycetes have been systematically underrepresented in taxonomical and ecological research. Since myxomycetes were generally considered a cryptic and less economically significant group, their taxonomy historically lagged compared to the state of the art in fungal taxonomy. Consequently, there is still the need of understanding phylogenetic relations, species boundaries, and developing of robust practices of species delimitation, description, and communication in myxomycetes. The ongoing revolution in species definitions in myxomycetes poses another challenge: bridging the biodiversity data accumulated in the past with current species inventories. The first stage of this process involves gathering previously reported data on species diversity and publishing them according to FAIR principles.

Given these challenges, this study aims to fill the gaps in our understanding of myxomycetes. It is a multiaspect study, comprised of two major parts. The first part of this thesis addresses phylogeny, evolution, and species delimitation in chosen groups of myxomycetes (papers **I**, **II**).

In our taxonomical studies **I** and **II** we used morphological and molecular methods to (1) establish a reliable taxonomical backbone for *Arcyria* and allied genera within the bright-spored myxomycetes, (2) reconstruct the evolutionary pathway of morphological characters and evaluate their application in taxonomy of bright-spored myxomycetes; (3) assess the barcoding gap applicability in myxomycetes. Additionally, we used exploratory and validaton species delimitation techniques to revise the genus *Arcyria* on the species level, however, this part of work is yet to be finished.

In the paper **I** we present phylogenies with wide taxonomical and geographical sampling across *Arcyria*, a genus of the order Trichiales that includes 265 published species and infraspecific taxa. The majority of species in this genus are problematic: representing taxonomic synonyms, taxa based on old and scarce descriptions, or relying on doubtful morphological differences. Phylogenies inferred from 18S–EF1–α–mitSSU datasets demonstrated that the genus *Arcyria* belongs to two evolutionary distant clades, confirming the conclusions of the previous studies about the polyphyly of the genus. In the paper **I** we emended the family *Arcyriaceae* s. str., established a new family *Hemitrichiaceae*, a new genus *Spiromyxa*, and resurrected the genus *Heterotrichia*.

The analyses of morphological traits demonstrated that neither of traits traditionally used to delimit the genus *Arcyria* s. l. is consistent with the phylogeny, being instead scattered across the branches of *Arcyriaceae* s. str. and

Hemitrichiaceae fam. nov. However, the colouration of spore masses in fresh condition, a trait, previously given minor attention in *Arcyria s. l.*, appeared to be partially consistent with the phylogeny. The character evolution analysis did not provide conclusive results about the origin of stalks in Trichiales. However, there was some evidence that the last common ancestor of *Arcyriaceae, Hemitrichiaceae* and *Trichiaceae* was stalked; the stalk filled with spore-like bodies perpetuated in *Arcyriaceae* and *Hemitrichiaceae*, but was lost in the common ancestor of *Trichiaceae*. The capillitium at the same node was reconstructed as elastic net attached to the stalk, and spore mass colouration as yellow.

We found out that the majority of morphospecies of *Arcyria* including most common ones represent either species complexes or para- or polyphyletic taxa, with the extreme case of *A. cinerea* scattered over at least 23 branches. Different automated species delimitation approaches resulted in competiting partition schemes that in some cases corresponded to species hypotheses relying on morphology (including 13 new provisional species names and excluding singletons), but in others were morphologically indistinguishable clusters, hypothetically corresponding to complexes of cryptic species.

Our paper **II** focuses on a genus *Lamproderma*, a comparatively lately-radiated, species-rich genus of *Columellomycetidae*. Apart from a taxonomical study and the description of a new species, in this publication and in a series of conference abstracts we address the application of the barcoding gap in myxomycetes. Most of the morphological species hypotheses of bright-spored and dark-spored myxomycetes included into the study appeared to be separated from the nearest neighbour by the local barcoding gap. However, in both groups there were exceptions representing i. morphologically indistinct lineages (cryptic species) and ii. morphologically distinct closely related species, where barcoding markers were extra conservative. The distribution of intraspecific distances in both groups partly overlapped with the distribution of interspecific distances thus demonstrating no clear-cut groupwise threshold, presumably due to the difference in coalescent depth between species.

The second part of this thesis summarizes our effort in collecting and publishing primary data about species diversity of myxomycetes. In papers (**III–V**) we demonstrate how the data obtained from various sources, may be reported according to FAIR (Findable, Accessible, Interoperable, Reusable) principles. The paper **V** reports 150 species representing 39 genera of myxomycetes of Estonia. The paper **IV** presents the occurrence-based checklist of myxomycetes of Ukraine and includes three datasets: Occurrences (5036 georeferenced occurrences), Checklist (339 taxa) and References (91 sources). The datasets, published on GBIF, are formatted in DarwinCore terms and linked between each other through the taxonID field. Seventy-one of the used literature sources were uploaded to Zenodo repositorium in open access. The paper **III** describes the worldwide occurrence dataset of 523 barcoded myxomycete specimens, including 36 types, gathered from five continents. The dataset encompassed 43 species and one subspecies of myxomycetes, including rare, endemic, and recently described taxa.

SUMMARY IN ESTONIAN

Limakute evolutsioon, liikide piiritlemine ning mitmekesisus *Arcyria* ja seotud perekondade näitel

Myxogastria (ehk limakud) sisaldab ligikaudu 1500 liiki, mis kuuluvad protistide riiki *Amoebozoa*. Limakutel on mitmeetapiline elutsükkel, mis hõlmab amöboidset staadiumi, mitmetuumalist liikuvat plasmoodiumi ja eoseid kandvaid struktuure. Limakud elavad amöboidses staadiumis substraatidel nagu muld, eluspuude koor, kõdupuit ja muu taimne varis. Seal toituvad nad bakteritest, vetikatest ja teistest protistidest ning on ise mardikate, nälkjate ja nematoodide toiduallikaks, omades maismaaökosüsteemide toitumisahela olulist rolli.

Vaatamata toitumisahela olulisele rollile on limakud taksonoomilistes ja ökoloogilistes uuringutes alaesindatud. Traditsiooniliselt on limakuid uurinud mükoloogid. Kuna neid peeti üldiselt vähem oluliseks taksoniks, jäi nende taksonoomia seentega võrreldes väheuurituks. Seetõttu on jätkuvalt oluline selle taksoni fülogeneesi ja liikide eristamise uurimine ning ökoloogilised uuringud. Limakute uurimine esitab veel ühe väljakutse: minevikus kogutud mitmekesisuse andmete ühendamine kaasaegsete liigi nimedega. Selle protsessi esimene etapp hõlmab liikide varem avaldatud andmete digitaliseerimist ja avaandmetena avaldamist FAIR (Findable=leitav, Accessible=ligipääsetav, Interoperable= koostalitlusvõimeline, Reusable=korduvkasutatav) põhimõtete kohaselt.

Neid väljakutseid arvestades on käesoleva doktoritöö eesmärk täiendada teadmisi limakute taksonoomiast ja evolutsioonist ning korrastada ja digitaliseerida limakute varasemaid uurimisandmeid. Doktoritöö koosneb peamiselt kahest osast: 1) valitud limaku taksonite fülogeneesi, evolutsiooni ja liikide piiritlemisega seotud uuringud (artiklid **I**, **II**); 2) limakute liikide varasemate andmete korrastamine, digitaliseerimine ja avaandmetena avaldamine (artiklid **III**–**V**).

Doktoritöö esimeses osas kasutame morfoloogilisi ja molekulaarseid meetodeid (**I**, **II**), et (1) luua perekond *Arcyria* ja teiste heledaeoseliste sõsarperekondade uus taksonoomiline süsteem, (2) luua evolutsiooniline morfoloogiliste tunnuste ontoloogia ja hinnata nende rakendamist heledaeoseliste limaku liikide eristamisel, (3) hinnata limakutel DNA triipkoodi geenmarkerite rakendatavust.

Artiklis **I** esitame fülogeneesi uurimistöö, mis hõlmab perekonna *Arcyria* laia taksonoomilise ja geograafilise valimi. Selles perekonnas on teadusele kirjeldatud 265 liiki ja liigisisest taksonit. Suur osa *Arcyria* liikidest vajab täiendavaid uuringuid: siin esineb palju taksonoomilisi sünonüüme, liigid põhinevad puudulikel kirjeldustel või tuginevad väikestele morfoloogilistele erinevustele. Kolme geenimarkeri (18S SSU, EF1–α ja mitSSU) põhine fülogenees näitas, et perekond *Arcyria* liigid kuuluvad kahte evolutsiooniliselt kaugesse taksonisse. Käesoleva töö tulemused kinnitasid varasemat hüpoteesi *Arcyria* polüfüleetilisusest. Artiklis **I** täiendasime sugukonna *Arcyriaceae* s. str. varasemat klassifikatsiooni, kirjeldasime uue sugukonna *Hemitrichiaceae*, uue perekonna *Spiromyxa* ja võtsime uuesti kasutusele perekonna *Heterotrichia*.

Morfoloogiliste tunnuste analüüs näitas, et kumbki perekonna *Arcyria* s. l. piiritlemiseks enim kasutatud tunnusest pole molekulaarse fülogeneesi tulemustega kooskõlas. Enamik kasutatud morfoloogilistest tunnustest esinevad sugukondade *Arcyriaceae* s. str. ja *Hemitrichiaceae* fam. nov. liikidel hajutatult. Kuid värskete eksemplaride eosmassi värvus (tunnus, millele on varem *Arcyria* s. l. vähe tähelepanu pööratud), on fülogeneesiga osaliselt kooskõlas. Seltsi *Trichiales* tunnuste evolutsiooni analüüs ei andnud lõplikke tulemusi eosla jala päritolu kohta. Siiski leidsime tõendeid selle kohta, et sugukondade *Arcyriaceae*, *Hemitrichiaceae* ja *Trichiaceae* ühisel esivanemal esines eosla jalg. Käesoleva uuringu põhjal on nimetatud jalg püsinud sugukondades *Arcyriaceae* ja *Hemitrichiaceae* tänapäevani, kuid on evolutsioonis kaduma läinud sugukonnas *Trichiaceae*. Seltsis Trichiales esinev kapilliitium kirjeldati kui eosla jala külge kinnitunud elastne võrk ja eosmassi värvus kollasena.

Selgitasime välja, et enamik perekonna *Arcyria* morfoloogilistel tunnustel põhinevad liigid on para- või polüfüleetilised liigikompleksid. Meie andmetel on näiteks liigi *Arcyria cinerea* eksemplarid molekulaarsete tunnuste põhjal fülogeneesi puu 23 erinevas harus. Erinevad statistilised meetodid nagu automatiseeritud liikide eristamise meetodid (STACEY, ASAP) andsid mõnel juhul tulemuse, mida toetasid ka morfoloogilised tunnused. Selle meetodi abil võib eristada 13 potentsiaalset uut liiki. Samas saadi selle meetodiga ka mitmeid krüptilisi liike, mis on morfoloogiliselt eristamata.

Doktoritöö **II** artikkel keskendub fülogeneetiliselt suhteliselt hiljuti eristunud liigirikkale perekonnale *Lamproderma*, mis kuulub sugukonda *Columellomycetidae*. Lisaks taksonoomilisele uuringule ja uue liigi kirjeldusele käsitleme DNA triipkoodi vahemiku rakendamist limakutel (**II**). Enamikel uuringusse kaasatud heleda- ja tumedaeoselistel morfoloogilistel tunnustel eristatud sõsarliikidel esineb DNA triipkoodi vahemik. Siiski oli mõlemas rühmas erandeid: (i) morfoloogiliselt ebaselged liinid (tõenäoliselt krüptilised liigid) ja (ii) morfoloogiliselt erinevad liigid, kus DNA triipkoodi markerid osutusid konservatiivseks. Liigisisese varieeruvuse suurus kattus osaliselt liikidevaheliste kauguste jaotusega, mis ei võimaldanud valida selget liikide eristamise läviväärtust.

Doktoritöö teises osas võetakse kokku uurimistöö limakute liigilise mitmekesisuse esmaste andmete kogumisel ja avaldamisel. Kolm käesoleva doktoritöö artiklit (**III–V**) käsitlevad kuidas saab erinevate allikate digitaliseeritud andmeid esitada vastavalt FAIR põhimõtetele. Artikkel **III** käsitleb 150 liiki, mis kuuluvad 39 eri limaku perekonda ja esinevad Eestis. **IV** artiklis esitatakse Ukraina limakute sageduspõhine nimekiri ja avaldatakse kolm andmekogumit: taksoni esinemised (5036 georefereeritud taksoni esinemist), liikide nimestik (339 taksonit) ja seotud kirjanduse viited (91 allikat). Globaalses elurikkuse portaali (GBIF) limakute avaldatud andmestikud on vormindatud vastavalt DarwinCore standardile ja omavahel seotud takson ID välja kaudu. Seitsekümmend üks kasutatud kirjandusallikat laeti avatud juurdepääsuga Zenodo digiarhiivi. Artiklis **V** kirjeldatakse viielt eri kontinendilt kogutud 523 DNA triipkoodiga limaku eksemplari (sealhulgas 36 tüüpeksemplari) põhjal nende liikide levikut. Andmekogum sisaldab 43 limaku liiki ja ühte alamliiki, sealhulgas ka haruldasi, endeemseid ja viimastel aastatel kirjeldatud taksoneid.

ACKNOWLEDGEMENTS

This work would not happen without my supervisor Urmas Kõljalg, whom I sincerely thank for inspiration and support provided in all possible ways. He demonstrated incredible patience, tolerance and created the atmosphere of academic freedom that boosted my abilities, not to mention that I enjoyed it very much. My co-supervisor Dmytro Leontyev was the person who first introduced me to slime moulds back in summer 2006. Since then, his passion and talents in studying nature always have been an example to me. Another special person, whom I want to thank, is Olexander Akulov from the Department of Mycology (V.N. Karazin Kharkiv National University), the supervisor of my BA and MA theses. From this brilliant lecturer I learned how to establsh collaborations, think strategically and, finally, stand my own ground. With warmest regards I remember my friends from the same university, with whom I shared a lot of expeditions and adventures, especially Oleh Prylutskyi and Yehor Yatsiuk.

I'm sincerely grateful to Kadri Põldmaa, Kadri Pärtel, Ave Suija, Margret Sisask, Rasmus Puusepp, Heidi Tamm, Sanni Färkkila, Jane Lees and other people from the University of Tartu for welcoming me in Estonia and assisting my work in different ways. Vladimir Mikryukov is cordially thanked for keeping his doors open for silly IT-related questions. I'm indebted to Anton Savchenko for making my life easier by step-by-step sharing his experience as a PhD student in TÜ, as well as tips and tricks in phylogenetics.

I extend my gratitude to Dag Endresen, Laura Russel, and whole BioData team for sharing knowledge in biodiversity data management.

I thank Martin Schnittler for discussions, critics, sharing research ideas and specimens with me. I'm also grateful for cooperation to all other co-authors, including Angela Lopez-Villalba, Veiko Kastanje, Grazina Adamonyte, Yuliia Leshchenko, Vitalii Viunnyk, Tyson Ehlers. Besides that, I'm most obliged to all scientists, citizen scientists and amateurs who sent specimens to me. Finally, Andrei Kazakov was a moral support to me during the last two years.

I dedicate this thesis to all fellow biologists who are now serving their duty in the Armed Forces of Ukraine.

This work was financed primarily by Estonian Research Council projects IUT20-30 and PRG1170. Other sources include Norwegian Agency for International Cooperation and Quality Enhancement in Higher Education (DIKU project CPEA-LT-2017/10049) and Kristjan Jaak foundation.

PUBLICATIONS

CURRICULUM VITAE

Name: Iryna Yatsiuk
Date of birth: 10 June 1988
Citizenship: Ukraine
Address: Institute of Ecology and Earth Sciences, University of Tartu, J. Liivi 2, 50409, Tartu, Estonia
Phone: +372 5670 9111
E-mail: yatsiuk@ut.ee

Language skills: English (C1), Ukrainian (native), Russian (native), Estonian (B1)

Education and degrees:

2019–	University of Tartu, PhD candidate in Botany and Ecology
2018–	Kandidat nauk degree: 3 December, 2018, the Institute of Botany, Academic of Sciences of Ukraine, Kyiv
2009–2010	V.N. Karazin Kharkiv National University (Ukraine), MSc in Biology
2006–2009	V.N. Karazin Kharkiv National University (Ukraine), BSc in Biology

Professional experience:

2023–2024	University of Tartu, Institute of Ecology and Earth Sciences, Junior Research Fellow in Mycology
2015–2019	V.N. Karazin Kharkiv National University, Department of Mycology and Plant Resistance, junior lecturer
2012–2013	National Nature Park 'Homilshansky lisy' (Kharkiv, Ukraine), researcher
2010–2015	V.N. Karazin Kharkiv National University, Department of Mycology and Plant Resistance, laboratory assistant

Publications:

Tedersoo, L., Hosseyni Moghaddam, M.S., Mikryukov, V., Hakimzadeh, A., Bahram, M., Nilsson, R.H., **Yatsiuk, I.**, Geisen, S., Schwelm, A., Piwosz, K., Prous, M., Sildever, S., Chmolowska, D., Rueckert, S., Skaloud, P., Laas, P., Tines, M., Jung, J.-H., Choi, J.H., Alkahtani, S., Anslan, S., 2024. EUKARYOME: the rRNA gene reference database for identification of all eukaryotes. *Database*, baae043. https://doi.org/10.1093/database/baae043

Yatsiuk, I., Leshchenko Yu., Viunnyk V., Leontyev, D., 2024. The comprehensive checklist of myxomycetes of Ukraine based on extended occurrence and reference datasets. *Biodiversity data journal*, 12: e120891 https://doi.org/10.3897/BDJ.12.e120891

Leontyev, D., **Yatsiuk**, I., 2024. Dataset of barcoded Reticulariaceae: ten years of DNA sequencing. *Biodiversity Data Journal* 12, e115630. https://doi.org/10.3897/BDJ.12.e115630

Yatsiuk, I., Leontyev, D., Lopez-Villalba, A., Schnittler, M., Koljalg, U., 2023. A new nivicolous species of *Lamproderma* (Myxomycetes) from lowland and mountainous regions of Europe. *Nova Hedwigia*, 116, 105–136. https://doi.org/10.1127/nova_hedwigia/2023/0807

Prylutskyi, O., **Yatsiuk, I.**, Savchenko, A., Kit, M., Solodiankin, O., Schigel, D., 2022. Strict substrate requirements alongside rapid substrate turnover may indicate an early colonization: A case study of *Pleurotus calyptratus* (Agaricales, Basidiomycota). *Fungal Ecology* 59, 101098. https://doi.org/10.1016/j.funeco.2021.101098

Pärtel, K., Suija, A., **Yatsiuk, I.**, 2021. The Estonian Mycological Collections of Heinrich August Dietrich (1820–1897). *Acta Baltica Historiae et Philosophiae Scientiarum* 9, 48–78. https://doi.org/10.11590/abhps.2021.2.03

Pärtel, K., Suija, A., **Yatsiuk, I.**, 2021. The mycological collection of G. C. Girgensohn from the middle of the 19th century. *Folia Cryptogamica Estonica* 58, 109–119. https://doi.org/10.12697/fce.2021.58.14

Yatsiuk, I., Leontyev, D., 2020. Two species of nivicolous myxomycetes that formed fruiting bodies during three spring seasons in the lowlands of the Eastern Ukraine. *Phytotaxa* 437, 147–155. https://doi.org/10.11646/phytotaxa.437.3.3

Yatsiuk, I., Adamonytė, G., Kastanje, V., 2020. A comprehensive checklist of Estonian myxomycetes. *Karstenia* 58, 239–247. https://doi.org/10.29203/ka.2020.497

Leontyev, D., **Yatsiuk, I.**, Kochergina, A., 2020. Inclusion of myxomycetes in the Red Data Book of Ukraine: feasibility, selection criteria and recommended species. *Ukrainian Botanical Journal* 77, 189–203. https://doi.org/10.15407/ukrbotj77.03.189

Kõljalg, U., Nilsson, H. R., Schigel, D., Tedersoo, L., Larsson, K.-H., May, T.W.; Taylor, A.F.S., Jeppesen, T.S., Frøslev, T.G., Lindahl, B.D., Põldmaa, K., Saar, I., Suija, A., Savchenko, A., **Yatsiuk, I.**, Adojaan, K., Ivanov, F., Piirmann, T., Pöhönen, R., Zirk, A., Abarenkov, K., 2020. The Taxon Hypothesis Paradigm – On the Unambiguous Detection and Communication of Taxa. *Microorganisms* 8, 1910. https://doi.org/10.3390/microorganisms8121910

Yatsiuk, I., Leontyev, D., Shlakhter, M., 2018. Myxomycetes of the National Nature Park Slobozhanskiy (Ukraine): biodiversity and noteworthy species. *Nordic Journal of Botany* 36, UNSP e01605. https://doi.org/10.1111/njb.01605

Prylutskyi, O., Akulov, O., Leontyev, D., Ordynets, A., **Yatsiuk, I.**, Usichenko, A., Savchenko, A., 2017. Fungi and fungus-like organisms of Homilsha forests national park, Ukraine. *Mycotaxon* 132, 1–56. https://doi.org/10.5248/132.705

Yatsiuk, I., Saar, I., Kalamees, K., Sulaymonov, S., Gafforov, Y., O'Donnell, K., 2016. Epitypification of *Morchella steppicola* (Morchellaceae, Pezizales), a morphologically, phylogenetically and biogeographically distinct member of the Esculenta Clade from central Eurasia. *Phytotaxa* 284, 31–40. https://doi.org/10.11646/phytotaxa.284.1.3

Morozova, I., 2014. New records of discomycetous fungi from Ukraine. *Turkish Journal of Botany* 38, 398–405. https://doi.org/10.3906/bot-1301-14.

Leontyev, D., Eliasson, U., Kochergina, A., **Morozova, I.**, 2009. New and rare myxomycetes of Ukraine. 1. East Forest-Steppe. *Karstenia* 49, 61–67. https://doi.org/10.29203/ka.2009.434

Conference presentations, talks:

Yatsiuk, I. Leontyev, D. *Arcyria* and allied genera: taxonomic backbone, diversity and charac-ters evolution. 11th International Congress on the Systematics and Ecology of Myxomycetes (ICSEM11), 28–31 August 2023, Tartu, Estonia.

Yatsiuk, I. Barcoding in species delimitation and otu-picking for dark-spored vs. bright-spored myxomycetes. 11th International Congress on the Systematics and Ecology of Myxomycetes (ICSEM11), 28–31 August 2023, Tartu, Estonia.

Yatsiuk, I., Leshchenko, Yu. Myxomycetes of Ukraine. The checklist from invisible sources. GBIF node meeting, 16 May 2023, online.

Yatsiuk, I., Shyriaeva, D., Prylutskyi, O. GBIF and open biodiversity data in Ukraine. BioDATA Final Conference, 13 November 2022, Oslo, Norway.

Yatsiuk, I., Prikhodko, I., Leontyev, D. Barcoding in bright-spored and dark-spored myxomycetes: no universal threshold. Poster. International Conference on DNA Barcoding and Biodiversity (ICDBB). 25–27 May, 2022, Sofia, Bulgaria.

Yatsiuk, I. Do "lowland nivicolous" myxomycetes fruitify more regularly than we think? 10th International Congress on the Systematics and Ecology of Myxomycetes (ICSEM10). 25–28 February 2020, Turrialba, Costa-Rica.

Yatsiuk, I. Molecular species definition in myxomycetes – where are we now? PhD Student Conference of the Department of Botany, 2020, UT.

Other publications: datasets, educational materials:

Prylutskyi, O., **Yatsiuk, I.**, Yatsiuk, Y., 2022. Records of *Sarcoscypha austriaca* and *Urnula craterium* from the territory of Eastern Ukraine. Version 1.5. V. N. Karazin Kharkiv National University. Occurrence dataset. https://doi.org/10.15468/budlyh

Mikryukov, V, Savchenko, A, **Yatsiuk, I.,** 2021. Phylogenetic reconstruction workshop. https://mycology-microbiology-center.github.io/Phylo2021/

Savchenko, A., Ordynets, A., Prylutskyi, O., **Yatsiuk, I.**, Akulov, O., Usichenko, A., 2017. V.N. Karazin Kharkiv National University herbarium, Department of Mycology and Plant Resistance. Occurrence dataset. https://doi.org/10.15468/kuspj6

Teaching, management:

2023	11th International Congress on the Systematics and Ecology of Myxomycetes (ICSEM11), 28–31 August 2023, Tartu, Estonia – president, organizer.
2021	Phylogenetic reconstruction workshop, Tartu – organizer, teacher
2019–2022	BioData, biodiversity data management skills for students, Norway–Ukraine, mentor
2018	Ukrainian Rufford Small Grants Conference “From monitoring to implementation”. Kharkiv, Ukraine, 23–25 April 2018 – conference organizer.

Grants and scholarships:

2024	Mobility grant of Estonian Doctoral School grant for the participation in the International Mycological congress, oral talk
2024	BiCIKL infrastructure, a grant for free of charge publication in the dedicated topical collection in the Biodiversity Data Journal within the project “Linking FAIR biodiversity data through publications: The BiCIKL approach”
2022	University of Oslo, BioDATA grant for data mobilization including digitization, data quality assurance, data preparation, and publication of collection specimen and other species data from Ukraine to GBIF, project “Deciphering Cyrillic: the checklist from invisible sources”
2021	Archimedes DORA Plus short-term mobility grant for attending the XXV Nordic Mycological Congress in Scania, Sweden – the event was cancelled due to COVID19 pandemic and grant declined by me.
2020	Kristjan Jaak National Scholarship for short study visits, attending 10th International Congress on the Systematics and Ecology of Myxomycetes, Costa-Rica.
2016	The Rufford Foundation, small grant for the project “Conservation of rare fungus *Pleurotus calyptratus* in aspen stands of Ukrainian Forest-Steppe”.

ELULOOKIRJELDUS

Nimi: Iryna Yatsiuk
Sünniaeg: 10. juuni 1988
Kodakondsus: Ukraina
Aadress: Ökoloogia ja maateaduste instituut, Tartu Ülikool,
J. Liivi 2, 50409, Tartu, Eesti
Telefon: +372 5670 9111
Meiliaadress: yatsiuk@ut.ee

Keeleoskused: inglise (C1), ukraina (emakeel), vene (emakeel), eesti (B1)

Haridus:

2019–	Tartu Ülikool, doktoriõpe botaanika ja ökoloogia erialal
2018–	Botaanika Instituut, Ukraina Rahvuslik Teaduste Akadeemia (Kiiev), teaduste kandidaadi kraad bioloogias
2009–2010	V.N. Karazini nimeline Harkivi Rahvuslik Ülikool (Ukraina), magistrikraad bioloogias
2006–2009	V.N. Karazini nimeline Harkivi Rahvuslik Ülikool (Ukraina), bakalaureusekraad bioloogias

Töökogemus:

2023–	Tartu Ülikool, Ökoloogia ja maateaduste instituut, Botaanika osakond, nooremteadur
2015–2019	V.N. Karazini nimeline Harkivi Rahvuslik Ülikool, Mükoloogia ja taimekaitse osakond, nooremõppejõud
2012–2013	Rahvuslik looduspark 'Homilsha mets', teadur
2010–2015	V.N. Karazini nimeline Harkivi Rahvuslik Ülikool, Mükoloogia ja taimekaitse osakond, laborant

Teadusartiklid:

Tedersoo, L., Hosseyni Moghaddam, M.S., Mikryukov, V., Hakimzadeh, A., Bahram, M., Nilsson, R.H., **Yatsiuk**, **I**., Geisen, S., Schwelm, A., Piwosz, K., Prous, M., Sildever, S., Chmolowska, D., Rueckert, S., Skaloud, P., Laas, P., Tines, M., Jung, J.-H., Choi, J.H., Alkahtani, S., Anslan, S., 2024. EUKARYOME: the rRNA gene reference database for identification of all eukaryotes. *Database*, baae043. https://doi.org/10.1093/database/baae043

Yatsiuk, I., Leshchenko Yu., Viunnyk V., Leontyev, D., 2024. The comprehensive checklist of myxomycetes of Ukraine based on extended occurrence and reference datasets. *Biodiversity data journal*, 12: e120891 https://doi.org/10.3897/BDJ.12.e120891

Leontyev, D., **Yatsiuk**, I., 2024. Dataset of barcoded Reticulariaceae: ten years of DNA sequencing. *Biodiversity Data Journal* 12, e115630. https://doi.org/10.3897/BDJ.12.e115630

Yatsiuk, I., Leontyev, D., Lopez-Villalba, A., Schnittler, M., Koljalg, U., 2023. A new nivicolous species of *Lamproderma* (Myxomycetes) from lowland and mountainous regions of Europe. *Nova Hedwigia*, 116, 105–136. https://doi.org/10.1127/nova_hedwigia/2023/0807

Prylutskyi, O., **Yatsiuk, I.**, Savchenko, A., Kit, M., Solodiankin, O., Schigel, D., 2022. Strict substrate requirements alongside rapid substrate turnover may indicate an early colonization: A case study of *Pleurotus calyptratus* (Agaricales, Basidiomycota). *Fungal Ecology* 59, 101098. https://doi.org/10.1016/j.funeco.2021.101098

Pärtel, K., Suija, A., **Yatsiuk, I.**, 2021. The Estonian Mycological Collections of Heinrich August Dietrich (1820–1897). *Acta Baltica Historiae et Philosophiae Scientiarum* 9, 48–78. https://doi.org/10.11590/abhps.2021.2.03

Pärtel, K., Suija, A., **Yatsiuk, I.**, 2021. The mycological collection of G. C. Girgensohn from the middle of the 19th century. *Folia Cryptogamica Estonica* 58, 109–119. https://doi.org/10.12697/fce.2021.58.14

Yatsiuk, I., Leontyev, D., 2020. Two species of nivicolous myxomycetes that formed fruiting bodies during three spring seasons in the lowlands of the Eastern Ukraine. *Phytotaxa* 437, 147–155. https://doi.org/10.11646/phytotaxa.437.3.3

Yatsiuk, I., Adamonytė, G., Kastanje, V., 2020. A comprehensive checklist of Estonian myxomycetes. *Karstenia* 58, 239–247. https://doi.org/10.29203/ka.2020.497

Leontyev, D., **Yatsiuk, I.**, Kochergina, A., 2020. Inclusion of myxomycetes in the Red Data Book of Ukraine: feasibility, selection criteria and recommended species. *Ukrainian Botanical Journal* 77, 189–203. https://doi.org/10.15407/ukrbotj77.03.189

Kõljalg, U., Nilsson, H. R., Schigel, D., Tedersoo, L., Larsson, K.-H., May, T.W.; Taylor, A.F.S., Jeppesen, T.S., Frøslev, T.G., Lindahl, B.D., Põldmaa, K., Saar, I., Suija, A., Savchenko, A., **Yatsiuk, I.**, Adojaan, K., Ivanov, F., Piirmann, T., Pöhönen, R., Zirk, A., Abarenkov, K., 2020. The Taxon Hypothesis Paradigm – On the Unambiguous Detection and Communication of Taxa. *Microorganisms* 8, 1910. https://doi.org/10.3390/microorganisms8121910

Yatsiuk, I., Leontyev, D., Shlakhter, M., 2018. Myxomycetes of the National Nature Park Slobozhanskiy (Ukraine): biodiversity and noteworthy species. *Nordic Journal of Botany* 36, UNSP e01605. https://doi.org/10.1111/njb.01605

Prylutskyi, O., Akulov, O., Leontyev, D., Ordynets, A., **Yatsiuk, I.**, Usichenko, A., Savchenko, A., 2017. Fungi and fungus-like organisms of Homilsha forests national park, Ukraine. *Mycotaxon* 132, 1–56. https://doi.org/10.5248/132.705

Yatsiuk, I., Saar, I., Kalamees, K., Sulaymonov, S., Gafforov, Y., O'Donnell, K., 2016. Epitypification of *Morchella steppicola* (Morchellaceae, Pezizales), a morphologically, phylogenetically and biogeographically distinct member of the Esculenta Clade from central Eurasia. *Phytotaxa* 284, 31–40. https://doi.org/10.11646/phytotaxa.284.1.3

Morozova, I., 2014. New records of discomycetous fungi from Ukraine. *Turkish Journal of Botany* 38, 398–405. https://doi.org/10.3906/bot-1301-14.

Leontyev, D., Eliasson, U., Kochergina, A., **Morozova, I.**, 2009. New and rare myxomycetes of Ukraine. 1. East Forest-Steppe. *Karstenia* 49, 61–67. https://doi.org/10.29203/ka.2009.434

Konverentsiettekanded:

Yatsiuk, I. Leontyev, D. *Arcyria* and allied genera: taxonomic backbone, diversity and charac-ters evolution. 11th International Congress on the Systematics and Ecology of Myxomycetes (ICSEM11), 28–31 August 2023, Tartu, Estonia.

Yatsiuk, I. Barcoding in species delimitation and otu-picking for dark-spored vs. bright-spored myxomycetes. 11th International Congress on the Systematics and Ecology of Myxomycetes (ICSEM11), 28–31 August 2023, Tartu, Estonia.

Yatsiuk, I., Leshchenko, Yu. Myxomycetes of Ukraine. The checklist from invisible sources. GBIF node meeting, 16 May 2023, online.

Yatsiuk, I., Shyriaeva, D., Prylutskyi, O. GBIF and open biodiversity data in Ukraine. BioDATA Final Conference, 13 November 2022, Oslo, Norway.

Yatsiuk, I., Prikhodko, I., Leontyev, D. Barcoding in bright-spored and dark-spored myxomycetes: no universal threshold. Poster. International Conference on DNA Barcoding and Biodiversity (ICDBB). 25–27 May, 2022, Sofia, Bulgaria.

Yatsiuk, I. Do "lowland nivicolous" myxomycetes fruitify more regularly than we think? 10th International Congress on the Systematics and Ecology of Myxomycetes (ICSEM10). 25–28 February 2020, Turrialba, Costa-Rica.

Yatsiuk, I. Molecular species definition in myxomycetes – where are we now? PhD Student Conference of the Department of Botany, 2020, UT.

Muud publikatsioonid:

Prylutskyi, O., **Yatsiuk, I.**, Yatsiuk, Y., 2022. Records of *Sarcoscypha austriaca* and *Urnula craterium* from the territory of Eastern Ukraine. Version 1.5. V. N. Karazin Kharkiv National University. Occurrence dataset. https://doi.org/10.15468/budlyh

Mikryukov, V, Savchenko, A, **Yatsiuk, I.,** 2021. Phylogenetic reconstruction workshop. https://mycology-microbiology-center.github.io/Phylo2021/

Savchenko, A., Ordynets, A., Prylutskyi, O., **Yatsiuk, I.**, Akulov, O., Usichenko, A., 2017. V.N. Karazin Kharkiv National University herbarium, Department of Mycology and Plant Resistance. Occurrence dataset. https://doi.org/10.15468/kuspj6

Õpetamine, juhtimine:

2023	11th International Congress on the Systematics and Ecology of Myxomycetes (ICSEM11), 28–31 August 2023, Tartu, Estonia – president, korraldaja.
2021	Phylogenetic reconstruction workshop, Tartu – korraldaja, mentor
2019–2022	BioData projekt– õpilaste bioloogilise mitmekesisuse andmehaldusoskused, mentor
2018	Ukraina Ruffordi sihtasutuse konverents “From monitoring to implementation”. Harkiv, Ukraina, 23–25 April 2018 – konverentsi korraldaja.

Uurimistoetused ja stipendiumid:

2024	BiCIKL infrastruktuur, Toetus artikli avaldamiseks ajakirjas projekti “Linking FAIR biodiversity data through publications: the BiCIKL approach” raames
2022	Oslo Ülikool, BioDATA toetus andmete koondamiseks, projekt „Kirillitsa dešifreerimine: nähtamatute allikate kontrollnimekiri“
2021	Archimedes DORA Plus lühiajalise liikuvustoetus XXV Põhjamaade mükoloogiakongressil Scanias, Rootsis osalemiseks. Üritus tühistati COVID19 pandeemia tõttu ning toetuse andmisest loobuti.
2020	Kristjan Jaagu nimelise õpirände stipendium, 10. rahvusvahelisel limakute süstemaatika ja ökoloogia konverentsil osalemine, toimumiskoht: Costa Rica
2016	Väike toetus Rufford sihtasutuselt projekti “Haruldase seene *Pleurotus calyptratus* kaitse Ukraina metsastepi haavametsades”

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.
400. **Ants Tull**. Domesticated and wild mammals as reservoirs for zoonotic helminth parasites in Estonia. Tartu, 2022, 152 p.

401. **Saleh Rahimlouye Barabi**. Investigation of diazotrophic bacteria association with plants. Tartu, 2022, 137 p.
402. **Farzad Aslani**. Towards revealing the biogeography of belowground diversity. Tartu, 2022, 124 p.
403. **Nele Taba**. Diet, blood metabolites, and health. Tartu, 2022, 163 p.
404. **Katri Pärna**. Improving the personalized prediction of complex traits and diseases: application to type 2 diabetes. Tartu, 2022, 190 p.
405. **Silva Lilleorg**. Bacterial ribosome heterogeneity on the example of bL31 paralogs in *Escherichia coli*. Tartu, 2022, 189 p.
406. **Oliver Aasmets**. The importance of microbiome in human health. Tartu, 2022, 123 p.
407. **Henel Jürgens**. Exploring post-translational modifications of histones in RNA polymerase II-dependent transcription. Tartu, 2022, 147 p.
408. **Mari Tagel**. Finding novel factors affecting the mutation frequency: a case study of tRNA modification enzymes TruA and RluA. Tartu, 2022, 176 p.
409. **Marili Sell**. The impact of environmental change on ecophysiology of hemiboreal tree species – acclimation mechanisms in belowground. Tartu, 2022, 163 p.
410. **Kaarin Hein**. The hissing behaviour of Great Tit (*Parus major*) females reflects behavioural phenotype and breeding success in a wild population. Tartu, 2022, 96 p.
411. **Maret Gerz**. The distribution and role of mycorrhizal symbiosis in plant communities. Tartu, 2022, 206 p.
412. **Kristiina Nõomaa**. Role of invasive species in brackish benthic community structure and biomass changes. Tartu, 2023, 151 p.
413. **Anton Savchenko**. Taxonomic studies in Dacrymycetes: *Cerinomyces* and allied taxa. Tartu, 2023, 181 p.
414. **Ahto Agan**. Interactions between invasive pathogens and resident mycobiome in the foliage of trees. Tartu, 2023, 155 p.
415. **Diego Pires Ferraz Trindade**. Dark diversity dynamics linked to global change: taxonomic and functional perspective. Tartu, 2023, 134 p.
416. **Madli Jõks**. Biodiversity drivers in oceanic archipelagos and habitat fragments, explored by agent-based simulation models. Tartu, 2023, 116 p.
417. **Ciara Baines**. Adaptation to oncogenic pollution and natural cancer defences in the aquatic environment. Tartu, 2023, 164 p.
418. **Rain Inno**. Placental transcriptome and miRNome in normal and complicated pregnancies. Tartu, 2023, 145 p.
419. **Daniyal Gohar**. Diversity, genomics, and potential functions of fungus-inhabiting bacteria. Tartu, 2023, 138 p.
420. **Sirli Rosendahl**. Fitness effects of chromosomal toxin-antitoxin systems in *Pseudomonas putida*. Tartu, 2023, 154 p.
421. **Mathilde Frédérique E. André**. New Guinea, a hotspot for Human evolution: settlement history and adaptation in northern Sahul. Tartu, 2023, 202 p.

422. **Vlad-Julian Piljukov**. Biochemical characterization of Irc3 helicase. Tartu, 2023, 137 p.
423. **Gerli Albert**. Carbon use strategies of macrophyte communities in the northeastern Baltic Sea: implications for a high CO_2 environment. Tartu, 2023, 128 p.
424. **Mariann Koel**. The molecular interactions between trophoblast and endometrial cells in embryo implantation. Tartu, 2023, 171 p.
425. **Robin Gielen**. Diversity and ecological role of pathogenic fungi in insect populations. Tartu, 2023, 139 p.
426. **Kaspar Reier**. Quantity, stability and disparity of ribosomal components in *Escherichia coli* stationary phase. Tartu, 2023, 151 p.
427. **Linda Rusalepp**. The impact of environmental drivers and competition on phenolic metabolite profiles in hybrid aspen and silver birch. Tartu, 2023, 153 p.
428. **Eliisa Pass**. The effect of managed forest-wetland landscapes on forest grouse and nest predation. Tartu, 2023, 115 p.
429. **Sanni Färkkilä**. Methods for studying plant-fungal interactions – reflecting on the old, the new and the upcoming. Tartu, 2024, 147 p.
430. **Maarja Jõeloo**. Advances in microarray-based copy number variation discovery and phenotypic associations. Tartu, 2024, 209 p.
431. **Natàlia Pujol Gualdo**. Decoding genetic associations of female reproductive health traits. Tartu, 2024, 205 p.
432. **Sirelin Sillamaa**. The role of helicases Hmi1 and Irc3 in yeast mitochondrial DNA maintenance. Tartu, 2024, 189 p.
433. **Iris Reinula**. Genetic variation of grassland plants in changing landscapes. Tartu, 2024, 201 p.
434. **Vi Ngan Tran**. The cellular dynamics and epithelial morphogenesis in *Drosophila* wing development. Tartu, 2024, 158 p.
435. **Slendy Julieth Rodríguez Alarcón**. Intraspecific trait diversity in plants: characterizing effects of trait variation on community assembly and ecosystem functioning. Tartu, 2024, 129 p.
436. **Arun Kumar Devarajan**. Microbes and climate change: insights from plant-microbe interactions in rice phyllosphere and soil microbiomes in subarctic grasslands. Tartu, 2024, 224 p.
437. **Leonard Owuraku Opare**. Rearing density effects on a commercially important insect species. Tartu, 2024, 145 p.
438. **Siqiao Liu**. The effect of anthropogenic disturbance on soil fungal communities. Tartu, 2024, 172 p.
439. **Kertu Liis Krigul**. The gut microbiome at the interface of human health and disease. Tartu, 2024, 158 p.
440. **Danat Yermakovich**. The evolutionary history of complex traits: implications of archaic admixture. Tartu, 2024, 153 p.
441. **Yiming Meng**. Plant mycorrhizal type and status in the global flora. Tartu, 2024, 200 p.