DISSERTATIONES
BIOLOGICAE
UNIVERSITATIS
TARTUENSIS
383

JHONNY CAPICHONI MASSANTE

Phylogenetic structure of plant communities along environmental gradients: a macroecological and evolutionary approach

DISSERTATIONES BIOLOGICAE UNIVERSITATIS TARTUENSIS

383

DISSERTATIONES BIOLOGICAE UNIVERSITATIS TARTUENSIS

383

JHONNY CAPICHONI MASSANTE

Phylogenetic structure of plant communities along environmental gradients: a macroecological and evolutionary approach

UNIVERSITY OF TARTU
Press

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

Dissertation was accepted for the commencement of the degree of *Doctor philosophiae* in Plant Ecology and Ecophysiology at the University of Tartu on 08 March 2021 by the Scientific Council of the Institute of Ecology and Earth Sciences University of Tartu.

Supervisor: Prof. Pille Gerhold, University of Tartu, Estonia

Opponent: Prof. Zdeňka Lososová, Masaryk University, Czech Republic

Commencement: MS Teams or Zoom, on 11 May 2021 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
ISBN 978-9949-03-579-3 (print)
ISBN 978-9949-03-580-9 (pdf)

University of Tartu Press
www.tyk.ee

CONTENTS

LIST OF ORIGINAL PUBLICATIONS

This thesis is based on the following papers, which are referred to in the text by Roman numerals:

I) **Massante, J.C.**, Götzenberger, L., Takkis, K., Hallikma, T., Kaasik, A., Laanisto, L., *et al.* (2019). Contrasting latitudinal patterns in phylogenetic diversity between woody and herbaceous communities. *Sci. Rep.*, 9, 6443.

II) **Massante, J.C.** & Gerhold, P. (2020). Environment and evolutionary history depict phylogenetic alpha and beta diversity in the Atlantic coastal white-sand woodlands. *J. Veg. Sci.*, 31, 634–645.

III) **Massante, J.C.**, Köbel, M., Pinho, P., Gerhold, P., Branquinho, C. & Nunes, A. (2020). Phylogenetic structure of understorey annual and perennial plant species reveals opposing responses to aridity in a Mediterranean biodiversity hotspot. *Sci. Total Environ.*, 144018.

IV) **Massante, J.C.** & Gerhol, P. (2021). Evolutionary history of marginal habitats influences the diversity of tree communities in the Atlantic Forest. *Manuscript under review.*

Published papers are reproduced with the permission of the publishers.

The author's contribution to the papers:
Was responsible for ***, contributed substantially **, contributed *

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

1. INTRODUCTION

1.1. Background

The distribution of biological diversity on Earth has fascinated naturalists for centuries, making the understanding of diversity patterns and their underlying mechanisms a long-standing goal in ecology and biogeography (Humboldt 1849; Whittaker 1956). Conversely, evolutionary biologists have deviated from that goal and focused on understanding evolutionary changes in organisms rather than how they could influence entire ecological communities. This decoupling between ecological and evolutionary studies prevailed until the second half of the 20th century, when ecologists and evolutionary biologists started investigating both mechanisms and diversity patterns (McGill *et al.* 2019). However, historically, studies addressing diversity patterns have focused on how the number of species is distributed along environmental gradients and across habitat types. For example, one of the earliest and most ubiquitous patterns on Earth is the latitudinal diversity gradient (LDG), in which the number of species decreases polewards (Hillebrand 2004; Mittelbach *et al.* 2007; Schemske & Mittelbach 2017; Kinlock *et al.* 2018). This striking pattern has been found in different taxa both from terrestrial and marine realms (Jablonski *et al.* 2013; Kerkhoff *et al.* 2014; Rolland *et al.* 2014; Piel 2018), although recent evidence has shown that it might not be universal (Fragnière *et al.* 2015; Gaucherel *et al.* 2018). Another conspicuous pattern is the decreasing species richness towards high elevations (Rahbek 1995; Antonelli *et al.* 2018). A clear clue of elevation gradients is the vegetation zonation in mountains, which varies at a far smaller spatial extent relative to LDG (Sanders & Rahbek 2012). It is evident that neither latitude nor elevation are real drivers of species richness. They are instead proxies for gradients in climatic variables, especially temperature (Willig *et al.* 2003). Moreover, species richness patterns along latitude and elevation depend on the way coexisting species are evolutionarily related to each other (phylogenetic relatedness), and how they are adapted to different climatic conditions. However, despite the recognition that ecological and evolutionary mechanisms are intertwined, and the balance between them underlies contemporary species diversity in ecological communities, integrating them to unravel diversity patterns is still challenging (Mouquet *et al.* 2012; Weber *et al.* 2017; McGill *et al.* 2019).

The implementation of the phylogenetic approach in community ecology over the last 20 years has offered a promising alternative to overcome the shortcomings of the classical approach of species richness to understand diversity patterns (Webb 2000; Webb *et al.* 2002; Cavender-Bares *et al.* 2009; Mouquet *et al.* 2012). Specifically, it is assumed that evolution plays a crucial role in the assembly of ecological communities, as coexisting species share evolutionary information that can be measured by the phylogenetic structure of a community (Webb *et al.* 2002). Two communities may have the same number of coexisting species but differ considerably in community phylogenetic structure due to the difference in the way species have evolved and responded to different factors (Fig. 1). A community is phylogenetically clustered when coexisting species are evolutionarily closely related, whereas coexistence of distantly related species results in a phylogenetically overdispersed community (Cavender-Bares *et al.* 2009). The interpretation of these phylogenetic community structure patterns has been overly simplistic, focusing on ecological factors only, namely on the duality between environmental filtering and biotic interactions (Webb *et al.* 2002). Thus, assuming that species traits are conserved throughout evolutionary time, studies have suggested the environment and the interplay between competition and facilitation as drivers of non-random phylogenetic structure of coexisting species (Webb *et al.* 2002; Cavender-Bares *et al.* 2009; Vamosi *et al.* 2009; Valiente-Banuet & Verdú 2013). In communities where environmental filtering prevails,

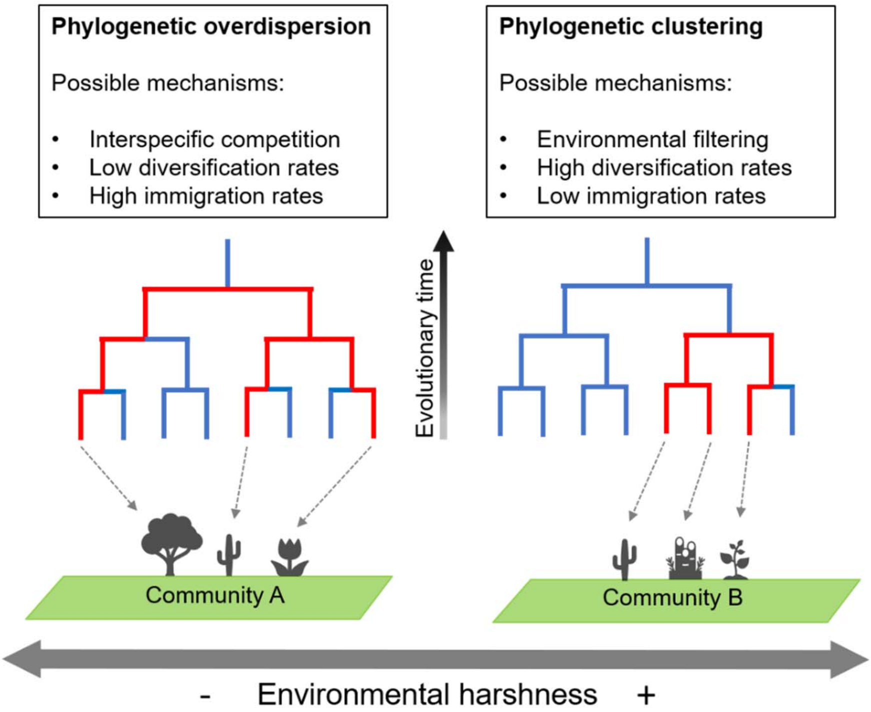

Fig. 1. Schematic representation of phylogenetic community structure patterns. Both communities A and B display the same number of coexisting species. However, species in community A are phylogenetically distantly related (phylogenetic overdispersion), whereas species in community B are closely related (phylogenetic clustering). Some mechanisms that may be involved in the generation of these patterns are presented in the boxes. Red lines indicate the evolutionary path connecting extant coexisting species in communities, whereas blue lines indicate species that either were excluded or did not reach the community. Branch lengths were set to 1. The arrow between the two phylogenies indicates the evolutionary time before present. Copy of Fig. 1 in **III**.

phylogenetic clustering is expected because only a subset of evolutionary lineages may cope with the environmental stress. In contrast, in communities where competition between species is the most relevant factor, phylogenetic overdispersion is expected because closely related species often compete for the same resources, ultimately excluding weaker competitors (Webb *et al.* 2002).

However, traits may not always be conserved, nor competition necessarily leads to overdispersion (Mayfield & Levine 2010; Bennett *et al.* 2013; Gerhold *et al.* 2015). Additionally, in communities located under more extreme environmental conditions, facilitation may prevail over competition (Bertness & Callaway 1994) because some species may increase the realised niche of distantly related less tolerant species, therefore, increasing overdispersion (Butterfield *et al.* 2013; Pistón *et al.* 2016). The phylogenetic structure of communities may also depend on topo-edaphic variables such as soil fertility through habitat specialisation of lineages (Fine & Kembel 2011) and historical and macroevolutionary factors that have shaped the regional species pool (e.g., immigration and diversification, Ricklefs, 1987; Wiens, 2017; Zobel, 2016). Therefore, investigating diversity patterns through an integrative approach involving both ecological and evolutionary mechanisms offers the opportunity to understand how communities have been assembled and ultimately foster the improvement of predictions in ecology (Mouquet *et al.* 2012; Gerhold *et al.* 2018).

Climate is a powerful predictor of both species richness, phylogenetic diversity (i.e., the sum of evolutionary paths connecting species in a given community; Faith 1992) and phylogenetic structure of communities, globally (Kubota *et al.* 2018) and regionally (Kerkhoff *et al.* 2014; Qian & Sandel 2017). The phylogenetic diversity of mammals is unevenly distributed worldwide due to the variation in biogeographic history and diversification rate, with both processes reflecting global climatic gradients (Davies & Buckley 2011). Likewise, amphibian phylogenetic diversity can be traced back to past climate change, being unusually low on islands due to recent radiation of a few lineages and high in biogeographic contact areas (i.e. ecotones) due to high immigration or *in situ* diversification, combined with long-term persistence of old lineages (Fritz & Rahbek 2012). Angiosperm woody plant communities tend to be phylogenetically clustered in drier and historically unstable regions, probably due to tropical niche conservatism (Kubota *et al.* 2018). At a regional scale, phylogenetic diversity of woody angiosperms is low in temperate regions of the American continent (Kerkhoff *et al.* 2014) as an outcome of the tropical conservatism of lineages (Wiens & Donoghue 2004). Tropical niche conservatism has also been suggested as the mechanism underlying the phylogenetic structure of tree angiosperms in North America, where increasing phylogenetic clustering towards regions with extremely dry and cold climates has been shown (Qian & Sandel 2017). However, studies addressing the phylogenetic structure of plant communities were so far focused on a specific taxonomic group (e.g. woody angiosperms) and did not consider other taxonomic groups (e.g. gymnosperms). Gymnosperms occupy large areas both in the Southern Hemisphere (e.g. Podocarpaceae and Araucariaceae) and Northern Hemisphere (e.g. Pinaceae) and show a physiological advantage over angiosperms in cold and dry regions (Bond 1989). Additionally, the presence of different growth forms (i.e. woody and herbaceous species) along the latitudinal gradient depends on their response to climatic variables that correlate with latitude (Engemann *et al.* 2016). Therefore, plant communities of different growth forms may show different responses to latitude. However, there is still insufficient knowledge about plant communities worldwide, with no global-scale study undertaken to examine variation in the phylogenetic structure across a wide taxonomic range of plant communities.

Recently, an increasing number of studies focus on how species are affected by contemporary climate change and anthropogenic factors (e.g. desertification and habitat fragmentation). It has been proposed that changes in species immigration due to climate change will likely affect the phylogenetic diversity of plants, birds, and mammals in Southern Europe in the coming decades (Thuiller et al., 2011). Likewise, rapid climate change may drive spatial phylogenetic homogenisation of woody species (Saladin *et al.* 2020). Among several threatened regions worldwide, coastal plant communities are perhaps the most critical. For example, the coastal vegetation of the South American Atlantic forest domain (hereafter AFD), also called restinga, has undergone massive fragmentation due to human occupation (Neves *et al.* 2017), and the number of extinct species and their evolutionary history is still unknown. Restingas originated in the Quaternary as a result of climatic instability and sea-level rise, and occur in Pleistocene and Holocene sandy sediments of marine origin along over 3,000 km of the Brazilian coast (Martin *et al.* 1993; Scarano 2002). Since climatic instability promoted forest contraction in the southern part of the AFD, whereas large forests remained historically stable in their central range (Carnaval & Moritz 2008), it might be expected that restingas have been influenced by the presence of both temperate and tropical lineages in southern Brazil (Duarte *et al.* 2014) in contrast to central regions of the AFD dominated by tropical lineages. As restingas comprise a geologically young ecosystem, there has been no time for local diversification (Scarano 2002); thus, the contemporary phylogenetic structure may reflect dispersal from neighbouring rainforests. Restingas have also experienced high soil salinity as the major environmental filter for plant species (Neves *et al.* 2017), and there are significant differences in phylogenetic community structure due to edaphic heterogeneity (Oliveira *et al.* 2014). However, no study has been undertaken to understand broad-scale patterns of phylogenetic structure in restingas and their relationship with contemporary and historical climatic variables.

An aspect of the current climatic threat is the risk of desertification due to increasing water scarcity (i.e., aridity) in some regions of the globe. Aridity is a critical factor for species diversity, especially in drylands that occupy ca. 41% of the land surface on Earth (Reynolds et al., 2007). Recent evidence shows that different aspects of drylands are lost with increasing aridity, starting with plant productivity, followed by soil fertility and plant cover and richness (Berdugo *et al.* 2020). Comparably important for ecosystem functioning (Cadotte *et al.* 2009), but with controversies (Venail *et al.* 2015), the phylogenetic diversity and structure of plant communities in drylands have been far less understood than species richness. Studies commonly address the influence of aridity on the phylogenetic structure of either perennial (e.g., Soliveres *et al.* 2012; Gong *et al.* 2019) or annual species (e.g., García-Camacho *et al.* 2017) separately and in different drylands. Annual and perennial species are found co-occurring along aridity gradients and are subjected to an interplay between facilitation and competition (Holzapfel *et al.* 2006). The difference in their life history strategies requires specific adaptations to environmental conditions that lead to an establishment-longevity tradeoff (Tilman 1994). For example, annuals are strongly affected by interannual climatic variability (Tielbörger & Kadmon 1997), which ultimately interfere in seed germination, establishment and dispersal (Facelli *et al.* 2005). As opposed to annuals, perennials must endure stressful conditions during the summer drought in drylands, and do so through a balance between conservative and acquisitive strategies (Liancourt *et al.* 2005). Given the intertwined co-occurrence of annuals and perennials, understanding how their phylogenetic structure responds to aridity is essential to predict diversity in drylands under scenarios of increasing aridity worldwide (Dai 2013).

Predicted scenarios of climate change may also influence species diversity along elevation gradients. It has been shown that the number of plant species in mountains has dramatically increased due to the increase in temperature over the last 145 years (Steinbauer *et al.* 2018). Such a modification has profound consequences on different taxa's phylogenetic structure, especially plants (Zhu *et al.* 2020), as it may inevitably drive mountaintop extinctions (Colwell *et al.* 2008). Studies on phylogenetic community structure along elevation gradients have shown that patterns might be contingent on the taxon investigated and differences in habitat types, especially in the tropics (e.g., Graham *et al.* 2009; Kluge & Kessler 2011; Dehling *et al.* 2014; Bose *et al.* 2019). Such a remarkable discrepancy of patterns in tropical areas may be linked to the fact that habitat types within a specific region display contrasting evolutionary histories based on lineages from different geological epochs (Bartish *et al.* 2016). However, understanding how phylogenetic community structure varies between habitat types along tropical elevation gradients is still challenging (Bose *et al.* 2019). Such information is crucial to understanding the evolution of these habitat types and how they are evolutionarily connected. Ultimately it will allow a more comprehensive understanding of how these systems respond to the effects of climate change.

1.2. Objectives of the thesis

The main objective of this thesis is to address potential ecological and evolutionary mechanisms underlying phylogenetic plant community structure along environmental gradients, with particular attention to possible differences between different growth forms (i.e., woody and herbaceous species worldwide; Massante *et al.* 2019, **I**) and life-history strategies (i.e., annual and perennial species in drylands; Massante *et al.* 2020, **III**). In **I**, data were extracted from original published papers and combined into a global dataset, whereas in **III**, data were previously collected by co-authors in southwest Europe. The thesis also addresses the phylogenetic structure of angiosperm tree species in response to environmental variables and climatic stability (Massante & Gerhold 2020, **II**) as well as elevation and different habitat types (Massante & Gerhold manuscript, **IV**). In both **II** and **IV**, data were retrieved from Tree Flora of the Neotropical region database (NeoTropTree; Oliveira-Filho 2017). Two complementary metrics of phylogenetic community structure were used to reflect the variation at basal (mean pairwise phylogenetic distance, MPD) and terminal phylogenetic levels (mean nearest taxon distance, MNTD) coupled with null models to control for the effect of species richness gradients (Swenson 2014b). Specifically, the thesis addresses the following questions:

Paper **I**: How does the phylogenetic community structure of different growth forms (i.e., woody and herbaceous plant species) relate to latitude?
Paper **II**: What are the relative effects of the current climate, historical climatic stability, and edaphic factors on the phylogenetic structure of angiosperm tree communities in geologically young restinga habitats along the Atlantic coast of Brazil?
Paper **III**: How does the phylogenetic structure of annual and perennial plant communities respond to aridity in Mediterranean semi-natural dryland?
Paper **IV**: How does the phylogenetic structure of angiosperm tree communities respond to elevation in different habitat types in the tropical South American Atlantic forest domain?

2. MATERIAL AND METHODS

2.1. Data collection

A global dataset was compiled from papers indexed in the libraries JSTOR (from 1700 until 1945) and ISI of Web of Knowledge (1945–2016) to investigate latitudinal patterns in the phylogenetic structure of plant communities (paper **I**). Simultaneous occurrence of the keywords "community", "vegetation", "species list", and "plant" were used. To be included in the analysis, papers must have had a full species list regardless of the sampling method (plots, transects, regional surveys). A community was recognised when there were coexisting species recorded in the sampling units. The dataset was further separated into woody communities (trees and shrubs) and herbaceous communities based on the information provided by the authors of the original studies. There were 223 woody communities added from Alwyn Gentry's dataset (Phillips & Miller 2002), previously available from http://salvias.net/pages/database_info.php, now maintained by the Botanical Information and Ecology Network (BIEN – https://bien.nceas.ucsb.edu/bien/). Sampling unit size ranged from < 1 m^2 in herbaceous communities to > 1 km^2 in woody communities. Communities composed of both woody and herbaceous species and partial species lists (e.g. list of dominant species) were excluded from the analysis. Aquatic communities, communities located in anthropogenic habitats, and communities with fewer than three species were also excluded. Overall, there were 459 woody communities with 8,753 species and 589 herbaceous communities with 1,847 species. Woody communities included forests, scrublands and savannas, whereas herbaceous communities included the herbaceous layers of forests, grasslands, meadows, outcrops, salt marshes and dunes. Communities were located between the latitudes of 54.79ºS and 60.67ºN of the equator (Fig. 1 in **I**).

In paper **II** and **IV,** data were retrieved from the Tree Flora of the Neotropical Region database (NeoTropTree – NTT; Oliveira-Filho, 2017). In paper **II**, the phylogenetic diversity of coastal white-sand plant communities (called *Restingas* in Brazil) was analysed. In general, restingas are a mosaic of vegetation that originated in the Quaternary, occurring in Pleistocene and Holocene sandy sediments (Martin *et al.* 1993). Data of 136 restinga communities with 960 tree species, spanning 20º of latitude (Fig. 1 in **II**) were retrieved from the database. Communities were classified as northern, central, and southern restingas based on biogeographic and ecological information (Oliveira-Filho 2017). Southern restingas are considered older than restingas of central Brazil (Delaney 1962; Roncarati & Menezes 2005). Therefore southern restingas have experienced larger climatic instability due to stronger effects of the Quaternary sea-level rise (Delaney 1962). As paper **IV** investigated elevation gradients and differences in species richness and phylogenetic structure between the Atlantic rainforest and its marginal habitat types, data were retrieved for 108 communities within an area of ~44.000 km^2 (Fig. 1 in **IV**) that included 2,074 tree species. These communities are located in a gradient spanning more than 2,000 meters above sea level and four different habitat types (including the rainforest, cloud forest, semideciduous forest and restinga). In both papers **II** and **IV**, the community is a circular area of 10k diameter in which species presence/absence was recorded.

In paper **III,** data were previously collected by members of the Environmental Changes (eChanges) workgroup from the University of Lisbon, with whom the study was developed. The data comprises 54 sites selected through a stratified random selection approach based on the United Nations aridity index (AI; Middleton and Thomas, 1997). These sites are located in Mediterranean drylands dominated by Holm-oak (*Quercus ilex*) woodlands in the southwestern Iberian Peninsula (Fig. S1 in **III**). The sampling of the understorey of Holm-oak woodlands was performed in April-June 2012 to optimise species identification. The point-intercept method was used to estimate plant cover. Six 20 m transects were systematically arranged over an area of ca. 1000 m^2 and 10 m apart from each other, with points spaced every 50 cm (246 points per site) (Nunes *et al.* 2015). At each point, a rod of 5 mm diameter was stuck to the ground with a 90º angle, and all plant species touching the rod only once at each point were recorded. Then, the species cover as the proportion of points intercepted along the six transects was estimated. There were 282 species from 41 families. The original dataset was separated into datasets composed of 191 annual species and 91 perennial species, respectively.

In all papers, species names were standardised according to The Plant List (http://www.theplantlist.org/) using the R package 'Taxonstand' (Cayuela *et al.* 2012) to match the nomenclature available in megaphylogenies. Synonyms of species were merged to their accepted names before further analysis.

2.2. Phylogeny and phylogenetic diversity

2.2.1. Phylogenetic trees

A megaphylogeny approach was used to produce the phylogenetic trees of interest in all papers. The use of megaphylogenies has been demonstrated to be a powerful tool in community phylogenetic analysis because the results obtained with them strongly correlate with the results obtained with precise purpose-built phylogenies (Li *et al.* 2019).

In paper **I,** the most updated megaphylogeny for seed plants available at that time was used, which comprised 79,881 taxa (Smith & Brown 2018), as a backbone to construct a phylogenetic tree containing all species in the dataset. The R function 'S.PhyloMaker' (Qian & Jin 2016) was used to bind species into the backbone within their parental taxa with dated branch lengths. Further, the complete phylogenetic tree was pruned down to two phylogenies that only included either woody or herbaceous species. In paper **II**, **III**, and **IV**, an updated version of the megaphylogeny proposed by Smith and Brown (2018) was used, including plant species from 479 monophyletic families (Jin & Qian 2019).

Species were bounded into the backbone using the same approach as in paper **I** but using the new R package ‘V.PhyloMaker’ (Jin & Qian 2019). Because gymnosperm and pteridophyte species were rare in all communities in papers **II** and **IV**, they were removed from the dataset to prevent bias in the phylogenetic analysis (Massante *et al.* 2019). Gymnosperms and pteridophytes were absent in paper **III**.

2.2.2. Phylogenetic structure

The term phylogenetic diversity was used in papers **I** and **II** for simplicity**.** However, as the used indices reflect the community phylogenetic structure of coexisting species, in paper **III** and **IV,** this term was updated to the most commonly used term, “phylogenetic structure”, and kept in the present thesis. Two complementary indices were used to investigate the variation in the phylogenetic structure at both basal and terminal phylogenetic levels: mean pairwise phylogenetic distance (MPD) and mean nearest taxon distance (MNTD), respectively. MPD is considered a ‘basal phylogenetic metric’ because it estimates phylogenetic distances across the whole phylogenetic tree by averaging all species pairwise distances (Swenson 2014a). MNTD estimates phylogenetic distances at the phylogenetic tree tips, i.e. between each species and its closest relative, thus being considered a ‘terminal phylogenetic metric’ (Swenson 2014a). Gradients in species richness often influence phylogenetic indices (Miller *et al.* 2017). For example, MPD does not correlate with species richness, but its variance decreases with an increase in species richness, whereas MNTD decreases with species richness (Miller *et al.* 2017). Therefore, the standardised effect size of both indices (SESmpd and SESmntd) was calculated to account for the influence of species richness on community phylogenetic analysis. The observed indices values in the communities were compared to a null distribution of randomised communities (N = 1000 randomisations) with equal species richness (eq. 1). Because there was information on the relative abundance of species in paper **III**, the abundance was taken into account using the argument ‘abundance.weighted = TRUE’ implemented in the R package ‘picante’ (Kembel *et al.* 2010). The standardised values of MPD and MNTD are opposite in sign to the common used net related index (NRI) and nearest taxon distance index, respectively (Webb 2000).

$$\mathrm{SESmpd} = \frac{\mathrm{MPDobserved} - \mathrm{MPDnull}}{\mathrm{sd(MPDnull)}} \qquad (1),$$

where MPDobserved is the observed MPD in the community, MPDnull is the average of the expected MPD in the randomised communities (n = 1000 randomisations), and sd(MPDnull) is the standard deviation of 1000 MPDnull values. SESmntd was calculated based on equation (1) by replacing MPD with MNTD.

2.2.2. Taxonomic and phylogenetic beta diversity

Patterns of phylogenetic beta diversity were investigated in paper **II**, and taxonomic and phylogenetic spatial turnover in papers **III** and **IV**. In paper **II**, phylogenetic beta diversity was calculated at basal phylogenetic levels using mean phylogenetic dissimilarity between species in pairs of communities (Dpw, equivalent to the phylogenetic alpha diversity index MPD; Swenson, 2011). The mean nearest taxon distance separating species in two communities (Dnn, equivalent to the phylogenetic alpha diversity index MNTD; Swenson 2011) was used to capture phylogenetic beta diversity variation at terminal phylogenetic levels. Both indices were calculated in the R package 'picante' (Kembel *et al.* 2010). The focus in papers **III** and **IV** was on how species and lineages are replaced along environmental gradients as well as between different habitat types. The turnover component from the Sørensen pairwise dissimilarity, known as Simpson dissimilarity index, is not influenced by species richness gradients (i.e. nestedness – when communities with a low number of species are a subset of communities with a high number of species; Baselga 2010; Leprieur *et al.* 2012) was used as a measure of species turnover between communities. The R functions' beta.pair' and 'phylo.beta.pair' in the R package 'betapart' (Baselga & Orme 2012) were used to calculate taxonomic and phylogenetic turnover, respectively. Further, in paper **IV**, the effects of nestedness on the overall taxonomic and phylogenetic beta diversity were accessed by calculating the relative importance of the nestedness-resultant component (BDratio and PBDratio, respectively) as follows:

$$\text{BDratio} = \frac{\text{BDnestedness}}{\text{BD}} \qquad (2),$$

where BDnestedness is the nestedness-resultant component of the Sorensen pairwise dissimilarity index, and BD is the full Sorensen index (Baselga 2010). Values lower than 0.5 indicate that the variation in BD is basically influenced by spatial turnover. Values higher than 0.5 indicate that variation in BD results from differences in species richness between communities (Dobrovolski *et al.* 2012; Peixoto *et al.* 2017). PBDratio was calculated by replacing values in (2) with those produced with 'phylo.beta.pair'. In that case, PBDnestedness represents the difference in Faith's phylogenetic diversity(PD) between communities.

2.3. Environmental variables

The climatic variables used in most papers were originally retrieved from the database WorldClim at 1 km^2 resolution (Hijmans *et al.* 2005). In paper **II** and **IV,** environmental variables, including climatic and topo-edaphic measures, were already available from the NTT database (Oliveira-Filho 2017). In paper **II**, annual mean temperature and annual precipitation for the Last Glacial Maximum

(LGM, ~21,000 years before present; Hijmans *et al.* 2005) were also extracted and then used to calculate the absolute difference between current and past variables as a proxy for climatic stability to test its influence on the phylogenetic community structure of tree communities. The aridity index (AI) data used in paper **III** were retrieved from the global aridity database (http://www.cgiar-csi.org/data/global-aridity-and-pet-database; Trabucco and Zomer, 2009). The AI represents the ratio of annual precipitation to annual potential evapotranspiration, and its values increase with the decrease in aridity. The complement of the AI (1-AI, hereafter aridity) was used to ease interpretation. In that case, lower values indicate lower aridity (Delgado-Baquerizo *et al.* 2013). In paper **III**, the local slope and its standard deviation within a 250 m radius circular area around the site centroid were estimated as a measure of topographic roughness, based on digital elevation models with 10 m resolution using ArcGIS 10.1 (ESRI 2010). Edaphic variables were obtained by collecting soil samples at each site from the upper 10 cm (composite samples of 5 subsamples) and used to calculate soil nutrient content (soil organic matter, soil N, soil C, and C/N ratio).

The analysis of phylogenetic beta diversity in paper **II** and taxonomic and phylogenetic turnover in papers **III** and **IV** requires dissimilarity matrices between communities, in which the dissimilarity may be calculated using a variety of spatial and environmental variables. A matrix of geographic distance between communities was calculated using the function ‘spDists’ in the R package ‘sp’ (Pebesma & Bivand 2005; Bivand *et al.* 2013) and the Great Circle distance (WGS84 ellipsoid). Then a matrix of the environmental distance between communities was calculated in two steps. First, a principal component analysis (PCA) was applied on environmental variables relevant for the study system, available from each dataset (15 climatic variables in paper **II**, 20 in paper **III**, and 16 in paper **IV**) using the R function ‘prcomp’ (R Core Team 2017). All variables were scaled to have unit variance before calculation. The scores of the first three PCA axes were retrieved. A dissimilarity matrix was then calculated using the ‘dist’ R function (R Core Team 2017) coupled with the ‘Euclidian’ distance method.

2.4. Data analysis

In papers **I**, **II**, and **IV**, there was spatial autocorrelation in the data, and it was accounted for by fitting all models with an additional term describing the correlation structure using the ‘corExp’ function in the R package ‘nlme’ (Pinheiro *et al.* 2017). All continuous variables were centred and scaled to have zero mean and unit variance before parameter estimation to make them comparable within the models.

Due to the hierarchical nature of the data in paper **I**, patterns of SESmpd and SESmntd in both woody and herbaceous communities along the latitudinal gradient were analysed with linear mixed-effect models (LMM) using the function ‘lme’ in the R package ‘nlme’ (Pinheiro *et al.* 2017). Alternative models including combinations of latitude with biogeographic realms (Afrotropical, Australasian, Indo-Malayan, Nearctic, Neotropical, Palearctic) as well as habitat types as fixed effects factors, and study identity as a random factor were built and compared using Akaike Information Criterion values (AIC; Burnham & Anderson 2004). Sampling unit size was included as a covariate in the fixed effects variables of all models to account for its influence on the response variables.

In paper **II**, the effect of latitude and climatic and edaphic factors on SESmpd and SESmntd was explored with generalised least square models (GLS) using the 'gls' function in the R package 'nlme' (Pinheiro *et al.* 2017). A model selection approach with the lowest Akaike Information Criterion values (AIC; Burnham and Johnson, 2004) was used as an indicator of the most parsimonious models. The final models were then refitted using restricted maximum likelihood (REML). Latitudinal patterns of the overall species richness and species richness in the ten most diverse families in restingas were also investigated using GLS.

In papers **III** and **IV,** *a priori* decision based on ecological relevance and collinearity (Pearson's correlation < 0.7) was used to select variables for statistical analysis, reaching out to six and five variables, respectively. Further, a model averaging approach based on Akaike Information Criterion (AIC; Burnham and Johnson, 2004) was applied to the variables using the R package 'MuMIn' (Barton 2019). Coefficients of each variable were estimated by averaging them across all models, then weighted according to the probability associated with each model. As there was no spatial autocorrelation in the data of paper **III**, they were analysed using ordinary least square models (OLS). In paper **IV,** data were analysed using GLS.

Because the use of partial Mantel tests on dissimilarity matrices has been criticised (Legendre & Legendre 2012), a residual approach was adopted to analyse phylogenetic beta diversity in paper **II** and taxonomic and phylogenetic spatial turnover in papers **III** and **IV**. First, linear models were fitted with dissimilarity matrices of diversity as a dependent variable and either the geographic or environmental dissimilarity matrices between communities, including both linear and quadratic terms, as an independent variable (e.g. phylogenetic beta diversity vs geographic distance). Each of these models' residuals was extracted, representing the amount of phylogenetic beta diversity or taxonomic and phylogenetic spatial turnover not explained by geographic or environmental dissimilarity matrices. Mantel tests with 1000 randomisations were used to test the correlation between phylogenetic beta diversity and taxonomic and phylogenetic turnover with geographic and environmental dissimilarity matrices after accounting for each other's effects (residuals from each linear model), using the 'mantel' function on the 'ecodist' R package (Goslee & Urban 2007). In paper **III**, the total variance in taxonomic and phylogenetic spatial turnover was partitioned into fractions explained by space (PCMN vectors; Borcard and Legendre, 2002), climate (matrix including aridity, winter temperature, and summer precipitation), and topo-edaphic variables (slope SD, soil nutrients, and soil C/N ratio) using the function 'varpart' in the 'vegan' R package (Oksanen *et al.* 2019). In paper **IV**, both taxonomic and phylogenetic spatial turnover across different habitat types were visualised using non-metric multidimensional scaling (NMDS). Differences between habitat types were tested using analysis of similarity (ANOSIM) with 1000 permutations in the ‘vegan’ R package (Oksanen *et al.* 2019).

All statistical analyses performed in papers **I–V** were carried out in R version 3.4.3 (R Core Team 2017), and figures were produced using the R package ‘ggplot2’ (Wickham 2016).

3. RESULTS

3.1. Woody and herbaceous communities display contrasting latitudinal patterns of phylogenetic structure

There were contrasting latitudinal patterns in woody and herbaceous plant communities. In woody communities, SESmpd, which estimates variation at basal levels of phylogeny, showed a concave-up relationship with latitude, whereas SESmntd (variation at terminal levels of phylogeny) increased linearly (Fig. 2a, c). In herbaceous communities, SESmpd showed a concave-down relationship with latitude, whereas SESmntd did not show a clear relationship (Fig. 2b, d).

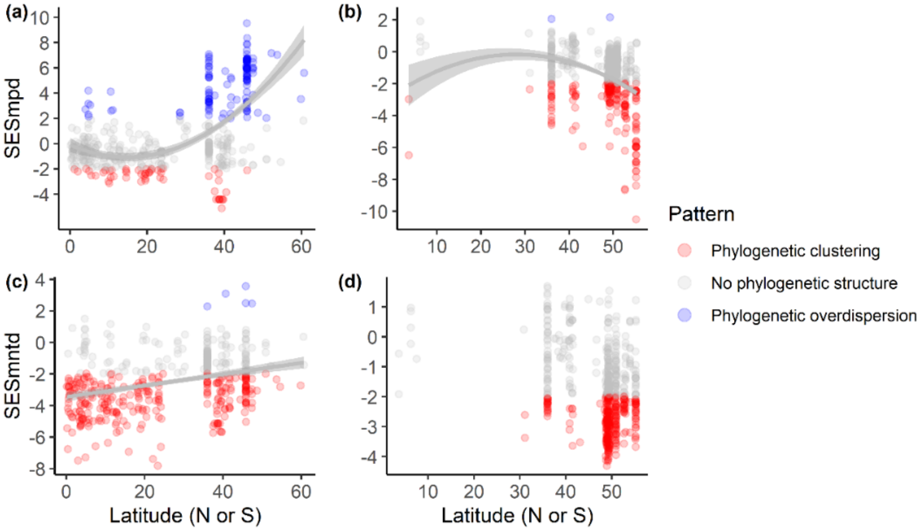

Figure 2. Effect of latitude on the phylogenetic structure of plant communities. The standardised effect size of mean pairwise distance (SESmpd) in woody (**a**) and herbaceous (**b**) communities. The standardised effect size of mean nearest taxon distance (SESmntd) in woody (**c**) and herbaceous (**d**) communities. Lines represent the top-ranked models' predicted values (Full parameter estimates are available in Table 2 in **I**). Shaded areas represent 95% confidence intervals. Modified from figure 2 in **I**.

While habitat type (closed, semi-open, open) influenced patterns of SESmpd in woody communities, it was the most crucial variable for both SESmpd and SESmntd in herbaceous communities, in which both indices were comparably lower in open habitats than in closed ones (Table 2 in **I**; Fig. S2b and d in **I**). Despite an overall phylogenetic clustering in SESmpd, herbaceous communities showed lower values of SESmpd in the Neotropical and Palearctic biogeographic realms than in the Afrotropical realm (Table 2 in **I**; Table S2 and Fig. S2a in **I**). Once gymnosperm species were removed from woody communities, an opposite pattern of SESmpd related to latitude appeared: SESmpd decreased towards higher latitudes (Fig. 3a), whereas SESmntd was not affected by the removal of gymnosperms (Fig. 3b).

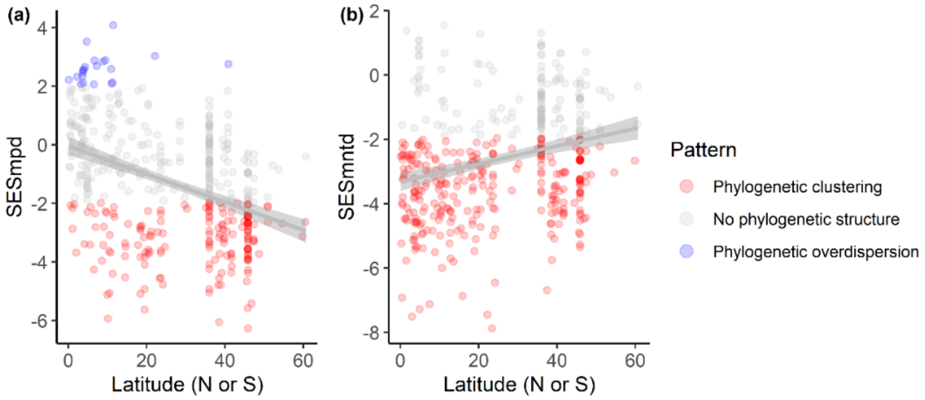

Figure 3. Effect of latitude on the phylogenetic structure of woody communities without gymnosperm species. **(a)** The standardised effect size of mean pairwise distance (SESmpd). **(b)** The standardised effect size of mean nearest taxon distance (SESmntd). Lines represent the top-ranked models' predicted values (Full parameter estimates are available in Table S3 in **I**). Shaded areas represent 95% confidence intervals. Modified from figure S3 in **I**.

3.2. Taxonomic and phylogenetic patterns of Atlantic white-sand coastal vegetation (restingas) in response to differences in climate and soil

The overall angiosperm tree species richness and species richness in the most dominant families showed a unimodal relationship with latitude in restingas (Fig. 2 and 3 in **II**). Both indices of phylogenetic structure showed an overall positive relationship with latitude towards southernmost restingas (Fig. S2 in **II**). SESmpd was lower in northern restingas (Fig. S5c in **II**) than in central and southern restingas. SESmntd was lower in northern and central restingas than in southern restingas (Fig. S5d in **II**).

After accounting for other environmental variables, the phylogenetic structure of restinga communities was no longer correlated with latitude, at least in SESmntd. While SESmpd correlated with precipitation of the driest month and latitude (Fig. 4a), SESmntd positively correlated with the maximum temperature of the warmest month and precipitation of the driest month, as well as historical temperature instability (Fig. 4b). SESmntd also tended to be higher in communities with more fertile and less saline soils (Fig.4b). There was no correlation between phylogenetic beta diversity at basal phylogenetic levels (Dpw) and spatial or environmental distances between communities (Fig. 5a and b in **II**). At terminal phylogenetic levels (Dnn), phylogenetic beta diversity correlated with spatial and environmental distances between communities (Fig. 5c and d in **II**).

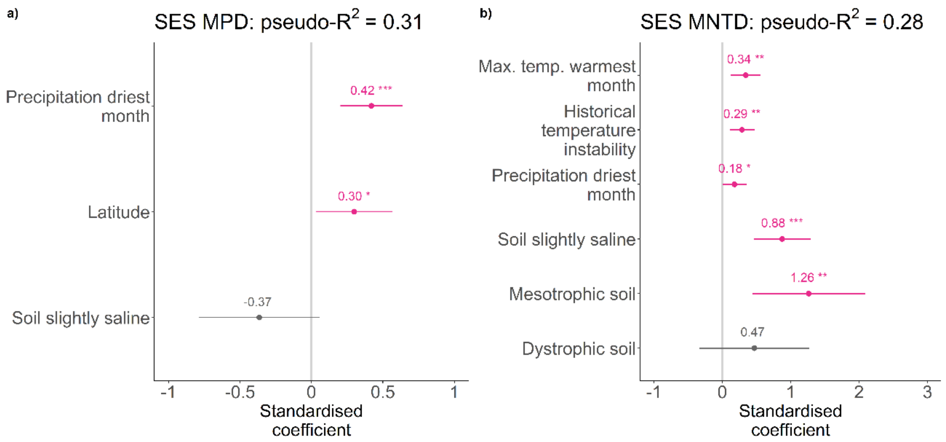

Figure 4. Standardised regression coefficients of model predictors and associated 95% confidence intervals (CI) for the phylogenetic structure of angiosperm tree communities in the Atlantic white-sand coastal woodlands (restingas). **(a)** The standardised effect size of the mean pairwise distance (SESmpd) and **(b)** the standardised effect size of the mean nearest taxon distance (SESmntd). CIs that do not cross the zero line are coloured in green and indicate a statistically significant effect (***, $p < 0.0005$, **, $p < 0.005$; *, $p < 0.05$) on changes in the phylogenetic structure. Pseudo-R^2 values were calculated as the square of the correlation between fitted and observed values in the models. Full parameter estimates are available in Table S5.1 and S5.2 in **II**. Copy of Fig. 4 in **II**.

3.3. Phylogenetic structure of annual and perennial species along an aridity gradient in a Mediterranean dryland

Annual species richness did not show a clear pattern along the aridity gradient, whereas perennials showed a unimodal relationship (Fig. 2a and b in **III**). In both cases, there was a high dispersion of values at intermediate aridity levels. After accounting for other climatic and topo-edaphic variables, annual richness decreased with topographic heterogeneity, whereas that of perennials decreased with aridity and increased with winter temperature (Fig. 4a and b in **III**).

The phylogenetic structure of annuals and perennials showed opposite relationships with aridity. In annuals, SESmpd showed a quadratic relationship (quadratic slope = 3.81 ± 1.63, p = 0.024; Fig. 5a), and SESmntd decreased linearly with aridity (linear slope = –7.06 ± 2.92, p = 0.019; Fig. 5c). Both indices showed phylogenetic clustering at intermediate to high aridity level. In perennials, both SESmpd and SESmntd showed a positive linear relationship with aridity, being more clustered in communities with lower aridity (SESmpd, linear slope = 20.53 ± 6.17, p = 0.001; SESmntd, linear slope = 19.30 ± 4.32, p < 0.001; Fig. 5b and d).

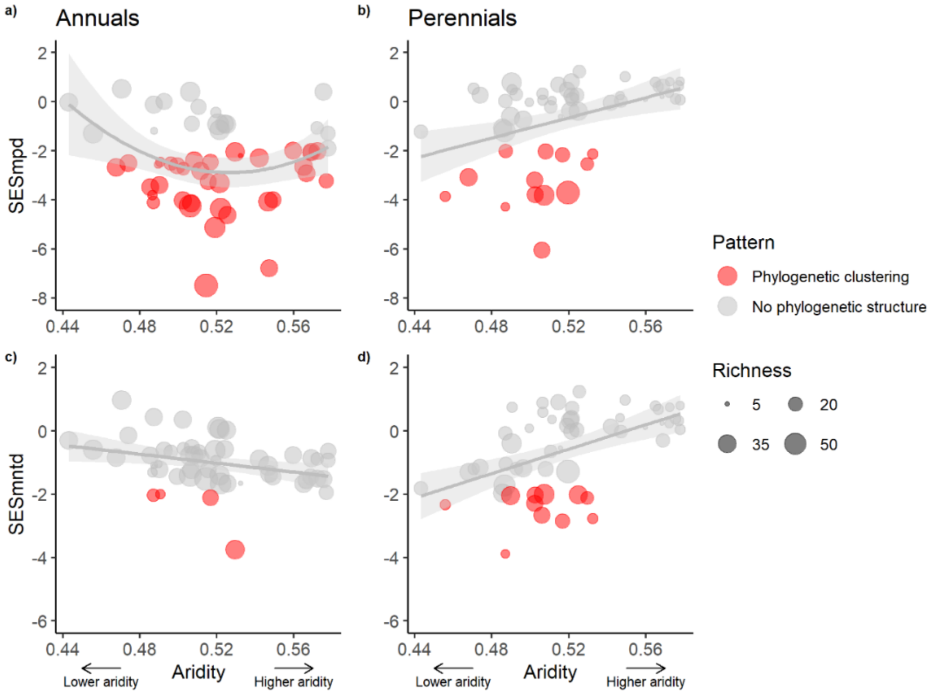

Figure 5. Phylogenetic structure of plant communities along the aridity gradient in Mediterranean drylands. SESmpd = the standardised effect size of the mean pairwise phylogenetic distance, and SESmntd = the standardised effect size of the mean nearest taxon distance. Lines and shaded areas represent the fitted values from linear regression with a quadratic **(a)** and a linear term **(b, c, d)**, and their 95% confidence intervals, respectively. The size of the circle is proportional to the number of species in the community.

After combining aridity with other climatic and topo-edaphic variables, aridity was still a strong predictor of the phylogenetic structure of both annual and perennial communities. Both SESmpd and SESmntd of annuals negatively correlated with aridity and soil nutrient content, indicating clustering in drier communities and communities with higher soil nutrient content (Fig. 4c, e in **III**). In contrast, SESmpd and SESmntd of perennials were more clustered at both phylogenetic levels (SESmpd and SESmntd) in communities located at low to medium aridity and high soil C/N ratio (Fig. 4b, f in **III**).

There was a high taxonomic and phylogenetic turnover between plant communities in both annual and perennial species. After accounting for spatial effects, taxonomic and phylogenetic turnover of both annuals and perennials correlated with the environmental distance between communities (Table 1). Once controlled for the environmental effects, there was no correlation with the spatial distance between communities in either case (Table 1).

Table 1. Mantel test results comparing taxonomic and phylogenetic turnover of annual and perennial components of plant communities with spatial and environmental distances between communities. The relationship between taxonomic and phylogenetic turnover and spatial distance was calculated after accounting for the effect of the environmental distance (i.e. residuals of turnover ~ Env). The relationship between taxonomic and phylogenetic turnover and environmental distance was calculated after accounting for the spatial distance effect (i.e. residuals of turnover ~ spatial).

Life-history strategy	Response	Predictor	Mantel R [95% CI]	p-value
Annuals	Taxonomic turnover	Spatial|Env	0.006 [–0.0 – 0.02]	0.801
		Env|Spatial	**0.36 [0.33 – 0.41]**	**0.001**
	Phylogenetic turnover	Spatial|Env	0.007 [–0.01 – 0.03]	0.780
		Env|Spatial	**0.25 [0.21 – 0.29]**	**0.001**
Perennials	Taxonomic turnover	Spatial|Env	–0.008 [–0.02 – 0.01]	0.765
		Env|Spatial	**0.22 [0.18 – 0.27]**	**0.001**
	Phylogenetic turnover	Spatial|Env	–0.017 [–0.03 – 0.00]	0.531
		Env|Spatial	**0.17 [0.12 – 0.21]**	**0.001**

3.4. Phylogenetic structure of tree communities in the southeast Atlantic forest

Angiosperm tree species richness displayed a tremendous variation across communities in the southeast Atlantic forest domain, ranging from 85 species in restinga to 755 species in rainforest (mean = 285.5, sd = 137.5). Species richness peaked at middle elevations (Fig. 3a in **IV**) and was higher in rainforest and cloud forest than in semideciduous forest and restinga (Fig. 4a and Table S1 in **IV**). Once controlled for elevation and other environmental variables, species richness responded negatively to salinity and water deficit severity and increased with annual precipitation (Fig. 6a in **IV**). Phylogenetic endemism (PE) increased with elevation (Fig. 3b in **IV**) and was higher in cloud and semideciduous forests (Fig. 4b and Table S1 in **IV**). PE did not vary with annual precipitation but was negatively correlated with precipitation seasonality and positively correlated with all other variables (Fig. 6b in **IV**).

The phylogenetic structure of communities at different phylogenetic levels revealed opposing directions along the elevation gradient. SESmpd increased with elevation: communities consisted of species from rather distantly related lineages at high elevations (linear slope = 8.77 ± SE 1.42, $p < 0.001$; Fig. 6a), whereas SESmntd decreased with elevation, with communities consisting of more close relatives at high elevations (linear slope = –6.63 ± 1.13, $p < 0.001$, Fig. 6b). After accounting for other environmental variables, elevation was still a relevant predictor of SESmpd, together with salinity and water deficit: communities located in areas with high salinity and water deficit consisted of close relatives (Fig. 6c in **IV**). SESmntd responded negatively to precipitation seasonality and increased with water deficit, i.e. communities consisted of close relatives at the tips of phylogeny in areas of high precipitation seasonality and distant relative in areas with high water deficit (Fig. 6d in **IV**).

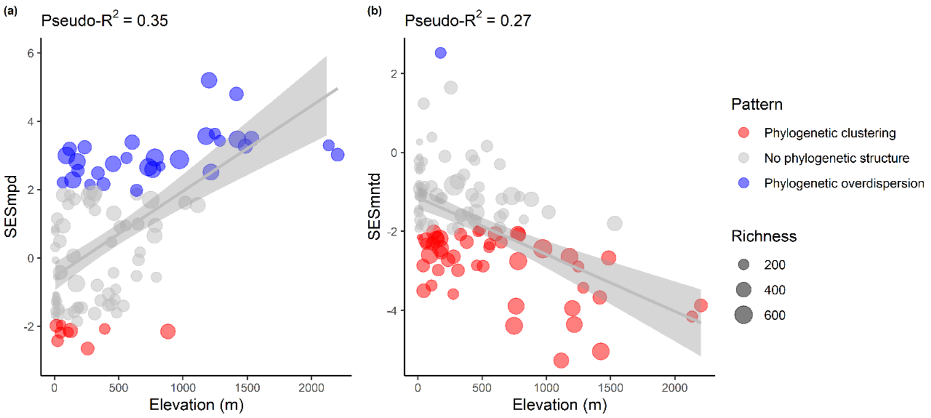

Figure 6. Phylogenetic structure of angiosperm tree communities along elevation gradients in the southeast Atlantic forest domain. **(a)** the standardised effect size of the mean pairwise phylogenetic distance (SESmpd); **(b)** the standardised effect size of the mean nearest taxon distance (SESmntd). Lines were drawn from generalised least squares (GLS), accounting for spatial autocorrelation between communities. Shaded areas represent 95% confidence intervals. Pseudo-R^2 values were calculated as the square of the correlation between fitted and observed values in the models.

Community phylogenetic structure differed significantly across habitat types. While SESmpd was higher in cloud forest and rainforest than in semideciduous forest and restinga (Fig. 7a; Table S1 in **IV**), SESmntd was lower in cloud forest and rainforest compared to semideciduous forest and restinga (Fig. 7b; Table S1 in **IV**). Both indices showed no difference in phylogenetic structure between semideciduous forest and restinga.

The taxonomic and phylogenetic beta diversity analyses showed that the restinga tree communities are likely a subset of rainforest and semideciduous forest communities due to the nestedness effect (i.e. loss of species richness and phylogenetic diversity, respectively; Fig. 7a and b in **IV**). The spatial turnover of species and lineages was the main determinant of the overall habitat types dissimilarity, indicating a high degree of species replacement between them (Fig. 7a and b in **IV**). There was a significant difference in the taxonomic (ANOSIM R = 0.87, p = 0.001) and phylogenetic turnover between habitat types (ANOSIM R = 0.65, p = 0.001, Fig. 7c and d in **IV**). Overall, there was an overlap of 128 species (6% of the total) between all habitat types (Fig. 7e in **IV**). Rainforest and cloud forest showed the highest number of species that did not occur elsewhere

(14% and 13%, respectively), followed by semideciduous forest (4%) and restinga (1.7%). Rainforest shared comparably more species with semideciduous forest and cloud forest (17% and 13.7%, respectively) than with restinga (2.3%, Fig.7e in **IV**).

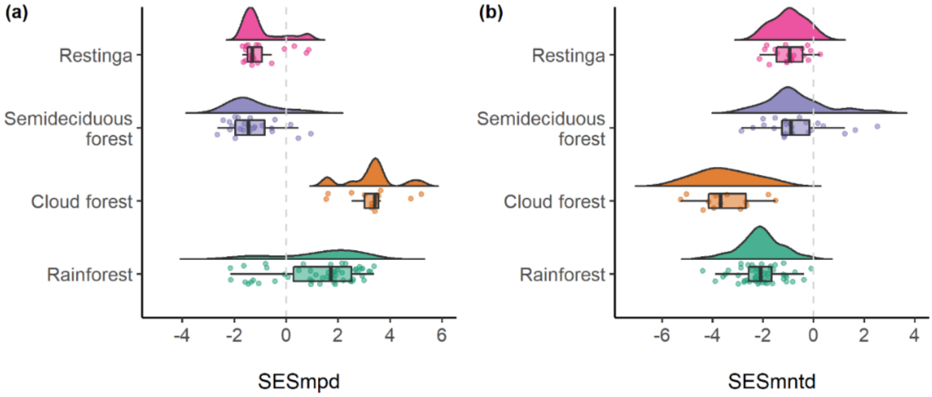

Figure 7. Phylogenetic structure of angiosperm tree communities across habitat types in the southeast Atlantic forest domain. **(a)** the standardised effect size of the mean pairwise phylogenetic distance (SESmpd); **(b)** the standardised effect size of the mean nearest taxon distance (SESmntd). Curves show the probability distribution of the variables, dots represent the real data points, and boxplots show their median and the interquartile ranges.

4. DISCUSSION

Over the past decades, many studies have shown the potential to address the evolutionary history of coexisting species to understand contemporary patterns in ecological communities. However, most of the approaches focused on ecological mechanisms only, either biotic interactions or environmental filtering as drivers of species diversity patterns (Webb *et al.* 2002; Cavender-Bares *et al.* 2009). Some studies have recently defended that both evolutionary and ecological mechanisms are intertwined and contribute to explaining diversity patterns (Kerkhoff *et al.* 2014; Gerhold *et al.* 2015, 2018; Carlucci *et al.* 2017; Weber *et al.* 2017; Kubota *et al.* 2018). By adopting a broader hypothesis formulation in which both evolutionary and ecological mechanisms are considered factors that influence species richness and phylogenetic structure of plant communities, the results in this thesis reinforce this integrated view.

This thesis shows that on a global scale, woody and herbaceous communities display contrasting patterns of phylogenetic structure along the latitudinal gradient and that species of both growth forms tend to be more closely related in open habitat types, probably due to recent colonisation (paper **I**). In geologically young restingas, where local diversification is unlikely to have occurred, the current phylogenetic structure of angiosperm tree communities probably results from the coexistence of Gondwanan restricted lineages with species from widespread families in historically unstable areas of southern Brazil. Phylogenetic clustering in restingas in historically more stable areas likely results from local diversification in the neighbouring rainforest with subsequent dispersal to restingas (paper **II**). In semi-natural drylands, where water availability is the most limiting factor, annual plant species are phylogenetically clustered in communities with intermediate to high aridity levels, whereas clustering in perennials is found at low to intermediate aridity levels. This contrasting response to aridity probably results from historical environmental filtering and endemism of recent diversified annual species and local dominance of a few perennial species in more mesic areas (paper **III**). Finally, the variation in the phylogenetic structure of angiosperm tree species along elevation and across habitat types in the Atlantic forest domain largely depends on whether the basal or terminal phylogenetic level is considered. For example, higher SESmpd and phylogenetic endemism and lower SESmntd at high elevations show that cloud forest is phylogenetically more distinct from rainforest, semideciduous forest and restinga due to local diversification in a few lineages. In contrast, higher SESmntd in semideciduous forest and restinga demonstrates that these habitat types are likely colonised by lineages that underwent past diversification and are adapted to harsh environmental conditions such as water limitation and high salinity, respectively (paper **IV**).

4.1. Latitudinal patterns of phylogenetic structure in woody and herbaceous plant communities suggest an effect of local diversification and habitat age

Woody plant communities were phylogenetically more clustered at low latitudes and tended to become overdispersed at high latitudes. The decreasing relatedness between species towards high latitudes contrasts with previous studies showing phylogenetic clustering in colder and drier regions. The latter pattern has been proposed to result from tropical lineages retaining their ancestral niches and failing to disperse into temperate regions (Qian *et al.* 2013; Kerkhoff *et al.* 2014; Kubota *et al.* 2018). The present study suggests, however, that tropical niche conservatism might not be the most important mechanism for assembling plant communities when a broad taxonomic scale is considered (e.g. including gymnosperm species). In the present study, gymnosperms were considered in the woody communities because they occupy and dominate many communities worldwide (e.g. the Podocarpaceae and Araucariaceae in the Southern Hemisphere, and the Pinaceae in the Northern Hemisphere) and have physiological advantages over angiosperms in cold and dry regions (Bond 1989). Therefore, phylogenetically distant gymnosperms at high latitudes contribute significantly to the phylogenetically overdispersed pattern in woody communities. Since most woody species originated in warm tropical regions (Axelrod 1966; Richards 1996; Ricklefs 2005), the pattern of increasing overdispersion towards high latitudes probably results from high diversification of angiosperms at low latitudes due to larger area and greater time for diversification (Fine & Ree 2006), and from temperate niche conservatism of gymnosperms at high latitudes due to their physiological advantage over angiosperms in cold and nutrient-poor environments (Bond 1989; Berendse & Scheffer 2009). Considering only angiosperms in the analysis, SESmpd decreases towards high latitudes, supporting the findings in previous studies (Qian *et al.* 2013; Kerkhoff *et al.* 2014; Kubota *et al.* 2018). SESmntd is not affected by the exclusion of gymnosperms because the division between angiosperms and gymnosperms deep in the phylogeny does not affect the relationships at the tips of the phylogeny.

The relationship between the phylogenetic structure of herbaceous communities and latitude is less evident than in woody communities. The lack of relationship probably arises because, despite the unimodal relationship between SESmpd and latitude, both SESmpd and SESmntd are most influenced by differences in habitat types, with more closely related species coexisting in open habitats. Therefore, phylogenetic clustering of herbaceous communities at high latitudes may reflect recent geological origin of temperate and boreal habitat types relative to the tropics (Fine & Ree 2006), together with the presence of evolutionarily young lineages that diversified following the rise of angiosperm-dominated herbaceous flora in open habitats during global cooling in the Late Cretaceous and Eocene-Oligocene transition, such as C_4 Poaceae, Brassicaceae and Ranunculaceae (Couvreur *et al.* 2010; Linnert *et al.* 2014; Spriggs *et al.* 2014; Wang *et al.* 2016).

Phylogenetic clustering has also been attributed to recent radiation of lineages in relatively young fynbos and grasslands vegetation in South Africa (Proches *et al.* 2006). Alternatively, phylogenetic clustering in local herbaceous communities may result from historical environmental filtering acting in evolutionarily young species pools, such as grasslands of Tertiary origin, in which only a few lineages had enough time to establish (Lososová *et al.* 2015). This result finds support in the coexistence of more closely related species in the Nearctic and Neotropical biogeographic realms than in the Afrotropical realm, probably because herbaceous communities in the first two realms are located at high latitudes, where only species adapted to cold conditions are expected to coexist. However, the weaker relationship between phylogenetic structure and biogeographic realm probably resulted from the fact that the Afrotropical realm was underrepresented in the dataset. Furthermore, results in herbaceous communities must be interpreted with caution because of spatial limitation in the distribution of the original studies and a comparably higher number of communities in Central Europe than in other regions.

4.2. Phylogenetic structure of angiosperm tree communities in the Atlantic coastal white-sand vegetation (restingas) is contingent on climate and evolutionary history of the neighbouring rainforest

The unimodal relationship between species richness and latitude reflects the distribution of the most dominant families with higher species richness in the central region of restingas. The central region of restingas is characterised by a stable historical climate (Carnaval & Moritz 2008) and high endemism rates (Werneck *et al.* 2011), which may have contributed to the high total number of species in restingas. Species richness in restingas is generally lower than in the Atlantic rainforest because only a few lineages have traits to cope with environmental harshness (Scarano 2002). Recent studies have argued that dioecy, fleshy fruit formation and asexual reproduction are the traits related to the successful colonisation of species in restingas (Matallana *et al.* 2005; Scarano 2009). However, the processes by which restingas have been colonised remain little understood.

Contrary to species richness, the phylogenetic structure (both SESmpd and SESmntd) positively correlates with latitude, with species becoming more distantly related in the southernmost and wetter restingas. The coexistence of distantly related species in southern restingas may be related to the availability of forest remnants in periods of unfavourable climatic conditions during Quaternary (Behling *et al.* 2007). These remnants were crucial for maintaining old Gondwanan lineages (Segovia & Armesto 2015). Therefore, the results in paper **II** suggest that species in southern restingas belong to old and restricted Gondwanan lineages and species from lineages widespread in the Atlantic forest domain.

Even after including environmental variables such as temperature, precipitation, soil salinity and soil fertility, SESmpd is still correlated with latitude. SESmpd also correlates with precipitation, indicating the presence of distantly related lineages in wetter restingas. SESmntd, on the other hand, positively correlates with more variables after accounting for latitude. SESmntd increases with temperature, precipitation, and displays high values in more fertile and less saline soils. These variables are related to the main limiting environmental factors proposed for species distribution in restingas (Scarano 2002). Thus, lower values of SESmntd indicate the coexistence of closely related species in more stressful communities due to adaptations of a few lineages to extreme conditions, supporting previous studies (Kubota *et al.* 2018). Additionally, phylogenetic clustering towards more stable regions may reflect regional diversification in the neighbouring rainforest with subsequent dispersal to restingas nearby (Fernandes & Queiroz 2015). Higher values of SESmntd in historically unstable regions indicate a lack of recent radiation among close relatives and may have resulted from close relatives evolving early in the evolutionary time and persisting in stable refugia (Behling *et al.* 2007; Leonhardt & Lorscheitter 2010).

Phylogenetic beta diversity at terminal levels of the phylogeny is more pronounced than at basal levels across restingas, supporting previous studies in other Atlantic forest habitat types (Duarte *et al.* 2014). This pattern may result from the availability of several local species pools nested within a large lineage pool along the latitudinal gradient in the Atlantic forest, in which tropical species adapted to local conditions fail in colonising colder and wetter subtropical restingas. This hypothesis finds support in the correlation between phylogenetic beta diversity and both geographic and environmental dissimilarities between communities, indicating that dispersal limitation and niche conservatism seem to be the factors underlying high phylogenetic beta diversity at terminal levels in the geologically young restingas (Daru *et al.* 2017). In the dispersal limitation scenario, species that evolved in the rainforest and colonised nearby restingas probably had insufficient time to disperse to other regions, especially during climatic oscillation events (Carnaval & Moritz 2008). In the niche conservatism scenario, species may have found suitable empty niches in restingas similar to those in the rainforest, and through slow evolution of niches, species remained in their area of origin, regardless of their dispersal capacity (Daru *et al.* 2017). As expected, the lack of correlation between phylogenetic beta diversity at basal levels and either geographic or environmental distances between communities reflects widespread plant families in the Atlantic forest domain that probably colonised restingas during the Quaternary, homogenising the phylogenetic structure deep in the phylogeny. Low phylogenetic beta diversity at basal levels has also been found in the Atlantic rainforest due to sympatric speciation (Gastauer *et al.* 2015) and in white-sand forests of the Amazonian basin due to recent diversification (Guevara *et al.* 2016), supporting the hypothesis of older lineages tending to be uniformly distributed in lowland habitat types.

4.3. Phylogenetic structure of annual and perennial species responds contrastingly to aridity in a Mediterranean dryland

Species richness of annuals does not correlate with aridity, whereas that of perennials shows a unimodal relationship. Annual species have a short life-span and high potential for seed dispersal and dormancy, and their germination and establishment are strongly dependent on interannual water availability (Gutterman 2002). Therefore, neutral processes such as dispersal and stochastic colonisation (Hubbell 2001) as well as seed germination strategies to increase seedling survival (Gutterman 2002; Volis & Bohrer 2013) are likely the factors related to the lack of pattern in annuals. Unlike annuals, perennial species have a longer life-span and must endure summer droughts over the years and do so through conservative or acquisitive strategies (Liancourt *et al.* 2005). Thus, environmental filtering at the drier extreme of the gradient selects species that can cope with harsh conditions such as water limitation. In contrast, at the other extreme of the gradient, a few dominant species such as those from the genera *Cistus* and *Cynodon* are probably strong competitors and exclude other species from communities, thus contributing to the unimodal pattern in perennials (Michalet *et al.* 2006). Despite the lack of relationship between annuals and aridity, the greater number of both annual and perennial species at intermediate levels of aridity may indicate the presence of an ecotone where both species of the aridest and those of the least arid communities still find conditions to live.

The phylogenetic structure of annuals and perennials responded contrastingly to aridity. Both SESmpd and SESmntd decreased with aridity in annuals, with phylogenetic clustering occurring at intermediate to high aridity. Two different processes may explain this pattern. Firstly, phylogenetic clustering in SESmpd indicates that environmental filtering affects entire lineages in the regional species pool, selecting species from dry-adapted lineages and excluding those lacking mechanisms to cope with water scarcity. Secondly, assuming that lineages were already filtered out (low SESmpd), clustering in SESmntd is likely dependent on annuals' capacity to disperse to neighbouring communities coupled with endemism of recently diversified species within dry-adapted lineages (Verdú & Pausas 2013). Additionally, in Mediterranean ecosystems, species may descend from lineages adapted to specific soil conditions, therefore outcompeting other less specialised species (Fine & Kembel 2011).

In contrast to that found in annuals, SESmpd and SESmntd in perennials decrease towards regions with lower aridity, and communities tend to be phylogenetically clustered at intermediate to low aridity. Aridity has increased over geological time in the Mediterranean basin and contributed to local diversification (Valente *et al.* 2010; Verdú & Pausas 2013). Therefore, lineages have already been filtered out regionally, reflecting the phylogenetic clustering found at intermediate to low aridity. The coexisting closely related species in these regions likely display traits that may reduce competitive exclusion in the absence of niche differentiation (e.g. among the above mentioned *Cistus* species) (Mayfield & Levine 2010) or high trait dissimilarity (Prinzing et al., 2008), allowing better partitioning of resources. Even after accounting for other environmental variables such as temperature, precipitation and soil nutrient availability, aridity is still a strong predictor of phylogenetic structure. Additionally, SESmpd and SESmntd negatively correlate with soil C/N ratio, indicating that locally dominant species (e.g. those from the genus *Cistus*) may have more efficient use of scarce nitrogen than other species in areas with low aridity and high soil C/N ratio (Zhang *et al.* 2020).

Spatial phylogenetic turnover (i.e. the replacement of lineages across communities) did not correlate with geographic distance between communities in either annuals or perennials, indicating that species in the Mediterranean basin may not be dispersal limited or that there has been enough time for species sorting to occur despite dispersal limitation. In contrast, phylogenetic turnover correlated with the environmental distance between communities, which shows that even within a filtered group of lineages, species may still have specific adaptations to different environmental conditions and are mostly related to variables at a finer scale such as soil specificity (Fine & Kembel 2011).

4.4. Evolutionary history of marginal habitats influences the diversity of tree communities in the Atlantic Forest

Angiosperm tree species richness in the southeast Atlantic forest domain shows a unimodal pattern along the elevation gradient, peaking at middle elevations, reinforcing previous studies (Rahbek 1995; McCain & Grytnes 2010). Species richness is higher in rainforest and cloud forest than in semideciduous forest and restinga. Therefore, the unimodal relationship between species richness and elevation may reflect environmental filtering at both extremes of the gradient. Salinity may filter species in restingas, and water scarcity in semideciduous forests at low elevations, whereas temperature could filter species in cloud forests at high elevations.

Unlike species richness, phylogenetic endemism increases with elevation, highlighting mountainous regions as areas of high endemism rates (Hoorn *et al.* 2013; Rahbek *et al.* 2019). Interestingly, rainforests show lower phylogenetic endemism despite their high number of species, suggesting that rainforests' richness may partly depend on the species generated in cloud forests. As expected, restingas do not show either lower or higher phylogenetic endemism levels, mainly because restingas did not have sufficient time for plant diversification (Scarano 2002).

SESmpd and SESmntd show contrasting relationships with elevation and across habitat types. SESmpd increases with elevation and is higher in rainforest and cloud forest than in restinga and semideciduous forest. The increasing phylogenetic distance at basal levels along the elevation gradient is probably related to the Atlantic forest domain's evolutionary history. The Atlantic forest domain is the oldest forest in South America (Rizzini 1997), and it holds a mix of species and higher-level taxa that evolved while South America was separating from Africa during the last 165 million years (Sanmartín *et al.* 2004). Throughout the geological time, lineages had sufficient time to disperse from lowlands towards other habitat types such as cloud forests. Therefore, communities at higher elevations may be composed of pre-adapted distantly related lineages dispersed from other mountainous regions and lowland lineages in the same region. Similar findings have been shown in other tropical regions such as Malesian mountain forests (Culmsee & Leuschner 2013) and the Indian Western Ghats (Bose *et al.* 2019), reinforcing the idea that species in tropical elevation gradients are sorted from lineages with different biogeographical and evolutionary histories (Duarte *et al.* 2014; González-Caro *et al.* 2020). The decreasing of SESmntd with elevation indicates diversification within lineages adapted to the mountainous climate and topographic heterogeneity. Therefore, mountains in the Atlantic forest domain could be considered a 'Cradle' (Stebbins 1974) of angiosperm tree species, indicated by the high level of phylogenetic endemism and phylogenetic clustering in SESmntd. On the other side of the gradient, SESmntd tends to increase towards semideciduous forest and restinga, indicating a lack of recent diversification. Diversification may have happened before species arrive in these habitat types, and only lineages able to cope with high temperatures, dry seasons and saline soils were able to colonise them, indicating environmental filtering and possibly phenotypic plasticity in anatomical and physiological traits beneficial in the specific environment (Herzog *et al.* 1999; Rôças *et al.* 2001; Scarano *et al.* 2001; Scarano 2009). The tendency of no phylogenetic structure or clustering in restinga may also be related to the geologically young age of the habitat type, as discussed in more detail in section 4.2. Furthermore, SESmpd decreasing with salinity and water deficit severity indicates that not all lineages can tolerate such constraints.

The high degree of tree species and lineages replacement across habitat types, indicated by spatial taxonomic and phylogenetic turnover, is the main factor of overall taxonomic and phylogenetic beta diversity in the southeast Atlantic forest. An exception was found between rainforest and restinga and between semideciduous forest and restinga, in which taxonomic and phylogenetic beta diversity are mainly driven by the nestedness effect (i.e. loss of species richness and phylogenetic diversity, respectively). In that case, restinga communities are likely a subset of more species-rich habitat types such as rainforest and semideciduous forest. High phylogenetic beta diversity has been found in other regions of the Atlantic forest domain. It has been argued to result from the presence of lineages with different biogeographical origin (Duarte *et al.* 2014), such as those native to Gondwana (Segovia & Armesto 2015). These results contradict the idea that habitat types such as cloud forest and semideciduous forest are a subset of species from the rainforest (Scarano 2002). According to the results presented in paper **IV**, restinga is the only habitat type that can be considered a subset of the rainforest, probably because species are still dispersing into this coastal vegetation.

5. CONCLUSIONS

The results presented in this thesis showed that on a global scale, plant communities' phylogenetic structure along the latitudinal gradient might depend on the plant growth form and phylogenetic scale considered (i.e. basal and terminal diversifications in the phylogeny). Patterns of phylogenetic structure in woody communities changed from overdispersed to clustered in high latitudes once gymnosperm species were excluded from analysis, highlighting that only a few angiosperm lineages can cope with environmental harshness. Phylogenetic clustering in herbaceous communities at high latitudes may be related to the young geological age of open habitat types. However, further studies must consider broader global sampling. In geologically young ecosystems (restingas), where angiosperm tree species had no time for diversification, plant communities' phylogenetic structure strongly depends on the available lineage pool that comprises different habitat-specific species pools across the Atlantic forest domain. Moreover, environmental harshness and the presence of Quaternary refugia also influence whether coexisting species are more closely or distantly related to each other. The age of restingas also prevents more derived species from dispersing from their local distribution, increasing phylogenetic beta diversity at terminal levels of the phylogeny. In the historically dry Mediterranean basin, annual and perennial plant species' phylogenetic structure responds contrastingly to aridity and can be important in land use management and restoration strategies. Furthermore, species with both life-history strategies seem not to be dispersal limited across the region but instead are adapted to specific local climatic and edaphic conditions. In the Atlantic forest domain, tree communities tend to show basal phylogenetic overdispersion and terminal clustering towards higher elevations, highlighting the influence of the Atlantic forest domain's evolutionary history on the contemporary communities. More specifically, the coexistence of distantly related lineages towards high elevations reflects the assembly of lineages with different biogeographic histories that once reached mountainous regions and underwent local diversification, reflected in terminal clustering. Results also show that not all habitat types should be considered marginal to the rainforest, for example, cloud forest and semideciduous forest. Restinga, instead, contains species that occur in both rainforest and semideciduous forest.

Overall, the results in this thesis add insights into the use of phylogenetic information to investigate the origin and maintenance of diversity patterns. These results have relevant implications for future studies aiming to predict how species diversity patterns will be affected under climate change scenarios (Colwell et al. 2008; Thuiller et al. 2011) and should be explored in more detail in the context of conservation and restoration strategies of ecological communities.

6. SUMMARY

The accelerated climate change and habitat destruction have affected biological diversity in ways never seen before. Preventing a species from its extinction goes beyond counting numbers. It also means conserving the evolutionary history it shares with its relatives. Evolution plays an important role in the way species are assembled into communities of different habitat types and along environmental gradients. For example, two grasslands may have the same number of herbaceous species but differ enormously in their constituent species' evolutionary history. Species that evolved in distantly related lineages may live together in one grassland because closely related species often compete for the same resources, thus causing the exclusion of the weaker species. It generates a pattern of phylogenetic structure, which in the first grassland is called phylogenetic overdispersion. In the second grassland, closely related species may share characters that give them a competitive advantage over others and allow them to outcompete distantly related species. Thus, the grassland where closely related species live together is considered phylogenetically clustered. Because patterns of biological diversity (e.g. phylogenetic overdispersion or clustering) result from complex processes that happen both on the contemporary time scale (e.g. species interactions and requirements to specific environmental conditions) and the evolutionary time scale (e.g. generation of new species), understanding how these processes act to shape community's diversity adds valuable insights into the way species will respond to future changes. This thesis investigates how plant communities' phylogenetic structure responds to changes in the environment such as elevation, climate, nutrients in the soil, and changes driven by humans such as desertification. Specifically, this thesis asks the following questions:

1) How does the phylogenetic community structure of different growth forms (i.e., woody and herbaceous plant species) relate to latitude, biogeographic realms and habitat types worldwide?
2) What are the relative effects of the current climate, historical climatic stability, and edaphic factors on the phylogenetic structure of angiosperm tree communities in geologically young restinga habitats along the Atlantic coast?
3) How does the phylogenetic structure of annual and perennial plant communities respond to aridity in Mediterranean semi-natural dryland?
4) How does the phylogenetic structure of angiosperm tree communities respond to elevation in different habitat types in the tropical Atlantic forest domain?

The analysis of woody and herbaceous plant communities worldwide (1) showed that their phylogenetic structure responds contrastingly to latitude, considered a surrogate for temperature. Woody communities become phylogenetically overdispersed towards high latitudes, probably because most woody species originated in warm and stable tropical regions. However, due to a lack of adaptations to cope with freezing, they did not reach cold regions at high latitudes. Only a few woody species, including both flowering plants and the evolutionarily distant related gymnosperms, have physiological adaptations to cope with freezing, thus contributing to the phylogenetic overdispersion. Once gymnosperms are removed from the analysis, communities become clustered because those flowering species that are adapted to cold climate come from closely related lineages. Herbaceous communities do not show a clear pattern along the latitudinal gradient. Instead, they are more sensitive to the habitat type, being more phylogenetically clustered in open habitats (e.g. grassland) than in closed habitat types (e.g. forest). That difference may be related to some lineages' recent origin, including herbaceous species such as grasses.

In the analysis of how species with different life-cycle strategies respond to desertification (i.e. increasing aridity) (3), communities of species that complete their life-cycle within one year (annual species) become phylogenetically clustered in drier areas. This result reflects historical environmental filtering acting on the dry-adapted lineages available in the region and the limited dispersal of young species adapted to specific soil conditions. Communities of species with a longer lifespan, that is, those that must endure stressful conditions during the summer drought (perennial species), become phylogenetically clustered at intermediate to low levels of aridity, indicating the presence of closely related species with specific characters that allow them to outcompete weaker distantly related competitors.

Analyses in (2) and (4) were carried out in the Atlantic Forest biodiversity hotspot and focused exclusively on tree species communities in coastal vegetation and along elevation, respectively. Using a metric that explores deep past evolutionary events, (2) coastal communities become phylogenetically overdispersed towards southernmost areas, suggesting the coexistence of distantly related and cold-adapted species with species that come from widespread lineages in the Atlantic Forest. Once the phylogenetic structure is calculated using a metric that explores recent evolutionary events, communities become clustered in areas of great climatic stability with a high number of spatially restricted species, indicating a potential limitation in the dispersal of the coexisting species and *in situ* diversification. Communities are also clustered in drier areas with high soil salinity and low soil fertility, indicating environmental filtering. The phylogenetic structure of tree communities responds contrastingly to elevation gradients (4). Considering deep past evolutionary events, communities become overdispersed towards high elevations, indicating a process of long-term colonisation of distantly related lowland lineages that share common characters to cope with cold temperatures. These lineages probably generated new species in the mountains because communities are clustered in high elevations when considering recent evolutionary events. Additionally, in communities associated with water limitation and high salinity, there is phylogenetic clustering when using the deep past metric and nearly no phylogenetic structure when using the metric that accounts for recent events. This result indicates that only a few lineages were able to establish in harsh conditions, and most lineages did not generate new species in these communities.

This thesis shows how the phylogenetic structure of plant communities responds to variation in different environmental variables. These results add insights into the use of phylogenetic information to investigate the origin and maintenance of diversity patterns. Additionally, these results are significant in the context of current climate change and habitat destruction because these events threaten the number of species that live in different biological communities, their function and the evolutionary history that they share.

7. REFERENCES

Antonelli, A., Kissling, W.D., Flantua, S.G.A., Bermúdez, M.A., Mulch, A., Muellner-Riehl, A.N., *et al.* (2018). Geological and climatic influences on mountain biodiversity. *Nat. Geosci.*, 11, 718–725.

Axelrod, D.I. (1966). Origin of deciduous and evergreen habits in temperate forests. *Evolution (N. Y).*, 20, 1–15.

Bartish, I. V., Ozinga, W.A., Bartish, M.I., Wamelink, G.W.W., Hennekens, S.M. & Prinzing, A. (2016). Different habitats within a region contain evolutionary heritage from different epochs depending on the abiotic environment. *Glob. Ecol. Biogeogr.*, 25, 274–285.

Barton, K. (2019). MuMIn: multi-model inference. R package version 1.43.15. https://cran.r-project.org/package=MuMIn.

Baselga, A. (2010). Partitioning the turnover and nestedness components of beta diversity. *Glob. Ecol. Biogeogr.*, 19, 134–143.

Baselga, A. & Orme, C.D.L. (2012). betapart : an R package for the study of beta diversity. *Methods Ecol. Evol.*, 3, 808–812.

Behling, H., Dupont, L., DeForest Safford, H. & Wefer, G. (2007). Late Quaternary vegetation and climate dynamics in the Serra da Bocaina, southeastern Brazil. *Quat. Int.*, 161, 22–31.

Bennett, J.A., Lamb, E.G., Hall, J.C., Cardinal-Mcteague, W.M. & Cahill, J.F. (2013). Increased competition does not lead to increased phylogenetic overdispersion in a native grassland. *Ecol. Lett.*, 16, 1168–1176.

Berdugo, M., Delgado-Baquerizo, M., Soliveres, S., Hernández-Clemente, R., Zhao, Y., Gaitán, J.J., *et al.* (2020). Global ecosystem thresholds driven by aridity. *Science (80-.).*, 367, 787–790.

Berendse, F. & Scheffer, M. (2009). The angiosperm radiation revisited, an ecological explanation for Darwin's "abominable mystery." *Ecol. Lett.*, 12, 865–872.

Bertness, M.D. & Callaway, R. (1994). Positive interactions in communities. *Trends Ecol. Evol.*

Bivand, R.S., Pebesma, E. & Gomez-Rubio, V. (2013). *Applied spatial data analysis with R, Second edition*. Springer, NY.

Bond, W.J. (1989). The tortoise and the hare: ecology of angiosperm dominance and gymnosperm persistence. *Biol. J. Linn. Soc.*, 36, 227–249.

Borcard, D. & Legendre, P. (2002). All-scale spatial analysis of ecological data by means of principal coordinates of neighbour matrices. *Ecol. Modell.*, 153, 51–68.

Bose, R., Ramesh, B.R., Pélissier, R. & Munoz, F. (2019). Phylogenetic diversity in the Western Ghats biodiversity hotspot reflects environmental filtering and past niche diversification of trees. *J. Biogeogr.*, 46, 145–157.

Burnham, K.P. & Anderson, D.R. (2004). Multimodel inference: Understanding AIC and BIC in model selection. *Sociol. Methods Res.*

Burnham, R.J. & Johnson, K.R. (2004). South American palaeobotany and the origins of neotropical rainforests. *Philos. Trans. R. Soc. B Biol. Sci.*, 359, 1595–1610.

Butterfield, B.J., Cavieres, L.A., Callaway, R.M., Cook, B.J., Kikvidze, Z., Lortie, C.J., *et al.* (2013). Alpine cushion plants inhibit the loss of phylogenetic diversity in severe environments. *Ecol. Lett.*, 16, 478–486.

Cadotte, M.W., Cavender-Bares, J., Tilman, D. & Oakley, T.H. (2009). Using phylogenetic, functional and trait diversity to understand patterns of plant community productivity. *PLoS One*, 4, 1–9.

Carlucci, M.B., Seger, G.D.S., Sheil, D., Amaral, I.L., Chuyong, G.B., Ferreira, L. V., *et al.* (2017). Phylogenetic composition and structure of tree communities shed light on historical processes influencing tropical rainforest diversity. *Ecography (Cop.).*, 40, 521–530.

Carnaval, A.C. & Moritz, C. (2008). Historical climate modelling predicts patterns of current biodiversity in the Brazilian Atlantic forest. *J. Biogeogr.*, 35, 1187–1201.

Cavender-Bares, J., Kozak, K.H., Fine, P.V.A. & Kembel, S.W. (2009). The merging of community ecology and phylogenetic biology. *Ecol. Lett.*, 12, 693–715.

Cayuela, L., Granzow-de la Cerda, Í., Albuquerque, F.S. & Golicher, D.J. (2012). taxonstand: An r package for species names standardisation in vegetation databases. *Methods Ecol. Evol.*, 3, 1078–1083.

Colwell, R.K., Brehm, G., Cardelús, C.L., Gilman, A.C. & Longino, J.T. (2008). Global warming, elevational range shifts, and lowland biotic attrition in the wet tropics. *Science (80-.).*, 322, 258–261.

Couvreur, T.L.P.P., Franzke, A., Al-Shehbaz, I.A., Bakker, F.T., Koch, M.A. & Mummenhoff, K. (2010). Molecular phylogenetics, temporal diversification, and principles of evolution in the mustard family (Brassicaceae). *Mol. Biol. Evol.*, 27, 55–71.

Culmsee, H. & Leuschner, C. (2013). Consistent patterns of elevational change in tree taxonomic and phylogenetic diversity across Malesian mountain forests. *J. Biogeogr.*, 40, 1997–2010.

Dai, A. (2013). Increasing drought under global warming in observations and models. *Nat. Clim. Chang.*, 3, 52–58.

Daru, B.H., Elliott, T.L., Park, D.S. & Davies, T.J. (2017). Understanding the Processes Underpinning Patterns of Phylogenetic Regionalization. *Trends Ecol. Evol.*, 32, 845–860.

Davies, T.J. & Buckley, L.B. (2011). Phylogenetic diversity as a window into the evolutionary and biogeographic histories of present-day richness gradients for mammals. *Philos. Trans. R. Soc. B Biol. Sci.*, 366, 2414–2425.

Dehling, D.M., Fritz, S.A., Töpfer, T., Päckert, M., Estler, P., Böhning-Gaese, K., *et al.* (2014). Functional and phylogenetic diversity and assemblage structure of frugivorous birds along an elevational gradient in the tropical Andes. *Ecography (Cop.).*, 37, no-no.

Delaney, P.J. V. (1962). Quaternary geologic history of the coastal plain of Rio Grande do Sul, Brazil. In: *South American Coastal Studies Technical Report*. Coastal Studies Institute, Lousiana State University, Baton Rouge, pp. 1–63.

Delgado-Baquerizo, M., Maestre, F.T., Gallardo, A., Bowker, M.A., Wallenstein, M.D., Quero, J.L., *et al.* (2013). Decoupling of soil nutrient cycles as a function of aridity in global drylands. *Nature*, 502, 672–676.

Dobrovolski, R., Melo, A.S., Cassemiro, F.A.S. & Diniz-Filho, J.A.F. (2012). Climatic history and dispersal ability explain the relative importance of turnover and nestedness components of beta diversity. *Glob. Ecol. Biogeogr.*, 21, 191–197.

Duarte, L.D.S., Bergamin, R.S., Marcilio-Silva, V., Seger, G.D.D.S. & Marques, M.C.M. (2014). Phylobetadiversity among Forest Types in the Brazilian Atlantic Forest Complex. *PLoS One*, 9, e105043.

Engemann, K., Sandel, B., Enquist, B.J., Jørgensen, P.M., Kraft, N., Marcuse-Kubitza, A., *et al.* (2016). Patterns and drivers of plant functional group dominance across the Western Hemisphere: a macroecological re-assessment based on a massive botanical dataset. *Bot. J. Linn. Soc.*, 180, 141–160.

ESRI, E. (2010). ArcMap 10.1. *Redlands, USA*.

Facelli, J.M., Chesson, P. & Barnes, N. (2005). Differences in seed biology of annual plants in arid lands: A key ingredient of the storage effect. *Ecology*, 86, 2998–3006.

Faith, D.P. (1992). Conservation evaluation and phylogenetic diversity. *Biol. Conserv.*, 61, 1–10.

Fernandes, M.F. & Queiroz, L.P. (2015). Floristic surveys of Restinga Forests in southern Bahia, Brazil, reveal the effects of geography on community composition. *Rodriguésia*, 66, 51–73.

Fine, P.V.A. & Kembel, S.W. (2011). Phylogenetic community structure and phylogenetic turnover across space and edaphic gradients in western Amazonian tree communities. *Ecography (Cop.)*., 34, 552–565.

Fine, P.V.A. & Ree, R.H. (2006). Evidence for a Time-Integrated Species-Area Effect on the Latitudinal Gradient in Tree Diversity. *Am. Nat.*, 168, 796–804.

Fragnière, Y., Bétrisey, S., Cardinaux, L., Stoffel, M. & Kozlowski, G. (2015). Fighting their last stand? A global analysis of the distribution and conservation status of gymnosperms. *J. Biogeogr.*, 42, 809–820.

Fritz, S.A. & Rahbek, C. (2012). Global patterns of amphibian phylogenetic diversity. *J. Biogeogr.*, 39, 1373–1382.

García-Camacho, R., Metz, J., Bilton, M.C. & Tielbörger, K. (2017). Phylogenetic structure of annual plant communities along an aridity gradient. Interacting effects of habitat filtering and shifting plant-plant interactions. *Isr. J. Plant Sci.*, 64, 122–134.

Gastauer, M., Saporetti-Junior, A.W., Magnago, L.F.S., Cavender-Bares, J. & Meira-Neto, J.A.A. (2015). The hypothesis of sympatric speciation as the dominant generator of endemism in a global hotspot of biodiversity. *Ecol. Evol.*, 5, 5272–5283.

Gaucherel, C., Tramier, C., Devictor, V., Svenning, J.-C. & Hély, C. (2018). Where and at which scales does the latitudinal diversity gradient fail? *J. Biogeogr.*, 45, 1905–1916.

Gerhold, P., Cahill, J.F., Winter, M., Bartish, I. V. & Prinzing, A. (2015). Phylogenetic patterns are not proxies of community assembly mechanisms (they are far better). *Funct. Ecol.*, 29, 600–614.

Gerhold, P., Carlucci, M.B., Procheş, Ş. & Prinzing, A. (2018). The Deep Past Controls the Phylogenetic Structure of Present, Local Communities. *Annu. Rev. Ecol. Evol. Syst.*, 49, 477–497.

Gong, Y., Ling, H., Lv, G., Chen, Y., Guo, Z. & Cao, J. (2019). Disentangling the influence of aridity and salinity on community functional and phylogenetic diversity in local dryland vegetation. *Sci. Total Environ.*, 653, 409–422.

González-Caro, S., Duque, Á., Feeley, K.J., Cabrera, E., Phillips, J., Ramirez, S., *et al.* (2020). The legacy of biogeographic history on the composition and structure of Andean forests. *Ecology*, 101, 1–11.

Goslee, S.C. & Urban, D.L. (2007). The ecodist Package for Dissimilarity-based Analysis of Ecological Data. *J. Stat. Softw.*, 22, 1–19.

Graham, C.H., Parra, J.L., Rahbek, C. & McGuire, J.A. (2009). Phylogenetic structure in tropical hummingbird communities. *Proc. Natl. Acad. Sci.*, 106, 19673–19678.

Guevara, J.E., Damasco, G., Baraloto, C., Fine, P.V.A., Peñuela, M.C., Castilho, C., *et al.* (2016). Low Phylogenetic Beta Diversity and Geographic Neo-endemism in Amazonian White-sand Forests. *Biotropica*, 48, 34–46.

Gutterman, Y. (2002). Minireview: Survival adaptations and strategies of annuals occurring in the judean and negev deserts of israel. *Isr. J. Plant Sci.*, 50, 165–175.

Herzog, B., Hübner, C., Ball, E., Bastos, R. do N., Franco, A.C., Scarano, F.R., *et al.* (1999). Comparative Study of the C 3 /CAM Intermediate Species Clusia parviflora Saldanha et Engi. and the Obligate CAM Species Clusia hilariana Schlecht. Growing Sympatrically Exposed and Shaded in the Coastal Restinga of Brazil. *Plant Biol.*, 1, 453–459.

Hijmans, R.J., Cameron, S.E., Parra, J.L., Jones, P.G. & Jarvis, A. (2005). Very high resolution interpolated climate surfaces for global land areas. *Int. J. Climatol.*, 25, 1965–1978.

Hillebrand, H. (2004). On the generality of the latitudinal diversity gradient. *Am. Nat.*, 163, 192–211.

Holzapfel, C., Tielbörger, K., Parag, H.A., Kigel, J. & Sternberg, M. (2006). Annual plant-shrub interactions along an aridity gradient. *Basic Appl. Ecol.*, 7, 268–279.

Hoorn, C., Mosbrugger, V., Mulch, A. & Antonelli, A. (2013). Biodiversity from mountain building. *Nat. Geosci.*, 6, 154.

Hubbell, S.P. (2001). *The unified neutral theory of biodiversity and biogeography*. Princeton University Press.

Humboldt, A. von. (1849). *Aspects of nature, in different lands and different climates; with scientific elucidations. Asp. nature, Differ. lands Differ. Clim. with Sci. elucidations. Transl. by Mrs. Sabine.* Lea and Blanchard, Philadelphia,.

Jablonski, D., Belanger, C.L., Berke, S.K., Huang, S., Krug, A.Z., Roy, K., *et al.* (2013). Out of the tropics, but how? Fossils, bridge species, and thermal ranges in the dynamics of the marine latitudinal diversity gradient. *Proc. Natl. Acad. Sci.*, 110, 10487–10494.

Jin, Y. & Qian, H. (2019). V.PhyloMaker: an R package that can generate very large phylogenies for vascular plants. *Ecography (Cop.).*, ecog.04434.

Kembel, S.W., Cowan, P.D., Helmus, M.R., Cornwell, W.K., Morlon, H., Ackerly, D.D., *et al.* (2010). Picante: R tools for integrating phylogenies and ecology. *Bioinformatics*, 26, 1463–1464.

Kerkhoff, A.J., Moriarty, P.E. & Weiser, M.D. (2014). The latitudinal species richness gradient in New World woody angiosperms is consistent with the tropical conservatism hypothesis. *Proc. Natl. Acad. Sci.*, 111, 8125–8130.

Kinlock, N.L., Prowant, L., Herstoff, E.M., Foley, C.M., Akin-Fajiye, M., Bender, N., *et al.* (2018). Explaining global variation in the latitudinal diversity gradient: Meta-analysis confirms known patterns and uncovers new ones. *Glob. Ecol. Biogeogr.*, 27, 125–141.

Kluge, J. & Kessler, M. (2011). Phylogenetic diversity, trait diversity and niches: Species assembly of ferns along a tropical elevational gradient. *J. Biogeogr.*, 38, 394–405.

Kubota, Y., Kusumoto, B., Shiono, T. & Ulrich, W. (2018). Environmental filters shaping angiosperm tree assembly along climatic and geographic gradients. *J. Veg. Sci.*, 29, 607–618.

Legendre, P. & Legendre, L. (2012). *Numerical Ecology*. 3 rd. Elsevier, Amsterdam.

Leonhardt, A. & Lorscheitter, M.L. (2010). The last 25,000 years in the Eastern Plateau of Southern Brazil according to Alpes de São Francisco record. *J. South Am. Earth Sci.*, 29, 454–463.

Leprieur, F., Albouy, C., de Bortoli, J., Cowman, P.F., Bellwood, D.R. & Mouillot, D. (2012). Quantifying phylogenetic beta diversity: Distinguishing between "true" turnover of lineages and phylogenetic diversity gradients. *PLoS One*, 7.

Li, D., Trotta, L., Marx, H.E., Allen, J.M., Sun, M., Soltis, D.E., *et al.* (2019). For common community phylogenetic analyses, go ahead and use synthesis phylogenies. *Ecology*, 100.

Liancourt, P., Callaway, R.M. & Michalet, R. (2005). Stress tolerance and competitive-response ability determine the outcome of biotic interactions. *Ecology*, 86, 1611–1618.

Linnert, C., Robinson, S.A., Lees, J.A., Bown, P.R., Pérez-Rodríguez, I., Petrizzo, M.R., *et al.* (2014). Evidence for global cooling in the Late Cretaceous. *Nat. Commun.*, 5.

Lososová, Z., Šmarda, P., Chytrý, M., Purschke, O., Pyšek, P., Sádlo, J., *et al.* (2015). Phylogenetic structure of plant species pools reflects habitat age on the geological time scale. *J. Veg. Sci.*, 26, 1080–1089.

Martin, L., Suguio, K. & Flexor, J.M. (1993). As flutuações de nível do mar durante o quaternário superior e a evolução geológica de "deltas" brasileiros. *Bol. IG-USP. Publicação Espec.*, 0, 01.

Massante, J.C. & Gerhold, P. (2020). Environment and evolutionary history depict phylogenetic alpha and beta diversity in the Atlantic coastal white-sand woodlands. *J. Veg. Sci.*, 31, 634–645.

Massante, J.C., Götzenberger, L., Takkis, K., Hallikma, T., Kaasik, A., Laanisto, L., *et al.* (2019). Contrasting latitudinal patterns in phylogenetic diversity between woody and herbaceous communities. *Sci. Rep.*, 9, 6443.

Massante, J.C., Köbel, M., Pinho, P., Gerhold, P., Branquinho, C. & Nunes, A. (2020). Phylogenetic structure of understorey annual and perennial plant species reveals opposing responses to aridity in a Mediterranean biodiversity hotspot. *Sci. Total Environ.*, 144018.

Matallana, G., Wendt, T., Araujo, D.S.D. & Scarano, F.R. (2005). High abundance of dioecious plants in a tropical coastal vegetation. *Am. J. Bot.*, 92, 1513–1519.

Mayfield, M.M. & Levine, J.M. (2010). Opposing effects of competitive exclusion on the phylogenetic structure of communities. *Ecol. Lett.*, 13, 1085–1093.

McCain, C.M. & Grytnes, J.-A. (2010). Elevational Gradients in Species Richness. In: *Encyclopedia of Life Sciences*. John Wiley & Sons, Ltd.

McGill, B.J., Chase, J.M., Hortal, J., Overcast, I., Rominger, A.J., Rosindell, J., *et al.* (2019). Unifying macroecology and macroevolution to answer fundamental questions about biodiversity. *Glob. Ecol. Biogeogr.*, 28, 1925–1936.

Michalet, R., Brooker, R.W., Cavieres, L.A., Kikvidze, Z., Lortie, C.J., Pugnaire, F.I., *et al.* (2006). Do biotic interactions shape both sides of the humped-back model of species richness in plant communities? *Ecol. Lett.*

Middleton, N. & Thomas, D. (1997). *World atlas of desertification.. ed. 2.* Arnold, Hodder Headline, PLC.

Miller, E.T., Farine, D.R. & Trisos, C.H. (2017). Phylogenetic community structure metrics and null models: a review with new methods and software. *Ecography (Cop.).*, 40, 461–477.

Mittelbach, G.G., Schemske, D.W., Cornell, H. V., Allen, A.P., Brown, J.M., Bush, M.B., *et al.* (2007). Evolution and the latitudinal diversity gradient: Speciation, extinction and biogeography. *Ecol. Lett.*, 10, 315–331.

Mouquet, N., Devictor, V., Meynard, C.N., Munoz, F., Bersier, L.F., Chave, J., *et al.* (2012). Ecophylogenetics: Advances and perspectives. *Biol. Rev.*, 87, 769–785.

Neves, D.M., Dexter, K.G., Pennington, R.T., Valente, A.S.M., Bueno, M.L., Eisenlohr, P.V., *et al.* (2017). Dissecting a biodiversity hotspot: The importance of environmentally marginal habitats in the Atlantic Forest Domain of South America. *Divers. Distrib.*, 23, 898–909.

Nunes, A., Tápia, S., Pinho, P., Correia, O. & Branquinho, C. (2015). Advantages of the point-intercept method for assessing functional diversity in semiarid areas. *IForest*, 8, 471–479.

Oksanen, J., Blanchet, F.G., Friendly, M., Kindt, R., Legendre, P., McGlinn, D., *et al.* (2019). Vegan: community ecology package. R Package version 2.5-6. https://cran.r-project.org/package=vegan.

Oliveira-Filho, A.T. (2017). *NeoTropTree, Flora arbórea da Região Neotropical: Um banco de dados envolvendo biogeografia, diversidade e conservação. Universidade Federal de Minas Gerais*. Available at: http://www.neotroptree.info. Last accessed .

Oliveira, A.A., Vicentini, A., Chave, J., Castanho, C. de T., Davies, S.J., Martini, A.M.Z., *et al.* (2014). Habitat specialization and phylogenetic structure of tree species in a coastal Brazilian white-sand forest. *J. Plant Ecol.*, 7, 134–144.

Pebesma, E.J. & Bivand, R.S. (2005). Classes and methods for spatial data in R. *R News*, 5, 9–13.

Peixoto, F.P., Villalobos, F., Melo, A.S., Diniz-Filho, J.A.F., Loyola, R., Rangel, T.F., *et al.* (2017). Geographical patterns of phylogenetic beta-diversity components in terrestrial mammals. *Glob. Ecol. Biogeogr.*, 26, 573–583.

Phillips, O. & Miller, J.S. (2002). *Global patterns of plant diversity : Alwyn H. Gentry's forest transect data set*. Missouri Botanical Press.

Piel, W.H. (2018). The global latitudinal diversity gradient pattern in spiders. *J. Biogeogr.*, 45, 1896–1904.

Pinheiro, J., Bates, D., DebRoy, S., Sarkar, D. & R Core Team. (2017). nlme: Linear and Nonlinear Mixed Effects Models.

Pistón, N., Schöb, C., Armas, C., Prieto, I. & Pugnaire, F.I. (2016). Contribution of co-occurring shrub species to community richness and phylogenetic diversity along an environmental gradient. *Perspect. Plant Ecol. Evol. Syst.*, 19, 30–39.

Proches, S., Wilson, J.R.. & Cowling, R.M. (2006). How much evolutionary history in a 10×10 m plot? *Proc. R. Soc. B Biol. Sci.*, 273, 1143–1148.

Qian, H. & Jin, Y. (2016). An updated megaphylogeny of plants, a tool for generating plant phylogenies and an analysis of phylogenetic community structure. *J. Plant Ecol.*, 9, 233–239.

Qian, H. & Sandel, B. (2017). Phylogenetic structure of regional angiosperm assemblages across latitudinal and climatic gradients in North America. *Glob. Ecol. Biogeogr.*, 26, 1258–1269.

Qian, H., Zhang, Y., Zhang, J. & Wang, X. (2013). Latitudinal gradients in phylogenetic relatedness of angiosperm trees in North America. *Glob. Ecol. Biogeogr.*, 22, 1183–1191.

R Core Team, . (2017). R: A language and environment for statistical computing.

Rahbek, C. (1995). The elevational gradient of species richness: a uniform pattern? *Ecography (Cop.).*, 18, 200–205.

Rahbek, C., Borregaard, M.K., Antonelli, A., Colwell, R.K., Holt, B.G., Nogues-Bravo, D., *et al.* (2019). Building mountain biodiversity: Geological and evolutionary processes. *Science (80-.).*

Richards, P.W. (1996). *The tropical rain forest: an ecological study*. 2nd edn. Cambridge University Press, Cambridge.

Ricklefs, R.E. (2005). Historical and ecological dimensions of global patterns in plant diversity. *Biol. Skr.*, 55, 583–603.

Rizzini, C.T. (1997). *Tratado de fitogeografia do Brasil.* 2nd edn. Ambito Cultural Edições Ltda.

Rôças, G., Scarano Fls, F.R. & Barros, C.F. (2001). Leaf anatomical variation in Alchornea triplinervia (Spreng) Müll. Arg. (Euphorbiaceae) under distinct light and soil water regimes. *Bot. J. Linn. Soc.*, 136, 231–238.

Rolland, J., Condamine, F.L., Jiguet, F. & Morlon, H. (2014). Faster Speciation and Reduced Extinction in the Tropics Contribute to the Mammalian Latitudinal Diversity Gradient. *PLoS Biol.*, 12.

Roncarati, H. & Menezes, L.F.T. (2005). Marambaia, Rio de Janeiro: origem e evolução. In: *Historia Natural da Marambaia* (eds. Menezes, L.F.T., Peixoto, A.L. & Araujo, D.S.D.). Universidade Federal Rural do Rio de Janeiro, Seropédica, pp. 15–38.

Saladin, B., Pellissier, L., Graham, C.H., Nobis, M.P., Salamin, N. & Zimmermann, N.E. (2020). Rapid climate change results in long-lasting spatial homogenization of phylogenetic diversity. *Nat. Commun.*, 11, 4663.

Sanders, N.J. & Rahbek, C. (2012). The patterns and causes of elevational diversity gradients. *Ecography (Cop.).*, 35, 1–3.

Sanmartín, I., Ronquist, F. & Cunningham, C. (2004). Southern Hemisphere Biogeography Inferred by Event-Based Models: Plant versus Animal Patterns. *Syst. Biol.*, 53, 216–243.

Scarano, F.R. (2002). Structure, function and floristic relationships of plant communities in stressful habitats marginal to the Brazilian Atlantic rainforest. *Ann. Bot.*, 90, 517–524.

Scarano, F.R. (2009). Plant communities at the periphery of the Atlantic rain forest: Rare-species bias and its risks for conservation. *Biol. Conserv.*, 142, 1201–1208.

Scarano, F.R., Duarte, H.M., Ribeiro, K.T., Rodrigues, P.J.F.P., Barcellos, E.M.B., Franco, A.C., *et al.* (2001). Four sites with contrasting environmental stress in southeastern Brazil: Relations of species, life form diversity, and geographic distribution to ecophysiological parameters. *Bot. J. Linn. Soc.*, 136, 345–364.

Schemske, D.W. & Mittelbach, G.G. (2017). "Latitudinal Gradients in Species Diversity": Reflections on Pianka's 1966 Article and a Look Forward. *Am. Nat.*, 189, 599–603.

Segovia, R.A. & Armesto, J.J. (2015). The Gondwanan legacy in South American biogeography. *J. Biogeogr.*, 42, 209–217.

Smith, S.A. & Brown, J.W. (2018). Constructing a broadly inclusive seed plant phylogeny. *Am. J. Bot.*, 105, 302–314.

Soliveres, S., Torices, R. & Maestre, F.T. (2012). Environmental conditions and biotic interactions acting together promote phylogenetic randomness in semi-arid plant communities: New methods help to avoid misleading conclusions. *J. Veg. Sci.*, 23, 822–836.

Spriggs, E.L., Christin, P.-A. & Edwards, E.J. (2014). C4 Photosynthesis Promoted Species Diversification during the Miocene Grassland Expansion. *PLoS One*, 9, e97722.

Stebbins, G.L. (1974). *Flowering plants: evolution above the species level.* 6th edn. Mass: Belknap Press of Harvard University Press, Cambridge.

Steinbauer, M.J., Grytnes, J.-A., Jurasinski, G., Kulonen, A., Lenoir, J., Pauli, H., *et al.* (2018). Accelerated increase in plant species richness on mountain summits is linked to warming. *Nature*, 556, 231–234.

Swenson, N.G. (2011). Phylogenetic beta diversity metrics, trait evolution and inferring the functional beta diversity of communities. *PLoS One*, 6.

Swenson, N.G. (2014a). *Functional and Phylogenetic Ecology in R. Use R!*

Swenson, N.G. (2014b). Phylogenetic imputation of plant functional trait databases. *Ecography (Cop.).*, 37, 105–110.

Tielbörger, K. & Kadmon, R. (1997). Relationships between shrubs and annual communities in a sandy desert ecosystem: A three-year study. *Plant Ecol.*, 130, 191–201.

Tilman, D. (1994). Competition and biodiversity in spatially structured habitats. *Ecology*, 75, 2–16.

Trabucco, A. & Zomer, R. (2009). *Global aridity index (global-aridity) and global potential evapo-transpiration (global-PET) geospatial database. CGIAR Consort. Spat. Inf.* Available at: https://cgiarcsi.community/data/global-aridity-and-pet-database/. Last accessed .

Valente, L.M., Savolainen, V. & Vargas, P. (2010). Unparalleled rates of species diversification in Europe. In: *Proceedings of the Royal Society B: Biological Sciences*. Royal Society, pp. 1489–1496.

Valiente-Banuet, A. & Verdú, M. (2013). Plant facilitation and phylogenetics. *Annu. Rev. Ecol. Evol. Syst.*

Vamosi, S.M., Heard, S.B., Vamosi, J.C. & Webb, C.O. (2009). Emerging patterns in the comparative analysis of phylogenetic community structure. *Mol. Ecol.*, 18, 572–592.

Venail, P., Gross, K., Oakley, T.H., Narwani, A., Allan, E., Flombaum, P., *et al.* (2015). Species richness, but not phylogenetic diversity, influences community biomass production and temporal stability in a re-examination of 16 grassland biodiversity studies. *Funct. Ecol.*, 29, 615–626.

Verdú, M. & Pausas, J.G. (2013). Syndrome-driven diversification in a mediterranean ecosystem. *Evolution (N. Y).*, 67, 1756–1766.

Volis, S. & Bohrer, G. (2013). Joint evolution of seed traits along an aridity gradient: seed size and dormancy are not two substitutable evolutionary traits in temporally heterogeneous environment. *New Phytol.*, 197, 655–667.

Wang, W., Lin, L., Xiang, X.G., Ortiz, R.D.C., Liu, Y., Xiang, K.L., *et al.* (2016). The rise of angiosperm-dominated herbaceous floras: Insights from Ranunculaceae. *Sci. Rep.*, 6, 6–13.

Webb, C.O. (2000). Exploring the Phylogenetic Structure of Ecological Communities: An Example for Rain Forest Trees. *Am. Nat.*, 156, 145–155.

Webb, C.O., Ackerly, D.D., McPeek, M.A. & Donoghue, M.J. (2002). Phylogenies and Community Ecology. *Annu. Rev. Ecol. Syst.*, 33, 475–505.

Weber, M.G., Wagner, C.E., Best, R.J., Harmon, L.J. & Matthews, B. (2017). Evolution in a Community Context: On Integrating Ecological Interactions and Macroevolution. *Trends Ecol. Evol.*, 32, 291–304.

Werneck, M. de S., Sobral, M.E.G., Rocha, C.T.V., Landau, E.C. & Stehmann, J.R. (2011). Distribution and endemism of angiosperms in the Atlantic forest. *Nat. Conserv.*, 9, 188–193.

Whittaker, R.H. (1956). Vegetation of the Great Smoky Mountains. *Ecol. Monogr.*, 26, 1–80.

Wickham, H. (2016). *Ggplot2 : elegant graphics for data analysis*. Springer.

Wiens, J.J. & Donoghue, M.J. (2004). Historical biogeography, ecology and species richness. *Trends Ecol. Evol.*, 19, 639–644.

Willig, M.R., Kaufman, D.M. & Stevens, R.D. (2003). Latitudinal Gradients of Biodiversity: Pattern, Process, Scale, and Synthesis. *Annu. Rev. Ecol. Evol. Syst.*, 34, 273–309.

Zhang, J., He, N., Liu, C., Xu, L., Chen, Z., Li, Y., *et al.* (2020). Variation and evolution of C:N ratio among different organs enable plants to adapt to N-limited environments. *Glob. Chang. Biol.*, 26, 2534–2543.

Zhu, J., Zhang, Y., Yang, X., Chen, N., Li, S., Wang, P., *et al.* (2020). Warming alters plant phylogenetic and functional community structure. *J. Ecol.*, 108, 2406–2415.

8. SUMMARY IN ESTONIAN

Taimekoosluste fülogeneetiline struktuur piki keskkonnagradiente makroökoloogilisest ja evolutsioonilisest vaatepunktist

Kliimamuutus ja elupaikade kadu ohustavad bioloogilist mitmekesisust, mille tõttu kahaneb liigirikkus ning kaob ka evolutsiooniline pärand, mis on geenides liigitunnustes. Tänased taimkattetüüpide kooslused keskkonnagradiendil on kujunenud evolutsiooniliste protsesside tulemil. Näiteks võib kahel niidul olla sarnane taimede liigirikkus, kuid erinev liikide evolutsiooniline pärand. Kauges suguluses olevad liigid võivad koosluses koos elada sellepärast, et lähisugulased konkureerivad tihti sarnaste ressursside pärast, mistõttu nõrgem konkurent välja tõrjutakse – areneb fülogeneetiliselt üledisperseerunud kooslus. Lähisugulased võivad koosluses koos olla, kui neil esinevad tunnused, mis annavad konkurentsis eelise kauges suguluses olevate liikide ees. Lähisugulaste kooseksisteerimisel tekib fülogeneetiliselt klasterdunud kooslus. Kuna bioloogilise mitmekesisuse mustrid (sh fülogeneetiline üledispersioon ja klasterdumine) arenevad nii tänapäevaste (nt biootilised interaktsioonid ja liikide nõudlused keskkonnaparameetrite suhtes) kui ka evolutsiooniliste protsesside (nt liigitekke) tulemil, on bioloogilise mitmekesisuse säilitamiseks oluline teada, milline on nende protsesside suhteline roll. Dissertatsioon uuribki, kuidas mõjutavad taimekoosluste fülogeneetilist struktuuri keskkonnategurid nagu näiteks kõrgus merepinnast, kliima, mulla toitainete sisaldus ja inimtekkeline kõrbestumine. Täpsemalt otsitakse vastuseid küsimustele:

1) Kuidas on koosluse eri kasvuvormide (st puittaimed ja rohttaimed) fülogeneetiline struktuur seotud laiuskraadi, biogeograafilise piirkonna ja taimkattetüübiga globaalsel skaalal?
2) Kuidas mõjutavad piki Atlandi ookeani kallast leviva *restinga* taimkattetüübi puittaimede fülogeneetilist struktuuri tänane kliima, ajalooline klimaatiline stabiilsus ja kasvukoha mulla omadused?
3) Kuidas mõjutab kõrbestumine ühe- ja mitmeaastaste rohttaimede fülogeneetilist struktuuri poollooduslikes kuivades Vahemere kooslustes?
4) Kuidas mõjutab kõrgus merepinnast puittaimede fülogeneetilist struktuuri erinevates taimkattetüüpides bioloogilise mitmekesisuse tulipunktis Atlantilise vihmametsa kompleksis?

Puit- ja rohttaimeliikide uurimine globaalsel skaalal (1) näitas, et laiuskraad mõjutab koosluste fülogeneetilist struktuuri erinevalt. Puittaimeliikide lähisugulus on suurem väiksematel laiuskraadidel tõenäoliselt sellepärast, et enamus puittaimi arenes soojas ja stabiilses troopikas. Külmumise vastaste kohastumuste puudumise tõttu ei levinud paljud liigid jahedamasse parasvöötmesse. Ainult mõnedel puittaimeliikidel, sh nii õis- kui ka kaugemas suguluses olevatel paljasseemnetaimedel, on külmumise vastased füsioloogilised kohastumused. Selliste liikide kooseksisteerimisel tekib koosluses fülogeneetiline üledispersioon. Paljasseemnetaimede mitte arvestamise tulemusel klasterdub koosluse fülogeneetiline struktuur, mille tingib külmumise vastaste kohastumustega õistaimeliikide omavaheline lähisugulus. Rohttaimeliikide fülogeneetiline struktuur koosluses piki laiuskraadi ei ole nii selge kui puittaimedel. Rohttaimeliikide fülogeneetilist struktuuri mõjutab pigem taimkattetüüp: rohttaimed on omavahel lähemas suguluses avatud (nt niidud) kui suletud võradega (nt mets) kasvukohtades. See tulemus võib olla seotud mõnede rohttaimeklaadide (nt kõrrelised) evolutsioonilise noorusega.

Erineva elustrateegiaga rohttaimeliikide uurimine kõrbestuvas piirkonnas (3) näitas, et üheaastased rohttaimed on lähemas suguluses kuivemates tingimustes. See on tõenäoliselt tingitud pikaajalisest liikide selekteerimiseste regionaalsest liigifondist kuivadesse kooslustesse. Pikema elueaga, st mitmeaastased liigid, mis peavad taluma kuivastressi suvise põua ajal, on fülogeneetiliselt lähemas suguluses niiskemates oludes. See on tõenäoliselt võimalik sellepärast, et neil on sarnased tunnused, mis annavad neile eelise kaugemalt sugulastest konkurentide ees.

Uurides evolutsioonilisi liikide lahknemisi Atlantilise vihmametsa kompleksi puittaimekooslustes rannikul (2) ja kõrgusvööndites (4) selgus, et (2) kaugmineviku lahknemiste valguses on rannikukoosluste liigid omavahel kaugemas suguluses lõunapoolsematel aladel. See on ilmselt tingitud kauges suguluses olevate ja jahedale kliimale kohastunud ning laialt levinud Atlantilise vihmametsa liikide kooseksisteerimisest. Lähimineviku liikide lahknemine näitab, et liigid on lähemas suguluses klimaatiliselt stabiilsemates piirkondades; neis piirkondades esineb ka palju ainuomaseid liike. See viitab võimalikule levimistõkkele ja kohapealsele liigitekkele. Liigid on lähemas suguluses ka kuivadel ning kõrge soolsuse ja väheviljaka mullaga aladel, mis viitab sugulasliikide spetsiaalsete kohastumuste selekteerimisele nendes kooslustes. Puittaimede fülogeneetiline struktuur erines kõrgusgradiendil (4). Kauges minevikus toimunud liikidevahelised lahknemised näitavad, et merepinnast kõrgemate taimekattetüüpide kooslustes on liigid omavahel pigem kauges suguluses. See näitab tõenäoliselt pikaajalist kauges suguluses olevate ning jaheda temperatuuriga kohastunud liikide levimist kõrgusgradiendil ülespoole. Neist liikidest arenes tõenäoliselt mägedes uusi liike, sest lähimineviku liikidevahelist lahknemist uurides selgus, et kõrgemal asuvate koosluste liigid on omavahel lähisugulased. Kuivas ja kõrge soolsusega mullal levivates kooslustes on liigid lähisugulased, kui vaadata kaugmineviku lahknemisi, kuid fülogeneetiline struktuur on juhuslik lähiminevikus toimunud lahknemiste valguses. Tulemus näitab, et vaid vähesed liigid suutsid minevikus karmide keskkonnatingimustega kooslusi asustada ning neist liikidest ei arenenud kohapeal uusi liike.

Dissertatsioon näitab, kuidas keskkonnategurid mõjutavad taimekoosluste fülogeneetilist struktuuri. Tulemused toetavad fülogeneetiliste andmete laialdasemat kasutamist, et uurida eluslooduse mitmekesisuse mustrite päritolu ja säilimise mehhanisme. Tulemused on olulised ka tänaste kliimamuutuste ja elupaikade kao kontekstis, sest liikide väljasuremine tähendab ka evolutsioonilise ajaloo kadumist looduslikes kooslustes.

ACKNOWLEDGEMENTS

I am deeply grateful to my wife for embarking with me on the journey to Estonia and for being supportive and kind in all moments, including the darkest ones. I sincerely thank my supervisor Pille Gerhold for accepting me as a PhD student and for her guidance and support throughout this important period of my life. I thank Lauri and Lars for scientific and sometimes emotional advice and Alice, Francesco and Triin for collaboration opportunities. A deep and special thank goes to the University of Tartu and its staff. One of the best things about doing a PhD at UT is to feel welcome and interact with lovely, efficient and detail-oriented people.

My special thank goes to Helen Kaptein, who kindly accommodated me in her house when I arrive in Tartu and Nemailla Bonturi, a Brazilian who found me talking to my wife on the street and introduced us to the unexpected lusophone community in Tartu. Life in Tartu would have been very hard without friends and colleagues from all over the world that made some moments easier. I thank everyone, especially Sofia, Lisandra, Guilherme, Jerome, Diego, Jessica, Paola, Marina, Raul, Lena, Inga, Aurele, Guille, John, Marge, and Mickael, for words of advice or for simply being there listening to my complainings and, of course, for a few fun and relaxing moments. I could not forget to thank all colleagues and friends I met at the University of South Bohemia in the Czech Republic, especially my roommate Guillaume for the fun statistical related moments in our apartment, and Anibal, Lindsay, and Nina.

Finally, a profound and special thank goes to my family and friends back in Brazil, who always supported and encouraged me, even though they do not understand exactly what I do. I am especially grateful to my parents, sisters, father-in-law, and mother-in-law for always being supportive; my friends Alan, Andreia, Wanderson and Bianca for the fun moments. I thank you for understanding why I was not present in important moments. I love you all!

***

The research included in this thesis was funded by the Estonian Research Council [PUT 1006], European Regional Development Fund (Contract No. 36.9-6.1/1476) and University of Tartu.

PUBLICATIONS

CURRICULUM VITAE

Jhonny Capichoni Massante

ORCID: https://orcid.org/0000-0003-2764-4976
University of Tartu – Institute of Ecology and Earth Sciences
Vanemuise 46, Tartu, Estonia, 51014
Email: jhonny.massante@ut.ee
Tel: +351 912522287
Last updated December 2020

Education

2016–present,	**Ph.D.** Institute of Ecology and Earth Sciences, University of Tartu, Estonia.
2014–2016,	**M.S.** Marine Biology and Coastal Environments, Fluminense Federal University, Brazil.
2007–2013,	**B.S.** Biology, State University of Rio de Janeiro, Brazil.

Professional appointments

2018–2018,	Fieldwork specialist, Department of Botaty, University of Tartu
2016–2018,	Teaching assistant, University of Tartu

Supervising

Annika Kumar (B.S.), "Variation in ecological and evolutionary drivers of phylogenetic beta diversity in plant communities" (at University of Tartu).

Publications

Jhonny C. Massante and Gerhold, P. Evolutionary history of marginal habitats influences the diversity of tree communities in the Atlantic Forest. M*anuscript under review.*

Mendes, G. et al. (including **Jhonny C. Massante**, 38/48). (2020). How much leaf area do insects eat? A dataset of insect herbivory sampled globally with a standardized protocol. *Accepted at Ecology.*

Jhonny C. Massante, Kobel, M., Pinho, P., Gerhold, P., Branquinho, C., Nunes, A. (2020). Phylogenetic structure of understorey annual and perennial plant species reveals opposing responses to aridity in a Mediterranean biodiversity hotspot. *Science of The Total Environment,* vol. 761, article 144018.

Blaus, A., Reitalu, T., Gerhold, P., Hiiesalu, H., **Jhonny C. Massante**, Veski, S. (2020). Modern pollen-plant diversity relationships inform palaeoecological reconstructions of functional and phylogenetic diversity in Calcareous fens. *Frontiers in Ecology and Evolution*, vol. 8, article 207.

Jhonny C. Massante and Gerhold, P. (2020). Environment and evolutionary history depict phylogenetic alpha and beta diversity in the Atlantic coastal white-sand woodlands. *Journal of Vegetation Science, 31 (4).*

Brown, J.J., Mennicken, S., **Jhonny C. Massante**, Dijoux, S., Telea, A., Benedek, A.M., Götzenberger, L., Májeková, M., Lepš, J., Šmilauer, P., Hrček, J., de Bello, F. (2019). A novel method to predict dark diversity using unconstrained ordination analysis. *Journal of Vegetation Science, 30 (4).*

Jhonny C. Massante, Götzenberger, L., Takkis, K., Hallikma, T., Kaasik, A., Laanisto, L. Hutchings, M.J., Gerhold, P. (2019). Contrasting latitudinal patterns in phylogenetic diversity between woody and herbaceous communities. *Scientific Reports, vol: 9, article 6443.*

Jhonny C. Massante. Mining disaster: restore habitats now. (2015). *Nature, 528 (7580).*

Awards and Grants

2020 Erasmus+ traineeship to work on phylogenetic structure of semi-natural and restored plant communities in Mediterranean drylands – Erasmus+ Programme of the European Union (2,880 EUR).

2019 Dora Plus activity 1.2 (PhD student mobility) to visit the University of Lisbon for a collaboration of 10 months – European Regional Development Fund and Archimedes Foundation (8,852 EUR).

2019 IAVS Travel grant, International Association for the Vegetation Science (550 EUR).

2019 Kristjan Jaak Scholarship for short study visits to attend the 15th European Ecological Federation Congress in Lisbon, Portugal – European Regional Development Fund and Archimedes Foundation (1,114 EUR).

2018 Doctoral Expedition to Reunion Island, University of Tartu (selected with the project: "Phylogenetic structure of plant communities along an elevational gradient in the tropical Reunion Island".

2018 Dora Plus activity 1.1 grant (short study visits) to attend the Meta-Analysis course delivered by dr. Wolfgang Viechtbauer at Maastricht University, The Netherlands – European Regional Development Fund and Archimedes Foundation (1,284 EUR).

2018 Dora Plus activity 1.1 grant (short study visits) to attend the Climate Change Biogeography meeting promoted by the International Biogeography Society in Évora, Portugal – European Regional Development Fund and Archimedes Foundation (1.355 EUR).

2017 Erasmus+ grant student mobility to attend the Quantitative Ecology Module at the University of South Bohemia, Czech Republic – Erasmus+ Programme of the European Union (1,983 EUR).

2017 IAVS Travel grant, International Association for the Vegetation Science (550 EUR).

2015 Field course: Ecology and Conservation the Brazilian Seasonally Dry Tropical Forest (Caatinga). Selected with the project: "Positive interactions among plants can increase regeneration niches in the Caatinga". (21 days of intensive training on sampling design, data analysis, scientific writing, and scientific presentation).

Selected presentations

Jhonny C. Massante, Neves, D., Gerhold, P. (July 2019). Environment and evolutionary history control phylogenetic turnover in Atlantic white-sand plant communities. *European Ecological Federation Congress – Ecology across borders: Embedding ecology in sustainable development goals*, Lisbon, Portugal. (Oral presentation).

Jhonny C. Massante, Götzenberger, L., Takkis, K., Hallikma, T., Laanisto L., Hutchings, M.J., Gerhold, P. (March 2018). Contrasting latitudinal patterns in phylogenetic diversity between woody and herbaceous communities. *Climate Change Biogeography – International Biogeographical Society meeting*, Évora, Portugal. (Poster).

Professional Service

Manuscript reviewer, 2019 –
Journal of Ecology, Journal of Biogeography, Journal of Vegetation Science (certified review record available at https://publons.com/researcher/3411727/jhonny-massante/peer-review/), *Ecological Indicators, Agronomy Research, Biodiversidade Brasileira.*

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 interannual patterns. Tartu, 2014, 115 p.
263. **Külli Lokko**. Seasonal and spatial variability of zoopsammon communities in relation to environmental parameters. Tartu, 2014, 129 p.
264. **Olga Žilina**. Chromosomal microarray analysis as diagnostic tool: Estonian experience. Tartu, 2014, 152 p.

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

285. **Ly Lindman**. The ecology of protected butterfly species in Estonia. Tartu, 2015, 171 p.
286. **Jaanis Lodjak**. Association of Insulin-like Growth Factor I and Corticosterone with Nestling Growth and Fledging Success in Wild Passerines. Tartu, 2016, 113 p.
287. **Ann Kraut**. Conservation of Wood-Inhabiting Biodiversity – Semi-Natural Forests as an Opportunity. Tartu, 2016, 141 p.
288. **Tiit Örd**. Functions and regulation of the mammalian pseudokinase TRIB3. Tartu, 2016, 182. p.
289. **Kairi Käiro**. Biological Quality According to Macroinvertebrates in Streams of Estonia (Baltic Ecoregion of Europe): Effects of Human-induced Hydromorphological Changes. Tartu, 2016, 126 p.
290. **Leidi Laurimaa**. *Echinococcus multilocularis* and other zoonotic parasites in Estonian canids. Tartu, 2016, 144 p.
291. **Helerin Margus**. Characterization of cell-penetrating peptide/nucleic acid nanocomplexes and their cell-entry mechanisms. Tartu, 2016, 173 p.
292. **Kadri Runnel**. Fungal targets and tools for forest conservation. Tartu, 2016, 157 p.
293. **Urmo Võsa**. MicroRNAs in disease and health: aberrant regulation in lung cancer and association with genomic variation. Tartu, 2016, 163 p.
294. **Kristina Mäemets-Allas**. Studies on cell growth promoting AKT signaling pathway – a promising anti-cancer drug target. Tartu, 2016, 146 p.
295. **Janeli Viil**. Studies on cellular and molecular mechanisms that drive normal and regenerative processes in the liver and pathological processes in Dupuytren's contracture. Tartu, 2016, 175 p.
296. **Ene Kook**. Genetic diversity and evolution of *Pulmonaria angustifolia* L. and *Myosotis laxa sensu lato* (Boraginaceae). Tartu, 2016, 106 p.
297. **Kadri Peil**. RNA polymerase II-dependent transcription elongation in *Saccharomyces cerevisiae*. Tartu, 2016, 113 p.
298. **Katrin Ruisu**. The role of RIC8A in mouse development and its function in cell-matrix adhesion and actin cytoskeletal organisation. Tartu, 2016, 129 p.
299. **Janely Pae**. Translocation of cell-penetrating peptides across biological membranes and interactions with plasma membrane constituents. Tartu, 2016, 126 p.
300. **Argo Ronk**. Plant diversity patterns across Europe: observed and dark diversity. Tartu, 2016, 153 p.
301. **Kristiina Mark**. Diversification and species delimitation of lichenized fungi in selected groups of the family Parmeliaceae (Ascomycota). Tartu, 2016, 181 p.
302. **Jaak-Albert Metsoja**. Vegetation dynamics in floodplain meadows: influence of mowing and sediment application. Tartu, 2016, 140 p.
303. **Hedvig Tamman**. The GraTA toxin-antitoxin system of *Pseudomonas putida*: regulation and role in stress tolerance. Tartu, 2016, 154 p.

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

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

344. **Teivi Laurimäe**. Taxonomy and genetic diversity of zoonotic tapeworms in the species complex of *Echinococcus granulosus* sensu lato. Tartu, 2018, 143 p.
345. **Tatjana Jatsenko**. Role of translesion DNA polymerases in mutagenesis and DNA damage tolerance in Pseudomonads. Tartu, 2018, 216 p.
346. **Katrin Viigand**. Utilization of α-glucosidic sugars by *Ogataea* (*Hansenula*) *polymorpha*. Tartu, 2018, 148 p.
347. **Andres Ainelo**. Physiological effects of the *Pseudomonas putida* toxin grat. Tartu, 2018, 146 p.
348. **Killu Timm**. Effects of two genes (DRD4 and SERT) on great tit (*Parus major*) behaviour and reproductive traits. Tartu, 2018, 117 p.
349. **Petr Kohout**. Ecology of ericoid mycorrhizal fungi. Tartu, 2018, 184 p.
350. **Gristin Rohula-Okunev**. Effects of endogenous and environmental factors on night-time water flux in deciduous woody tree species. Tartu, 2018, 184 p.
351. **Jane Oja**. Temporal and spatial patterns of orchid mycorrhizal fungi in forest and grassland ecosystems. Tartu, 2018, 102 p.
352. **Janek Urvik**. Multidimensionality of aging in a long-lived seabird. Tartu, 2018, 135 p.
353. **Lisanna Schmidt**. Phenotypic and genetic differentiation in the hybridizing species pair *Carex flava* and *C. viridula* in geographically different regions. Tartu, 2018, 133 p.
354. **Monika Karmin**. Perspectives from human Y chromosome – phylogeny, population dynamics and founder events. Tartu, 2018, 168 p.
355. **Maris Alver**. Value of genomics for atherosclerotic cardiovascular disease risk prediction. Tartu, 2019, 148 p.
356. **Lehti Saag**. The prehistory of Estonia from a genetic perspective: new insights from ancient DNA. Tartu, 2019, 171 p.
357. **Mari-Liis Viljur**. Local and landscape effects on butterfly assemblages in managed forests. Tartu, 2019, 115 p.
358. **Ivan Kisly**. The pleiotropic functions of ribosomal proteins eL19 and eL24 in the budding yeast ribosome. Tartu, 2019, 170 p.
359. **Mikk Puustusmaa**. On the origin of papillomavirus proteins. Tartu, 2019, 152 p.
360. **Anneliis Peterson**. Benthic biodiversity in the north-eastern Baltic Sea: mapping methods, spatial patterns, and relations to environmental gradients. Tartu, 2019, 159 p.
361. **Erwan Pennarun**. Meandering along the mtDNA phylogeny; causerie and digression about what it can tell us about human migrations. Tartu, 2019, 162 p.
362. **Karin Ernits**. Levansucrase Lsc3 and endo-levanase BT1760: characterization and application for the synthesis of novel prebiotics. Tartu, 2019, 217 p.
363. **Sille Holm**. Comparative ecology of geometrid moths: in search of contrasts between a temperate and a tropical forest. Tartu, 2019, 135 p.

364. **Anne-Mai Ilumäe**. Genetic history of the Uralic-speaking peoples as seen through the paternal haplogroup N and autosomal variation of northern Eurasians. Tartu, 2019, 172 p.
365. **Anu Lepik**. Plant competitive behaviour: relationships with functional traits and soil processes. Tartu, 2019, 152 p.
366. **Kunter Tätte**. Towards an integrated view of escape decisions in birds under variable levels of predation risk. Tartu, 2020, 172 p.
367. **Kaarin Parts**. The impact of climate change on fine roots and root-associated microbial communities in birch and spruce forests. Tartu, 2020, 143 p.
368. **Viktorija Kukuškina**. Understanding the mechanisms of endometrial receptivity through integration of 'omics' data layers. Tartu, 2020, 169 p.
369. **Martti Vasar**. Developing a bioinformatics pipeline gDAT to analyse arbuscular mycorrhizal fungal communities using sequence data from different marker regions. Tartu, 2020, 193 p.
370. **Ott Kangur**. Nocturnal water relations and predawn water potential disequilibrium in temperate deciduous tree species. Tartu, 2020, 126 p.
371. **Helen Post**. Overview of the phylogeny and phylogeography of the Y-chromosomal haplogroup N in northern Eurasia and case studies of two linguistically exceptional populations of Europe – Hungarians and Kalmyks. Tartu, 2020, 143 p.
372. **Kristi Krebs**. Exploring the genetics of adverse events in pharmacotherapy using Biobanks and Electronic Health Records. Tartu, 2020, 151 p.
373. **Kärt Ukkivi**. Mutagenic effect of transcription and transcription-coupled repair factors in *Pseudomonas putida*. Tartu, 2020, 154 p.
374. **Elin Soomets**. Focal species in wetland restoration. Tartu, 2020, 137 p.
375. **Kadi Tilk**. Signals and responses of ColRS two-component system in *Pseudomonas putida*. Tartu, 2020, 133 p.
376. **Indrek Teino**. Studies on aryl hydrocarbon receptor in the mouse granulosa cell model. Tartu, 2020, 139 p.
377. **Maarja Vaikre**. The impact of forest drainage on macroinvertebrates and amphibians in small waterbodies and opportunities for cost-effective mitigation. Tartu, 2020, 132 p.
378. **Siim-Kaarel Sepp**. Soil eukaryotic community responses to land use and host identity. Tartu, 2020, 222 p.
379. **Eveli Otsing**. Tree species effects on fungal richness and community structure. Tartu, 2020, 152 p.
380. **Mari Pent**. Bacterial communities associated with fungal fruitbodies. Tartu, 2020, 144 p.
381. **Einar Kärgenberg**. Movement patterns of lithophilous migratory fish in free-flowing and fragmented rivers. Tartu, 2020, 167 p.
382. **Antti Matvere**. The studies on aryl hydrocarbon receptor in murine granulosa cells and human embryonic stem cells. Tartu, 2021, 163 p.