DISSERTATIONES
BIOLOGICAE
UNIVERSITATIS
TARTUENSIS
458

VINEESH NEDUMPALLY

Assembling the phylogenetic tree of northern European macroheteroceran moths

DISSERTATIONES BIOLOGICAE UNIVERSITATIS TARTUENSIS
458

DISSERTATIONES BIOLOGICAE UNIVERSITATIS TARTUENSIS
458

VINEESH NEDUMPALLY

Assembling the phylogenetic tree of northern European macroheteroceran moths

UNIVERSITY OF TARTU
Press
1632

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

Dissertation was accepted for the commencement of the degree of *Doctor philosophiae* in zoology and ecology at the University of Tartu on November 10, 2025 by the Scientific Council of the Institute of Ecology and Earth Sciences, University of Tartu.

Supervisors: Dr. Erki Õunap, University of Tartu, Estonia

Prof. Toomas Tammaru, University of Tartu, Estonia

Opponent: Dr. Kyung Min Lee, University of Helsinki, Finland

Commencement: Oecologicum (J. Liivi 2, Tartu), room 127, on the 30th of January 2026 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 978-9908-57-083-9 (print)
ISSN 2806-2140 (pdf)
ISBN 978-9908-57-084-6 (pdf)

University of Tartu Press
www.tyk.ee

CONTENTS

LIST OF PUBLICATIONS

This dissertation is the summary of the following articles, which are referred to in the text by Roman numerals. All published articles are reproduced with the permission of the publishers.

I. **Nedumpally, V**., Õunap, E., & Tammaru, T. (2024). An insight into the molecular phylogeny of Drepanidae (Lepidoptera) with an emphasis on the European fauna. *European Journal of Entomology*, 121, 385–391. https://www.eje.cz/pdfs/eje/2024/01/41.pdf

II. Õunap, E., **Nedumpally, V**., Yapar, E., Lemmon, A. R., & Tammaru, T. (2025). Molecular phylogeny of north European Geometridae (Lepidoptera: Geometroidea). *Systematic Entomology*, 50, 32–67. https://doi.org/10.1111/syen.12638

III. **Nedumpally, V**., Zilli, A., Yapar, E., Tammaru, T., Lemmon, A. R., & Õunap, E. (2025). Elaborating the phylogeny of Noctuidae by focusing on relationships between north European taxa. *Systematic Entomology*, published online. https://doi.org/10.1111/syen.70010

IV. **Nedumpally, V**., Õunap, E., & Tammaru, T. Questioning the early Miocene origin of grass-feeding noctuids: evidence from a phylogenomic dataset. (Manuscript).

The author's contribution to each of the the articles (* denotes a moderate, ** a high contribution, *** a leading role).

	I	II	III	IV
Study design	**	*	**	***
Laboratory work	***	**	***	***
Analysis and interpretation	***	**	**	***
Manuscript writing	***	**	**	***

1. INTRODUCTION

Insects are the most species-rich animal class on the Earth and comprise over half of all described species (May, 1986). They play a vital role in e. g. nutrient cycling, pollination, seed dispersal, population regulation of other organisms, and serve as a major food source for many taxa (Scudder, 2017). Comprehending their evolutionary relationships is thus key to understanding the evolution of life. In recent decades, our understanding of the history and diversification of insects has grown substantially (Kristensen, 1981; Misof et al., 2014; Hailay Gebremariam, 2024). Technological improvements in DNA sequencing and computational analysis have increasingly clarified phylogenetic relationships between insect clades (Trautwein et al., 2012; Misof et al., 2014), notably resolving the relationships within Holometabola, clarifying the placement of Strepsiptera relative to Coleoptera, and refining divergence estimates for Hymenoptera, among other breakthroughs (Trautwein et al., 2012; Zhang et al., 2025).

Among insects, Lepidoptera represent one of the most successful lineages, occurring on all continents except Antarctica and occupying a wide variety of habitats (Grimaldi & Engel, 2005; Perveen & Khan, 2018). With nearly 160,000 described species worldwide (Kristensen, 2007; van Nieukerken et al., 2011; Zhang, 2013), Lepidoptera represent one of the most species-rich insect orders and have been the subject of particularly extensive phylogenetic investigation. Because Lepidoptera include several model organisms (e.g. *Bombyx mori* (Linnaeus, 1758), *Manduca sexta* (Linnaeus, 1763), and *Plutella xylostella* (Linnaeus, 1758)), serious agricultural pests, and many species most familiar to the wider audience, studies of their phylogeny and evolution are of both scientific and public importance (Timmermans et al., 2014). Over the years, numerous landmark contributions have progressively shaped our understanding of lepidopteran systematics. For instance, Packard, (1895) divided Lepidoptera into suborders Laciniata and Glossata based on the morphology of their mouthparts, Börner (1925, 1939) established a division of Lepidoptera into Monotrysia and Ditrysia according to the structure of the female genitalia, and Minet (1986) introduced the concept of Obtectomera for a large subsection of ditrysians based on pupal characters. The most recent comprehensive treatment of the order in the Handbook of Zoology (Kristensen, ed. 1998, 2003) recognized 124 lepidopteran families, 52 of which were further subdivided into subfamilies. Significant advances on the higher classification of Lepidoptera have continued in the 21th century, with van Nieukerken (2011) reporting 134 families, and several discoveries resulting in descriptions of new families have been done after that (e.g. Kristensen et al., 2015; Rajaei et al., 2015; Kaila et al., 2020). The “LepTree project” and the “Ditrysia project” provided considerable new resolution to the higher phylogeny of Ditrysia (Timmermans et al., 2014 and references therein). Today, the monophyly of Lepidoptera is firmly established, and the position of the order within the insect phylogenetic hierarchy as sister to Trichoptera is strongly supported by comprehensive molecular datasets (e.g. Kristensen et al., 2007; Misof et al., 2014).

In recent years, the elucidation of Lepidoptera phylogeny has made remarkable progress, driven by advances in phylogenetic methods, sequencing technologies, and bioinformatic tools. The following sections offer a brief insight into these developments.

1.1. Historical roots: Linnaean classification

The foundations of modern biosystematics were laid down by works of Carl Linnaeus, with the 10th edition of the Systema Naturae (Linnaeus, 1758) being universally recognized as the starting point of current zoological nomenclature. For over two centuries, systematists primarily relied on morphological characters in delimiting species and higher groups. Remarkably, the vast majority of currently recognized genera and higher taxonomic units were introduced during this morphology-based era. Along with a systematic treatment of all organisms known at his time, Linnaeus (1758) also provided the first family level classification of Lepidoptera, followed by a major contribution from Denis & Schiffermüller (1775), who published a faunistic list of the Lepidoptera of Vienna based on Linnaeus' classification. Subsequently, Hübner (1796–1838) described and illustrated numerous species of European moths and butterflies, introducing many generic names that remain still in use today. Later Herrich-Schäffer (1843–1856) provided numerous original descriptions of European Lepidoptera and carried out extensive studies on venation and other morphological features. Further landmark publications include Pierce's detailed studies on the genital structures of Noctuidae (1909) and Geometridae (1914) of British Islands, Janse's (1932, 1933–1935) richly illustrated overview on South African Geometridae, and Beck's (2000) insight to the systematics of Noctuidae based on larval characters. Morphology-based studies have been carried on in the 21st century as well, providing well-justified hypotheses on the classification of particular groups of Lepidopterans (e.g. Sihvonen & Kaila 2004, Fibiger & Lafontaine 2005).

1.2. From taxonomy to phylogenetics

A major breakthrough in biological thinking came with the work of Charles Darwin and his followers (Darwin, 1859; Haeckel, 1866; Weismann, 1893; Haldane, 1990; Hennig, 1950, 1966, 1982; Dobzhansky, 1951). Darwin (1859) introduced a unifying evolutionary framework for understanding biological diversity, demonstrating that all organisms share common ancestry and evolve through natural selection. As a consequence, in many taxonomic publications of late 19th and early 20th century, great emphasis was put on classifying known species into "natural" groups, which adequately reflect their relatedness (e.g. Prout 1912–1916). Hennig (1950, 1966, 1982), laid the foundation for modern approaches to classifying life based on their evolutionary history. He is widely regarded as the father of phylogenetic systematics (or cladistics) and brought a major shift to the

field by developing a method for grouping species and lineages that is both scientifically testable and reproducible. Hennig (1950, 1953) introduced the key idea of distinguishing between ancestral (plesiomorphic) and shared derived (synapomorphic) traits. He showed that synapomorphies could be used to identify sister groups and introduced the idea that only groups including a common ancestor and all its descendants (monophyletic groups) should be recognized as taxa and named as such (Schmitt, 2013), and developed methods for phylogenetic reconstruction.

1.3. Morphology based phylogenetics

The morphological structures of living organisms are highly diverse, and inferring phylogenetic relationships based solely on visual examination is often challenging. Consequently, numerous analytical approaches have been developed over time to resolve these relationships between organisms, including Lepidopterans. An early example of such practice can be seen in a work by Sterneck (1941), whose preliminary application of character coding grouped Sterrhinae (Lepidoptera: Geometridae) into smaller units that are almost fully compatible of modern concept of tribes in that subfamily. During the 1970s and 1980s, lepidopteran phylogenetics emerged through detailed anatomical studies combined with the early adoption of Hennigian phylogenetics (Kristensen, 1976; Kristensen, 1984;). For instance, Kristensen (1976) re-evaluated butterfly family-level relationships using the principles of phylogenetic (cladistic) systematics, providing important insights into their higher-level evolutionary relationships. Kristensen (1984) focused on understanding the evolutionary relationships and characteristics of the early-diverging moth and butterfly lineages, later updated by Kristensen & Skalski (1998), and they identified several traits unique to Lepidoptera. Although morphological phylogenetics offers advantages – such as its usefulness in studying museum specimens and fossil taxa, it also has drawbacks, including a limited number of informative characters, the prevalence of homoplasy, subjectivity in character definition and coding, and many more (see Sanderson & Donoghue, 1989; Wiens, 2001; Scotland et al., 2003). For over two centuries, morphology nevertheless served as the primary data source for reconstructing relationships across all taxonomic levels, with undeniable success.

1.4. Molecular phylogenetics

Since the 1960s, scientists have increasingly relied on various forms of molecular data–such as allozymes, DNA–DNA hybridization, and amino acid or nucleotide sequences for phylogenetic inference (Lee & Palci, 2015). These data allow researchers to compare homologous molecules across organisms, enabling them to measure genetic similarity and infer evolutionary relationships, which can be visualized as a phylogenetic tree. Molecular phylogenetics came into the spotlight

and gained prominence with the landmark study by Woese and Fox (1977), who used ribosomal RNA sequences to propose that the overall phylogenetic structure of the living world comprises three domains. Ever since then, molecular data have become central to evolutionary biology. Molecular phylogenetic studies on Lepidoptera started in the early 1990s and used the highly abundant sequences of the mitochondrial genome and nuclear ribosomal DNA (Sperling, 1993; Brower, 1994; Sperling & Hickey 1994). However, widespread incongruence often arises between phylogenies inferred from different single-gene datasets, and it is now widely accepted that building a phylogeny using only one gene and a single reconstruction method is generally unreliable (Rokas et al., 2003; Wahlberg & Wheat 2008). Therefore, increasing the length of gene fragments and number of genes (often termed as markers or loci) included in phylogenetic analyses is essential for producing more robust and stable evolutionary hypotheses.

1.4.1. Multigene phylogenies using Sanger sequencing

Although Friedlander et al. (1992) identified 14 single-copy nuclear protein-coding genes potentially useful for phylogeny inference in early 1990s, multigene phylogenetic analysis gained significant momentum several years later, in the early 2000s. This progress was driven by the increasing availability of nuclear protein-coding genes that greatly enhanced the resolution of phylogenetic relationships, for example, in arthropods (e.g. Giribet et al., 2001; Kopp & True, 2002; Peña et al., 2006). Later, Savard et al. (2006) conducted a phylogenomic analysis of four holometabolous insect orders, utilizing 185 nuclear genes made available through emerging genome sequencing projects. In the context of Lepidoptera, Wahlberg and Wheat (2008) proposed a set of eleven genetic markers for phylogenetic research, including six newly designed ones. These so-called "legacy genes" have since become a widely adopted and reliable tools for lepidopteran phylogenetics. Over the following years, the number of markers used in Lepidoptera studies expanded to 19–26 in more recent research (Cho et al., 2011; Zwick et al., 2011; Regier et al., 2013), and this increase in the amount of sequence data has contributed to improve resolution and support for higher-level relationships (Cho et al., 2011). Despite these advances, multigene phylogenetic analyses revealed that while relationships among non-ditrysian superfamilies and early-diverging lineages within Ditrysia were well supported and aligned with morphology-based hypotheses, deeper relationships within Apoditrysia, a large and highly diverse clade, remained weakly supported, underscoring the challenges of resolving rapid radiations in this group (Regier et al., 2013). Moreover, generating multilocus datasets through traditional PCR-based approaches remained labor-intensive, requiring extensive amplification and sequencing efforts.

1.4.2. Phylogenomics using next-generation sequencing

The emergence of next-generation sequencing (NGS) platforms has revolutionized phylogenetic studies by enabling the rapid and cost-effective generation of large-scale molecular data, facilitating the analysis of hundreds to thousands of loci across diverse taxa. Recent studies show that resolving species relationships despite gene tree variation often requires sequencing of hundreds of loci per sample, often exceeding million base pairs to infer both deep and shallow phylogenetic nodes (Lemmon et al., 2012; Espeland et al., 2018; Lee et al., 2018; Kawahara et al., 2019). Various sequencing methods, such as whole-genome sequencing, target enrichment, and transcriptome sequencing, have been introduced and have subsequently helped to meet this demand, thereby significantly advancing phylogenomics (Mamanova et al., 2010; Ekblom & Wolf, 2014; Kawahara & Breinholt 2014; Breinholt et al., 2018; Zhang et al., 2018; Kawahara et al., 2019). Anchored Hybrid Enrichment (AHE; Lemmon et al., 2012) is a target enrichment sequencing method that has become widely used in phylogenetic studies. It has proven effective for non-model taxa, ethanol-preserved tissues, stored DNA extractions, and, in some cases, also older museum specimens (Lemmon et al., 2012; Guschanski et al., 2013; Blaimer et al., 2016). AHE has been successfully applied across various insect orders (see Dietrich et al., 2017; Breinholt et al., 2018; Espeland et al., 2018; Kawahara et al., 2019; Buenaventura et al., 2020; Homziak et al., 2023; Cruaud et al., 2024; St Laurent et al., 2024, 2025)

Misof et al. (2014) conducted a landmark phylogenomic analysis of insects, using 1,478 single-copy nuclear protein-coding genes across 144 taxa (all extant hexapod orders along with few other arthropods used as outgroup) to resolve long-standing controversies in higher-level insect evolutionary relationships and providing a robust evolutionary framework for future comparative studies. Kawahara and Breinholt (2014) presented the first robust transcriptome-based phylogeny of Lepidoptera, which strongly challenged the traditional placement of butterflies and established a new evolutionary framework for genomic, developmental, and ecological studies of this diverse insect order. Later, Kawahara et al. (2019) provided most comprehensive phylogenomic insight to date, and traced the origin of major lepidopteran traits – from the evolution of the proboscis to the rise of day-flying butterflies and sonar-detecting moths, redefining our understanding of their diversification. Although lepidopteran phylogenomics has made significant advanced in recent years (e.g. Mitter et al., 2017 and reference therein: Zahiri et al., 2019: Kawahara et al., 2023), majority of families, including Drepanidae, Geometridae, and Noctuidae have received relatively little attention, particularly with respect to relationships at the subfamily and tribal levels.

1.5. Advancements in phylogeny reconstruction

1.5.1. Evolution of phylogenetic inference methods

In addition to increasing availability of genome-scale datasets which has facilitated the growth of phylogenetic research, further advances have become possible by the refinement of methods for tree construction. In phylogenetic inference, optimization principles are applied to identify the most likely tree topology. Over time, numerous approaches have been developed for reconstructing phylogenetic trees; however, the most widely used ones include Maximum Parsimony, Neighbor-Joining, Maximum Likelihood, and Bayesian inference.

Maximum parsimony (MP) seeks the phylogenetic tree that explains the observed data with the minimum number of character-state changes. However, MP may yield misleading results when evolutionary processes deviate from the principle of parsimony. Specifically, MP relies on the assumption that substitution rates are uniform across sites, nucleotide or amino acid types, and evolutionary lineages – assumptions that are often violated in real datasets (Yang, 1996). Another problem of using MP is that the analysis often results in numerous different, but equally good trees. In the Neighbor-Joining (NJ) method, phylogenetic trees are reconstructed from evolutionary distance data (Saitou & Nei, 1987), and this algorithm is widely appreciated for its ability to reconstruct phylogenetic trees with reasonable accuracy while relying on relatively few assumptions. It also offers rapid computation by employing a stepwise clustering approach instead of attempting an exhaustive search for the optimal topology. However, with larger datasets, the exponential growth of possible topologies reduces the probability of identifying the most accurate tree (Zou et al., 2024).

Maximum Likelihood (ML) inference is a widely used and statistically robust approach in phylogenetic analysis that identifies the tree topology and branch lengths most likely to explain the observed sequence data under a given model of molecular evolution (Patané et al., 2024). The topology with the highest likelihood value is selected as the optimal evolutionary tree. ML methods are statistically consistent and less prone to systematic errors, such as long-branch attraction, compared to approaches discussed above. The main limitations of ML are its high computational demands and dependence on the chosen evolutionary model (Zou et al., 2024).

Bayesian inference (BI) is a probabilistic approach to phylogenetic analysis that applies Bayes' theorem to estimate the posterior probability distribution of trees, integrating both the observed sequence data and prior assumptions about evolutionary processes (Huelsenbeck & Ronquist, 2001). Bayesian inference (BI) can incorporate complex models of sequence evolution, naturally handle parameter uncertainty, and simultaneously estimate topology, branch lengths, and model parameters. However, it is highly computationally demanding, its results may be sensitive to the choice of priors, and assessing the convergence of Markov chain Monte Carlo (MCMC) sampling is often challenging, with poor convergence potentially leading to misleading inferences (Barido-Sottani et al., 2024; Tay et al., 2024).

1.5.2. Open-source databases and their use for phylogenetic works

With the rapid development of sequencing technologies, vast numbers of gene sequences and complete genomes are being deposited into GenBank at an accelerating pace. This provides researchers unique opportunity to expand their datasets without the need for extensive sequencing. A cost-effective approach to acquire sequence data is to download, combine, filter, and analyze these datasets to construct a robust phylogenetic tree (Kjer et al., 2016). This approach has become widely used in multilocus phylogenetics, where individual genes are retrieved from public repositories and integrated into original datasets (e.g., Keegan et al., 2019, 2021). For whole-genome data, target loci can be extracted through sequence similarity searches using specialized bioinformatic tools (e.g., Zhang et al., 2019; He et al., 2024). The retrieved sequences can then be combined with newly generated data from one's own sequencing efforts and processed to construct a phylogenomic tree (Fonseca & Lohmann, 2018; He et al., 2024). However, the resulting phylogenies may still be limited by the quality and correct annotation of sequences in GenBank data (Kjer et al., 2016).

1.5.3. Backbone phylogenies

Modern phylogenetic software such as RAxML (Stamatakis et al., 2014) and IQ-TREE (Nguyen et al., 2015) support backbone constraint specifications, allowing to incorporate a well-established phylogeny from robust prior studies as a fixed "backbone" for further analyses. Such constraint trees are particularly useful for placing taxa of interest for which only short DNA sequences are available (Percy et al., 2018). In this approach, the constraint tree serves as a fixed higher-level topology during tree reconstruction from multilocus or genomic datasets. The software then restricts the search to topologies that preserve these predefined relationships, while still freely estimating the branching patterns within each constrained group. Using a backbone tree can significantly speed up phylogenetic analyses, as constrained topologies reduce the search space by limiting the number of alternative arrangements the software must evaluate. A backbone tree, derived from robust phylogenomic studies, can serve as a fixed higher-level framework for divergence time estimation (Espeland et al., 2018; Kawahara et al., 2019). This approach allows for more accurate and reliable estimates of evolutionary timelines, as the backbone phylogeny provides a well-supported framework onto which fossil data can be mapped, improving the precision of divergence time analyses (see Kawahara et al., 2019, Molleman et al., 2025).

1.6. Aim of the Thesis

The primary aim of this study was to infer the phylogenetic relationships among selected macroheteroceran moth families from northern Europe. While large-scale molecular analyses have significantly improved our understanding of lepidopteran classification at broader taxonomic levels (Misof et al., 2014; Kawahara et al., 2019), finer-scale phylogenetic relationships remain largely unresolved. Europe, and particularly Northern Europe, is exceptionally well suited for phylogenetic and comparative research due to its extensive and long-standing natural history data on moth ecology and life history. However, the lack of comprehensive molecular phylogenies continues to constrain such research. Among macroheteroceran families, for example, Drepanidae remained largely unexamined, whereas Geometridae were relatively well represented, with most Northern European genera (127 out of 153) included in recent molecular studies. In contrast, Noctuidae exhibited more limited phylogenetic coverage, with substantial gaps persisting within the subfamily Noctuinae (Davis et al., 2022). This gap provided the key motivation for the present work, in which we aimed to address it by constructing a robust phylogenetic tree for three families, Drepanidae, Geometridae and Noctuidae based on north European fauna. To illustrate the usability of recovered phylogenies, we used the one inferred for Noctuidae in a follow-up analysis focusing on timing of the major diversification events in the tribe Apameini.

To achieve the goals listed below (**I, II, III & IV**), we employed multiple strategies to acquire sequence data. These included Sanger sequencing, where individual genes were amplified and sequenced separately (**I**, **II**), next-generation sequencing using the Anchored Hybrid Enrichment (AHE) method (**II, III, IV**), which has proven effective for resolving phylogenetic relationships in diverse insect groups, and data mining from public resources (National Center for Biotechnology Information (NCBI), Barcode of Life Data System (BOLD)) to further enhance species and sequence coverage (**I, II, III, IV**). In addition to original material, we obtained DNA samples for critical species from Canadian Centre for DNA Barcoding (CCDB) and sequenced the "legacy" genes from these isolates (**I, II**).

1.6.1. Revealing the phylogenetic relationships of European Drepanidae (I)

The family Drepanidae comprises approximately 650 species worldwide (Minet & Scoble, 1999; van Nieukerken et al., 2011) and is divided into four subfamilies: Cyclidiinae, Drepaninae, Oretinae and Thyatirinae (Wu et al., 2010; Song et al., 2012; Jiang et al., 2016). However, beyond that, very little was known about the phylogeny of Drepanidae (Davis et al., 2022), even for the well-known and uncontroversial European drepanid fauna. To address this, we analyzed 21 of the 22 European species across all 14 genera using Sanger sequencing of 11 protein-coding genes. In addition to originally collected material, DNA samples obtained

from the CCDB, complemented with molecular data mined from public repositories were used to provide the results in a broader evolutionary context. The phylogenetic tree generated enhances our understanding of Drepanidae diversification and provides a foundation for future taxonomic and evolutionary studies.

1.6.2. Inferring the evolutionary relationships of northern European Geometridae (II)

The family Geometridae is the second largest family of Lepidoptera, comprising nearly 24,000 described species (Rajaei et al., 2022). The systematics of the family Geometridae has advanced significantly in recent decades, particularly due to making use of the progress in DNA sequencing technologies (Ban et al., 2018; Brehm et al., 2019; Murillo-Ramos et al., 2019 & Õunap et al., 2016, 2020). However, phylogenetic relationships at lower systematic levels of geometrids are still rather poorly known, as many genera have not been included in molecular phylogenetic studies, and their placement is considered uncertain. Additionally, numerous previous phylogenetic studies on geometrid moths have relied on the same set of sequences available from the NCBI GenBank, supplemented by varying amounts of newly generated data in each study. Until recently, no phylogenomic studies with large datasets had been conducted on Geometridae, except for the pioneering work of Murillo-Ramos et al. (2023). The present study first aimed to construct a phylogenomic tree for more than hundred species of Geometridae based on the AHE sequencing method, which subsequently served as a backbone tree for a follow-up larger-scale analysis relying on Sanger sequencing. Thereafter, molecular data for the "legacy genes" were generated for more than 130 species of Geometridae using Sanger sequencing, to ensure that there was enough data to place all the 376 north European geometrids into a comprehensive phylogenetic framework. Additionally, publicly available sequences of "legacy genes" were retrieved from GenBank, either downloaded directly as individual genes or extracted from whole genomes using bioinformatic tools. As a result, this study provided a high-quality phylogenetic tree including all species of Geometridae of the north European fauna.

1.6.3. Elaborating the phylogeny of north European Noctuidae (III)

Noctuidae are one of the most diverse families of Lepidoptera with more than 12,000 described species (Keegan et al., 2021). Although there are phylogenetic studies using a limited number of molecular markers which have helped in resolving evolutionary relationships within Noctuidae, there are many groups that have still received very little attention. The primary aim of the study was to infer the phylogenetic relationships within the family Noctuidae occurring in northern Europe, as these moths had got little attention in earlier phylogenetic studies (Davis et al., 2022). The AHE sequencing method was employed to sequence multiple nuclear protein coding loci for each species examined. Additionally,

whole genome assemblies of noctuids not present in our original material were downloaded from NCBI GenBank, and AHE loci were retrieved from these datasets using bioinformatic tools developed in article **II**. This comprehensive molecular dataset allowed to provide higher resolution of evolutionary relationships within several groups of Noctuidae, and helped to evaluate the taxonomic composition of the family in the phylogenetic context, as more than 130 genera were represented by their type species.

1.6.4. Time-calibrated phylogeny of Apameini with evolutionary implications (IV)

A major foundation to this study was laid by article **III**, where an unprecedentedly detailed phylogeny of north European noctuids was recovered. The tree inferred in this article allowed us to address conflicting estimations regarding the timing of the diversification events within the tribe Apameini. Recent studies have indicated that Miocene grassland expansion played a significant role in the radiation of grass-feeding herbivore lineages. The family Noctuidae, which includes numerous grass-feeding clades, provides an ideal target taxon for testing these hypotheses. The tribe Apameini, encompassing more than 850 species, almost exclusively comprises grass feeders with only few exceptions. A pioneering study using limited number of genetic markers suggested that the tribe Apameini emerged at least 29 million years ago, potentially coinciding with the expansion of grasslands during the late Oligocene or early Miocene (Toussaint et al. 2012). However, the time of emergence and diversification pattern of Apameini reported in a subsequent study appeared to be contradictory, around 22 million years ago in Kergoat et al. (2018), prompting our study to clarify the discrepancy. This study aimed to assess the age of Apameini and potential changes in diversification rate within this tribe utilizing the recently inferred phylogenetic tree of Noctuidae (**III**).

2. MATERIALS AND METHODS

2.1. Sample collection, species identification and DNA extraction

The study is based on moth specimens collected mainly from Estonia, but in cases where material from this country was not available, collection specimens originating from other regions were occasionally used. The moths were identified based on their external morphology (relying on expertise of some of the authors of respective papers); when necessary, genitalia dissection and DNA barcoding were performed for a reliable identification. Moths were stored as dry specimens at room temperature or as frozen samples at –20 °C until DNA extraction. Six drepanids, 375 geometrids, 243 noctuids and 27 species belonging to other (outgroup) families of Lepidoptera were included, with the age of the specimens varying between 2 months to 31 years. The genomic DNA was isolated (from the legs or abdomen of the moths) using the DNEasy Blood and Tissue kit (Qiagen N.V., Venlo, Netherlands) following the guidelines provided by the manufacturer. DNA concentration was determined by using the Qubit ™ 1X dsDNA HS Assay Kit on Qubit ™ 4 fluorometer (ThermoFisher Scientific).

2.2. Sequencing by the Sanger method

The eleven "legacy" genes were amplified using the Sanger sequencing method. These markers have frequently been used in phylogenetic and evolutionary studies of different families of Lepidoptera (Chazot et al., 2021; Murillo-Ramos et al., 2019; Õunap et al., 2016). Eleven "legacy" markers were sequenced from freshly extracted DNA (**I, II**) or DNA extracts obtained from CCDB (**I, II**). These markers include cytochrome oxidase subunit I [COI], elongation factor 1 alpha [EF-1α], wingless [WGL], glyceraldehyde3-phosphate dehydrogenase [GAPDH], ribosomal protein S5 [RPS5], isocitrate dehydrogenase [IDH], carbamoyl phosphate synthetase [CAD], malate dehydrogenase [MDH], arginine kinase [ArgK], sarco/endoplasmic reticulum calcium ATPase [Ca-ATPase] and nexin-9-likeprotein [Nex9]. Primer details, as well as PCR and cycle sequencing conditions are described in Articles **I** and **II**.

2.3. Sequencing by the AHE method

Target loci suitable for reliable enrichment across Geometridae (**II**) and Noctuidae (**III, IV**) were identified using the AHE sequencing method developed by Lemmon et al. (2012), and later extended to Lepidoptera by Breinholt et al. (2018). This probe set targeted 794 loci, including the 10 legacy genes. The Translational Laboratory at Florida State University, USA, performed library sequencing

at a coverage of 10–30× (equivalent to 20–60 gigabases) using an Illumina HiSeq 2500 sequencer employing the paired-end 150-base pair protocol. The sequence data generated using the AHE method were processed as described in Articles **II** and **III** to construct a phylogenetic tree.

2.4. Data mining from public repositories

To broaden taxon sampling and increase the coverage of legacy genes, publicly available single gene fragments were downloaded from the NCBI GenBank (https://www.ncbi.nlm.nih.gov/) and incorporated into the data set (**I, II**). Additionally, genome assemblies were downloaded from the NCBI GenBank. Genes of interest (i.e., the 11 legacy markers) were retrieved from the downloaded whole genomes using an in-house pipeline using MetaEuk (vb94867b, Levy Karin et al., 2020), HMMER v3.3.2 (http://hmmer.org/) and a custom python script (developed by Etka Yapar, one of the co-authors) for extraction written for this purpose and added to the dataset (**I, II**). Furthermore, AHE loci were mined from genome assemblies (**III**, **IV**), and to facilitate the gene mining process, the original AHE datasets were modified (see Article **III**). The AHE loci retrieved from the genome assemblies were incorporated into the original dataset.

2.5. Phylogenetic tree construction

Two different strategies were employed to construct phylogenetic trees using IQ-TREE v2.1.2 (Nguyen et al., 2015): (1) partitioning by loci (**I, II**), and (2) using the GHOST model (**III, IV**). In the partitioning-by-loci approach, each locus was initially treated as a separate partition, and substitution rates were calculated for each site to determine the most optimal partitioning scheme using ModelFinder (Kalyaanamoorthy et al., 2017) implemented in IQ-TREE v2.1.2. The parameters used for model selection and phylogenetic tree inference in IQ-TREE are described in Articles **I**, **II**, and **III**.

However, partitioning by loci assumes that the substitution rate for each site is constant across all lineages, or that heterotachy occurs exclusively between partitions rather than within them (Crotty et al., 2020). In reality, evolutionary processes are often both time and lineage-dependent (Crotty et al., 2020). To test the robustness of the tree search, in Article **III** we employed both the partitioning-by-loci method and the recently introduced GHOST model implemented in IQ-TREE (Crotty et al., 2020). The parameters used for the GHOST model are described in Article **III**. Phylogenetic trees inferred were visualized and edited in FigTree v1.4.3 software (Rambaut, 2018).

2.6. Dated phylogeny (IV)

For time calibration, the phylogenetic tree was constructed in IQ-TREE using 333 species (296 noctuids and 37 outgroup taxa) based on 548 protein-coding genes, totaling 249,138 nucleotides (see article **III**). This tree was used as a fixed topology for the time-calibration analyses, and was turned ultrametric using the R package ape (Paradis & Schliep, 2019). Due to software limitations, a reduced dataset was employed, comprising the 24 longest loci with at least 90% taxon coverage, totaling approximately 54,000 bp. Because node age estimation could not be performed on the full tree of 333 species, the tree was split into two subsets using the R package ape). In subset 1, majority of species from Xylenini and Apameini were excluded, while in subset 2, majority of species from Noctuini and Hadenini *s.l.* were excluded. In both subsets, 37 outgroup species from eight Macroheterocera families were retained along with ~90 Noctuidae species, resulting in 246 species in subset 1 and 227 in subset 2 (see Molleman et al., 2025). Optimal partitioning scheme based on predefined loci was calculated for both subsets using MODELFINDER (Kalyaanamoorthy et al., 2017) implemented in IQ-TREE 2.3.2 (Nguyen et al., 2015) in the CIPRES portal (Miller et al., 2010). The results suggested by MODELFINDER were taken into account, and the data were divided into 13 partitions for node age calculations for subset 1 and into 15 partitions for node age calculations for subset 2, respectively (Molleman et al., 2025).

To calibrate the tree in BEAST v1.10.4, five secondary calibration points were adopted from Kawahara et al. (2019). The ages (in millions of years) were as follows: root of the tree (normal distribution, mean 93.7 ± 11.1 SD), Noctuoidea (normal distribution, mean 77.6 ± 11.0 SD), Erebidae + Noctuidae clade (normal distribution, mean 68.6 ± 10.2 SD), *Chloridea* Duncan & Westwood, 1841 + *Helicoverpa* Hardwick, 1965 clade (normal distribution, mean 9.3 ± 5.6 SD), and *Spodoptera* Guenée, 1852 (normal distribution, mean 10.6 ± 5.7 SD) (see Molleman et al., 2025). As test runs with more complex clock models failed to converge, strict molecular clock was used, clock and tree priors were linked across all partitions, and birth-death tree prior with incomplete sampling (Stadler, 2009) was implemented for the final runs. For both subsets one analysis with BEAST was performed, with Bayesian MCMC running for 30 million generations and sampling every 1000th generation. The results were inspected in TRACER v1.7.2 (supplementary software to BEAST), and 3 million generations were discarded from each run as "burn-in". The final tree for both subsets were constructed using TREEANNOTATOR v1.10.4 (also a supplementary software to BEAST). The two trees were concatenated into a single 333-species tree using R package phytools (Revell 2012). For the follow-up analyses, only the tree of Apameini was used. To detect diversification rate heterogeneity across the tree, we employed the Bayesian Analysis of Macroevolutionary Mixtures (BAMM) software, version 2.5.0.

3. RESULTS & DISCUSSION

3.1. Phylogeny of Drepanidae at the European scale (I)

A phylogenetic tree of 37 Drepanidae species, including 21 of the 22 European representatives, was reconstructed using eleven legacy markers, with two Cimeliidae species as the outgroup, providing new insights into the evolutionary relationships within this group of moths. Sequencing of freshly collected specimens from six species yielded 7–10 markers per species, while DNA extracts from four species obtained from the CCDB yielded 3–8 markers per species. Mining of "legacy" markers from the downloaded genome assemblies recovered 10–11 markers per species. Retrieval of stored "legacy" markers from GenBank was variable, resulting in 2–7 markers per species. For three species included in the phylogeny, only DNA barcodes were available. Outgroup species were represented by eight (*Axia margarita* (Hübner, 1813)) and six (*A. theresiae* (Korb, 1900)) markers.

While constructing the phylogenetic tree, all five runs in IQ-TREE produced identical topologies, and the tree with the best likelihood score (Fig. 1) was selected as the basis for further discussion. In this phylogenetic analysis, all four subfamilies of Drepanidae formed statistically very well supported (SH-Like $\geq$ 97.7, UFBoot 2 $\geq$ 98) monophyletic groups, confirming the earlier finding of Wu et al. (2010) (Fig. 1). This analysis divided Drepanidae into two clades: one comprising Drepaninae and Oretinae, and the other comprising Thyatirinae and Cyclidiinae (see Article **I**). This sister relationship of Cyclidiinae with Thyatirinae had already been reported by Regier et al. (2009) and Kawahara et al. (2019), the latter study using more than 2,000 protein-coding genes, and it challenged earlier findings by Mutanen et al. (2010), Wu et al. (2010), and Regier et al. (2013), which placed Cyclidiinae as sister to all other drepanids. Our study confirmed the subfamily-scale phylogenetic structure of Drepanidae suggested by Regier et al. (2019) and Kawahara et al. (2019).

The phylogenetic tree reconstructed in this study provided insights into the evolutionary history of Drepanids. For instance, Drepanidae are characterized by variable forewing shapes, ranging from rounded or sharp tips to small or prominent hooks, which has earned respective species different vernacular names (e.g. the English "hook-tips", Estonian "sirptiiblased"). Our tree suggests that the hooked wingtips likely evolved once in the Oretinae + Drepaninae lineage and were subsequently lost multiple times in the course of the evolution of this clade, often in association with the evolution of white coloration, suggesting a shift in mimicry strategy from dry leaves to bird droppings. All Thyatirinae genera characterized by colorful (pink or orange blotches) forewing pattern were recovered as a distinct clade, indicating a potentially shared evolutionary origin of this trait.

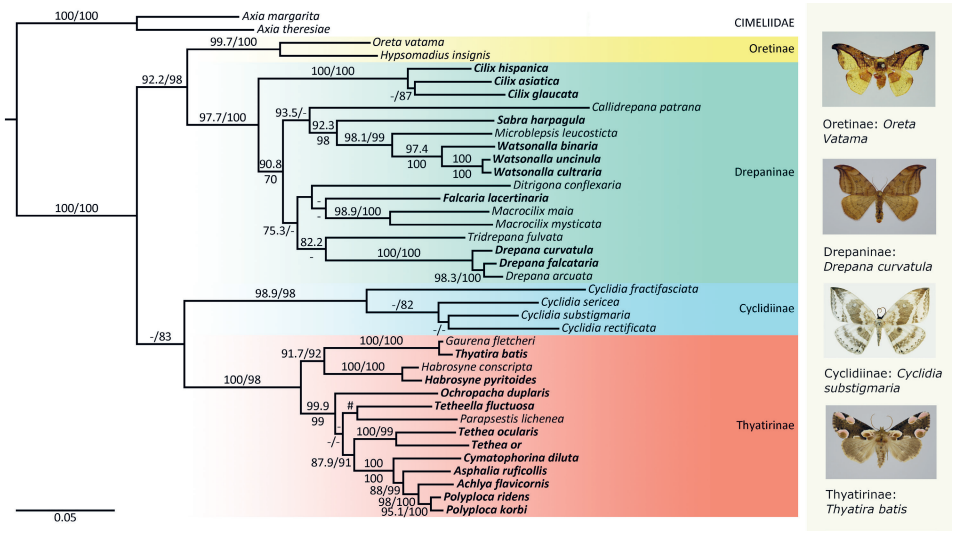

Fig 1. Maximum likelihood phylogeny of Drepanidae, modified from article **I**. Numbers above and below branches (separated by slashes) represent SH-like and UFboot2 support values, respectively. Support values below 70% are not shown. A very short branch with SH-like support of 84.4% and UFboot2 support of 94% is marked with the symbol #. European species are indicated in bold. Image credits: Cornelis Gielis (*Oreta vatama* Moore, 1866), Kenichiro Nakao (*Cyclidia substigmaria* (Hübner, 1831)), Egbert Friedrich (*Drepana curvatula* (Borkhausen, 1790), *Thyatira batis* (Linnaeus, 1758)).

Similarly, adult moths that are active very early or late in the year are known to exhibit correlated ecological traits, a phenomenon referred to as the "winter moth syndrome" (Hunter, 1995; Ude et al., 2025), and these species cluster closely together in the phylogenetic tree. Laszlo et al. (2007) divided Thyatiridae into two subfamilies, Thyatirinae and Polyplocinae; however, subsequent taxonomic revisions have downranked these groups to tribal level within a single subfamily. The phylogenetic results obtained in the present study are in conflict with the classification proposed by Laszlo et al. (2007). Specifically, the genera *Achlya* Billberg, 1820, *Asphalia* Hübner, 1821, *Cymatophorina* Spuler, 1908 and *Polyploca* Hübner, 1821 – previously assigned to Polyplocinae – form a distinct clade nested within Thyatirinae and were sister to *Tethea* Ochsenheimer, 1816. Furthermore, *Cymatophorina*, placed by Laszlo et al. (2007) in Demipsestini, was recovered as sister to the other three genera, indicating that Demipsestini sensu Laszlo et al. (2007) are paraphyletic. However, the present dataset almost exclusively includes European representatives, the taxon sampling is thus too limited to justify formal taxonomic revisions, and such changes were therefore not undertaken. In conclusion, this study offers further insights into the phylogeny of Drepanidae, enhancing our understanding of the evolutionary history of these moths while also contributing to knowledge about their ecological functions and adaptations. To elaborate on these outcomes, future research should broaden sampling efforts on a global scale and apply more sophisticated molecular approaches to further explore the evolutionary relationships within this fascinating family.

3.2. Molecular phylogeny of north European Geometridae (II)

A two-step analytical framework was employed to reconstruct an all-inclusive phylogeny of northern European Geometridae. In the first step, a backbone phylogeny was inferred from a dataset comprising 117 geometrid species and 35 outgroup taxa representing eight macroheteroceran families. The data matrix contained 209,499 base pairs from 648 protein-coding loci, generated using the anchored hybrid enrichment sequencing technique. This backbone was then used to construct a more comprehensive phylogeny of Geometridae, incorporating up to 11 traditional protein-coding genes for all 376 north European species, supplemented with data from 98 key taxa representing tribes occurring in other regions of the world. The combined maximum likelihood analysis, inferred using the phylogenomic backbone, produced a well-resolved tree, with majority of deeper nodes receiving maximum statistical support (SH-Like = 100%, UFBoot2 = 100%). Taxonomic changes were made if necessary, with due consideration given to previously proposed actions, including synonymizations and changes in rank; where appropriate, new synonymies were established. In cases where already existing names or previously revoked combinations were not available, new names or new combinations were proposed.

All outgroup families (Drepanidae, Erebidae, Lasiocampidae, Noctuidae, Notodontidae, Saturniidae, Sphingidae, Uraniidae) were recovered as monophyletic (**Fig 2**). Phylogenetic relationships among most subfamilies of Geometridae received maximum statistical support (SH-Like = 100%, UFBoot2 = 100%), except for the Epidesmiinae + Oenochrominae + Geometrinae clade (Fig. 2).

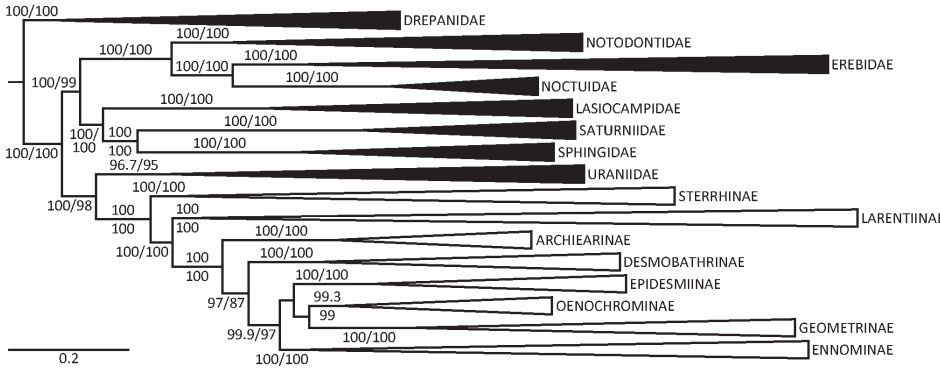

Fig 2. Maximum likelihood phylogeny of subfamilies of Geometridae (white triangles) and outgroup families (black triangles). Numbers above or below branches or slashes indicate SH-Like support and UFBoot2 support, respectively. Support indice values inferior to 70% are not shown. Figure adopted from article **II**.

In the present study, Sterrhinae were recovered as the sister group to all other Geometridae, with Larentiinae diverging next; all relevant nodes received maximum statistical support. Within Sterrhinae, the two informal groups termed as "Timandrini lineage" and "Scopulini lineage" (Sihvonen & Kaila, 2004) were also supported in the present study. Phylogenetic relationships between the tribes of Sterrhinae were recovered as fully concordant with Murillo-Ramos et al. (2019) and Sihvonen et al. (2020).

In Larentiinae, despite some notable discrepancies, this work was nevertheless largely concordant with earlier studies regarding its phylogenetic structure (Õunap et al., 2016, Murillo-Ramos et al., 2019). However, the new evidence suggests that some parts of this subfamily require taxonomic updates. Most importantly, two new tribes were described. First, the genera *Cosmorhoe* Hübner, 1825, *Lampropteryx* Stephens, 1831, and *Colostygia* Hübner, 1825 were recovered to form a well-supported monophyletic group sister to the rest of the "Xanthorhoini lineage" *sensu* Õunap et al. (2016). Consistent with earlier studies (Brehm et al., 2019; Murillo-Ramos et al., 2019), the phylogenomic analysis confirmed that this clade lies outside previously recognized tribes. As no close relationship with Cidariini or other recognized tribes was found, the group was formally described as tribe Lampropterygini (**Fig 3**)**.** Second, the genus *Pelurga* Hübner, 1825 was recovered as an isolated lineage branching off after Cidariini as sister to the derived part of the "Xanthorhoini lineage" with maximum statistical support (Fig. 3). Previous studies have also placed it outside of recognized tribes (Õunap et al., 2016, 2020), despite earlier classifications assigning it to Larentiini or Hydriomenini (Choi, 2006; Hausmann & Viidalepp, 2012; Beljaev, 2016). Consistent results across multiple molecular datasets confirm its distinct position and the group was thus described as Pelurgini.

Other rearrangements include reviving *Ochyria* Hübner, 1825 from a synonym of *Xanthorhoe* Hübner, 1825 and moving *Costaconvexa* Agenjo, 1949 to *Epirrhoini*, as explained below. The study found that *Phalaena quadrifasiata* Clerck, 1759 was more closely related to *Camptogramma* Stephens, 1831 than to *Xanthorhoe*, contrary to previous classifications (Hausmann & Viidalepp, 2012: Aarvik et al., 2017). Due to significant morphological differences, it cannot however be merged with *Camptogramma* (Hausmann & Viidalepp, 2012). As a result, the genus *Ochyria* was revived, with *P. quadrifasiata* reclassified as *Ochyria quadrifasiata* (Clerck 1759), making *Ochyria* a monotypic genus. For the first time, *Costaconvexa* Agenjo, 1949 was analyzed using molecular phylogenetic tools. The results showed it was sister to *Epirrhoe* Hübner, 1825, with moderate support, leading to its transfer from the tribe Xanthorhoini to Epirrhoini**.**

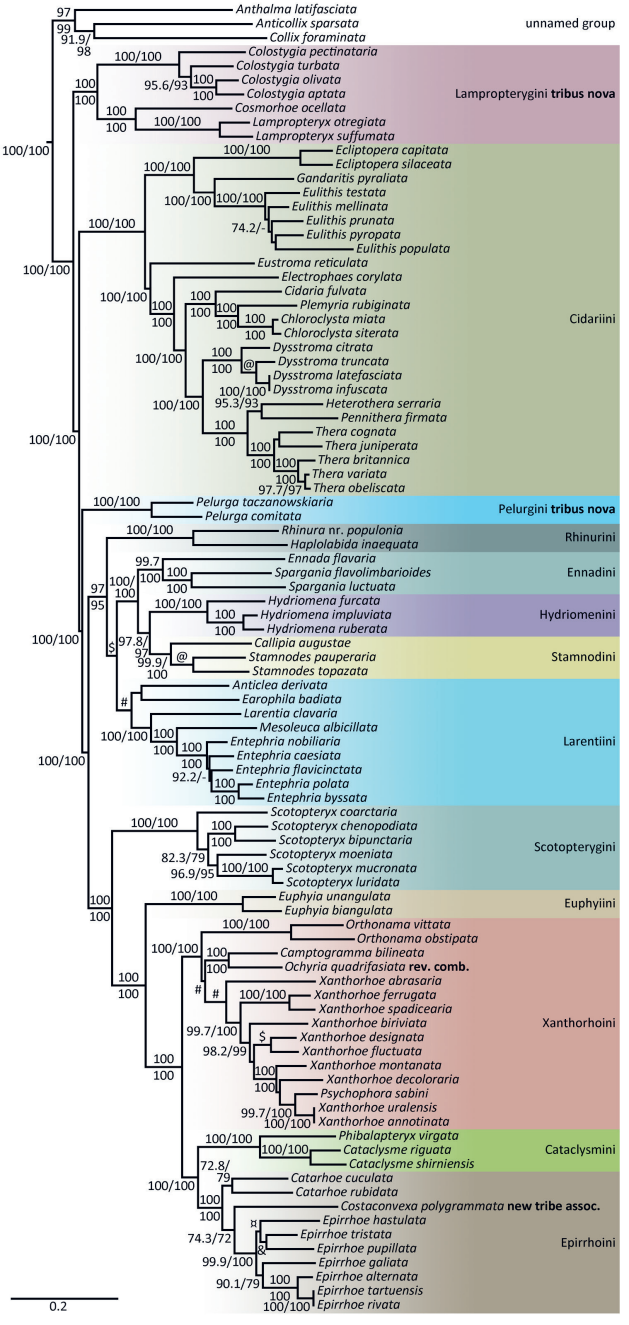

Fig 3. Maximum likelihood phylogeny of the "Xanthorhoini lineage" of the subfamily Larentiinae inferred from article **II**. Numbers above or below branches or slashes indicate SH-Like support and UFBoot2 support, respectively. Support indice values inferior to 70 are not shown. Supports to very short branches are indicated as follows: #, both indices 100%; @, both indices ≥ 95%; $, both indices ≥ 90%, &, both indices ≥ 80%; ¤, one indice ≥ 70%, the other <70%.

Present analysis recovered *Bombyx sabini* (Kirby, 1824), the type species of *Psychophora* Kirby, 1824, nested deeply within *Xanthorhoe* as sister to the *X. annotinata* (Zetterstedt 1839) + *X. uralensis* Choi, 2003 clade, with maximal support for the monophyly of *Xanthorhoe*. These results confirmed that *Psychophora* does not represent a distinct genus, consistent with earlier morphological assessments (Hausmann & Viidalepp, 2012). Formal synonymization of *Psychophora* under *Xanthorhoe* would render *Xanthorhoe* a junior subjective synonym, generating significant nomenclatural instability given the cosmopolitan distribution of the genus and extensive use of *Xanthorhoe* in the literature, in contrast to the limited representation of *Psychophora*. To address this, a case will be submitted to the ICZN to suppress *Psychophora* as senior synonym and retain *Xanthorhoe* as the valid name. Pending the Commission's decision, both genera are provisionally maintained, resulting in the paraphyly of *Xanthorhoe.*

The analysis revealed several conflicts with previous phylogenetic studies (Ban et al., 2018; Brehm et al., 2019 & Murillo-Ramos et al., 2019) in the subfamily Geometrinae. While Hemitheini have consistently been recovered as monophyletic, its placement varied between the studies. Archaeobalbini appeared paraphyletic and closely allied with Pseudoterpnini, contradicting earlier findings (Ban et al., 2018; Brehm et al., 2019: Murillo-Ramos et al., 2019). Other relationships, such as Neohipparchini + Geometrini and Agathiini + Comibaenini + Nemoriini, also received mixed support. Overall, the phylogeny of Geometrinae remains largely unresolved and requires further study with broader taxon sampling.

Our molecular phylogenetic analysis supported the informal division of Ennominae into two major lineages: the "Ennomine" and "Boarmiine" clades (Forbes, 1948; Holloway, 1994). Few conflicts with the existing classification that necessitated taxonomic updates were recovered in both clades; these will briefly be discussed below. *Lycia* Hübner, 1825 was found sister to *Artiora* Meyrick, 1892 and most Boarmiini (excluding the *Ectropis* Hübner, 1825 + *Cleora* Curtis, 1825 + *Ascotis* Hübner, 1825 clade), contrasting with earlier phylogenies that placed *Lycia* deeper within Boarmiini (Murillo-Ramos et al., 2019, 2021). With strong molecular support from five markers, *Artiora* was newly reassigned from Ennomini of uncertain placement (Skou & Sihvonen, 2015) to Boarmiini.

Within the tribe Macariini, the genus *Epelis* Hulst, 1896 was revived from synonymy with *Macaria* Curtis, 1826, and *Phalaena carbonaria* Clerck, 1759 was transferred from *Macaria* to *Epelis* as *Epelis carbonaria* (Clerck, 1759)**.** This revision was justified by the clear external morphological differences between *M. carbonaria* (Clerck, 1759) and *Narraga fasciolaria* (Hufnagel, 1767), which was recovered as its sister in our analysis. Moreover, *E. carbonaria* is externally highly similar to *Epelis truncataria* (Walker, 1862), the type species of *Epelis*, has similar diurnal lifestyle, and the small genetic distance between the two species' DNA barcodes was also small, only 0.059. This taxonomic change had been suggested previously, but was not formally implemented (Ferguson, 2008). The study also suggested reviving *Speranza* Curtis, 1828 from synonymy with *Macaria* to resolve paraphyly. As a result of this change following combinations appeared for the north European taxa: *Speranza fusca* (Thunberg, 1792), *Speranza artesiaria* (Denis & Schiffermüller, 1775), *Speranza brunneata* (Thunberg, 1784), *Speranza*

wauaria (Linnaeus, 1758) and *Speranza loricaria* (Eversmann, 1837). *Speranza* was justified as a separate genus based on its statistically well supported position away from *Macaria*, but also by morphological characters such as bipectinate male antennae and tendency towards female brachyptery in certain species, which are not known in *Macaria*.

The genus *Selenia* Hübner, 1823, traditionally placed in Ennomini (Viidalepp, 1996), had been moved to Epionini by Beljaev (2016). Sihvonen et al. (2015) classified *Selenia* as Ennomini of uncertain association, but also questioned its placement in that tribe. Based on phylogenomic evidence, *Selenia* was now reassigned to Epionini. The present analysis recovered *Selenia* as sister to *Apeira* Gistl, 1848 with maximum support, confirming this reassignment.

Opisthograptis Hübner, 1823 and *Epirranthis* Hübner, 1823 were recovered deep within Ennominae as sister genera with maximum support but without close relatives, as had been show by Sihvonen et al. (2011, 2015). To avoid treating them as two separate tribes which both comprise only one genus, our study proposed uniting them under a single tribe and therefore transferred *Epirranthis* Hübner, 1823 from Epirranthini to Rumiini**.** Consequently, Epirranthini were synonymized with Rumiini.

Overall, the expanded AHE dataset confirmed most previous subfamily- and tribe-level hypotheses while also supporting key taxonomic revisions, including the recognition of Lampropterygini and Pelurgini as new tribes and the placement of *Epirranthis* and *Opisthograptis* within Rumiini. The present study provides a robust phylogenetic framework for all northern European Geometridae species, offering a valuable resource for future comparative phylogenetic analyses like exploring patterns of diversification, trait evolution, and biogeography. For example, Ude et al. (2024) investigated the evolution of wing shape in Geometridae using a phylogenetic comparative approach encompassing 374 northern European species, employing the phylogenetic information generated in this study.

3.3. Molecular phylogeny of north European Noctuidae (III)

The phylogenetic tree of north European Noctuidae was inferred from a large dataset of 565 protein-coding genes, totaling 249,138 nucleotides, obtained through AHE technology and comprising 333 species (296 noctuids and 37 outgroup taxa). GHOST model implemented in IQ-TREE produced a well-resolved tree with maximum statistical support (SH-Like = 100%, UFBoot2 = 100%) for the vast majority of nodes (**Fig 4**). Many of the findings were concordant with previously published phylogenetic works (e.g. Zahiri et al., 2011, 2013: Rota et al., 2016: Keegan et al., 2019, 2021) and current classification of Noctuidae (Top et al., 2023), but this study also provided numerous new insights of relevance for the global phylogenetic context and taxonomy of the family. Taxonomic revisions were undertaken where necessary, with careful attention to previously published actions such as synonymizations and changes in rank. Where needed, new synonymies were established, and in cases lacking prior information, new names or combinations were proposed.

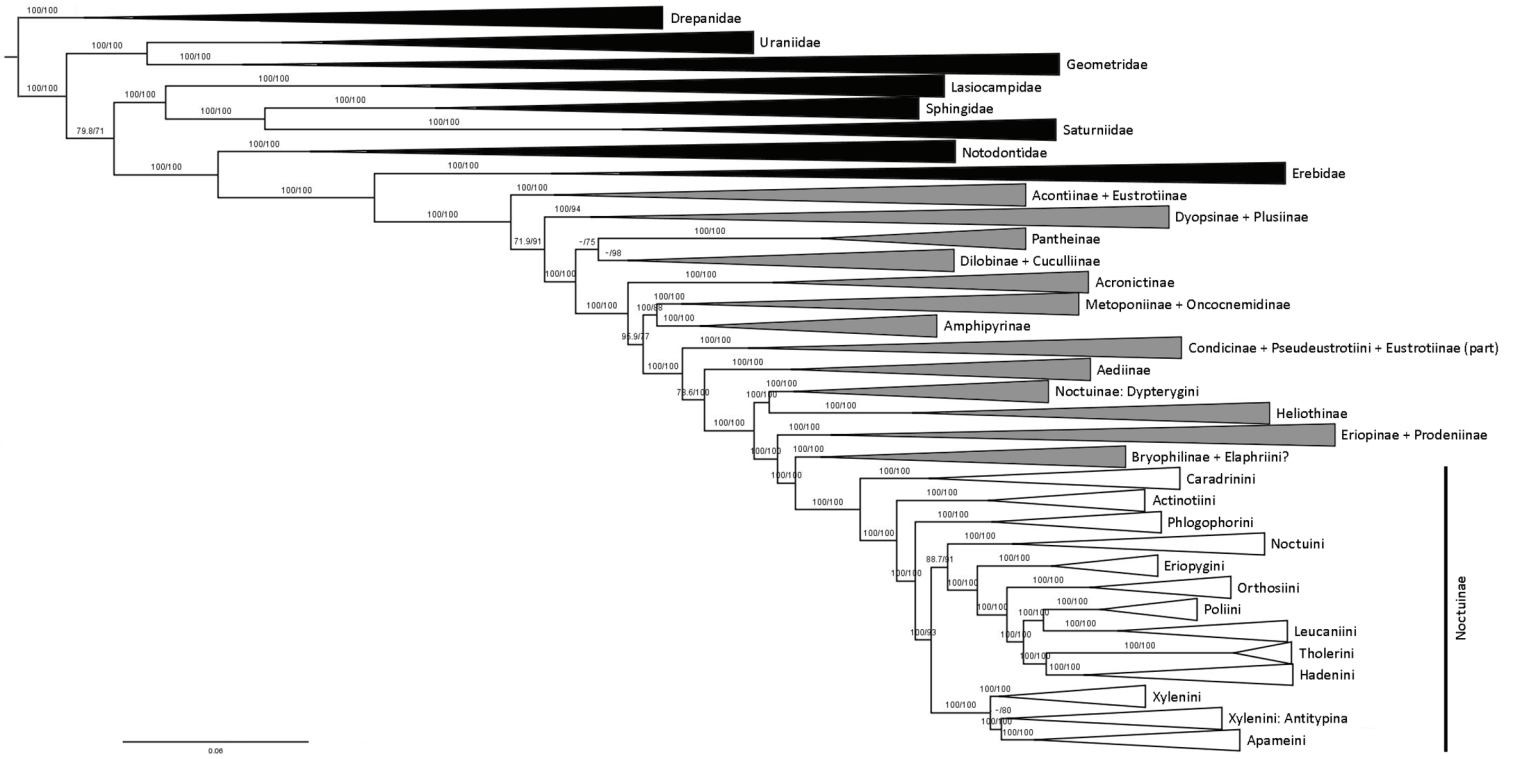

Fig 4. Maximum likelihood phylogeny of subfamilies of Noctuidae and outgroup families. Numbers with slashes indicate SH-Like support and UFBoot2 support, respectively. Support index values inferior to 70% are not shown. Black triangles: outgroup families; grey triangles: other subfamilies of Noctuidae; white triangles: tribes of subfamily Noctuinae.

In the present study, the Acontiinae + Eustrotiinae clade was recovered as sister to the rest of Noctuidae, identical to the results of Martinez (2022). The Plusiinae + Dyopsinae clade diverged next and was found to be sister to the remaining Noctuidae. One of the interesting findings of the analysis is the placement of *Cornutiplusia* Kostrowicki, 1961 within *Autographa* Hübner, 1821. Despite earlier distinctions based on genitalia, both morphology and phylogenetic results support its inclusion in *Autographa*. Hence, *Cornutiplusia* is hereby treated as a junior synonym of *Autographa,* and its only species, *Phalaena (Noctua) circumflexa* Linnaeus, 1761, was transferred to the latter genus as *Autographa circumflexa* (Linnaeus, 1761).

Our phylogenetic analyses recovered a strongly supported clade comprising Heliothinae and Dypterygiini (Noctuinae) as sister to the remaining part of Noctuidae. While the placement of Heliothinae was congruent with previous studies (Keegan et al., 2019, 2021; Li et al., 2024), the position of Dypterygiini differed from earlier hypotheses (Keegan et al., 2021). Both lineages were recovered as monophyletic with maximal statistical support. This represented the first evidence suggesting a sister-group relationship between Heliothinae and Dypterygiini. In the absence of corroborating morphological data, we refrain from proposing formal taxonomic changes but emphasize the need for further integrative analyses to validate this relationship.

The tribe Prodeniini, which includes several important agricultural pests, such as *Spodoptera exigua* (Hübner, 1808), *S. frugiperda* (Smith, 1797), and *S. littoralis* (Boisduval, 1833), has traditionally been treated within Noctuinae. However, species belonging to this tribe possess genitalia modified to such an extent that it is difficult to associate them with any other subgroup of Noctuidae (Fibiger, 1997). This study, together with those of Keegan et al. (2021), Kergoat et al. (2021), and Martinez (2022) indicates that Prodeniini should be removed from Noctuinae and treated as a separate subfamily. Therefore, Prodeniini were formally elevated to the subfamily rank: Prodeniinae.

Graphiphora subrosea Stephens, 1829, the type species of *Coenophila* Stephens, 1850, was placed within *Xestia* Hübner, 1818, as sister to *Xestia castanea* (Esper, 1798), with strong statistical support. Despite some distinctive genital traits, both external morphology and other genital features show affinities with other *Xestia* species. Therefore, *G. subrosea* was transferred to *Xestia* as *Xestia subrosea* (Stephens, 1829) and *Coenophila* was suggested to be treated as a subgenus: *Xestia* (*Coenophila*). The genus *Epilecta* Hübner, 1821 (type species *Noctua linogrisea* Denis & Schiffermüller, 1775) was recovered within *Noctua* Linnaeus, 1758, with strong statistical support, branching off the evolutionary lineage after *N. pronuba* (Linnaeus, 1758). This placement conflicts with earlier hypotheses linking *Epilecta* to *Spaelotis* Boisduval, 1840 (Fibiger, 1997). Despite the absence of the clasper, the genitalia of *N. linogrisea* fit within the extreme variation of *Noctua*. To avoid unnecessary splitting of *Noctua*, we treat *Epilecta* as a junior subjective synonym of *Noctua* and restore the original combination *Noctua linogrisea*, while noting the need for further morphological study. *Cryptocala* Benjamin, 1921 was another genus recovered within *Noctua* with maximum

support in this study. *Cryptocala* spp. are notably smaller than *Noctua* spp., with some distinct differences in male genitalia, but the latter are known to be extremely heterogenous in *Noctua* anyway (Fibiger 1997). Hence, *Cryptocala* was treated as a junior subjective synonym of *Noctua*, resulting with a combination *Noctua chardinyi* (Boisduval, 1829) for its sole European species.

Pachetra Guenée, 1841 and *Polia* Ochsenheimer, 1816 were recovered in a clade sister to Leucaniini rather than within Hadenini. We thus suggested elevating Poliina from a subtribe of Hadenini (e. g. Beck, 1996: Varga et al., 2020) to full tribe Poliini and excluded these genera from Hadenini. Present analysis placed *Noctua munda* Denis & Schiffermüller, 1775 (type species of *Anorthoa* Berio, 1980), within *Orthosia* Ochsenheimer, 1816 as sister to *O. incerta* (Hufnagel, 1766) with strong support. This demonstrated that *Anorthoa* does not merit separate generic status; *N. munda* was therefore transferred to *Orthosia* as *O. munda* (Denis & Schiffermüller, 1775), and *Anorthoa* was downgraded to a subgenus of *Orthosia*.

Additionally, the analysis strongly supported merging *Senta* Stephens, 1834 with *Leucania* Ochsenheimer, 1816, as *Melia flammea* Curtis, 1828 (type species of *Senta*) was recovered as sister to the rest of *Leucania*. This resulted in a combination *Leucania flammea* (Curtis, 1828) for its type species, with the genus forming a well-supported clade closely related to *Mythimna* Ochsenheimer, 1816. The analysis placed *Pseudaletia* Franclemont, 1951 as sister to the rest of the *Mythimna–Leucania* complex with strong support, confirming similar findings by Martinez et al. (2024). In contrast to its earlier treatment as a subgenus of *Mythimna* (Hacker et al., 2002), our evidence supported reinstating *Pseudaletia* as a valid genus, with *Leucania separata* transferred to this genus as *Pseudaletia separata* (Walker, 1865). Our analysis demonstrated that the genus *Sideridis* Hübner, 1821 as currently defined is not monophyletic. *Sideridis reticulata* (Goeze, 1781) is more closely related to the type species *S. lampra* (Schawerda, 1913) (Hacker et al., 2002), representing the "true" *Sideridis*, whereas *Noctua rivularis* Fabricius, 1775 was recovered outside this group as sister to *Conisania* Hampson, 1905 + *Hadena* Schrank, 1802 clade with strong statistical support. This finding also contradicts earlier treatments that associated *N. rivularis* with *Hadena* (e.g. Nowacki & Fibiger, 1996; Skou, 1991). To resolve this paraphyly, the genus *Aneda* Sukhareva, 1973 was revived from synonymy and reinstated at full genus rank, resulting in the combination *Aneda rivularis* (Fabricius, 1775) for its type species.

The remaining part of the phylogeny included Xylenini and Apameini with strong statistical support. However, contrary to current classifications, Xylenini was not recovered as monophyletic, since Antitypina formed a well-supported clade as sister to Apameini. The remaining lineages of Xylenini, comprising Xylenina and Cosmiina *sensu* Top et al. (2023), are therefore recognized here as Xylenini *sensu stricto*. Present analysis revealed that Cosmiina was placed near the root of Xylenina with strong support, rendering the latter paraphyletic. Since Cosmiina is most closely related to the *Fissipunctia* Beck, 1991 + *Parastichtis* Hübner, 1821 clade, and similar results were also reported by Martinez et al.

(2024), we proposed abandoning Cosmiina and treating it as a synonym of Xylenina to maintain monophyly.

The present study fills a major gap resulting from the poor representation of North European noctuids in earlier molecular research. This work sampled 140 genus-types, providing a robust phylogenetic and taxonomic framework for comparative evolutionary and ecological research (see **IV**, Molleman et al., 2025), particularly given the exceptionally well-documented life histories of northern European species.

3.4. Time-calibrated tree of Noctuidae and diversification of Apameini (IV)

Phylogeny of Noctuidae inferred in article **III** was well resolved in most nodes, with Apameini recovered as one of the well-supported clades. This tree was then used as a fixed topology for the time-calibrated analysis. The time-calibrated phylogeny inferred in this study indicates that the diversification of Apameini began approximately 8.66 (95% HPD 7.37–10.04) million years ago, i.e. substantially more recently than suggested in previous studies (**Fig 5**). Earlier studies in Apameini provided conflicting estimates: Toussaint et al. (2012) suggested that Apameini originated ~29 Ma, and linked this event with grassland expansion and rapid diversification in the Middle Miocene, whereas Kergoat et al. (2018) dated Apameini to ~22.3 Ma, with initially elevated speciation rates followed by a gradual slowdown.

The incongruences in node age estimates between the present and previous studies may be attributable to differences in dataset size and calibration approaches: Toussaint et al. (2012) used dataset with 1.9 kb and calibration points from Douglas & Stockey, (1996); Wolfe & Wehr, (1987) and Douglas, (1991). Kergoat et al. (2018) applied 4.7 kb with calibrations from Mutanen et al. (2010) and Wahlberg et al. (2013), whereas the present study employed 54 kb and more recent calibrations from Kawahara et al. (2019). Recent studies suggest that another major radiation of modern grasslands occurred between 3–9 Mya, driven by environmental changes (Edwards et al., 2010). Notably, present results place the diversification of Apameini precisely within this time window. BAMM analysis indicated a major radiation in Apameina, with diversification slowing after the tribe's formation but later accelerating independently in *Apamea* Ochsenheimer, 1816 (~4 Ma) and the crown group of predominantly endophagous Apameina (~5 Ma) (**Fig 6**).

It is widely hypothesized that the evolutionary shift from internal to external larval feeding in the Cretaceous was a key adaptation in Lepidoptera (Kawahara et al., 2019), as internal feeding imposes ecological and physiological constraints such as limited mobility, host specificity, and susceptibility to plant defenses (Kawahara et al., 2019; St Laurent et al., 2021). In Apameini, while *Apamea* larvae are mostly external feeders, the crown group of Apameina predominantly feeds internally (Zilli et al., 2005). Rather than limiting diversification, internal

feeding may have promoted it by providing ecological advantages such as niche expansion and predator protection, with host specialization further driving speciation. Future research should investigate whether the primary drivers of Apameini diversification are the ecological benefits associated with internal feeding itself, or rather the results of shifts and expansions in host plant use, particularly in relation to thriving grassland ecosystems.

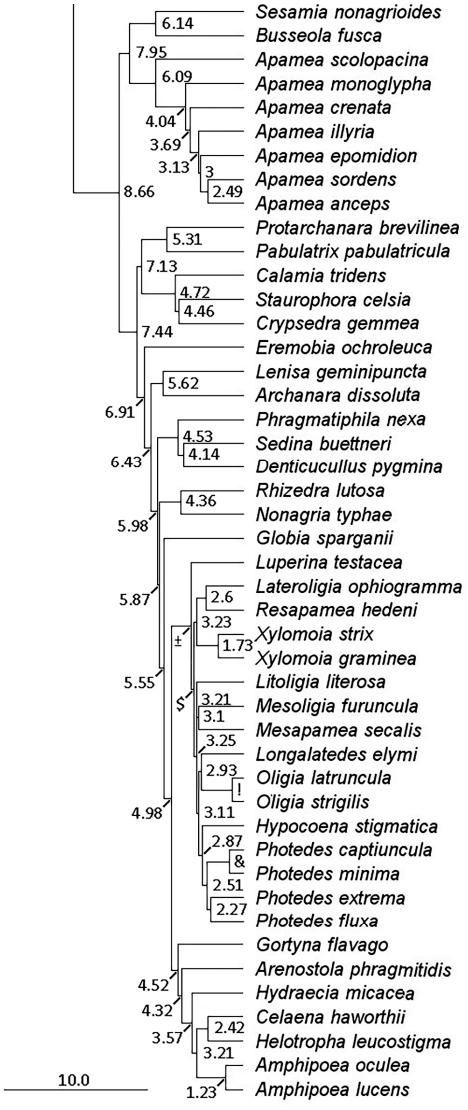

Fig 5. Time calibrated tree of the tribe Apameini constructed using Beast 1.10.4. Numbers indicate node ages in millions of years. Node ages of branches marked with symbols are as follows: $ = 3.43 Mya; ± = 3.63 Mya; & = 0.92 Mya; ! = 0.74 Mya.

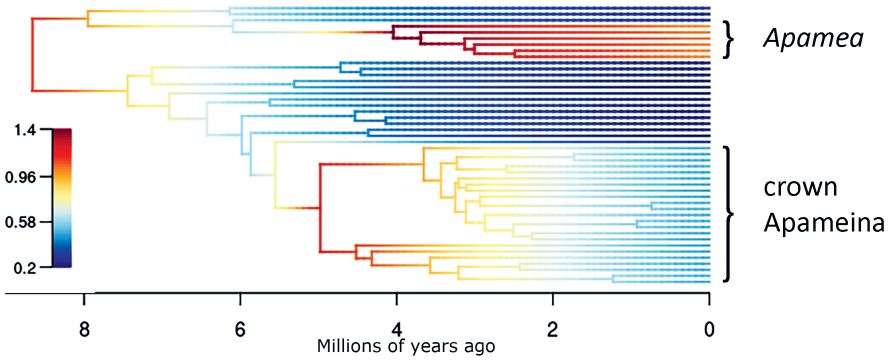

Fig 6. Mean phylo-rate plot from BAMM, indicating two instances of rapid radiation in Apameini, one in the genus *Apamea* and other in crown Apameina. Diversification rates are indicated using a gradual scale (cool colours = slow; warm colours = fast).

SUMMARY

The present study aimed to infer the phylogeny of Drepanidae, Geometridae and Noctuidae with special emphasis on the northern European fauna. It took advantage of recent advances in sequencing and phylogenetic methodologies which have the potential to greatly improve our understanding of phylogenetic relationships within Lepidoptera at all taxonomic levels. To infer the phylogenies of the target groups, this study combined data generated using Sanger sequencing and next-generation sequencing with publicly available sequences and genome assemblies.

The family Drepanidae includes around 650 species worldwide, yet it has received relatively little attention in phylogenetic research. In fact, no molecular phylogenies have been published even for the well-documented and uncontroversial European species. To address this gap, we investigated the phylogenetic relationships within Drepanidae using eleven molecular markers, totaling over 7,500 bp (**I**). Present analysis, based on 37 species – including 21 of the 22 European drepanid species – confirmed the monophyly of all four recognized subfamilies. The results further showed that Oretinae and Drepaninae form a sister-group within one major clade, whereas Cyclidiinae and Thyatirinae comprise the other. The analysis revealed that hooked wingtips, typical of the Drepaninae + Oretinae lineage, have been lost multiple times during evolution. Within Thyatirinae, the "winter moths" (species active very early in spring or late in the year) form a distinct and well-supported clade. In addition, the thyatirine genera characterized by pink or orange forewing blotches consistently formed a statistically well-supported clade.

A comprehensive phylogeny of northern European Geometridae was reconstructed using a two-step approach (**II**). In the first step, a backbone phylogeny was inferred using a dataset of 117 geometrid species and 35 outgroup species, comprising 648 protein-coding loci (209,499 bp) generated using the anchored hybrid enrichment (AHE) method. This backbone tree was then combined with a taxonomically wider dataset of 376 north European species, supplemented by 98 key taxa from other parts of the world, for which 11 traditional protein-coding genes were obtained using the Sanger sequencing method. The resulting maximum likelihood phylogeny was well-resolved, with most deeper nodes receiving maximal statistical support. Several taxonomic revisions were proposed: new tribes Lampropterygini and Pelurgini were described, *Ochyria* was revived as a monotypic genus, and genera such as *Costaconvexa*, *Artiora*, *Selenia* and *Epirranthis* were assigned to appropriate tribes based on phylogenomic and morphological evidence. Additional revisions included reviving genera from synonymy (e.g., *Ochyria*, *Epelis*, *Speranza*), transferring species to correct genera (e.g., *Xanthorhoe quadrifasiata* to *Ochyria quadrifasiata*, *Macaria carbonaria* to *Epelis carbonaria*) and redefining tribes to maintain monophyly (most importantly, moving *Epirranthis* to Rumiini). The study confirmed many previously proposed subfamily- and tribe-level relationships while resolving several conflicts,

particularly within Larentiinae and Ennominae. Overall, this study provides a robust phylogenetic framework for all northern European Geometridae and supports key taxonomic revisions that reflect both molecular and morphological evidence.

A phylogenetic analysis of 333 species (296 noctuid + 37 outgroup species) based on 565 protein-coding genes (249,138 bp, AHE data) produced a strongly supported tree for Noctuidae that both confirms earlier studies and introduces important taxonomic revisions (**III**). Acontiinae + Eustrotiinae were recovered as sister to all other Noctuidae, with Plusiinae + Dyopsinae diverging next. Several taxonomic rearrangements were made, including synonymizing *Cornutiplusia* with *Autographa, Senta* with *Leucania,* and *Epilecta* and *Cryptocala* with *Noctua. Coenophila* was ranked down as a subgenus of *Xestia*, and *Anorthoa* as a subgenus of *Orthosia*. Prodeniini were elevated to subfamily rank (Prodeniinae), Poliina to tribe (Poliini), Additional changes include reinstating *Pseudaletia* as a valid genus, reviving *Aneda* for *Sideridis rivularis*, and synonymizing Cosmiina with Xylenina to maintain monophyly of the latter. Together, these revisions refine noctuid systematics and provide a robust phylogenetic framework for future evolutionary and ecological research.

The phylogenetic tree obtained in article **III** was thereafter used for evolutionary analyses. First, it was time-calibrated in order to infer divergence times and evolutionary patterns. This time-calibrated phylogeny shows that Apameini diversified around 8.7 Mya (**IV**), much more recently than previous estimates (20–29 Mya). These differences likely reflect variation in dataset size and calibration approaches among studies. Current results place Apameini diversification within the major grassland radiation (3–9 Mya), with BAMM analyses indicating subsequent independent accelerations of diversification in *Apamea* and the endophagous Apameina. While *Apamea* larvae are mostly external feeders, the crown group Apameina feeds internally; rather than constraining diversification, internal feeding may have facilitated it through niche expansion, predator protection, and host specialization. Future work should clarify whether diversification was primarily driven by internal feeding itself or by shifts in host plant use linked to grassland expansion.

SUMMARY IN ESTONIAN

Põhja-Euroopa suurliblikate fülogeneesipuu koostamine

Käesoleva uurimuse eesmärk oli koostada kolme liblikasugukonna – sirptiiblaste, vaksiklaste ja öölaste – fülogeneesipuud, pöörates põhitähelepanu Põhja-Euroopa faunale. Uuringus tugineti viimase aja arengutele DNA sekveneerimise ja fülogeneetilise analüüsi meetodite vallas, millel on suur potentsiaal parandada meie arusaamist liblikaliste (*Lepidoptera*) sugulussuhetest kõigil taksonoomilistel tasemetel. Sihtrühmade fülogeneesipuude koostamiseks kombineeriti selles uuringus Sangeri sekveneerimise ning järgmise põlvkonna sekveneerimise abil saadud originaalandmeid avalikult kättesaadavate järjestuste ja genoomiandmetega.

Sugukonda sirptiiblased (*Drepanidae*) kuulub ligikaudu 650 liiki üle maailma, kuid senistes fülogeneetilistes uurimustes on sellele rühmale pööratud suhteliselt vähe tähelepanu. Isegi hästi tuntud ja ühemõtteliselt piiritletud Euroopa liikide kohta polnud avaldatud ainsatki molekulaarset fülogeneesipuud. Selle puuduse kõrvaldamiseks uuriti käesolevas töös sirptiiblaste sugulussuhteid, kasutades ühtteist molekulaarset markerit kogupikkusega üle 7 500 aluspaari (**I**). Analüüs, mis põhines 37 liigil – sealhulgas hõlmates 22-st Euroopa sirptiiblasest 21 – kinnitas kõigi nelja tunnustatud alamsugukonna monofüleetilisust. Lisaks näitasid tulemused, et alamsugukonnad *Oretinae* ja *Drepaninae* moodustavad sõsarrühmade paarina ühe põhiklaadi, samas kui alamsugukonnad *Cyclidiinae* ja *Thyatirinae* moodustavad teise. Analüüs näitas, et *Drepaninae* + *Oretinae* rühmale iseloomulikud sirpja kujuga tiivatipud on korra tekkinuna evolutsiooni käigus korduvalt kadunud. Alamsugukonna *Thyatirinae* sees moodustavad „talveliblikad" (liigid, mis on aktiivsed varakevadel või hilissügisel) selgelt eristuva ja tugevalt toetatud klaadi. Lisaks moodustasid statistiliselt hästi toetatud klaadi need *Thyatirinae* perekonnad, mille liikide eestiibadel leidub roosasid või oranže laike.

Põhja-Euroopa vaksiklaste (*Geometridae*) täielik fülogeneesipuu (**II**) rekonstrueeriti kaheetapilise lähenemise abil. Esmalt koostati aluspuu 117 vaksikuliigi ja 35 välisrühma liigi andmestiku põhjal, mis tugines hübriidse rikastamise (AHE) meetodil sekveneeritud 648 valke kodeerivale lookusele (209 499 bp). Saadud aluspuu ühendati seejärel taksonoomiliselt laiema andmestikuga, mis hõlmas 376 Põhja-Euroopa liiki ning täiendavalt 98 võtmetaksonit mujalt maailmast, mille jaoks sekveneeriti Sangeri meetodi abil 11 traditsioonilist valku kodeerivat geeni. Suurima tõepära meetodil saadud fülogeneesipuu oli hästi lahenenud, enamik sügavaid harusid sai maksimaalse statistilise toetuse. Tehti mitu taksonoomilist muudatust: kirjeldati uued triibused *Lampropterygini* ja *Pelurgini*, taastati *Ochyria* kui eraldiseisev monotüüpne perekond, mõned teised perekonnad (näiteks *Costaconvexa*, *Artiora*, *Selenia* ja *Epirranthis*) paigutati fülogenoomilistele ja morfoloogilistele tõenditele tuginedes teistesse triibustesse. Täiendavad muudatused hõlmasid seni sünonüümidena käsitletud perekondade „taaselustamist" (nt *Ochyria*, *Epelis*, *Speranza*), liikide üleviimist „õigesse" perekonda (nt *Xanthorhoe*

quadrifasiata on nüüd *Ochyria quadrifasiata*, *Macaria carbonaria* on nüüd *Epelis carbonaria*) ning triibuste ümberkujundamist monofüleetilisuse säilitamiseks (kõige olulisema sellise muutusena viidi *Epirranthis* triibusesse *Rumiini*). Uuring kinnitas paljusid varem oletatud fülogeneetilisi suhteid alamsugukondade ja triibuste vahel ning lahendas mitmeid vastuolusid, eriti alamsugukondades kirivaksiklased (*Larentiinae*) ja metsavaksiklased (*Ennominae*). Kokkuvõttes asetab see töö kõik Põhja-Euroopa vaksiklased usaldusväärsete andmetega toetatud fülogeneetilise raamistikku ning toetab võtmetähtsusega taksonoomilisi muudatusi, mis tuginevad nii molekulaarsetele kui morfoloogilistele tõenditele.

Järgmises töös (**III**) viidi fülogeneetiline analüüs läbi 296 öölaste (*Noctuidae*) sugukonna liigiga, kaasates lisaks lisaks 37 välisrühma liiki. Analüüs, mis põhines 565 valku kodeerival geenil (249 138 bp, AHE andmed), andis tugevalt toetatud sugupuu, mis kinnitab paljusid varasemaid arusaamu, kuid toob kaasa ka olulisi taksonoomilisi muudatusi. Alamsugukondi *Acontiinae* ja *Eustrotiinae* hõlmav klaad osutus kõigi teiste öölaste sõsarrühmaks, millele järgnes *Plusiinae* + *Dyopsinae* haru lahknemine ülejäänud öölastest. Tehti mitu taksonoomilist ümberkorraldust, sealhulgas *Cornutiplusia* sünonümiseerimine *Autographa*-ga, *Senta* sünonüümiseerimine *Leucania*-ga ning *Epilecta* ja *Cryptocala* ühendamine perekonnaga *Noctua*. Perekond *Coenophila* viidi *Xestia* alamperekonnaks ning *Anorthoa* omakorda *Orthosia* alamperekonnaks. Varasem triibus *Prodeniini* tõsteti alamsugukonna tasemele kui *Prodeniinae*, alamtriibus *Poliina* aga triibuse tasemele kui *Poliini*. Täiendavate muudatuste hulka kuulus *Pseudaletia* taastamine kehtiva perekonnana, *Aneda* taaselustamine liigi *Sideridis rivularis* jaoks ning alamtriibuse *Cosmiina* sünonüüminemine alamtriibusega *Xylenina.* Need muudatused täpsustavad öölaste süstemaatikat ja loovad tugeva fülogeneetilise raamistiku edasiseks evolutsiooni- ja ökoloogiaalasteks uuringuks.

Artiklis **III** konstrueeritud fülogeneesipuud kasutati seejärel evolutsiooniliste analüüside jaoks. Kõigepealt kalibreeriti puu ajas, et hinnata eri harude lahknemise aega ja evolutsioonilisi mustreid. Saadud ajaliselt kalibreeritud fülogeneesipuu näitab, et triibus *Apameini* kujunes välja umbes 8,7 miljonit aastat tagasi ehk oluliselt hiljem kui varem arvatud (20–29 miljonit aastat tagasi) (**IV**). Need erinevused peegeldavad tõenäoliselt erinevusi andmestike suuruses ja kalibreerimismeetodites. Käesoleva töö tulemused asetavad *Apameini* mitmekesistumise rohumaade suure laienemise perioodi (3–9 miljonit aastat tagasi), kusjuures BAMM-analüüsid näitavad sõltumatuid liigitekke kiirenemisi perekonnas *Apamea* ja alamtriibuses *Apameina*. Kui juureöölaste (*Apamea*) röövikud toituvad valdavalt väliselt, siis *Apameina* röövikud kaevandavad toidutaimede sees; niisugune toitumisviis ei pruukinud mitte piirata, vaid hoopis soodustada mitmekesisuse kasvu, võimaldades laiendada nišše ja toidutaimedele spetsialiseerumist ning pakkudes kaitset röövloomade eest. Edasised uuringud peaksid täpsustama, kas mitmekesisuse suurenemise ajendas eeskätt taimede sees toitumine ise või sellega kaasnenud toidutaimede vahetus, mis oli seotud rohumaade laienemisega.

REFERENCES

Aarvik, L., Bengtsson, B. Å., Elven, H., Ivinskis, P., Jürivete, U., Karsholt, O. Mutanen, M. & Savenkov, N. (2017). Nordic-Baltic checklist of Lepidoptera. *Norwegian Journal of Entomology*, Supplement 3: 1–236.

Ban, X., Jiang, N., Cheng, R., Xue, D. & Han, H. (2018). Tribal classification and phylogeny of Geometrinae (Lepidoptera: Geometridae) inferred from seven gene regions. *Zoological Journal of the Linnean Society*, 184: 653–672.

Barido-Sottani, J., Schwery, O., Warnock, R. C., Zhang, C. & Wright, A. M. (2024). Practical guidelines for Bayesian phylogenetic inference using Markov chain Monte Carlo (MCMC). *Open Research Europe*, 3: 204.

Beck, H. (1996). Systematische liste der Noctuidae Europas. *Neue Entomologische Nachrichten*, 36: 3–122.

Beck, H. (2000). Larvae of European Noctuidae. Revision of the systematics of the Noctuidae (Lepidoptera: Noctuidae). Herbipoliana 5/4. 512 pp.

Beljaev, E. A. (2016). Superfam. Geometroidea, fam. Geometridae – looper moths. In: Leley, A.S. (Ed.) Annotated catalogue of the insects of Russian Far East. Vol 2: Lepidoptera, Vol. 2. Vladivostok: Dalnauka, pp. 518–666 (in Russian).

Blaimer, B. B., Lloyd, M. W., Guillory, W. X. & Brady, S. G. (2016). Sequence capture and phylogenetic utility of genomic ultraconserved elements obtained from pinned insect specimens. *PLoS ONE,* 11: e0161531.

Börner, C. (1925). Lepidoptera, Schmetterlinge. In: Brohmer, P.: Fauna von Deutschland (3. edn), 358–387.

Börner, C. (1939). Die Grundlagen meines Lepidopterensystems. Verhandlungen des VIII. *Internationalen Kongresses für Entomologie Berlin*, 2: 1372–1424.

Brehm, G., Murillo-Ramos, L., Sihvonen, P., Hausmann, A., Schmidt, B. C., Õunap, E., Moser, A., Mörtter, R., Bolt, D., Bodner, F. & Lindt, A. (2019). New World geometrid moths (Lepidoptera: Geometridae): Molecular phylogeny, biogeography, taxonomic updates and description of 11 new tribes. *Arthropod Systematics and Phylogeny*, 77: 457–486.

Breinholt, J. W., Earl, C., Lemmon, A. R., Lemmon, E. M., Xiao, L. & Kawahara, A. Y. (2018). Resolving relationships among the megadiverse butterflies and moths with a novel pipeline for anchored phylogenomics. *Systematic Biology*, 67: 78–93.

Brower, A. V. Z. (1994). Phylogeny of *Heliconius* butterflies inferred from mitochondrial DNA sequences (Lepidoptera: Nymphalidae). *Molecular Phylogenetics and Evolution*, 3: 159–174.

Buenaventura, E., Szpila, K., Cassel, B. K., Wiegmann, B. M. & Pape, T. (2020). Anchored hybrid enrichment challenges the traditional classification of flesh flies (Diptera: Sarcophagidae). *Systematic Entomology*, 45: 281–301.

Chazot, N., Condamine, F. L., Dudas, G., Peña, C., Kodandaramaiah, U., Matos-Maraví, P., Aduse-Poku, K., Elias, M., Warren, A. D., Lohman, D. J. & Penz, C. M. (2021). Conserved ancestral tropical niche but different continental histories explain the latitudinal diversity gradient in brush-footed butterflies. *Nature Communications*, 12: 5717.

Cho, S., Zwick, A., Regier, J. C., Mitter, C., Cummings, M. P., Yao, J., Du, Z., Zhao, H., Kawahara, A. Y., Weller, S. & Davis, D. R. (2011). Can deliberately incomplete gene sample augmentation improve a phylogeny estimate for the advanced moths and butterflies (Hexapoda: Lepidoptera)? *Systematic Biology*, 60: 782–796.

Choi, S.-W. (2006). Taxonomic revision of the genera Pareulype Herbulot and Pelurga Hübner (Lepidoptera, Geometridae) in Korea. *Integrative Biosciences*, 10: 103–108

Crotty, S. M., Minh, B. Q., Bean, N. G., Holland, B. R., Tuke, J., Jermiin, L. S. & Haeseler, A. V. (2020). GHOST: recovering historical signal from heterotachously evolved sequence alignments. *Systematic Biology*, 69: 249–264.

Cruaud, A., Rasplus, J. Y., Zhang, J., Burks, R., Delvare, G., Fusu, L., Gumovsky, A., Huber, J. T., Janšta, P., Mitroiu, M. D. & Noyes, J. S. (2024). The Chalcidoidea bush of life: evolutionary history of a massive radiation of minute wasps. *Cladistics*, 40: 34–63.

Darwin, C. (1859). On the origin of species by means of natural selection, or the preservation of favoured races in the struggle for life. London, 502 pp

Davis, R. B., Õunap, E. & Tammaru, T. (2022). A supertree of Northern European macromoths. *PLoS ONE*, 17: e0264211.

Denis, M. & Schiffermüller, I. (1775). Ankundung eines systematischen Werkes von den Schmetterlingen der Wienergeged. Vienna, 324 pp.

Dietrich, C. H., Allen, J. M., Lemmon, A. R., Lemmon, E. M., Takiya, D. M., Evangelista, O., Walden, K. K., Grady, P. G. & Johnson, K. P. (2017). Anchored hybrid enrichment-based phylogenomics of leafhoppers and treehoppers (Hemiptera: Cicadomorpha: Membracoidea). *Insect Systematics and Diversity*, 1: 57–72.

Dobzhansky, T. (1951). Genetics and the origin of species. 2nd edition, Columbia University Press.

Douglas, S. D. (1991). Flower form and pollinator diversity in the Middle Eocene of British Columbia and Washington. M. Sc. thesis, University of Alberta, Edmonton. 342 p.

Douglas, S. D. & Stockey, R. A. (1996). Insect fossils in middle Eocene deposits from British Columbia and Washington State: faunal diversity and geological range extensions. *Canadian Journal of Zoology.* 74: 1140–1157.

Edwards, E. J., Osborne, C. P., Strömberg, C. A., Smith, S. A., C4 Grasses Consortium, Bond, W.J., Christin, P.A., Cousins, A.B., Duvall, M.R., Fox, D.L. & Freckleton, R.P. (2010). The origins of C4 grasslands: integrating evolutionary and ecosystem science. *Science*, 328: 587–591.

Ekblom, R. & Wolf, J. B. (2014). A field guide to whole-genome sequencing, assembly and annotation. *Evolutionary Applications*, 7: 1026–1042.

Espeland, M., Breinholt, J., Willmott, K. R., Warren, A. D., Vila, R., Toussaint, E. F., Maunsell, S.C., Aduse-Poku, K., Talavera, G., Eastwood, R. & Jarzyna, M.A. (2018). A comprehensive and dated phylogenomic analysis of butterflies. *Current Biology*, 28: 770–778.

Ferguson, D. C. (2008). Geometroidea, Geometridae (part): Ennominae (part): Abraxini, Cassymini, Macariini. In: Hodges, R. W., Brown, R. L., Davis, D. R., Lafontaine, J. D., Powell, J. A. & Solis, M. A. (Eds.) Themoths of North America, Fascicle 17.2. Washington: The Wedge Entomological Research Foundation, pp. 1–431.

Fibiger, M. & Lafontaine, J. D. (2005). A review of the higher classification of the Noctuoidea (Lepidoptera) with special reference to the Holarctic fauna. *Esperiana*, 11: 7–92.

Fibiger, M. (1997). Noctuinae III. Noctuidae Europaeae, volume 3. Sorø, 418 pp.

Fonseca, L. H. M. & Lohmann, L. G. (2018). Combining high-throughput sequencing and targeted loci data to infer the phylogeny of the "Adenocalymma-Neojobertia" clade (Bignonieae, Bignoniaceae). *Molecular Phylogenetics and Evolution*, 123: 1–15.

Forbes, W. T. M. (1948). Lepidoptera of New York and neighboring states. Part II: Memoirs of the Cornell University Agricultural Experiment Station, Vol. 274. Cornell University, Agricultural Experiment Station, pp. 1–263.
Friedlander, T. P., Regier, J. C. & Mitter, C. (1992). Nuclear gene sequences for higher level phylogenetic analysis: 14 promising candidates. *Systematic Biology*, 41: 483–490.
Giribet, G., Edgecombe, G. D. & Wheeler, W. C. (2001). Arthropod phylogeny based on eight molecular loci and morphology. *Nature*, 413: 157–161.
Grimaldi, D. & Engel, M. S. (2005). Evolution of the Insects. Cambridge University Press.
Guschanski, K., Krause, J., Sawyer, S., Valente, L. M., Bailey, S., Finstermeier, K., Sabin, R., Gilissen, E., Sonet, G., Nagy, Z. T., Lenglet, G., Mayer, F. & Savolainen, V. (2013). Next-generation museomics disentangles one of the largest primate radiations. *Systematic Biology*, 62: 539–554.
Hacker, H., Ronkay, L. & Hreblay, M. (2002) Hadeninae I. Noctuidae Europaeae, volume 4. Sorø, 419 pp.
Haeckel, E. (1866). Generelle Morphologie der Organismen: Bd. Allgemeine Anatomie der Organismen (Vol. 1). G. Reimer.
Hailay Gebremariam, G. (2024). A systematic review of insect decline and discovery: Trends, drivers, and conservation strategies over the past two decades. *Psyche: A Journal of Entomology*, 2024: 5998962.
Haldane, J. B. (1990). The causes of evolution (Vol. 5). Princeton University Press.
Hausmann, A. & Viidalepp, J. (2012). Larentiinae I. In: The geometrid moths of Europe, Vol. 3. Vester Skerninge: Apollo Books, p. 743.
He, R., Wang, S., Li, Q., Wang, Z., Mei, Y. & Li, F. (2024). Phylogenomic analysis and molecular identification of true fruit flies. *Frontiers in Genetics*, 15: 1414074.
Hennig W. (1950). Grundzüge einer Theorie der phylogenetischen Systematik. Deutscher Zentralverlag. 370 pp.
Hennig, W. (1953). Kritische Bemerkungen zum phylogenetischen System der Insekten. (Mit Beiträgen von H. Bollmann und J. Machatschke). Beiträge zur Entomologie= Contributions to Entomology, 3(Sonderheft), 1–85.
Henning W. (1966). Phylogenetic Systematics, University of Illinois Press, Urbana, Ill.
Hennig, W. (1982). Phylogenetische Systematik, Paul Parey, Berlin.
Herrich-Schäffer, G. A. W. (1843–1856). Systematische Bearbeitung der Schmetterlinge von Europa. – Resensburg, 6 vols.
Holloway, J. (1994). The moths of Borneo, part 11: family Geometridae, subfamily Ennominae. *Malayan Nature Journal*, 47: 1–309.
Homziak, N. T., Storer, C. G., Gall, L. F., Borth, R. & Kawahara, A. Y. (2023). Phylogenomics resolves major relationships of Catocala underwing moths. *Systematic Entomology*, 48: 633–643.
Hübner (1796–1838). Sammlung Europäischer Schmetterlinge. – Augsburg, 7 vols
Huelsenbeck, J. P. & Ronquist, F. (2001). MRBAYES: Bayesian inference of phylogenetic trees. *Bioinformatics*, 17: 754–755.
Hunter, A. F. (1995). The ecology and evolution of reduced wings in forest macrolepidoptera. *Evolutionary Ecology*, 9: 275–287.
Janse, A. J. T. (1932). The Moths of South Africa, Volume I: Sematuridae and Geometridae. E.P. & Commercial Printing Co., Ltd., Durban. 376 pp, 15 pls.
Janse, A. J. T. (1933–1935). The Moths of South Africa, Volume II: Geometridae (Concluded). E.P. & Commercial Printing Co., Ltd., Durban. 448 pp, 15 pls.

Jiang, N., Liu, S., Xue, D. & Han, H. (2016). A review of Cyclidiinae from China (Lepidoptera, Drepanidae). *ZooKeys*, 553: 119–148.

Kaila, L., Nupponen, K., Gorbunov, P. Y., Mutanen, M. & Heikkilä, M. (2020). Ustyurtiidae, a new family of Urodoidea with description of a new genus and two species from Kazakhstan, and discussion on possible affinity of Urodoidea to Schreckensteinioidea (Lepidoptera). *Insect Systematics and Evolution*, 51: 444–471.

Kalyaanamoorthy, S., Minh, B. Q., Wong, T. K., Von Haeseler, A. & Jermiin, L. S. (2017). ModelFinder: fast model selection for accurate phylogenetic estimates. *Nature Methods*, 14: 587–589.

Kawahara, A. Y. & Breinholt, J. W. (2014). Phylogenomics provides strong evidence for relationships of butterflies and moths. *Proceedings of the Royal Society B: Biological Sciences*, 281: 20140970.

Kawahara, A. Y., Plotkin, D., Espeland, M., Meusemann, K., Toussaint, E. F., Donath, A., Gimnich, F., Frandsen, P. B., Zwick, A., Dos Reis, M. & Barber, J. R. (2019). Phylogenomics reveals the evolutionary timing and pattern of butterflies and moths. *Proceedings of the National Academy of Sciences*, 116: 22657–22663.

Kawahara, A. Y., Storer, C., Carvalho, A. P. S., Plotkin, D. M., Condamine, F. L., Braga, M. P., Ellis, E. A., St Laurent, R. A., Li, X., Barve, V. & Cai, L. (2023). A global phylogeny of butterflies reveals their evolutionary history, ancestral hosts and biogeographic origins. *Nature Ecology and Evolution*, 7: 903–913.

Keegan, K. L., Lafontaine, J. D., Wahlberg, N. & Wagner, D. L. (2019). Towards resolving and redefining Amphipyrinae (Lepidoptera, Noctuoidea, Noctuidae): a massively polyphyletic taxon. *Systematic Entomology*, 44: 451–464.

Keegan, K. L., Rota, J., Zahiri, R., Zilli, A., Wahlberg, N., Schmidt, B. C., Lafontaine, J. D., Goldstein, P. Z. & Wagner, D. L. (2021). Toward a Stable Global Noctuidae (Lepidoptera) Taxonomy. *Insect Systematics and Diversity*, 5: 1–24.

Kergoat, G. J., Condamine, F. L., Toussaint, E. F., Capdevielle-Dulac, C., Clamens, A. L., Barbut, J., Goldstein, P. Z. & Le Ru, B. (2018). Opposite macroevolutionary responses to environmental changes in grasses and insects during the Neogene grassland expansion. *Nature Communications*, 9: 5089.

Kergoat, G. J., Goldstein, P. Z., Le Ru, B., Meagher, R. L., Zilli, A., Mitchell, A., Clamens, A.-L., Gimenez, S., Barbut, J., Nègre, N., d'Alençon, E. & Nam, K. (2021). A novel reference dated phylogeny for the genus Spodoptera Guenée (Lepidoptera: Noctuidae: Noctuinae): new insights into the evolution of a pest-rich genus. *Molecular Phylogenetics and Evolution*, 161: 107161.

Kjer, K. M., Simon, C., Yavorskaya, M. & Beutel, R. G. (2016). Progress, pitfalls and parallel universes: a history of insect phylogenetics. *Journal of the Royal Society Interface*, 13: 20160363.

Kopp, A. & True, J. R. (2002). Phylogeny of the Oriental Drosophila melanogaster species group: a multilocus reconstruction. *Systematic Biology*, 51: 786–805.

Kristensen, N. P., Scoble, M. J. & Karsholt, O. K. (2007). Lepidoptera phylogeny and systematics: the state of inventorying moth and butterfly diversity. *Zootaxa* 1668: 699–747

Kristensen, N. P. & Skalski, A.W. (1998). Phylogeny and palaeontology. In: Kristensen, N.P. (Ed) Lepidoptera, Moths and Butterflies, 1. Evolution, systematics and biogeography, Handbuch der Zoologie/ Handbook of Zoology, 4, De Gruyter, Berlin, New York, pp. 7–25

Kristensen, N. P. (1976). Remarks on the family-level phylogeny of butterflies (Insecta, Lepidoptera, Rhopalocera). *Journal of Zoological Systematics and Evolutionary Research*, 14: 25–33.
Kristensen, N. P. (1981). Phylogeny of insect orders. *Annual Review of Entomology*, 26: 135–157.
Kristensen, N. P. (1984). The male genitalia of Agathiphaga (Lepidoptera: Agathiphagidae) and the lepidopteran ground plan. *Insect Systematics and Evolution*, 15: 151–178.
Kristensen, N. P. (Ed). (1998). Lepidoptera, moths and butterflies. Volume 1: evolution, systematics and biogeography. Handbuch der Zoologie/ Handbook of Zoology, 4, De Gruyter, Berlin, New York, 487 pp.
Kristensen, N. P. (Ed.). (2003). Lepidoptera, moths and butterflies (Vol. 2). Berlin & New York, NY: Walter de Gruyter.
Kristensen, N. P., Hilton, D.J., Kallies, A., Milla, L., Rota, J., Wahlberg, N., Wilcox, S.A., Glatz, R.V., Young, D.A., Cocking, G. & Edwards, T. (2015). A new extant family of primitive moths from Kangaroo Island, Australia, and its significance for understanding early Lepidoptera evolution. *Systematic Entomology*, 40: 5–16.
Laszlo G. M., Ronkay G., Ronkay, L. & Witt T. (2007). The Thyatiridae of Eurasia including the Sundaland and New Guinea (Lepidoptera). In: Esperiana. Buchreihe zur Entomologie. Vol. 13. Bad Staff elstein, pp. 7–683.
Lee, K. M., Kivelä, S. M., Ivanov, V., Hausmann, A., Kaila, L., Wahlberg, N. & Mutanen, M. (2018). Information dropout patterns in restriction site associated DNA phylogenomics and a comparison with multilocus Sanger data in a species-rich moth genus. *Systematic Biology*, 67: 925–939.
Lee, M. S. & Palci, A. (2015). Morphological phylogenetics in the genomic age. *Current Biology*, 25: R922–R929.
Lemmon, A. R., Emme, S. A. & Lemmon, E. M. (2012). Anchored hybrid enrichment for massively high-throughput phylogenomics. *Systematic Biology*, 61: 727–744.
Levy Karin, E., Mirdita, M. & Söding, J. (2020). MetaEuk – sensitive, high-throughput gene discovery, and annotation for large-scale eukaryotic metagenomics. *Microbiome*, 8: 1–15
Linnaeus, C. (1758). Systema Naturae. 10th edn. Stockholm. 823 pp.
Mamanova, L., Coffey, A. J., Scott, C. E., Kozarewa, I., Turner, E. H., Kumar, A., Howard, E., Shendure, J. & Turner, D. J. (2010). Target-enrichment strategies for next-generation sequencing. *Nature Methods*, 7: 111–118.
Martinez, J. I. (2022). Discovering the origins of the noctuid moths and systematics of pantheid moths (Lepidoptera: Noctuoidea). A dissertation presented to the graduate school of the University of Florida in partial fulfillment of the requirements for the degree of Doctor of Philosophy. University of Florida. 318 pp.
Martinez, J. I., Homziak, N., Plotkin, D., Couch, C., Pierson, T., Weng, Y.-M. et al. (2024). A new molecular phylogeny of Noctuoidea reveals robust family-level relationships. https://www.royensoc.co.uk/wp-content/uploads/2024/09/Jose-Martinez-A-new-molecular-phylogeny-of-Noctuoidea-reveals-robust-family-level-relationships.pdf [Accessed 26th November 2024].
May, R. M. (1986). Biological diversity: How many species are there?. *Nature*, 324: 514–515.
Miller, M. A., Pfeiffer, W. & Schwartz, T. (2010). Creating the CIPRES science gateway for inference of large phylogenetic trees. Proceedings of the Gateway Computing Environments Workshop (GCE), 14 November 2010, New Orleans, Louisiana, IEEE. pp. 1–8.

Minet, J. & Scoble, M. J. (1999): The Drepanoid/Geometroid Assemblage. In Kristensen N.P. (ed.): Lepidoptera, Moths and Butterflies. Vol. 1. Evolution, Systematics and Biogeography. Handbook of Zoology IV. Arthropoda: Insecta. Part 35. Walter de Gruyter, Berlin, New York, pp. 301–320.

Minet, J. (1986). Ebauche d'une classification moderne de l'ordre des Lepidopteres. *Alexanor*, 14: 291–313.

Misof, B., Liu, S., Meusemann, K., Peters, R. S., Donath, A., Mayer, C., Frandsen, P. B., Ware, J., Flouri, T., Beutel, R.G. & Niehuis, O. (2014). Phylogenomics resolves the timing and pattern of insect evolution. *Science*, 346: 763–767.

Mitter, C., Davis, D. R. & Cummings, M. P. (2017). Phylogeny and evolution of Lepidoptera. *Annual Review of Entomology*, 62: 265–283.

Molleman, F., Wąsala, R., Tambay, A., Davis, R.B., Õunap, E. & Walczak, U. (2025). Larger and polymorphic noctuid moths tend to show less inter-annual abundance variation in the canopy of a temperate forest. *Agricultural and Forest Entomology*, 00, 000–000. Published online 08. August 2025.

Murillo-Ramos, L., Brehm, G., Sihvonen, P., Hausmann, A., Holm, S., Ghanavi, H. R., Õunap, E., Truuverk, A., Staude, H., Friedrich, E. Tammaru, T. & Wahlberg, N. (2019). A comprehensive molecular phylogeny of Geometridae (Lepidoptera) with a focus on enigmatic small subfamilies. *PeerJ*, 7: p.e7386.

Murillo-Ramos, L., Chazot, N., Sihvonen, P., Õunap, E., Jiang, N., Han, H., Clarke, J. T., Davis, R. B., Tammaru, T. & Wahlberg, N. (2021). Molecular phylogeny, classification, biogeography and diversification patterns of a diverse group of moths (Geometridae: Boarmiini). *Molecular Phylogenetics and Evolution*, 162, 107198.

Murillo-Ramos, L., Twort, V., Wahlberg, N. & Sihvonen, P. (2023). A phylogenomic perspective on the relationships of subfamilies in the family Geometridae (Lepidoptera). *Systematic Entomology*, 48: 618–632.

Mutanen, M., Wahlberg, N. & Kaila, L. (2010). Comprehensive gene and taxon coverage elucidates radiation patterns in moths and butterflies. *Proceedings of the Royal Society B: Biological Sciences*, 277: 2839–2848.

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. *Molecular Biology and Evolution*, 32: 268–274.

Õunap, E., Tammaru, T. & Truuverk, A. (2020). Perizomini (Lepidoptera: Geometridae: Larentiinae) are polyphyletic. *Insect Systematics and Evolution,* 51: 489–516.

Õunap, E., Viidalepp, J. & Truuverk, A. (2016). Phylogeny of the subfamily Larentiinae (Lepidoptera: Geometridae): Integrating molecular data and traditional classifications. *Systematic Entomology*, 41: 824–843.

Packard, A. S. (1895). On a new classification of the Lepidoptera. *The American Naturalist*, 29: 636–647.

Paradis, E. & Schliep, K. (2019). ape 5.0: an environment for modern phylogenetics and evolutionary analyses in R. *Bioinformatics*, 35: 526–528.

Patané, J. S. L., Martins, J. & Setubal, J. C. (2024). A Guide to Phylogenomic Inference. In: Setubal, J. C., Stadler, P. F., Stoye, J. (eds) Comparative Genomics. Methods in Molecular Biology, vol 2802. Humana, New York, NY. pp.267–345.

Peña, C., Wahlberg, N., Weingartner, E., Kodandaramaiah, U., Nylin, S., Freitas, A. V. & Brower, A. V. (2006). Higher level phylogeny of Satyrinae butterflies (Lepidoptera: Nymphalidae) based on DNA sequence data. *Molecular Phylogenetics and Evolution*, 40: 29–49.

Percy, D. M., Crampton-Platt, A., Sveinsson, S., Lemmon, A. R., Lemmon, E. M., Ouvrard, D. & Burckhardt, D. (2018). Resolving the psyllid tree of life: phylogenomic analyses of the superfamily Psylloidea (Hemiptera). *Systematic Entomology*, 43: 762–776.

Pierce, F. N. (1909). The Genitalia of the Group Noctuidae of the Lepidoptera of the British Islands. A. W. Duncan. Liverpool. 88 pp, 32 pls.

Pierce, F. N. (1914). The Genitalia of the Group Geometridae of the Lepidoptera of the British Islands. Northern Publishing Company. Liverpool. 86 pp, 48 pls.

Perveen, F. K. & Khan, A. (2018). Introductory Chapter: Moths. Moths-Pests of Potato, Maize and Sugar Beet; IntechOpen: London, UK.

Prout, L. B. (1912 – 1916). Die spanner des Palaearktischen Faunengebietes. In: Seitz, A. (Ed.) Die Gross-Schmetterlinge der Erde, Band 4. Stuttgart: Verlag A. Kernen, pp. 1–479.

Rajaei, H. S., Greve, C., Letsch, H., Stüning, D., Wahlberg, N., Minet, J. & Misof, B. (2015). Advances in Geometroidea phylogeny, with characterization of a new family based on Pseudobiston pinratanai (Lepidoptera, Glossata). *Zoologica Scripta*, 44: 418–436.

Rajaei, H., Hausmann, A., Scoble, M., Wanke, D., Plotkin, D., Brehm, G., Murillo-Ramos, L. & Sihvonen, P. (2022). An online taxonomic facility of Geometridae (Lepidoptera), with an overview of global species richness and systematics. Integrative Systematics: Stuttgart Contributions to Natural History, 5: pp.145–192.

Rambaut, A. (2018). FigTree: tree figure drawing tool (Version 1.4.4). Retrieved from http://tree.bio.ed.ac.uk/software/figtree.

Regier, J. C., Mitter, C., Zwick, A., Bazinet, A. L., Cummings, M. P., Kawahara, A. Y., Sohn, J. C., Zwickl, D. J., Cho, S., Davis, D. R. & Baixeras, J. (2013). A large-scale, higher-level, molecular phylogenetic study of the insect order Lepidoptera (moths and butterflies). *PLoS ONE*, 8: p.e58568.

Regier, J. C., Zwick, A., Cummings, M. P., Kawahara, A. Y., Cho, S., Weller, S., Roe, A., Baixeras, J., Brown, J. W., Parr, C. & Davis, D. R. (2009). Toward reconstructing the evolution of advanced moths and butterflies (Lepidoptera: Ditrysia): an initial molecular study. *BMC Evolutionary Biology*, 9: p.280.

Revell, L. J. (2012). phytools: an R package for phylogenetic comparative biology (and other things). *Methods in Ecology and Evolution,* 2: 217–223.

Rokas, A., Williams, B. L., King, N. & Carroll, S. B. (2003). Genome-scale approaches to resolving incongruence in molecular phylogenies. *Nature*, 425: 798–804.

Rota, J., Zacharczenko, B. V., Wahlberg, N., Zahiri, R., Schmidt, B. C. & Wagner, D. L. (2016). Phylogenetic relationships of Acronictinae with discussion of the abdominal courtship brush in Noctuidae (Lepidoptera). *Systematic Entomology*, 41: 416–429.

Saitou, N. & Nei, M. (1987). The neighbor-joining method: a new method for reconstructing phylogenetic trees. *Molecular Biology and Evolution*, 4: 406–425.

Sanderson, M. J. & Donoghue, M. J. (1989). Patterns of variation in levels of homoplasy. *Evolution*, 43: 1781–1795.

Savard, J., Tautz, D., Richards, S., Weinstock, G. M., Gibbs, R. A., Werren, J. H., Tettelin, H. & Lercher, M. J., (2006). Phylogenomic analysis reveals bees and wasps (Hymenoptera) at the base of the radiation of Holometabolous insects. *Genome Research*, 16: 1334–1338.

Schmitt, M. (2013). From taxonomy to phylogenetics–life and work of Willi Hennig. Brill. Boston. pp 208

Scotland, R. W., Olmstead, R. G. & Bennett, J. R. (2003). Phylogeny reconstruction: the role of morphology. *Systematic Biology*, 52: 539–548.
Scudder, G. G. (2017). The importance of insects. Insect biodiversity: science and society, R. G. Foottit, P. H. Adler, Eds. Wiley Blackwell, Oxford, United Kingdom, ed. 2, pp. 9–43.
Sihvonen, P. & Kaila, L. (2004). Phylogeny and tribal classification of Sterrhinae with emphasis on delimiting Scopulini (Lepidoptera: Geometridae). *Systematic Entomology*, 29: 324–358.
Sihvonen, P., Mutanen, M., Kaila, L., Brehm, G., Hausmann, A. & Staude, H. S. (2011). Comprehensive molecular sampling yields a robust phylogeny for geometrid moths (Lepidoptera: Geometridae). *PLoS ONE*, 6: e20356.
Sihvonen, P., Staude, H. S. & Mutanen, M. (2015). Systematic position of the enigmatic African cycad moths: an integrative approach to a nearly century old problem (Lepidoptera: Geometridae, Diptychini). *Systematic Entomology*, 40: 606–627.
Sihvonen, P., Murillo-Ramos, L., Brehm, G., Staude, H. & Wahlberg, N. (2020). Molecular phylogeny of Sterrhinae moths (Lepidoptera: Geometridae): towards a global classification. *Systematic Entomology*, 45: 606–634.
Song, W. H., Xue, D. Y. & Han, H. X. (2012). Revision of Chinese Oretinae (Lepidoptera, Drepanidae). *Zootaxa*, 3445: 1–36.
Sperling, F. A. (1993). Mitochondrial DNA phylogeny of the *Papilio machaon* species group (Lepidoptera: Papilionidae). *The Memoirs of the Entomological Society of Canada*, 125: 233–242.
Sperling, F. A. & Hickey, D. A. (1994). Mitochondrial DNA sequence variation in the spruce budworm species complex (*Choristoneura*: Lepidoptera). *Molecular Biology and Evolution*, 11: 656–665.
St Laurent, R. A., Carvalho, A. P. S., Earl, C. & Kawahara, A. Y. (2021). Food plant shifts drive the diversification of sack-bearer moths. *The American Naturalist*, 198: E170–E184.
St Laurent, R. A., Goldstein, P. Z., Miller, S. E. & Robbins, R. K. (2024). Hiding in plain sight: Phylogenomics reveals a new branch on the Noctuoidea tree of life. *Systematic Entomology*, 49: 258–278.
St Laurent, R. A., Goldstein, P. Z., Prada-Lara, L., Schintlmeister, A., Miller, S. E., Miller, J. S. & Robbins, R. K. (2025). Phylogenomics of Prominent Moths (Lepidoptera: Notodontidae): A Subfamily-Level Reclassification. *Smithsonian Contributions to Zoology*, 657: 1–133.
Stadler, T. (2009). On incomplete sampling under birth–death models and connections to the sampling-based coalescent. *Journal of Theoretical Biology*, 261: 58–66.
Stamatakis, A. (2014). RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. *Bioinformatics*, 30: 1312–1313.
Sterneck, J. V. (1941). Versuch einer Darstellung der systematischen Beziehungen bei den paläarktischen Sterrhinae (Acidaliinae), Studien über Acidaliinae (Sterrhinae) IX. Zeitschrift des Wiener Entomologen-Vereines, 26: 248–262.
Tay, J. H., Kocher, A. & Duchene, S. (2024). Assessing the effect of model specification and prior sensitivity on Bayesian tests of temporal signal. *PLOS Computational Biology*, 20: e1012371.
Timmermans, M. J., Lees, D. C. & Simonsen, T. J. (2014). Towards a mitogenomic phylogeny of Lepidoptera. *Molecular Phylogenetics and Evolution*, 79: 169–178.
Top, M., Fritsch, D. & Kononenko, V. (2023). Noctuidae Europaeae Essential. Bugbook Publishing. Oestermarie, Bornholm. 840 pp.

Toussaint, E. F., Condamine, F. L., Kergoat, G. J., Capdevielle-Dulac, C., Barbut, J., Silvain, J. F. & Le Ru, B. P. (2012). Palaeoenvironmental shifts drove the adaptive radiation of a noctuid stemborer tribe (Lepidoptera, Noctuidae, Apameini) in the Miocene. *PLoS ONE*, 7: e41377

Trautwein, M. D., Wiegmann, B. M., Beutel, R., Kjer, K. M. & Yeates, D. K. (2012). Advances in insect phylogeny at the dawn of the postgenomic era. *Annual Review of Entomology*, 57: 449–468.

Ude, K., Õunap, E., Davis, R. & Tammaru, T. (2025). Phylogenetic analysis of the "winter moth syndrome": ecological correlates of female flightlessness and cold-season activity in Geometridae. *Evolutionary Ecology*, in press.

Ude, K., Õunap, E., Kaasik, A., Davis, R.B., Javoiš, J., Nedumpally, V., Foerster, S. I. & Tammaru, T. (2024). Evolution of wing shape in geometrid moths: phylogenetic effects dominate over ecology. *Journal of Evolutionary Biology*, 37: 526–537.

van Nieukerken, E. J., Kaila, L., Kitching, I. J., Kristensen, N. P., Lees, D. C., Minet, J., Mitter, C., Mutanen, M., Regier, J. C., SSimonsen, T. J. et al. (2011). Zhang, Z.-Q. (ed.). "Order Lepidoptera Linnaeus, 1758" (PDF). Animal biodiversity: An outline of higher-level classification and survey of taxonomic richness. *Zootaxa*, 3148: 212–221.

Varga, Z., Ronkay, G., Gyulai, P., Kiss, A. & Ronkay, L. (2020). Noctuinae III. Poliina. Taxonomic Atlas of the Eurasian and North African Noctuoidea. Volume 11. Heterocera Press, Budapest, 313 pp.

Viidalepp, J. (1996). Checklist of the Geometridae (Lepidoptera) of the former U.S.S.R. Stenstrup: Apollo Books, p. 111.

Wahlberg, N. & Wheat, C. W. (2008). Genomic outposts serve the phylogenomic pioneers: designing novel nuclear markers for genomic DNA extractions of Lepidoptera. *Systematic Biology*, 57: 231–242.

Wahlberg, N., Wheat, C. W. & Peña, C. (2013). Timing and patterns in the taxonomic diversification of Lepidoptera (butterflies and moths). *PLoS ONE*, 8: e80875.

Weismann, A. (1893). The germ-plasm: a theory of heredity. Charles Scribner's Sons, New York, USA.

Wiens, J. J. (2001). Character analysis in morphological phylogenetics: problems and solutions. *Systematic Biology*, 50: 689–699.

Woese, C. R. & Fox, G. E. (1977). Phylogenetic structure of the prokaryotic domain: the primary kingdoms. *Proceedings of the National Academy of Sciences*, 74: 5088–5090.

Wolfe, J. A. & Wehr, W. (1987). Middle Eocene dicotyledonous plants from Republic, northeastern Washington. *US Geological Survey Bulletin*. 1597: 1–25.

Wu, C. G., Han, H. X. & Xue, D. Y. (2010). A pilot study on the molecular phylogeny of Drepanoidea (Insecta: Lepidoptera) inferred from the nuclear gene EF-1α and the mitochondrial gene COI. *Bulletin of Entomological Research,* 100: 207–216.

Yang, Z. (1996). Phylogenetic analysis using parsimony and likelihood methods. *Journal of Molecular Evolution*, 42: 294–307.

Zahiri, R., Kitching, I. J., Lafontaine, J. D., Mutanen, M., Kaila, L., Holloway, J. D. & Wahlberg, N. (2011). A new molecular phylogeny offers hope for a stable family level classification of the Noctuoidea (Lepidoptera). *Zoologica Scripta*, 40: 158–173.

Zahiri, R., Lafontaine, D., Schmidt, C., Holloway, J. D., Kitching, I. J., Mutanen, M. & Wahlberg, N. (2013). Relationships among the basal lineages of Noctuidae (Lepidoptera, Noctuoidea) based on eight gene regions. *Zoologica Scripta*, 42: 488–507.

Zahiri, R., Schmidt, B. C., Schintlmeister, A., Yakovlev, R. V. & Rindoš, M. (2019). Global phylogeography reveals the origin and the evolutionary history of the gypsy moth (Lepidoptera, Erebidae). *Molecular Phylogenetics and Evolution*, 137: 1–13.

Zhang, F., Ding, Y., Zhu, C. D., Zhou, X., Orr, M. C., Scheu, S. & Luan, Y. X. (2019). Phylogenomics from low-coverage whole-genome sequencing. *Methods in Ecology and Evolution*, 10: 507–517.

Zhang, H., He, L. & Cai, L. (2018). Transcriptome Sequencing: RNA-Seq. In: Huang, T. (eds) Computational Systems Biology. Methods in Molecular Biology, vol 1754. Humana Press, New York.

Zhang, Y. M., Bossert, S. & Spasojevic, T. (2025). Evolving perspectives in Hymenoptera systematics: Bridging fossils and genomes across time. *Systematic Entomology*, 50: 1–31.

Zhang, Z. Q. (2013). Phylum Arthropoda. In: Zhang, Z.-Q. (Ed.) Animal biodiversity: An outline of higher-level classification and survey of taxonomic richness (Addenda 2013). *Zootaxa*, 3703: 17–26.

Zilli, A., Ronkay, L. & Fibiger, M. (2005). Apameini. Noctuidae Europaeae, volume 8. Sorø, 323 pp.

Zou, Y., Zhang, Z., Zeng, Y., Hu, H., Hao, Y., Huang, S. & Li, B. (2024). Common methods for phylogenetic tree construction and their implementation in R. *Bioengineering*, 11: 480.

Zwick, A., Regier, J. C., Mitter, C. & Cummings, M. P. (2011). Increased gene sampling yields robust support for higher-level clades within Bombycoidea (Lepidoptera). *Systematic Entomology*, 36: 31–43.

ACKNOWLEDGEMENTS

I would like to express my deepest gratitude to my supervisors, Erki Õunap and Toomas Tammaru. My sincere gratitude goes to Erki Õunap, who has been involved in my work from its very beginning through to the final stage of this thesis. He has made numerous valuable contributions to my articles and the thesis, and I deeply appreciate the time and effort he has dedicated to guiding me. Beyond his scientific input, I have learned important academic and professional values from him, which will undoubtedly be a valuable asset throughout my career. Throughout my studies, he has always been kind and approachable, never showing the dark side of his face, which created an environment where I always felt supported, and I am truly grateful for his mentorship throughout my studies.

Toomas Tammaru has been a constant source of support and encouragement throughout my studies. His expertise and sharp scientific insight have been invaluable in shaping the direction of my research, and his patience and approachability made every stage of this journey smoother. I am especially grateful for his ability to foresee challenges – such as the mind-bending logic of a certain reviewer's comments, which could have delayed article acceptance – and to propose effective solutions (such as suggesting the preparation of an additional article) that ensured the timely completion of this thesis. His insightful feedback and dedication have not only strengthened my articles and thesis but have also deeply inspired me as a researcher.

I would like to take this opportunity to thank Niklas Wahlberg and Jadranka Rota for hosting me at Lund University. I am also grateful to Etka Yapar for guiding me from basic Linux skills to the final stages of my analysis, and for being such a kind and wonderful friend. Many thanks to our collaborator Alberto Zilli, whose valuable input greatly shaped my article III. I am also grateful to our collaborator Alan R. Lemmon for his contribution with sequencing, even though the results arrived much later than expected – better late than never. I sincerely acknowledge John Clarke and Robert B. Davis for their invaluable analytical support and guidance.

I would like to thank Sille Holm, who truly understands the challenges faced by a foreigner. During my early days in Estonia, she was kind enough to offer her help and invited all PhD students to her home, making me feel that I was not living in an alien world – a kindness and support that continues to this day. I would also like to thank Toomas Esperk for his valuable suggestions and comments during lab meetings and department seminars, as well as for giving me the opportunity to enjoy my first beach experience in Estonia at his summer house. I am equally grateful to Tiit Teder for his insightful suggestions and comments during lab meetings and department seminars, and for helping me explore the bogland, which I had never visited before.

The transition from the crowding effect (in India) to the low-density effect (in Estonia) was somewhat challenging. I am grateful to Nidal Fetnassi for her supportive friendship and unwavering encouragement. Her moral support and positive presence were invaluable throughout this period. Later, Kerli Kuusk joined

our circle, helping me recover from the low-density effect by giving candies and chocolate and guiding me to explore and learn more about Estonia, I take this opportunity to thank her for everything. I thank Hannah for her friendship, understanding and encouragement, provided invaluable support during my studies. I also take this opportunity to thank my good friends in Estonia: Stenio Foerster, Leonard Opare, Auli Veske, Tristan van Laar and Kadri Ude. Additionally, I am grateful to Margret Sisask and Eve Möls for their administrative support.

Last but not least, I am deeply grateful to the pillars of my life, my son Ivaan (whose every smile brightens my days) and my wife Anagha, whose unwavering support has been my greatest strength. I am forever thankful to Anagha for taking on the responsibility of looking after our son when I am away and for supporting my decision to pursue a PhD, despite its risks. I also admire her courage in taking a one-year leave from her job to join me in Estonia, which allowed us to create many wonderful memories together. I would also like to express my heartfelt gratitude to my parents, brothers, my parents-in-law and other family members for their constant love, support throughout my life. Additionally, I am thankful to social media for reducing the distance between us and helping me stay connected with them every day. This work is supported by the Estonian Research Council grants PRG741 and PRG2618.

PUBLICATIONS

CURRICULUM VITAE

Name: Vineesh Nedumpally
Date of birth: 21.01.1989
Citizenship: Indian
Contact: Department of Zoology, Institute of Ecology and Earth Sciences, J. Liivi 2, 50409, Tartu, Estonia,
E-mail: vineeshnedumpally@gmail.com

Education:

2021– Present	Ph.D. in Zoology and Hydrobiology, University of Tartu, Estonia.
2014–2018	Ph.D. in Biosciences, Mangalore University, India.
2009–2011	M.Sc. in Biotechnology, Bharathiar University, India.
2006–2009	B.Sc. in Biotechnology, University of Calicut, India.

Grants & Scholarships:

2023	Erasmus+ Grant for a three-month traineeship at Lund University, Sweden.
2023	Doctoral school mobility grant for NGS data analysis training at Lund University, Sweden.
2025	Doctoral school mobility grant to attend ESEB conference held in Barcelona, Spain.

Conference presentations

2025	Congress of the European Society for Evolutionary Biology (ESEB 2025), Barcelona, Spain. Poster: Questioning the early Miocene origin of grass-feeding noctuids: evidence from a phylogenomic dataset.
2023	XXIII European Congress of Lepidopterology, Orléans, France. Oral: Phylogenomics of North European Noctuidae based on Anchored Hybrid Enrichment technology.
2022	XXII European Congress of Lepidopterology, Laulasmaa, Estonia. Poster: Phylogenomics of North European Noctuinae based on anchored hybrid enrichment technology.

Research interests: Phylogenetics, population genetics, evolutionary biology, Lepidoptera, insects

Scientific publications:

Nedumpally, **V**., Zilli, A., Yapar, E., Tammaru, T., Lemmon, A. R. & Õunap, E. (2025). Elaborating the phylogeny of Noctuidae by focusing on relationships between north European taxa. *Systematic Entomology*. https://doi.org/10.1111/syen.70010

Nedumpally, **V**., Õunap, E. & Tammaru, T. (2024). An insight into the molecular phylogeny of Drepanidae (Lepidoptera) with an emphasis on the European fauna. *European Journal of Entomology*, 121: 385–391.

Õunap, E., **Nedumpally**, **V**., Yapar, E., Lemmon, A.R. & Tammaru, T. (2024). Molecular phylogeny of north European Geometridae (Lepidoptera: Geometroidea). *Systematic Entomology*, 50: 32–67.

Ude, K., Õunap, E., Kaasik, A., Davis, R. B., Javoiš, J., **Nedumpally**, **V**., Foerster, S. I. A. & Tammaru, T. (2024). Evolution of wing shape in geometrid moths: phylogenetic effects dominate over ecology. *Journal of Evolutionary Biology*, 37: 526–537.

Sajikumar, K. K., Sasikumar, G., Viswambharan, D., Rahuman, S., Jeena, N. S., **Vineesh, N**., Binesh, C. P., Koya, K. S., Mahesh, V., Rohit, P. & Asokan, P. K. (2024). Resolving taxonomic ambiguity and distribution of Tremoctopus gracilis (Cephalopoda: Tremoctopodidae) based on molecular evidence. *Marine Biology*, 171: 47.

Vineesh, **N**., Shihab, I., Akhilesh, K. V., Sajeela, K. A., Muktha, M. & Gopalakrishnan, A. (2023). Is *Lutjanus argentimaculatus* genetically connected along the Arabian Sea and Bay of Bengal? A study using microsatellite markers. *Aquaculture*, 562: 738863.

Gopalakrishnan, A., **Vineesh**, **N**., Shihab, I., Akhilesh, K. V., Bineesh, K. K., Menon, M. & Vijayagopal, P. (2021). An insight into the threadfin (Perciformes: Polynemidae) diversity of Indian waters using mitochondrial COI signatures. Thalassas: *An International Journal of Marine Sciences*, 37: 689–700.

Akhilesh, K. V., Rajan, P. T., **Vineesh**, **N**., Idrees Babu, K. K., Bineesh, K. K., Muktha, M., Chellappan, A., Manjebrayakath, H., Gladston, Y. & Nashad, M. (2021). Checklist of serranid and Epinephelid fishes (Perciformes: Serranidae & Epinephelidae) of India. *Journal of the Ocean Science Foundation*, 38: 35–65.

Shihab, I., **Vineesh**, **N**., Reynold, P., Vijayagopal, P. & Gopalakrishnan, A. (2019). Identification of microsatellite loci, gene ontology and functional gene annotations in Indian salmon (*Eleutheronema tetradctylum*) through Next-generation sequencing technology using Illumina platform. *Ecological genetics and genomics*, 100038.

Radhakrishnan, D. P., **Vineesh**, **N**., Kathirvelpandian, A., Basheer, V. S. & Gopalakrishnan. A. (2018). Population structure of Spanish mackerel *Scomberomorus commerson* (Lacepede 1800) in the Northern Indian Ocean determined using microsatellite markers. *Aquatic Living Resources*, 31: 22.

Shihab, I., **Vineesh**, **N**., Mohitha, C., Vijayagopal, P. & Gopalakrishnan, A. (2018). Development and validation of microsatellite markers in a protandrous fish species *Eleutheronema tetradactylum* (Shaw, 1804) through cross-species amplification. *Indian Journal of Fisheries,* 65: 47–51.

Vineesh, **N**., Divya, P. R., Kathirvelpandian, A., Mohitha, C., Shanis, C. P. R., Basheer, V. S., & Gopalakrishnan, A. (2017). Four evolutionarily significant units among narrow-barred Spanish mackerel (*Scomberomorus commerson*) in the Indo-West Pacific region. *Marine Biodiversity*, 48: 2025–2032.

Shihab, I., Gopalakrishnan, A., **Vineesh**, **N**., Muktha, M., Akhilesh, K. V., Jeena, N. S. & Vijayagopal, P. (2017). Histological profiling of gonads depicting protandrous hermaphroditism in *Eleutheronema tetradactylum. Journal of Fish Biology*, 90: 2402–2411.

Gopalakrishnan, A., **Vineesh**, **N**., Shihab, I., Muktha, M., Akhilesh, K.V., Jeena, N. S. & Vijayagopal, P. (2017). Mitochondrial signatures revealed panmixia in Lutjanus argentimaculatus (Forsskål 1775). *Journal of Genetics*, 97: 179–187

Basheer, V. S., **Vineesh**, **N**., Bineesh, K. K., Kumar, R. G., Mohitha, C., Venu, S., Kathirvelpandian, A. Gopalakrishnan, A. & Jena, J. K. (2017). Mitochondrial signatures for identification of grouper species from Indian waters, *Mitochondrial DNA Part A*, 28: 451–457

Divya, P. R., **Vineesh**, **N**., Kathirvelpandian, A., Mohitha, C., Basheer, V. S., Gopalakrishnan, A. & Jena, J. K. (2016). Identification and characterization of microsatellite markers in narrow barred Spanish mackerel, *Scomberomorus commerson* (Lacepede, 1800). *Indian Journal of Fisheries*, 63: 61–65.

Vineesh, **N**., Kathirvelpandian, A., Divya, P. R., Mohitha, C., Basheer, V. S., Gopalakrishnan, A & Jena, J. K. (2016). Hints for panmixia in *Scomberomorus commerson* in Indian waters revealed by mitochondrial ATPase 6 and 8 genes. *Mitochondrial DNA Part A*, 27: 2822–2824.

Bineesh, K. K., Gopalakrishnan, A., Jena J. K., Basheer, V. S., Mohitha, C., **Vineesh**, **N**., Joselet, M. & N. G. K. Pillai. (2015): Molecular identification of Bigeyes Perciformes, Priacanthidae) from Indian waters, *Mitochondrial DNA Part A*, 27: 4638–4642.

Bineesh, K. K., Mohitha, C., **Vineesh**, **N**., Basheer, V. S., Joselet, M. Akhilesh, K. V. Pillai, N. G. K. Jena, J. K. & Gopalakrishnan. A. (2015). Molecular identification of three deepsea fish species of the genus *Chelidoperca* (Perciformes: Serranidae) from Indian waters. *Indian Journal of Fisheries*, 62: 104–108.

Basheer, V. S., Mohitha, C., **Vineesh**, **N**., Divya, P. R., Gopalakrishnan, A. & Jena, J. K. (2014). Molecular phylogenetics of three species of the genus *Rastrelliger* using mitochondrial DNA markers. *Molecular biology reports*, 42: 873–879.

Vineesh, **N**., Mohitha, C., Bineesh, K. K., Kumar, R. G., Gopalakrishnan, A. & Basheer, V. S. (2014). DNA barcoding and taxonomic notes on the genus *Macolor* (Perciformes: Lutjanidae) from Indian waters. *Journal of the Ocean Science Foundation*, 13: 16–26.

ELULOOKIRJELDUS

Nimi: Vineesh Nedumpally
Sünniaeg: 21.01.1989
Kodakontsus: India
Kontaktandmed: Tartu Ülikooli ökoloogia ja maateaduste instituut, zooloogia osakond, J. Liivi 2, 50409, Tartu, Eesti
E-mail: vineeshnedumpally@gmail.com

Haridustee:

2021–	zooloogia ja hüdrobioloogia doktoriõpe, Tartu Ülikool, Eesti
2014–2018	bioteaduste doktoriõpe, Mangalore Ülikool, India
2009–2011	biotehnoloogia magistriõpe, Bharathiari Ülikool, India
2006–2009	biotehnoloogia bakalaureuseõpe, Calicuti Ülikool, India

Uurimistoetused ja stipendiumid:

2023	Erasmus+ stipendium kolmekuuliseks praktikaõppeks Lundi Ülikoolis Rootsis.
2023	Doktoriõppe mobiilsusgrant NGS-andmete analüüsi koolitusel osalemiseks Lundi Ülikoolis, Rootsis.
2025	Doktoriõppe mobiilsusgrant osalemiseks ESEB konverentsil Barcelonas Hispaanias.

Konverentsiettekanded:

2025	Congress of the European Society for Evolutionary Biology (ESEB 2025), Barcelona, Hispaania. Posterettekanne: Questioning the early Miocene origin of grass-feeding noctuids: evidence from a phylogenomic dataset.
2023	XXII European Congress of Lepidopterology, Orléans, Prantsusmaa. Suuline ettekanne: Phylogenomics of North European Noctuidae based on Anchored Hybrid Enrichment technology.
2022	XXII European Congress of Lepidopterology, Laulasmaa, Eesti. Posterettekanne: Phylogenomics of North European Noctuinae based on anchored hybrid enrichment technology.

Peamised uurimisvaldkonnad: fülogeneetika, populatsioonigeneetika, evolutsiooniline bioloogia, liblikalised, putukad

Teaduspublikatsioonid:

Nedumpally, **V**., Zilli, A., Yapar, E., Tammaru, T., Lemmon, A. R. & Õunap, E. (2025). Elaborating the phylogeny of Noctuidae by focusing on relationships between north European taxa. *Systematic Entomology*. https://doi.org/10.1111/syen.70010

Nedumpally, **V**., Õunap, E. & Tammaru, T. (2024). An insight into the molecular phylogeny of Drepanidae (Lepidoptera) with an emphasis on the European fauna. *European Journal of Entomology*, 121: 385–391.

Õunap, E., **Nedumpally**, **V**., Yapar, E., Lemmon, A.R. & Tammaru, T. (2024). Molecular phylogeny of north European Geometridae (Lepidoptera: Geometroidea). *Systematic Entomology*, 50: 32–67.

Ude, K., Õunap, E., Kaasik, A., Davis, R. B., Javoiš, J., **Nedumpally**, **V**., Foerster, S. I. A. & Tammaru, T. (2024). Evolution of wing shape in geometrid moths: phylogenetic effects dominate over ecology. *Journal of Evolutionary Biology*, 37: 526–537.

Sajikumar, K. K., Sasikumar, G., Viswambharan, D., Rahuman, S., Jeena, N. S., **Vineesh, N**., Binesh, C. P., Koya, K. S., Mahesh, V., Rohit, P. & Asokan, P. K. (2024). Resolving taxonomic ambiguity and distribution of Tremoctopus gracilis (Cephalopoda: Tremoctopodidae) based on molecular evidence. *Marine Biology*, 171: 47.

Vineesh, **N**., Shihab, I., Akhilesh, K. V., Sajeela, K. A., Muktha, M. & Gopalakrishnan, A. (2023). Is *Lutjanus argentimaculatus* genetically connected along the Arabian Sea and Bay of Bengal? A study using microsatellite markers. *Aquaculture*, 562: 738863.

Gopalakrishnan, A., **Vineesh**, **N**., Shihab, I., Akhilesh, K. V., Bineesh, K. K., Menon, M. & Vijayagopal, P. (2021). An insight into the threadfin (Perciformes: Polynemidae) diversity of Indian waters using mitochondrial COI signatures. Thalassas: *An International Journal of Marine Sciences*, 37: 689–700.

Akhilesh, K. V., Rajan, P. T., **Vineesh**, **N**., Idrees Babu, K. K., Bineesh, K. K., Muktha, M., Chellappan, A., Manjebrayakath, H., Gladston, Y. & Nashad, M. (2021). Checklist of serranid and Epinephelid fishes (Perciformes: Serranidae & Epinephelidae) of India. *Journal of the Ocean Science Foundation*, 38: 35–65.

Shihab, I., **Vineesh**, **N**., Reynold, P., Vijayagopal, P. & Gopalakrishnan, A. (2019). Identification of microsatellite loci, gene ontology and functional gene annotations in Indian salmon (*Eleutheronema tetradctylum*) through Next-generation sequencing technology using Illumina platform. *Ecological genetics and genomics*, 100038.

Radhakrishnan, D. P., **Vineesh**, **N**., Kathirvelpandian, A., Basheer, V. S. & Gopalakrishnan. A. (2018). Population structure of Spanish mackerel *Scomberomorus commerson* (Lacepede 1800) in the Northern Indian Ocean determined using microsatellite markers. *Aquatic Living Resources*, 31: 22.

Shihab, I., **Vineesh**, **N**., Mohitha, C., Vijayagopal, P. & Gopalakrishnan, A. (2018). Development and validation of microsatellite markers in a protandrous fish species *Eleutheronema tetradactylum* (Shaw, 1804) through cross-species amplification. *Indian Journal of Fisheries,* 65: 47–51.

Vineesh, **N**., Divya, P. R., Kathirvelpandian, A., Mohitha, C., Shanis, C. P. R., Basheer, V. S., & Gopalakrishnan, A. (2017). Four evolutionarily significant units among narrow-barred Spanish mackerel (*Scomberomorus commerson*) in the Indo-West Pacific region. *Marine Biodiversity*, 48: 2025–2032.

Shihab, I., Gopalakrishnan, A., **Vineesh**, **N**., Muktha, M., Akhilesh, K. V., Jeena, N. S. & Vijayagopal, P. (2017). Histological profiling of gonads depicting protandrous hermaphroditism in *Eleutheronema tetradactylum. Journal of Fish Biology*, 90: 2402–2411.

Gopalakrishnan, A., **Vineesh**, **N**., Shihab, I., Muktha, M., Akhilesh, K.V., Jeena, N. S. & Vijayagopal, P. (2017). Mitochondrial signatures revealed panmixia in Lutjanus argentimaculatus (Forsskål 1775). *Journal of Genetics*, 97: 179–187

Basheer, V. S., **Vineesh**, **N**., Bineesh, K. K., Kumar, R. G., Mohitha, C., Venu, S., Kathirvelpandian, A. Gopalakrishnan, A. & Jena, J. K. (2017). Mitochondrial signatures for identification of grouper species from Indian waters, *Mitochondrial DNA Part A*, 28: 451–457

Divya, P. R., **Vineesh**, **N**., Kathirvelpandian, A., Mohitha, C., Basheer, V. S., Gopalakrishnan, A. & Jena, J. K. (2016). Identification and characterization of microsatellite markers in narrow barred Spanish mackerel, *Scomberomorus commerson* (Lacepede, 1800). *Indian Journal of Fisheries*, 63: 61–65.

Vineesh, **N**., Kathirvelpandian, A., Divya, P. R., Mohitha, C., Basheer, V. S., Gopalakrishnan, A & Jena, J. K. (2016). Hints for panmixia in *Scomberomorus commerson* in Indian waters revealed by mitochondrial ATPase 6 and 8 genes. *Mitochondrial DNA Part A*, 27: 2822–2824.

Bineesh, K. K., Gopalakrishnan, A., Jena J. K., Basheer, V. S., Mohitha, C., **Vineesh**, **N**., Joselet, M. & N. G. K. Pillai. (2015): Molecular identification of Bigeyes Perciformes, Priacanthidae) from Indian waters, *Mitochondrial DNA Part A*, 27: 4638–4642.

Bineesh, K. K., Mohitha, C., **Vineesh**, **N**., Basheer, V. S., Joselet, M. Akhilesh, K. V. Pillai, N. G. K. Jena, J. K. & Gopalakrishnan. A. (2015). Molecular identification of three deepsea fish species of the genus *Chelidoperca* (Perciformes: Serranidae) from Indian waters. *Indian Journal of Fisheries*, 62: 104–108.

Basheer, V. S., Mohitha, C., **Vineesh**, **N**., Divya, P. R., Gopalakrishnan, A. & Jena, J. K. (2014). Molecular phylogenetics of three species of the genus *Rastrelliger* using mitochondrial DNA markers. *Molecular biology reports*, 42: 873–879.

Vineesh, **N**., Mohitha, C., Bineesh, K. K., Kumar, R. G., Gopalakrishnan, A. & Basheer, V. S. (2014). DNA barcoding and taxonomic notes on the genus *Macolor* (Perciformes: Lutjanidae) from Indian waters. *Journal of the Ocean Science Foundation*, 13: 16–26.

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 boreo-nemoral 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 inter-annual 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.

442. **Iryna Yatsiuk**. Evolution, species delimitation and diversity in myxomycetes: *Arcyria* and allied genera. Tartu, 2024, 193 p.
443. **Daniela León Velandia**. Mycorrhizal trait distribution and composition in plant communities under natural gradients. Tartu, 2024, 121 p.
444. **Bruno Paganeli**. Dark diversity methods for prioritization of areas and species in nature conservation. Tartu, 2024, 155 p.
445. **Mario Reiman**. Placental transcriptome in normal and complicated pregnancies. Tartu, 2025, 167 p.
446. **Maarja Kõrkjas**. Dynamics of tree-related microhabitats in live forest trees and its links with biodiversity. Tartu, 2025, 134 p.
447. **Eleonora Beccari**. Mapping and exploring trait spaces across the tree of life. Tartu, 2025, 190 p.
448. **Jack R. Hall**. Dissolved organic carbon dynamics of Baltic Sea macroalgae: production, bioavailability and ecosystem effects. Tartu, 2025, 135 p.
449. **Artjom Stepanjuk**. Function of adhesion molecules and signalling pathways in human endometrial and embryonic models. Tartu, 2025, 247 p.
450. **Marianne Kivastik**. Heterostylous plants in an era of global change: the role of local, landscape and climatic actors. Tartu, 2025, 167 p.
451. **Yehor Yatsiuk**. Large tree-cavities as key structures for forest biodiversity. Tartu, 2025, 215 p.
452. **Ovidiu Copoț**. Relevance of eDNA, citizen science, and species distribution modelling for fungal conservation. Tartu, 2025, 198 p.
453. **Tarmo Puurand**. Human genome studies with k-mer frequencies. Tartu, 2025, 184 p.
454. **Stênio Ítalo Araújo Foerster**. Phylogenetic comparative studies of body size in insects and arachnids: from predictions to applications. Tartu, 2025, 171 p.
455. **Hanna Maria Kariis**. Improving pharmacotherapy outcomes in psychiatric and cardiovascular conditions. Tartu, 2025, 193 p.
456. **Elisabeth Prangel**. The impact of land-use change and ecological restoration on biodiversity and ecosystem service supply in semi-natural grasslands. Tartu, 2025, 233 p.
457. **Nidal Fetnassi**. Determinants of moth assemblages across human-modified landscapes of Estonia and Morocco. Tartu, 2025, 162 p.