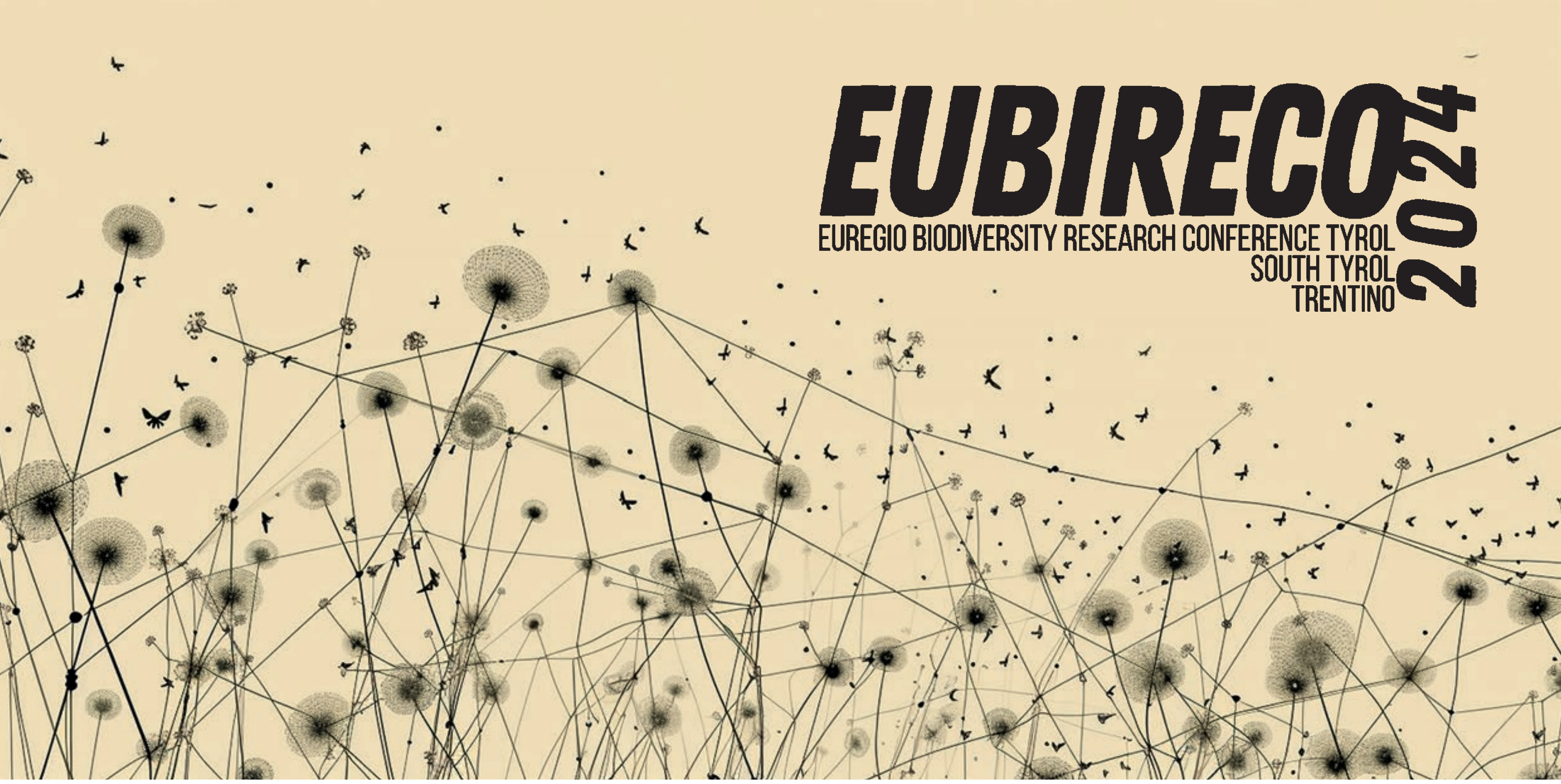

Landesmuseen Südtirol
Musei provinciali Alto Adige
Museums provinziai

NATURMUSEUM SÜDTIROL
MUSEO SCIENZE NATURALI ALTO ADIGE
MUSEUM NATÖRA SÜDTIROL
BIODIVERSITY CENTER

EUROPAREGION
EUREGIO
Tirol Südtirol Trentino
Tirolo Alto Adige Trentino

Proceedings of the

Euregio Biodiversity Research Conference (EUBIRECO) – 2024

Tyrol-South Tyrol-Trentino

November 22–23, 2024
Bozen/Bolzano, Italy

Petra Mair, David Gruber & Thomas Wilhalm

1. Introduction

From 2000 to 2022, the Museum of Nature South Tyrol regularly hosted the biennial conference „Zoologische und botanische Forschung in Südtirol/Ricerca zoologica e botanica in Alto Adige“ (Zoological and Botanical Research in South Tyrol). This appealed to academics and amateurs alike, to those working at universities and museums as well as purely private naturalists. However, with the establishment of the European Academy of Bolzano and the Free University of Bolzano, a new, increasingly scientifically oriented generation has grown up, and with it the need to give the traditional conference a new format.

From November 22–23, 2024, the Museum of Nature South Tyrol invited participants to Bolzano for the "Euregio Biodiversity Research Conference (Eubireco) 2024, Tyrol-South Tyrol-Trentino." The focus was on biodiversity research throughout the Tyrol-South Tyrol-Trentino Euroregion, as well as cross-border cooperation. The newly aligned conference was intended to lay the foundation for future cooperation in order to better protect and understand biodiversity in our region. It is the Museum's intention that this conference will not remain limited to Bolzano but will, in the future, be hosted in turn by research institutions and organizations across the entire Euroregion, thus strengthening shared responsibility and collaboration.

The conference is particularly encouraging young scientists to present their research findings to a wider specialist audience. At the same time, it is designed to provide a platform for the exchange of knowledge and experience, as well as to promote the development of networks for future research collaborations and the formulation of new research directions.

Around 120 researchers from across the Euregio responded to the call and took part in the conference.

2. Organization

Scientific Committee: Peter Huemer, Tiroler Landesmuseen-Betriebsges. m.b.H., Sammlungs- und Forschungszentrum, Hall i. Tirol (Austria); Chiara Paniccia, Institute for Alpine Environment, Eurac Research, Bolzano (Italy); Claudio Varotto, Research and Innovation Centre, Fondazione Edmund Mach (FEM), San Michele all'Adige (Italy); Camilla Wellstein, Free University of Bozen-Bolzano and Thomas Wilhalm, Museum of Nature South Tyrol, Bolzano (Italy)

Organizing Committee: Sonia Cossarini, Petra Mair, Thomas Wilhalm

Coordination: Petra Mair

3. Acknowledgements

We gratefully acknowledge the patronage of the Amt der Europaregion/Ufficio Euregio of the Autonomous Province of Bolzano-South Tyrol. Our sincere thanks go in particular to the Secretary General of the Euregio Tyrol-South Tyrol-Trentino, Christoph von Ach, for his support. We also wish to thank the Euregio for providing the venue at the Waaghaus and for kindly sponsoring the coffee break, as well as the members of the scientific committee for their efforts in reviewing and selecting the presentations.

4. Conference Program

The 75 lectures and poster presentations covered the following broader topics:

- Biodiversity: recording and monitoring (fungi, animals, plants incl. pollen)
- Systematics & biogeography
- Biodiversity & nature conservation
- Ecology, environment & global change

The venues were located in Bolzano, i.e., on November 22 at the Haus der Kultur/Casa della Cultura „Walther von der Vogelweide“ (Schlernstraße/Via Sciliar 1) and on November 23 simultaneously at the Museum of Nature South Tyrol (Bindergasse/Via Bottai 1) and the Waaghaus (Kornplatz/Piazza del Grano 12).
Extended abstracts of several oral presentations are provided in Chapter 5, short abstracts of all both oral and poster presentations are given in Chapter 6.

Friday, November 22, 2024

Oral presentations

9:20 – 10:00	**Keynote:** **Integrating genetic diversity into biodiversity conservation** Martin Fischer; Institute of Integrative Biology, ETH Zürich (CH)

Session: Biodiversity: recording and monitoring (fungi, animals, plants incl. pollen) 1
Chair: Chiara Paniccia – Institute for Alpine Environment, Eurac Research, Bolzano

10:00 – 10:20	**Five years of Biodiversity Monitoring South Tyrol – report on the first monitoring cycle** Ulrike Tappeiner; Institute for Alpine Environment, Eurac Research, Bozen (I), Department of Ecology, University of Innsbruck (A)
10:20 – 10:40	**Caddisflies (Trichoptera) diversity in South Tyrol: From historical records to new findings** Francesca Vallefuoco; Institute for Alpine Environment, Eurac Research, Bolzano (I)
10:40 – 11:00	**Monitoring of the Alpine Salamander, *Salamandra atra*, in Trentino: a Double Observer approach** Luca Roner; MUSE – Museo delle Scienze, Trento (I)

Session: Biodiversity: recording and monitoring (fungi, animals, plants incl. pollen) 2
Chair: Peter Huemer – Sammlungs- und Forschungszentrum, Hall i. Tirol

11:40 – 12:00	**The City Nature Challenge in Innsbruck – Exploring the Potential of Citizen Science Initiatives to Strenghten Regional Biodiversity Datasets in Museums** Petra Schattanek-Wiesmair & Christian Anich; Sammlungs- und Forschungszentrum, Hall i. Tirol (A)
12:00 – 12:20	**The MonitAnt project: towards a European standardized protocol for red wood ants monitoring** Elia Nalini; Institute for Alpine Environment, Eurac Research, Bolzano (I)
12:20 – 12:40	**Developing a standardized monitoring scheme of the I Annex Bird Directive species breeding in South Tyrol: methods and first results** Francesco Ceresa; Museo di Scienze Naturali dell’Alto Adige, Bolzano (I)
12:40 – 13:00	**Large-scale passive acoustic monitoring of birds in an Alpine ecosystem** Jarek Scanferla; Institute for Alpine Environment, Eurac Research, Bolzano (I)

Session: Biodiversity: recording and monitoring (fungi, animals, plants incl. pollen) 3
Chair: Mauro Gobbi – MUSE – Museo delle Scienze, Trento

14:30 – 14:50	**Soil fauna on mountaintops: first results from the GLORIA Extended samplings in South Tyrol** Michael Steinwandter; Institute for Alpine Environment, Eurac Research, Bozen (I)
14:50 – 15:10	**Soil biodiversity in protected, near-natural forests** Julia Seeber; Institute for Alpine Environment, Eurac Research, Bozen (I)
15:10 – 15:30	**Long-term study of heavy metal and nitrogen concentrations in moss species *Hylocomium splendens* in South Tyrol** Renate Alber; Biologisches Labor – Landesagentur für Umwelt und Klimaschutz, Leifers (I)

15:30 – 15:50 **Genetic variability of the chestnut blight fungus *Cryphonectria parasitica* in different populations of northern Italy**
Sanja Baric; Free University of Bozen-Bolzano (I)

15:50- 16:10 **Grasslands4Biodiversity (G4B) – How can we protect biodiversity-rich grasslands in the Central Alps?**
Jonas Sommer; Institute for Alpine Environment, Eurac Research, Bozen (I)

Session: Ecology, environment & global change 1
Chair: Camilla Wellstein – Free University of Bozen-Bolzano

16:40 – 17:00 **Rivers Run Through It – Exploring Aquatic Macrobenthos Diversity in the Vinschgau/Venosta Valley**
Thea Schwingshackl; Institute for Alpine Environment, Eurac Research, Bozen (I)

17:00 – 17:20 **A long-term perspective on hypolimnetic dissolved oxygen and surface CO_2? Case study mountain Lake Tovel**
Ulrike Obertegger; Fondazione Edmund Mach, San Michele all'Adige (I)

17:20 – 17:40 **Does global change make high-elevation plant communities of the European Alps richer but less unique?**
Pau Carnicero Campmany; Department of Botany, University of Innsbruck (A)

17:40 – 18:00 **Alpine flora at the extremes: the distribution of plants on mountain peaks**
Giulia Tomasi; Fondazione Museo Civico di Rovereto (I)

18:00 – 18:20 **Cold-adapted species in the warming Alps: who will survive?**
Mauro Gobbi; MUSE – Museo delle Scienze, Trento (I)

Poster presentations

Session: Biodiversity: recording and monitoring (fungi, animals, plants incl. pollen)

Biodiversa+ Habitat Pilot: Finding a shared method for mapping and monitoring grasslands and wetlands using Remote Sensing data
Albin Bjärhall; Institute for Alpine Environment, Eurac Research, Bozen (I)

Diversity of stink bugs and their egg parasitoids in South Tyrol
Sara Bortolini; Laimburg Research Centre, Vadena/Pfatten (I)

Biodiversa+: a European Biodiversity Partnership for a transnational network of harmonized biodiversity monitoring schemes
Michele Bresadola; Institute for Alpine Environment, Eurac Research, Bozen (I)

Unraveling the biology of the invasive apricot aphid (*Myzus mumecola*)
Marta Chignola; Free University of Bozen-Bolzano (I)

Remarkable bryophyte discoveries in the area of the "Alter See" natural monument in the Lienz Dolomites (East Tyrol, Austria)
Felix Faltner; Revital Integrative Naturraumplanung GmbH, Nußdorf-Debant (Osttirol) (A)

Species Distribution Modeling for Farmland Birds in South Tyrol Using Remote Sensing Data
Lena Josephina Jäger; Institute for Earth Observation, Eurac Research, Bozen (I)

Monitoring invertebrates included in the Habitats Directive in South Tyrol: First results and future strategies
Audrey Marsy; Institute for Alpine Environment, Eurac Research, Bozen (I)

A survey of larval parasitoids of *Drosophila suzukii* (Matsumura) (Diptera: Drosophilidae) in semi-natural habitats and ecotones in South Tyrol
Martina Melchiori; Laimburg Research Centre, Vadena/Pfatten (I)

DNA barcoding of minor fish fauna in South Tyrol
Massimo Morpurgo; Museo di Scienze Naturali dell'Alto Adige, Bolzano (I)

Orthopterological highlights from the Biodiversity Monitoring South Tyrol
Emanuele Repetto; Institute for Alpine Environment, Eurac Research, Bozen (I)

On the composition of the apple's Sooty Blotchs pathobiome
Filippo Rey; Free University of Bozen-Bolzano (I)

Advancing biomonitoring through automated image and sound recognition: two European pilot studies
Jarek Scanferla; Institute for Alpine Environment, Eurac Research, Bozen (I)

South Tyrol's bat guardians: Citizen science for Barbastelle bat conservation in settlements
Hanna Steigleder; Institute for Alpine Environment, Eurac Research, Bozen (I)

Saturday, November 23, 2024

Oral presentations

Parallel Sessions

Biodiversity & nature conservation **Chair: Philipp Kirschner – Department of Botany, University of Innsbruck**	***Biodiversity: recording and monitoring (fungi, animals, plants incl. pollen) 4*** **Chair: Renate Alber – Biologisches Labor, Landesagentur für Umwelt und Klimaschutz, Leifers-Laives**
8:30 – 8:50 **Preliminary Results on the Analysis and Conservation of Natural and Semi-natural Habitats in South Tyrol (LEST Project)** Camilla Wellstein; Free University of Bozen-Bolzano (I)	8:30 – 8:50 **Airborne pollen biodiversity: changes in 30 years of data at San Michele all'Adige (North Italy)** Fabiana Cristofolini; Fondazione Edmund Mach, San Michele all'Adige (I)
8:50 – 9:10 **Peatlands in Trentino: an overview based on surveys covering 224 hectares conducted since 2011** Daniel Spitale; BioMonitoring Team, Tre Ville, TN (I)	8:50 – 9:10 **Tiny but mighty – Pollen of South Tyrol** Magdalena Widmann; Biologisches Labor – Landesagentur für Umwelt und Klimaschutz, Leifers (I)
9:10 – 9:30 **Wolf depredation on livestock in Trentino: an analysis of dynamics and prevention strategies** Giulia Bombieri; MUSE – Museo delle Scienze, Trento (I)	9:10 – 9:30 **The air as a means to assess plant biodiversity in Alpine environments** Franziska Zemmer; Fondazione Edmund Mach, San Michele all'Adige (I)
9:30 – 9:50 **The landscape of fear in cow farms: breeding barn swallows reduce housefly activity in cattle sheds** Francesca Roseo; LIPU, Parma (I); MUSE – Museo delle Scienze, Trento (I)	9:30 – 9:50 **AtlasFloraAlpina – towards a first online flora atlas for the entire Alpine arc** Thomas Wilhalm; Naturmuseum Südtirol, Bozen (I)
9:50 – 10:10 **Extensive management practices and natural structural elements enhance bat conservation in mountain agricultural landscapes** Chiara Paniccia; Institute for Alpine Environment, Eurac Research, Bolzano (I)	9:50 – 10:10 **Introducing „naturamonta“: A New Scientific Journal Dedicated to Biodiversity and related Research In The EUREGIO Tyrol, South Tyrol, Trentino** Christian Anich; Sammlungs- und Forschungszentrum, Hall i. Tirol (A)
	Session: Ecology, environment & global change 2 **Chair: Franziska Zemmer – Fondazione Edmund Mach (FEM), San Michele all'Adige**
10:10 – 10:30 **Crowded mountains: large-scale and long-term responses of mammals to human outdoor activity in mountainous areas** Marco Salvatori; MUSE – Museo delle Scienze, Trento (I); Università di Firenze (I)	10:10 -10:30 **Carbon Inventory South Tyrol – Quantification of Soil Organic Carbon (SOC) stocks and assessment of their stability for agricultural areas of South Tyrol, Italy** Alexander Schönafinger; Institute for Alpine Environment, Eurac Research, Bozen (I)
Session: Systematics & biogeography (taxonomy, phylogenetics & evolution) 1 **Chair: Claudio Varotto – Fondazione Edmund Mach (FEM), San Michele all'Adige**	***Session: Ecology, environment & global change 2*** **Chair: Franziska Zemmer – Fondazione Edmund Mach (FEM), San Michele all'Adige**
11:10 – 11:30 **A few more tiny steps towards a better understanding of the flora of the Euregio region** Peter Schönswetter; Department of Botany, University of Innsbruck (A)	11:10 – 11:30 **Impact of land management and elevation on composition and structure of alpine flower-visiting arthropod communities** Marco Caccianiga; Università degli Studi di Milano (I)
11:30 – 11:50 **Distribution of polyploid plants in the Eastern Alps: a preliminary report** Teresa Zeni; Department of Botany, University of Innsbruck (A)	11:30 – 11:50 **Evaluating the impact of grassland management on wild bee communities along an elevational gradient** Lisa Obwegs; University of Innsbruck (A)
11:50 – 12:10 **Cryptic evolution and diversification of the agmatoploid-polyploid species complex *Luzula* sect. *Luzula* (Juncaceae) in the Eastern Alps** Valentin Heimer; Institute for Alpine Environment, Eurac Research, Bozen (I); University of Innsbruck (A)	11:50 – 12:10 **Assessing the impact of habitat and landscape heterogeneity on mountain bird communities** Matteo Anderle; Institute for Alpine Environment, Eurac Research, Bolzano (I)

12:10 – 12:30 **Genomic Insights into Evolution and Refugial Dynamics of Endemic Vascular Plants in the Southeastern Limestone Alps** Philipp Kirschner; Free University of Bozen-Bolzano (I); Department of Botany, University of Innsbruck (A)	12:10 – 12:30 **Functional diversity of alpine dragonfly communities: The interplay between thermal adaptations and habitat requirements** Felix Puff; University of Vienna (A); Institute for Alpine Environment, Eurac Research, Bozen (I)
12:30 – 12:50 **Evolution and range formation of the threatened steppe plant *Astragalus exscapus* and its relatives** Clemens Maylandt; Department of Botany, University of Innsbruck (A)	12:30 – 12:50 **Insect community simplification across land-use and elevational gradients deliver conservation insights from South Tyrol** Elia Guariento; Institute for Alpine Environment, Eurac Research, Bozen (I)
Session: Systematics & biogeography (taxonomy, phylogenetics & evolution) 2 **Chair: Peter Schönswetter – Department of Botany, University of Innsbruck**	***Session: Ecology, environment & global change 3*** **Chair: Christian Anich – Sammlungs- und Forschungszentrum, Hall i. Tirol**
14:30 – 14:50 **Phylogenetic remarks on hexaploid varicoloured fescues in the Southern Alps** Peter Englmaier; OECONSULT, Sachverständigenbüro für ökologische Wissenschaften, Wien (A)	14:30 – 14:50 **Chironomid microbiome: new insights for cold adapted species from DNA metabarcoding analysis** Valeria Lencioni; MUSE – Museo delle Scienze, Trento (I)
14:50 – 15:10 **Glacial legacies: Refugial dynamics of the endemic bush cricket *Anonconotus italoaustriacus*** Philipp Kirschner; Naturmuseum Südtirol, Bozen (I); Department of Botany, University of Innsbruck (A)	14:50 – 15:10 **Rock glaciers as climate refuge: Preserving aquatic biodiversity in the face of glacier loss in the Eastern Italian Alps** Magdalena Vanek; Institute for Alpine Environment, Eurac Research, Bozen (I)
15:10 – 15:30 **Population genomics and invasion history of a Neartic Leafhopper in Europe *Scaphoideus titanus*** Lapo Ragionieri; Free University of Bozen-Bolzano (I)	15:10 – 15:30 **Drivers and patterns of arthropod colonization of recently deglaciated terrains in the Dolomites (North-eastern Italian Alps** Ivan Petri; MUSE – Museo delle Scienze, Trento (I); University of Milan (I)
15:30 – 15:50 **A DNA barcode library of Austrian Geometridae (Lepidoptera) reveals high potential for DNA-based species identification** Benjamin Schattanek-Wiesmair; Sammlungs- und Forschungszentrum, Hall i. Tirol (A)	15:30 – 15:50 **Climate-driven shifts in the population dynamics of the invasive tiger mosquito (*Aedes albopictus*) in the European Alpine region** Margo Blaha; Università di Trento (I)
15:50 – 16:10 **Disentangling evolutionary relationships within *Euphorbia angulata* (Euphorbiaceae)** Alexander Ulbrich; Department of Botany, University of Innsbruck (A)	15:50 – 16:10 **The nematode community of the spruce bark beetle in South Tyrol** Veronika Rau; Free University of Bozen-Bolzano (I)

Poster Presentations

Session: Biodiversity & nature conservation

Morphological and DNA metabarcoding approaches to identify reliable metrics for the assessment of trout farming-related effects on biological water quality in Alpine rivers
Andrea Chemello; Fondazione Edmund Mach, San Michele all'Adige (I)

Session: Systematics & biogeography (taxonomy, phylogenetics & evolution)

Factors influencing intraspecific variation in wing morphology in high-elevation specialist birds
Francesco Ceresa; Museo di Scienze Naturali dell'Alto Adige, Bolzano (I)

A bibliometric analysis to discuss taxonomic bias in studies of Italian fauna
Emanuele Miccolis; University of Padua (I); University of Palermo (I)

The freshwater jellyfish *Craspedacusta sowerbii* species complex (Cnidaria, Olindiidae) in Italy: distribution and genetic lineages
Massimo Morpurgo; Museo di Scienze Naturali dell'Alto Adige, Bolzano (I)

Session: Ecology, environment & global change

High temperature thresholds for membranes, proteins, photosystem II, and whole leaf tissues in different mountain species
Clara Bertel; Universität Innsbruck, Department of Botany (A)

Alien species in Lake Garda
Cristina Cappelletti; Fondazione Edmund Mach, San Michele all'Adige (I)

Trait space occupancy of ants, butterflies, carabid beetles, grasshoppers and vascular plants along elevation in Val Mazia / Matschertal
Veronika Fontana; Institute for Alpine Environment, Eurac Research, Bozen (I)

Is better living upward or downward? Spatial segregation of water shrews *Neomys fodiens* and *Neomys milleri* in South Tyrol
Eva Ladurner; Naturmuseum Südtirol, Bozen (I)

Research on CLIMATE and ECOLOGY at the MUSE – Science Museum of Trento
Valeria Lencioni; MUSE – Museo delle Scienze, Trento (I)

The new MUSE biotope: ecological survey for the study of aquatic biodiversity
Francesca Paoli; MUSE – Museo delle Scienze, Trento (I)

Impact of land-use intensity on spider communities: A study on the taxonomic resolution effect
Julia Plunger; Institute for Alpine Environment, Eurac Research, Bozen (I)

Do dissolved heavy metals enter the food webs of Alpine streams?
Monica Tolotti; Fondazione Edmund Mach, San Michele all'Adige (I)

Effects of global warming on the alpine vegetation of four peaks in the Texel Group, South Tyrol, as part of the GLORIA project
Friederike Westrich; Department of Botany, University of Innsbruck (A)

5. Extended abstracts

Both extended and short abstracts (see Chapter 6) are listed alphabetically by the first author.

Suggested citation for the extended abstracts (example):
Marsy A., Guariento E., Hilpold A. & Ligazzolo G., 2025: Monitoring invertebrates included in the Habitats Directive in South Tyrol: First results and future strategies. In: Mair P., Gruber D. & Wilhalm T. (eds.), Proceedings of the Euregio Biodiversity Research Conference (EUBIRECO) – 2024, Tyrol-South Tyrol-Trentino, November 22–23, 2024, Bolzano, Italy. Gredleriana, 25: 13–16.

Audrey Marsy[1], Elia Guariento[1], Andreas Hilpold[1], Giulia Ligazzolo[2]

Monitoring invertebrates included in the Habitats Directive in South Tyrol: First results and future strategies.

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[2] Office of Nature of the Autonomous Province of Bolzano-South Tyrol, Landhaus/Palazzo 11, Rittner Straße/Via Renon 3, I-39100 Bozen/Bolzano, Italy

Introduction

The Birds Directive (2009) and the Habitats Directive (1992) require Member States, as well as their autonomous regions and provinces, to report on protected species every six years. The fifth Habitats Directive report planned for 2025 mandates detailed data on distribution ranges, population trends, and conservation measures for species listed in Annexes II, IV and V.
In this context, the “Species Monitoring” project was launched in 2023, bringing together regional partners such as the University of Bolzano, the Museum of Nature South Tyrol, Eurac Research, and the Office of Nature of the Autonomous Province of Bolzano-South Tyrol, which acts as the project coordinator. The primary aim of this project is to monitor and update the distribution of species listed in the two directives, filling knowledge gaps and taking the first steps towards the development of a long-term monitoring strategy for their conservation in South Tyrol. This contribution will outline the initial results of the project, focusing on invertebrate species listed in the Habitats Directive.

Monitoring and first results

Butterflies

Butterfly species listed in the Habitats Directive are monitored across various sites in South Tyrol and include *Euphydryas aurinia* monitored at three sites and *Parnassius apollo* and *Phengaris arion* monitored at four sites. These locations were selected before the “SpeciesMonitoring” project began, based on existing knowledge of the species presence and the availability of suitable larval habitat (Figure 1). Additional sites will

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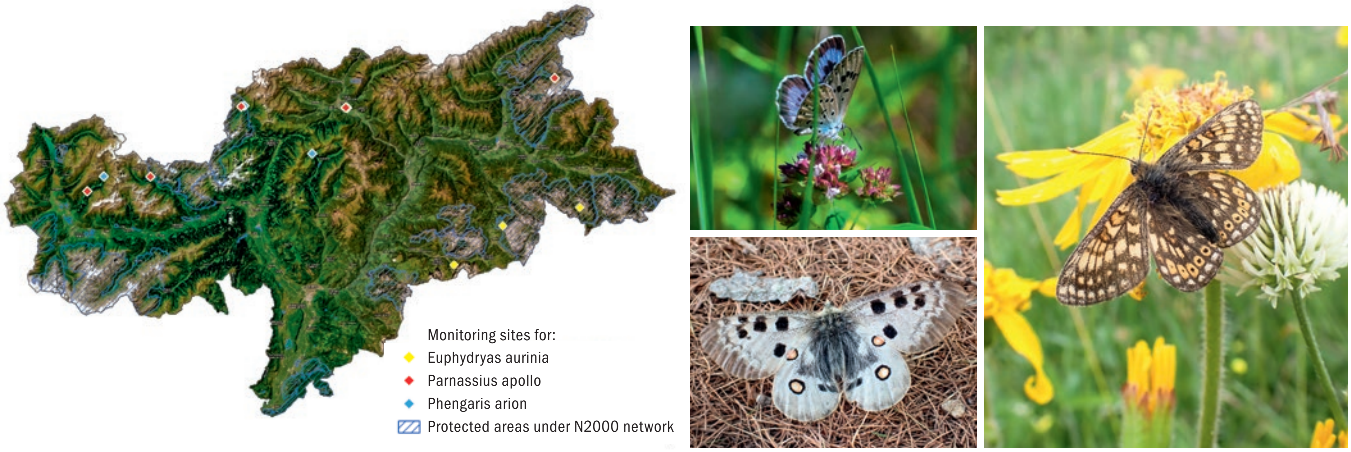

Figure 1: Monitoring sites within the SpeciesMonitoring project for the three butterfly species; *Phengaris arion* © E. Repetto, *Parnassius apollo* and *Euphydryas aurinia*, © A. Marsy (from top to bottom and left to right)

Figure 2: *Vertigo moulinsiana* found in upper vegetation during the monitoring of the Castelfeder sites. © A. Marsy

be identified and included in the coming years to increase the number of monitoring locations. The entire study area was monitored exhaustively over a set time interval (which varies depending on the site). Following national recommendations (Stoch et al. 2016), monitoring is carried out in the selected sites for two consecutive years. While most focus is on adults, larval habitats are also investigated to assess habitat conservation status. The two-year monitoring cycle has been completed only for *Euphydryas aurinia*, confirming a single population in Val Gardena, with 5 and 6 adult individuals observed in 2023 and 2024, respectively.

Snails/Vertigo

Four *Vertigo* species included in the Habitats Directive occur in South Tyrol: *Vertigo moulinsiana*, *V. angustior*, *V. genesii*, and *V. geyeri*, with the latter two being exclusive to South Tyrol within Italy. Monitoring efforts carried out so far (in 2023 and 2024) involved sampling of 13 sites with known *Vertigo* occurrences (Kiss et al. 2011); additional sites will be surveyed in the future. The methodology, following German national recommendation (BFN 2017), included collecting four litter samples from suitable microhabitat at each site and analyzing them in the laboratory. Only *V. moulinsiana* (Figure 2) was monitored by visual survey along a 30 m transect. (Moorkens et al. 2011; Książkiewicz-Parulska et al. 2017). *Vertigo* species were confirmed at 9 of the 13 surveyed sites. Individual densities varied greatly depending on the site and species.

Beetles

In 2023, *Osmoderma eremita* and *Cerambyx cerdo* populations at the Castelfeder site were monitored following standardised protocols (Campanaro et al. 2011; Maurizi et al. 2017; Redolfi de Zan et al. 2017a) and ISPRA recommendations (Stoch et al. 2016). The use of pheromone traps for *O. eremita* and mainly visual encounter surveys for *C. cerdo*

Figure 3: From left to right: *Osmoderma eremita* ©G. V. Mörl, *Cerambyx cerdo* and pheromone trap for *O. eremita* monitoring at Castelfeder © A. Marsy.

(Figure 3) resulted in the detection of 6 and 42 individuals, respectively, which underlines the site's significance for their conservation. In 2024, the expert entomologist Georg von Mörl assisted in discovering a new *O. eremita* population near Brixen/Bressanone during an explorative survey using pheromone traps.

Other species

Further directive invertebrate species with well-documented distributions are present in South Tyrol, such as *Lucanus cervus*, *Helix pomatia*, and *Euplagia quadripunctaria*. For these species, most records were obtained and validated through citizen science initiatives and the online platform iNaturalist, further enriching the distribution data. This approach proved effective: in 2024 alone, 38 new records of *Lucanus cervus* were collected through these channels.

Conclusions

These preliminary findings underscore the importance of continued monitoring and conservation efforts for invertebrate species listed in the Habitats Directive. The “Species Monitoring” project provides crucial baseline data that will contribute to the 2025 Habitats Directive report.

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Climate-driven shifts in the population dynamics of the invasive tiger mosquito (*Aedes albopictus*) in the European Alpine region

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Introduction

Mountain regions are among the most sensitive environments to climate change, and the European Alps are no exception. Despite covering only 1.8 % of the continent (approximately 190,000 km²), the Alps host a remarkable diversity of ecosystems, landscapes, and socio-economic activities. Anthropogenic greenhouse gas emissions have led to an average global near-surface temperature increase of +1.1°C compared to pre-industrial levels (1850–1900), with Europe warming at twice the global average rate (IPCC 2021; C3S 2024). This accelerated warming has already resulted in an average temperature increase of around 2°C in the European Alps, accompanied by subtle shifts in precipitation seasonality, generally towards wetter winters and drier summers in some areas (Dumont et al. 2025). Such climatic changes are altering ecological balances and opening doorways for species previously limited by colder temperatures, including invasive disease vectors such as *Aedes albopictus* (Skuse, 1894), the Asian tiger mosquito. *Aedes albopictus* has emerged as a significant global health concern due to its role in transmitting mosquito-borne viral diseases. Native to tropical and subtropical Southeast Asia, *Aedes albopictus* has demonstrated a remarkable plasticity, successfully expanding its range to every continent except Antarctica. Its introduction to Europe, first recorded in Italy in 1990, has led to widespread establishment across the Italian peninsula, including parts of the Alps (Battistin et al. 2024).

This expansion has been facilitated by several biological and environmental factors. *Aedes albopictus* possesses cold-tolerant diapausing eggs, allowing it to overwinter in temperate climates. It is highly adaptable to urban and peri-urban habitats, with a preference for container breeding that abounds in human-modified environments, and it has a lifecycle tightly linked to climatic cues. Milder winters and changes in precipitation patterns are making previously inhospitable areas increasingly suitable for mosquito colonization, raising concerns about vector-borne disease emergence in mountain communities. Its upward expansion into mid-elevation Alpine zones, now documented up to 600 m above sea level, is closely linked to ongoing climate change (Hawley 1988; Medlock et al. 2015; Battistin et al. 2024).

Despite the growing presence of *Aedes albopictus* in mountainous Europe, our understanding of how climate change will shape its future dynamics in these areas remains limited. While both correlative and mechanistic approaches have been used to explore the potential effects of climate change on mosquito distributions (Proestos et al. 2015), no study has yet provided a comprehensive, spatially and temporally explicit analysis of *Aedes albopictus* dynamics in the European Alps.

In this study, we address this gap by applying a spatio-temporal machine learning framework that integrates a large, standardized ovitrap dataset with environmental

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predictors such as temperature, precipitation, and photoperiod. Our model leverages both observed mosquito data and future climate projections specific to the Alps to forecast changes in *Aedes albopictus* abundance and seasonal activity.

Specifically, our objectives are to:

- Map current and projected spatial patterns of *Aedes albopictus* colonization and establishment in Alpine and pre-Alpine areas.
- Evaluate temporal shifts in seasonal abundance under three distinct climate scenarios for mid-century (2040–2050) and late-century (2070–2080) periods.
- Explore the relationship between elevation and predicted changes in mosquito abundance to assess altitudinal trends in future colonization risk.

Our results aim to explore how *Aedes albopictus* populations may respond to climate-driven environmental change in mountain landscapes, particularly in areas historically considered unsuitable for invasive mosquito species.

Methodology

Our study focuses on the European Alps and surrounding lowland areas, spanning portions of Italy, France, Switzerland, Austria, and Slovenia. Geographically, the region is bounded between 43°N and 49°N latitude and 5°E to 18°E longitude. The landscape is characterized by strong altitudinal gradients, ranging from coastal plains to peaks exceeding 4,000 meters, which in turn drive sharp climatic transitions over relatively short spatial distances. These gradients, coupled with accelerating regional warming (Gobiet et al. 2014; Hock et al. 2019; Boe et al. 2020), make the Alps an ideal setting for examining how climate change influences the spatial and temporal dynamics of *Aedes albopictus*.

Ovitrap data

A unified database of *Aedes albopictus* observations was assembled from multiple monitoring programs. Firstly, we gathered a comprehensive collection of ovitrap observations within the study area (Da Re et al. 2024), specifically 31951 georeferenced observations in 77 locations. For data integration into the machine learning model, the egg counts of *Aedes albopictus* were set as the target variable. Temporal resolution is standardized to a weekly period, while spatial resolution is set at 0.1° (~8–11 km), consistent with the E-OBS climatic datasets v28.0. (Cornes et al. 2018), which provide a temporal coverage from January 1950 to June 2023. These data were aggregated to weekly values by computing median temperatures and cumulative precipitation, aligned with the temporal resolution of the entomological observations. Each observational record was aligned with the corresponding environmental data based on its geographic coordinates and sampling week.

Stacked machine learning model

To model egg abundance, we adopted a stacked ensemble learning approach (Wolpert 1992), which is an ensemble learning technique that combines predictions from multiple base models using a meta-learner to improve accuracy and robustness[14]. Following the method established in Da Re et al. (2025), we implemented a stacked model using three base algorithms: XGBoost (Chen & Guestrin, 2016), Random Forest (Breiman, 2001), and Cubist (Kuhn et al., 2024). These models were then combined into a unified ensemble using a linear meta-learner, implemented with the *mlr3* library (Bischl et al. 2016; Lang et al. 2019). Once the ensemble was constructed and tuned, it underwent training and testing.

Model validation and projection

The final observational dataset, linking mosquito egg abundance to environmental conditions, was partitioned into training and testing subsets. We used two independent sets to rigorously assess model performance across both spatial and temporal dimensions: the spatial test set included locations withheld entirely from training, while the temporal test set excluded entire years of data across all sites. This setup evaluates the model's ability to extrapolate to geographic areas unrepresented in the training dataset and future periods. Performance metrics included Root Mean Squared Error (RMSE) and coefficient of determination (R^2), computed separately for training, spatial, and temporal subsets.

Once validated, the trained model was applied to a gridded dataset of climatic covariates covering the study area for the 2010–2023 period. These weekly predictions were averaged over time to generate a baseline map of current mosquito egg abundance and distribution.

Climate change scenarios and future predictions

Future climate change data are based on EURO-CORDEX (Jacob et al. 2020) (the European branch of the World Climate Research Programme's Coordinated Regional Climate Downscaling Experiment), which offers ensembles of regional climate models (RCMs), generated by dynamically downscaling general circulation models (GCMs) from CMIP5 (Coupled Model Intercomparison Project Phase 5). From the large ensemble of RCMs (over 50 GCM-RCM combinations), we selected a sub-ensemble that maximizes the range of expected changes (Cannon 2015) in summer and winter temperature and precipitation over the study period in order to ease computation and interpretability of results. Regarding emission scenarios, we focused only on RCP8.5 (representative concentration pathway), which implies continuously increasing greenhouse gas concentrations. While it might not be the most plausible scenario from a political point of view, it offers the strongest climate change forcing. Together with the sub-ensemble selection, it is a mixed approach to consider model and scenario uncertainty by relating the three selected models to their expected changes in temperature and precipitation. It could also be considered as a sensitivity analysis of different climate futures.

The future environmental datasets were generated by adjusting the historical baseline (observations) with monthly climate change factors based on the RCM data. This approach is sometimes referred to as delta approach, because it adds the modelled climate change (delta) directly onto the observations. Temperature was modified using additive shifts, while precipitation changes were applied as multiplicative factors. Change factors were spatially explicit based on the RCM resolution of 0.11°, bilinearly remapped to the spatial scale of E-OBS, and applied separately month-by-month. Altogether, this is an approach to generate future climate data that is based on physically plausible spatiotemporal changes derived from climate models and unbiased, which is important for impact models, since RCMs can exhibit non-negligible biases (Matiu et al. 2024).

Two projection periods were examined: mid-century (2036–2055) and late-century (2066–2085), each evaluated under three possible futures:

1. A baseline change scenario, reflecting moderate warming with minimal seasonal redistribution.
2. A warmer-wetter scenario, with milder winters and increased summer rainfall.
3. A warmer-drier scenario, featuring rising winter temperatures but significant summer drying.

The resulting dataset was thus structured into six distinct environmental datasets (2 time periods times 3 future scenarios). The trained model was applied independently to each of the six future datasets, allowing us to generate mosquito abundance predictions for different periods and possible climatic futures. Combining these with the results based on the past observations, this approach allows direct comparisons between current and future predictions of *Aedes albopictus* egg distribution and abundance.

Results

The model showed a strong fit on the training dataset, with an R^2 of 0.92. When applied to the spatial and temporal test sets, the model fitted with R^2 values of 0.50 and 0.45, respectively.

The predictions of the model under historical climate conditions reveal that *Aedes albopictus* is well-established across much of the lowland and pre-Alpine areas, with consistently high egg abundance in northern Italy, the southern Swiss Plateau, and parts of southeastern France. These areas exhibit long activity periods, with oviposition beginning in late March and extending into early November.

Egg abundance follows a distinct seasonal pattern: low values in early spring, followed by a steep rise in late May, peaking during July and August. The decline begins in September and becomes more pronounced through October, in line with decreasing temperatures and photoperiod.

Following the assessment of the model performance, we proceeded to apply it to the six new datasets representing future environmental conditions. Predictions for mid-century and late-century scenarios reveal a marked increase in both the spatial extent and temporal duration of *Aedes albopictus* activity. Under all future climate scenarios, our model predicts a significant increase in *Aedes albopictus* egg abundance, accompanied by upward altitudinal expansion. These changes are already evident by mid-century (2036–2055) and become more pronounced by late-century (2066–2085) (Figure 1).

Notably, the Autonomous Province of Trento and the Canton of Ticino, which currently exhibit marginal seasonal presence, are projected to host significantly higher mosquito activity under both average and warm scenarios. In contrast, changes are less dramatic in Emilia-Romagna, a region that already hosts dense mosquito populations.

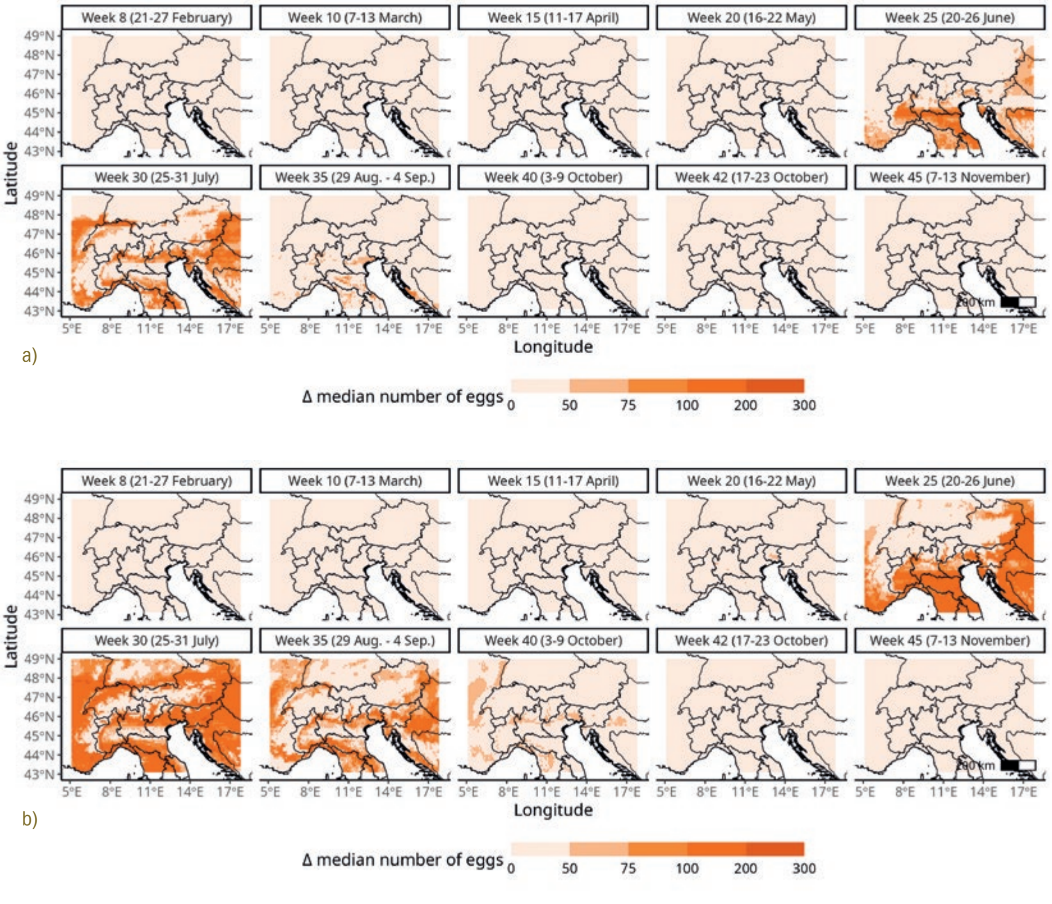

Figure 1: Projected changes in *Aedes albopictus* egg abundance under future climate conditions. Maps show the difference in median predicted egg abundance between the future climate scenarios (moderate warming with minimal seasonal redistribution) in (a) 2036–2055 and (b) 2066–2085, and the current baseline (2010–2023) for 10 weeks of the year. Darker colors indicate regions with increased egg abundance.

Discussion

The model's high training accuracy and moderate generalization performance suggest that it effectively captures the main ecological drivers of *Aedes albopictus* abundance. Specifically, the model reproduces known seasonal and spatial distribution patterns, indicating it has internalized the species' sensitivity to temperature, photoperiod, and precipitation. These variables are well-established determinants of *Aedes albopictus* population dynamics, influencing development rates, survival, diapause induction, and oviposition behavior (Hawley 1988; Medlock et al. 2012). Performance decreased on test datasets, particularly when projecting across space or time, as expected. This is because the test set includes environmental conditions not fully represented in the training data, and these extrapolative settings pose a greater challenge to any empirical model, as they require inference beyond the conditions used for parameter estimation.

Nonetheless, the model's projections of increased egg abundance and expanded seasonal activity under future climate scenarios are ecologically plausible and consistent with the species' thermal and photoperiodic limits (Hawley 1988). This species thrives in warm, humid environments with sufficient precipitation to sustain container-breeding habitats. It is limited by cold temperatures, especially in overwintering stages, and its activity is constrained by photoperiodic cues that induce diapause. The model reflects these constraints, projecting northward and altitudinal expansion under warming trends, consistent with observed climate-driven range shifts in other mosquito vectors (Caminade et al. 2012).

As climate warming reduces thermal limitations in previously unsuitable higher-elevation areas, the model predicts a progressive upward expansion, particularly into mid-montane zones. While our climate input data may not capture fine-scale topographic variability or microclimatic effects, it is adequate for identifying broad elevational trends at the regional scale. Moreover, our altitudinal analyses were conducted across a broad spatial extent, which minimizes the influence of localized topographic anomalies and reinforces the robustness of the projected elevational patterns.

Regional disparities in predicted change are also informative, such as the muted response in Emilia-Romagna, which may reflect ecological saturation, where current climatic conditions already support near-maximal mosquito densities (Angelini et al. 2008; Carrieri et al. 2011). This highlights the importance of considering baseline conditions when interpreting climate sensitivity.

Ongoing efforts include the integration of additional ovitrap data from the Province of Bolzano (2013–2024) and Switzerland (2021–2024), which will extend the environmental gradient represented in the training data and are expected to improve the model's ability to capture the spatio-temporal dynamics within the observational dataset. This expansion is expected to increase both the accuracy and robustness of predictions, providing a stronger basis for future climate projections.

Conclusions

This study aimed to quantify the current and future distributions of *Aedes albopictus* across the European Alps, pinpointing where populations are established and how abundances vary in space, and to characterize spatio-temporal shifts under climate scenarios of the mid and late 20th century, identifying expansions northward and upward and changes in seasonal activity windows. Our findings show a substantial increase in abundance and altitudinal expansion under climate change scenarios, particularly in pre-Alpine and currently marginal areas.

Our work demonstrates the effectiveness of a spatio-temporal ensemble machine learning framework in modelling the current and future distribution of *Aedes albopictus* across the Alps. Moreover, the modelling framework is transferable to other ecologically sensitive systems facing climate-driven threats.

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Developing a standardized monitoring scheme of the Annex I Birds Directive species breeding in South Tyrol: methods and first results

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Introduction

The Birds Directive (2009/147/EC) is a milestone in wildlife conservation in Europe, and aims to protect all bird species naturally occurring in the European Union, plus their most important habitats (https://environment.ec.europa.eu/topics/nature-and-biodiversity/birds-directive_en). The Annex I of the Birds Directive includes species and subspecies that are subject to special conservation measures concerning their habitats, which implies the creation of Special Protection Areas, that are part of the Natura 2000 network. The member States are committed to regularly forward to the EU a report about the implementation of the Directive, the status and trends of species and threats to them; this implies a regular monitoring of bird populations. In South Tyrol (north-eastern Italy), 26 species included in the Annex I breed regularly, and for some of them this region covers a relevant proportion of their national range (Nardelli et al. 2015). We had relatively good information about the breeding distribution of the Annex I species breeding in South Tyrol, except for a few ones with secretive habits or low population density. Differently, for population sizes and trends in most cases we relied on scarce or no information (Ceresa & Kranebitter 2020). To fill these knowledge gaps, which represent a strong limit for conservation, during the years 2023 and 2024 we started planning and implementing a standardized monitoring scheme targeted at the Annex I bird species breeding in South Tyrol.

Methods

We selected different field methods for different species or groups of species, based on their behavioural and ecological characteristics. Surveys were repeated for all species (usually twice) during the same breeding season, because this enables us to calculate and account for detectability during data analysis (MacKenzie et al. 2002; Royle et al. 2005), as well as species occupancy/abundance, which can change throughout the breeding season (e.g., Ceresa et al. 2020). The methods' choice was supported by the experience gained during previous research and monitoring projects carried out in South Tyrol, but also by previous methodological proposals for local bird monitoring (Clementi 2019), by the guidelines adopted in neighbouring regions (Pedrini et al. 2014) and by more general literature about bird censuses (e.g., Gibbs & Gregory 2006). More in detail:

- For the woodpeckers listed in Annex I (black woodpecker *Dryocopus martius*, grey-headed woodpecker *Picus canus*, three-toed woodpecker *Picoides tridactylus*), we adopted point counts placed along transects in forested areas, with acoustic stimulation at each point using recorded calls. This method allows to collect data also for other forest species of high conservation interest such as other woodpeckers, the hazel grouse *Bonasa bonasia* (an Annex I species) and forest raptors such as the

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goshawk *Accipiter gentilis*. From 2025 onwards, we will adopt a similar procedure along the same transects for the boreal owl *Aegolius funereus* and the Eurasian pygmy-owl *Glaucidium passerinum* (both listed in Annex I), which allows to collect data also for other nocturnal birds like the tawny owl *Strix aluco*.

- For diurnal raptors, we adopted standardized observations from panoramic points with broad view on potential breeding areas, lasting 1.5 hours. We focused on those Annex I species for which we had larger knowledge gaps (black kite *Milvus migrans*, red kite *Milvus milvus*, short-toed snake-eagle *Circaetus gallicus*, European honey buzzard *Pernis apivorus*, and peregrine falcon *Falco peregrinus*), but the method is suited for all diurnal raptors. For the honey buzzard, an elusive forest raptor for which the information about breeding population is scarce in Italy (Nardelli et al. 2015), we experimented a specific protocol based on long-lasting observation points (4 hours) allowing a broad view over large areas of potentially suitable forests. The choice of panoramic points for diurnal raptors was supported by visibility analysis in QGIS (https://qgis.org/), which also allows a precise estimation of the potential breeding area surveyed.
- For meadow and shrubland birds, a monitoring scheme was already developed slightly earlier than for the other species and implemented from 2022, thanks to the efforts of a specific working group integrated by the Autonomous Province of Bolzano/Bozen, Eurac Research and the Museum of Nature South Tyrol. This is subdivided in three parts: i) diurnal point counts to monitor a wide set of meadow birds including three Annex I species (red-backed shrike *Lanius collurio*, woodlark *Lullula arborea*, and barred warbler *Sylvia nisoria*); ii) territory mapping for especially rare species such as the barred warbler, the woodlark and the ortolan bunting *Emberiza hortulana*; and iii) nocturnal point counts with acoustic stimulation mainly targeted at the corncrake (*Crex crex*) and the European nightjar (*Caprimulgus europaeus*), but suited also for other, mainly nocturnal species.

Sampling areas were selected with the aim to adequately represent the local distributions and the ecological needs of the target species. To support this selection, for some species we are also developing landscape-scale habitat suitability models based on a maximum entropy approach (MaxEnt; Phillips et al. 2006), by relating bird observations with the available environmental and climatic layers. Of course, the number of sampling areas and of visits are also resource-dependent and need to be optimized to achieve a cost-effective long-term monitoring, that means, obtaining as much detailed information as possible given the resources available for fieldwork (e.g., Ficetola et al. 2018).

First results and discussion

During the first two years (2023–2024) we collected 839 observations of Annex I bird species and 1,717 observations of other breeding bird species of high conservation interest. For most target species, we strongly improved the information available about their distribution and population size, also discovering several previously unknown breeding areas. All surveyed forest transects hosted one to three Annex I woodpecker species, and we also detected several hazel grouses, a particularly elusive species for which we had to rely on scarce data so far. For diurnal raptors, our observation points covered most or a relevant proportion of the potentially suitable areas for the target species in South Tyrol, and in several cases, we exactly localized nests or nesting forest patches. Also, many breeding territories of non-Annex I raptors were detected (e.g., goshawk, Eurasian sparrowhawk *Accipiter nisus*, Eurasian buzzard *Buteo buteo*, common kestrel *Falco tinnunculus*, Eurasian hobby *Falco subbuteo*); such data are very relevant because these species are good biodiversity indicators. The specific field protocol adopted for the honey buzzard proved to be effective, with 12 identified breeding territories according to a conservative estimate. For meadow and shrubland species, we substantially improved the information available especially for the nocturnal species (corncrake and nightjar), but also for rare passerines such as the barred warbler. Unfortunately, we could also confirm the local extinction of the ortolan bunting as a regular breeder, consistently with previous recent specific surveys (years 2019–2022).

All collected data were stored into the Database of the Museum of Nature South Tyrol, and are automatically visible into a WebGIS tool for technicians and decision-makers of the local public administration, so that they can be taken into account in habitat management and conservation. These data are also visible in a publicly accessible platform, Flora Fauna South Tyrol (https://www.florafauna.it/), which could help to raise public awareness of local wildlife. Importantly, the data collected strongly contributed to the latest Birds Directive reporting (period 2019–2024) for South Tyrol, leading (together with the information collected in other projects/by other institutions) to a substantial improvement in the information provided for several bird species compared to the previous report. Furthermore, we have developed habitat suitability models for some species (e.g., black and grey-headed woodpeckers, hazel grouse, nightjar, barred warbler) and we are using them to better focus the specific monitoring scheme, and the resulting suitability maps can be also potentially useful for their conservation.

In conclusion, during the two first years we laid the groundwork for the long-term monitoring of the target species, successfully identifying representative sets of sampling areas for many species and strongly improving the information about their distributions and population sizes. Despite this, we still must improve the sets of sampling areas especially for some low density and low detectable species, e.g., the three-toed woodpecker and nocturnal raptors. Implementing these improvements and ensuring that the identified sampling areas are surveyed frequently enough to properly calculate population trends will be the priorities of the next years.

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Phylogenetic remarks on hexaploid varicoloured fescues (*Festuca* sect. *Eskia*, Poaceae) in the Southern Alps

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Introduction

Varicoloured fescues (*Festuca varia*-group, *Festuca* sect. *Eskia*) are widespread throughout the South European and Southwestern Asian mountain ranges. Although many different taxa were described in the early days of intensive botanical research, the knowledge of their characteristics is rather limited. Most of the taxa have been confused either among each other or with other species with varicoloured spikelets.

Ploidy levels and reliable data on distribution of several taxa throughout the Alps are known even for a quarter of a century (Wallossek 1999, 2000). First data on molecular phylogeny exist since 2002 (Torrecilla & al. 2002; Catalán & al. 2004; de Nova & al. 2006).

In addition to the diploid *Festuca acuminata*, two hexaploid taxa (*F. scabriculmis* subsp. *luedii* and subsp. *handel-mazzettii*) occur in the Southern Alps, whose morphology suggests relationships to each other and to the Western Alpine *F. scabriculmis* subsp. *scabriculmis*. Based on these considerations, an adapted taxonomic concept has already been presented (Englmaier 2020).

However, questions about the origin of these hexaploid taxa and their ancestors remain unresolved.

Thus, they were target of a high resolution molecular genetic exploration, which included not only nuclear (ITS) and plastid markers (*trn*L-F) but also other markers already tested on the genus *Festuca* (especially microsatellite loci, Segarra-Moragues & Catalan 2011). This required extensive methodological considerations, which ultimately led to a selection of 9 primer pairs already tested on *Festuca* or *Lolium*. 7 of these provided amplicons whose sequences have now been subjected to an initial evaluation.

Materials and methods

Plant collection, cultivation and sampling

Accessions of each of the two hexaploid taxa (*Festuca scabriculmis* subsp. *luedii* (West), *F. scabriculmis* subsp. *luedii* (East) and *F. scabriculmis* subsp. *handel-mazzettii*) were selected, plus accessions of each of the diploid species *F. acuminata* and *F. alpestris*, as well as of a further hexaploid taxon, *F. varia* subsp. *winnebachensis* for comparative purposes. *F. laevigata* was selected as an outgroup (see Figure 1 for sampling sites).

Each accession represents one single plant. Parts of the huge tufts were removed for cultivation in the Botanical Garden (HBV), University of Vienna and conserved as a herbarium voucher.

Fresh leaves were taken from cultivated plants for analysis and stored at approx. 200 K up to processing.

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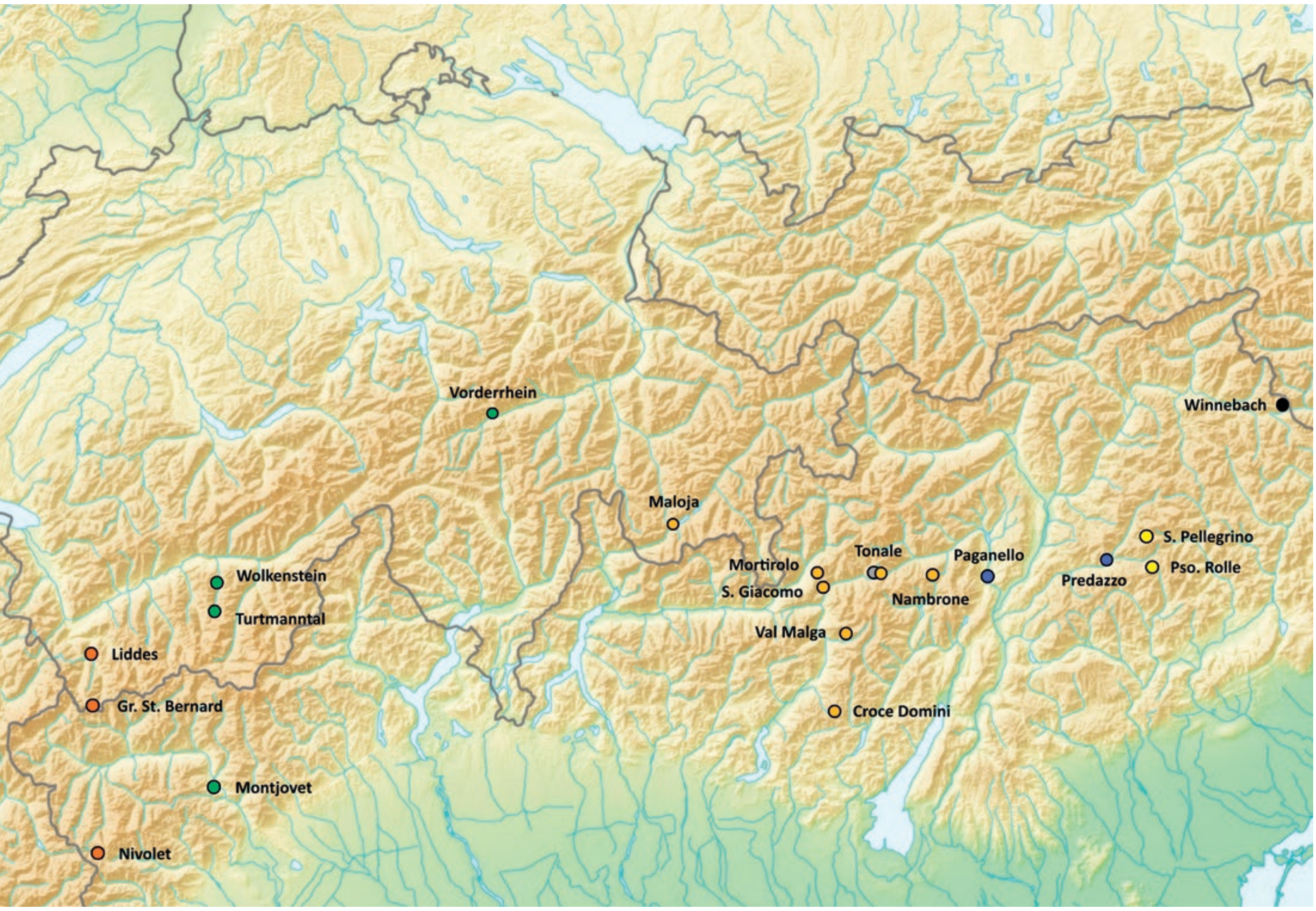

Figure 1: Taxa and sampling sites.
Festuca alpestris (blue signs): 2 populations, 10 accessions
Festuca acuminata (green signs): 4 populations, 15 accessions
Festuca scabriculmis subsp. *luedii*, western area (red signs): 3 populations, 11 accessions
Festuca scabriculmis subsp. *luedii*, eastern area (orange signs): 7 populations, 11 accessions
Festuca scabriculmis subsp. *handel-mazzettii* (yellow signs): 2 populations, 10 accessions
Festuca varia subsp. *winnebachensis*, for comparison (black sign): 1 population, 5 accessions
Festuca laevigata s. l., outgroup (grey sign): 1 population, 5 accessions
(Basemap source: Wikimedia commons, Lencer/Pechristener, CC-BY-SA3.0)

Sample preparation, sequencing and data analysis strategy

The following regions were selected for comparability with published studies:
Plastid *trn*L-F, using already tested primers „c“, and „f“ (Taberlet & al. 1991: 1106).
Nuclear ITS, using primer „18S-KRC“ (Torrecilla & Catalan 2002: 243) and „ITS-p4“ (Cheng & al. 2016: 14;, Kolter & Gmeinholzer 2021: 135), with a 4-bp-shift towards 5’ compared with common ITS4 as used by Torrecilla & Catalan (2002), to avoid interferences caused by endophytic DNA.
In addition, microsatellite targets were selected, according to Segarra-Moragues & Catalan (2011: 361) and Tomczyk & al (2020): A101, A 104, A115, A117, B101, B104, and C 105.
After DNA extraction, indexing and amplification, sequencing was done on an AVITI instrument (Element Biosciences, San Diego, CA) using 300-bp paired-end mode.
All labwork was done by IGAtech, Udine, Italy.
Results were generated by analysis of amplicon sequence variants (ASV).

Results

Analysis of the plastid-*trn*L-F region revealed a total of 7 ASV. One is exclusively represented in *F. acuminata* (with exception of the Vorderrhein population [c1-c5], 85 %), exclusively in *F. s.* subsp. *handel-mazzettii* [r, s], in subsp. *luedii* (exclusively, with the exception of the Gran Paradiso population [h], 85 % and populations from the Pso. Mortirolo area [l, m], 65 %) and in *F. v.* subsp. *winnebachensis* [t], 30 %. Another one is represented in small proportions in *F. s.* subsp. *luedii* (from Gran Paradiso [h], 15 %, from the area around P.so Mortirolo [l, m], 30 %) and in *F. acuminata* (from Vorderrhein [c1-c5], 15 %. Four ASV are exclusively represented in *F. alpestris*, one of them exclusively in the Predazzo population [a1-a5].

Analysis of the nuclear ITS region also revealed a total of 7 ASV. One is present in all taxa and all accessions, in varying frequencies: in *F. alpestris* [a1-5, b1-5] exclusively, in *F. acuminata* (from the Aosta Valley [f1-f5 50 %, all others exclusively), in *F. scabriculmis* subsp. *handel-mazzettii* 60 %, in subsp. *luedii* generally 25–60 % (from the Maloja Pass [n] 80 %), in *F. varia* subsp. *winnebachensis* [t] 80 %, in *F. laevigata* [u, outgroup] 85 %. Others were detected in individual taxa or populations.

Among microsatellite loci, A104 showed by far the greatest diversity and was therefore preferred for analysis. 18 ASV were identified. Two of these were exclusively found in each of the two diploid taxa (*F. alpestris* [a, b] and *F. acuminata* [c-f]. Five of these were found in individual populations of all taxa analyzed, the others are characteristics of different provenances of certain taxa. Clear differentiations between the two subareas of *F. s.* subsp. *luedii* are recognizable neither in this nor in other ms loci used in this study.

For all taxa, variability of all markers within populations was significantly lower than even between neighboring populations.

Discussion

Our results clearly point out, that *F. scabriculmis* subsp. *luedii* and subsp. *handel-mazzettii* are closely related to each other and to *F. acuminata* and result from hybridization with *F. acuminata* as the only maternal ancestor, as they have nearly identical plastid ASV composition. In contrast, the third hexaploid, *F. varia* subsp. *winnebachensis*, is clearly distinct. According to Mucko & al. (2024), a connection to taxa occurring in the Eastern Alps (*F. calva* and *F. varia* subsp. *varia)* is probable, but requires further confirmation.

It is also noticeable that there is a remarkable variability of microsatellite markers within *F. scabriculmis* subsp. *luedii*, which is seen both in spatial (populations around the Adamello Mts.) and in altitudinal scales (adjacent populations up to the Mortirolo Pass and along the Valle dell'Orco up to the Col de Nivolet), but not any significant differences were recognizable between the two conspicuous sub-areas of subsp. l*uedii*. Only the isolated population around the Maloja Pass is clearly separated.

Within *F. acuminata*, the northern (Rhine valley) and southern (Aosta valley) populations are slightly different from the Valais populations.

Outlook

Further investigations should show to what extent the populations in the Southern Alps are embedded in the overall Alpine diversity of varicoloured fescues, i.e., whether the *F. acuminata* populations of the Western and Maritime Alps, as well as *F. scabriculmis* subsp. *scabriculmis* occurring sympatrically there, correspond to the related Southern Alpine taxa.

Likewise, the position of *F. pumila* in relation to these taxa will also be of interest, whether the findings of Mucko & al. (2024) will be confirmed on closer examination and whether this morphologically variable taxon also shows a relatively high intraspecific genetic variability.

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Alpine dragon- and damselfly communities of anthropogenic habitats. An interplay between habitat requirements and temperature.

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Keywords: Alpine environments, artificial habitats, Bergman's rule, freshwater biodiversity, elevational gradient, habitat filtering.

Introduction

Alpine environments harbor a large diversity of natural habitats and thus are hotspots of global biological diversity (Steinbauer et al. 2016; Antonelli et al. 2018; Pinkert et al. 2024). Concerningly, while natural habitats are on the decline worldwide (Sala et al. 2000) human habitat modification has extended up to alpine elevations spurred on by demands of tourism, energy production and recently conservation (Fait et al. 2020; Brosse et al. 2022; Gerfand et al. 2024). Peatlands and freshwater habitats harbor a large part of the Alpine threatened biodiversity, but remain underrepresented in conservation efforts (Bragazza 2009). Artificial ponds have been proposed as stepping-stone or substitute habitats, that could boost population sizes of alpine freshwater species and assist them in shifting their ranges and better track climate change (Ilg & Oertli 2014; Oertli et al. 2014; Fait et al. 2020; Gerfand et al. 2024) and hundreds of pond creation and restoration projects have been carried out across several countries to establish habitats for biodiversity, with costs amounting to millions of Euros (Bartrons et al. 2024). However, little is known about the interactive effect of temperature and anthropogenic disturbance on invertebrate communities, with alpine species often being particularly vulnerable to human impacts (Negro et al. 2010; Kašák et al. 2013; Assandri & Bazzi 2022). Thus, the conservation value of alpine artificial water bodies remains therefore unclear.

Methods

Focusing on dragonflies and damselflies, whose semi-aquatic life cycle and ectothermic nature make them particularly sensitive to temperature (Hassall 2015) and habitat conditions (Bílková et al. 2025), we examined the taxonomic and functional composition on 28 natural and 13 anthropogenically altered sites spanning a 2000-meter elevational gradient in the European Alps. This altitudinal gradient comprises a wide heterogeneity of habitats (Assandri 2019), which range from natural alpine wetlands harbouring boreo-alpine specialists like *Aeshna subarctica* and *A. caerulea* (Assandri et al. 2022) to large and warm lakes, harbouring thermophilous species like *Trithemis annulata* (Puff et al. 2023). Our aim was to assess how diversity, abundance and functional traits change along elevation and if natural and anthropogenic habitats follow similar trends.

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Results & Discussion

Our results demonstrate that, similar to continental scales (Pinkert et al. 2017; Zeuss et al. 2017; Acquah-Lamptey et al. 2020; Mähn et al. 2023), dragonflies follow trends in morphology and life history at a regional scale, along an elevational gradient, as expected by Bergmann's rule (Shelomi 2012) and thermal melanism hypothesis (Clusella Trullas et al. 2007). In damselflies however, functional responses to temperature, especially morphology, are different and their abundances strongly declined below moderate temperatures, while those of dragonflies were unaffected by temperature (Figure 1). This suggests that dragonflies are better adapted to the cold temperatures of higher elevations, while damselflies seem far less able to adapt their morphology to cold environments. Additionally, both dragon- and damselfly communities at anthropogenic alpine sites were composed of more thermophile species than at natural alpine sites, indicating poor support of the natural and unique faunal elements via artificial water bodies (Figure 1). This must be considered for conservation aimed at maintaining and improving the status of alpine specialists (Ilg & Oertli 2014; Oertli et al. 2014), which not only constitute certain odonate lineages but also distinct parts of the functional diversity, as we show. The ecological dynamics of alpine artificial water bodies stem from the additive constrains of temperature and anthropogenic disturbance. This dual constraint appears to hinder typical alpine species from colonising these man-made environments, posing a challenge for their role in biodiversity conservation amid global warming and biodiversity decline. See Puff et al. (2025) for more details.

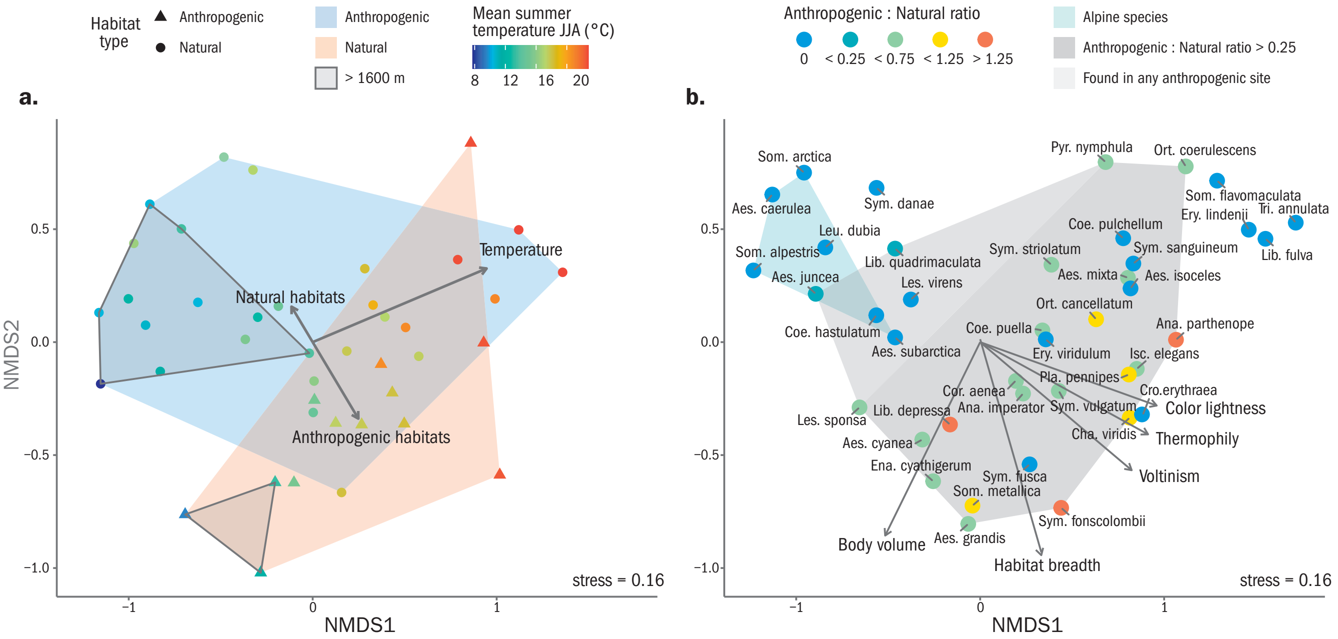

Figure 1: NMDS ordination of species communities. Panel (a) shows site scores with arrows indicating site variable loadings; panel (b) shows scaled species scores with trait loadings. The ratio of anthropogenic to natural sites was calculated from study data. Alpine species are defined as those with a Temperature Index < 6 (Termaat et al. 2019). Genus names in (b) are abbreviated to the first three letters. Modified from Puff et al. (2025).

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Species distribution modeling for farmland birds in South Tyrol

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Introduction

Agricultural biodiversity is rapidly declining due to the intensification of farming practices (Emmerson et al. 2016). In particular, habitat loss due to e.g. reduced crop type variability, the disappearance of structural elements such as hedges, or early and frequent mowing is a major challenge for many species in these ecosystems (Benton et al. 2003). In this context, birds are considered environmental indicators and play a key role in the assessment of agricultural landscapes (Morelli et al. 2014). As birds are sensitive to environmental changes, their condition reflects the health of the ecosystem (Gottschalk et al. 2010), and they are also one of the most monitored taxonomic groups (Engler et al. 2017). Therefore, understanding bird habitats and the environmental factors that shape them is crucial for assessing the impacts on land use in agroecosystems. However, especially farmland bird species are facing severe declines, as shown by recent abundance trends (European Environment Agency 2024).

This study models the habitat of six farmland bird species in South Tyrol: *Alauda arvensis* (Eurasian Skylark), *Emberiza citrinella* (Yellowhammer), *Lanius collurio* (Red-backed Shrike), *Passer montanus* (Eurasian Tree Sparrow), *Saxicola rubetra* (Whinchat) and *Sturnus vulgaris* (European Starling). Using ensemble species distribution models (SDMs), we linked bird occurrences to remotely sensed environmental features including climatic, satellite-derived and and other spatial variables to model the occurrence probability of these species in spatially complex terrain.

Material and Methods

South Tyrol is the most northern province of Italy within the Alpine region. The region is characterized by highly heterogenous mountainous landscapes and elevation ranges from 194 m to 3893 m, with about 40 % of the land above 2000 m sea level. Although agriculture covers approximately 69.5 % of the total area, only 26.6 % is classified as utilized agricultural area, mainly consisting of permanent meadows and pastures (ASTAT Landesinstitut für Statistik 2025).

Species distribution models (SDMs) are a commonly used modelling tool in ecological applications (Guisan et al. 2017). By combining data on the occurrence of species and environmental characteristics (features), they estimate the relationship between the two data sources and predict the suitability of habitats over space and time. To account for model selection bias and map the main trend and overall variation across several models, we used an ensemble modeling approach (Araújo & New 2007; Roilo et al. 2022). We used five modeling algorithms, namely, generalized linear models, generalized additive models, boosted regression trees, random forest, and maxent. We used breeding bird occurrence data from 2017–2023, provided by the Museum of Nature South Tyrol and the Institute of Alpine Environment at Eurac Research and environmental data accounting for topography, climate, land cover, vegetation and land management. Specifically, we derived spectral indices to characterize vegetation conditions and mapped the timing and frequency of mowing events to indicate land management intensity using freely available high-resolution satellite data from the European Coper-

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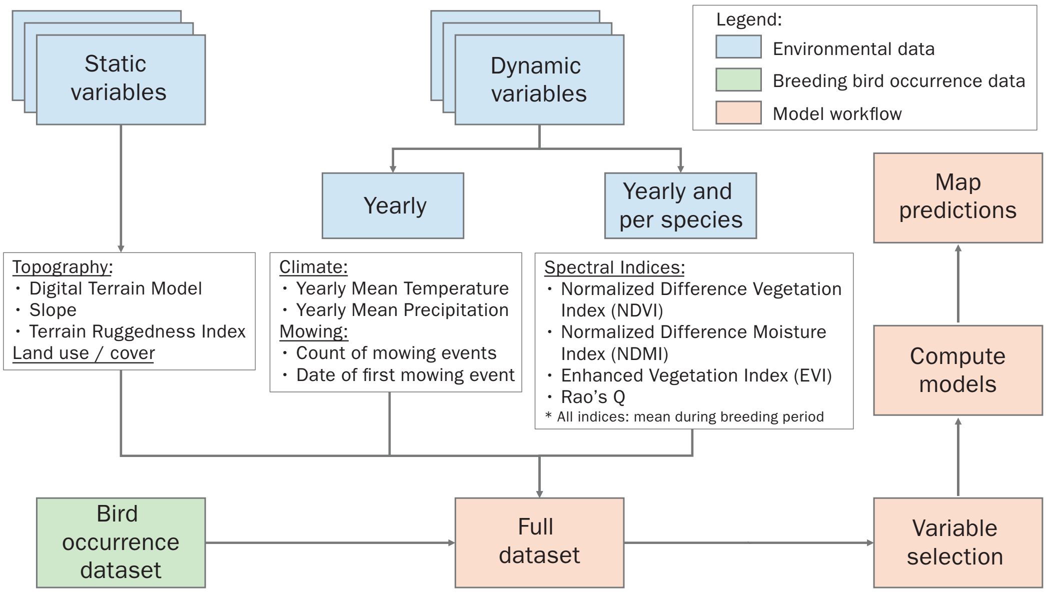

Figure 1: Schematic overview of the preprocessing and modeling workflow.

nicus Program. Milanesi et al. (2019) emphasize the importance of using dynamic environmental variables, to account for changing environmental or land use conditions. Consequently, we categorized our environmental variables as static or dynamic, with dynamic variables further divided into year- and species-specific data (Figure 1) which allowed us to model species-specific habitat suitabilities.

To assess cross correlation among environmental features and to only retain the most meaningful variables in the models, we employed the approach by Roilo et al. (2023) by fitting simple linear models for each variable and ranked them by the corrected Akaike information criterion (AICc) score. In addition, the number of presence points was set to a minimum number of 10 occurrences per variable to avoid overfitting. Final predictions were obtained by calculating the mean, weighted mean and median probabilities for models with a TSS (True Skill Statistic) value higher than 0.7.

Results

From the ensemble species distribution models, we obtained presence probability maps and variable importance statistics for each of the six modeled bird species across South Tyrol.

The probability maps showed that species-specific habitat preferences based on environmental and land use variables are effectively captured. Figure 2 shows exemplarily the produced maps for the Vinschgau valley with the Mals Heath as area with high predicted probabilities for all six species. *Alauda arvensis* (Skylark) and *Saxicola rubetra* (Whinchat) showed a high presence probability in open meadows and grasslands. In contrast, transition zones with a mixture of landscape features (i.e. hedgerows) and open meadows increased the presence probability of *Emberiza citrinella* (Yellowhammer) and *Lanius collurio* (Red-backed Shrike).

All selected variables in the models included land use and management variables, illustrating their importance for all species (Table 1). In particular, the timing of the first mowing event is a key information that can be accurately captured by remote sensing data. Overall, model accuracy was high for all species, with AUC (Area under ROC curve) values above 0.91 and TSS (True Skill Statistic) values higher than 0.7, indicating strong predictive power.

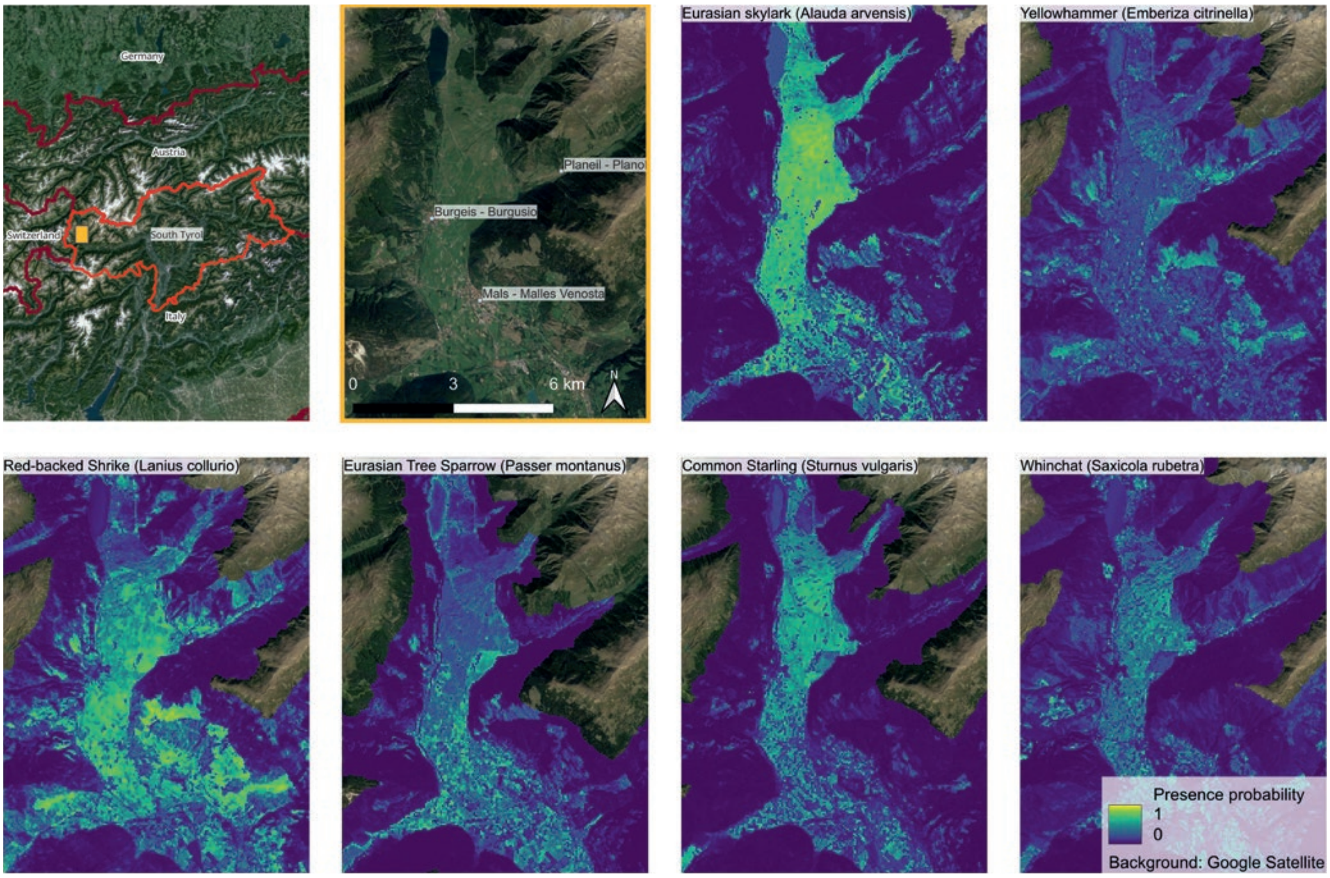

Figure 2: Habitat suitability in the upper Vinschgau valley (South Tyrol, Italy) for six farmland bird species.

Table 1: Selected variables in the models, sorted by importance.

Alauda arvensis	***Emberiza citrinella***	***Lanius collurio***	***Passer montanus***	***Saxicola rubetra***	***Sturnus vulgaris***
Precipitation	Precipitation	Precipitation	Precipitation	Date of first mowing event	Date of first mowing event
Slope	Land use/land cover	Land use/land cover	Slope	Precipitation	Slope
Land use/land cover	Slope	Date of first mowing event	Land use/land cover	EVI	Land use/land cover
Date of first mowing event	Date of first mowing event	EVI	Digital Terrain Model	Slope	EVI
EVI	Digital Terrain Model	Digital Terrain Model	NDMI	Land use/land cover	Precipitation
NDMI	NDMI	Slope	Rao'sQ		Digital Terrain Model
Rao'sQ	EVI	NDMI	Count of mowing events		Temperature
	Rao'sQ	Rao'sQ	EVI		NDVI
					Rao'sQ
occurrences: 83	**occurrences: 166**	**occurrences: 282**	**occurrences: 212**	**occurrences: 55**	**occurrences: 140**

Discussion

Our findings underline the value of high-resolution remote sensing data for habitat suitability assessments. Since land use and land management variables were among the most important parameters, our results reflect that early mowing can destroy the nests and chicks of ground breeding species during their rearing time (Grüebler et al. 2008). This is a strong factor in modeling ecologically realistic habitat probabilities. Furthermore, the contrasting habitat preferences of the different species align with expert knowledge, nicely illustrated by the Mals Heath (Figure 2). The open meadows and grasslands north of Burgeis show a high probability of occurrence of Skylarks, whereas transition zones with a mix of landscape features and open meadows increase the probability of occurrence of the Yellowhammer. Overall, the Mals Heath stands out with high presence probability of different species. This is partly explained by a relatively late first mowing date of many meadows in the area, incentivized at least partly also by existing political efforts promoting biodiversity protection (Südtiroler Landesverwaltung 2024). This emphasizes the potential of SDMs to critically assess land use and management practices, and to provide support for decision-making regarding biodiversity conservation.

Summary

This study represents an effective modeling of farmland bird species in South Tyrol, reflecting species-specific ecological requirements. It also shows how remote sensing can significantly improve the quality of SDMs with additional high-resolution data. In particular, land use and management information derived from satellite data can improve our understanding of spatio-temporal land use dynamics and support a more dynamic modeling approach. This further highlights the value of interdisciplinary work between ecologists and remote sensing experts to identify critical areas for biodiversity conservation and targeted conservation measures.

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Carbon Inventory South Tyrol Quantitative analysis and stability assessment of SOC stocks in South Tyrol's agricultural areas

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Introduction

The European Union (EU) aims to achieve climate neutrality by 2050, as outlined in the Paris Agreement and the European Green Deal (European Commission 2019). The Land Use, Land-Use Change, and Forestry (LULUCF) sector, which includes agriculture, has set an even more ambitious goal of climate neutrality by 2035 (Vikolainen 2022; European Parliament and Council of the European Union 2023). Understanding the interrelationship between major carbon pools is crucial for effective carbon emission management. According to the Guidelines for National Greenhouse Gas Inventories (IPCC 2019), these pools comprise living biomass, dead organic matter, and soil carbon within the biosphere. Although estimating carbon in biomass is relatively straightforward and may only be a minor contributor to certain land uses, such as grasslands, the quantification and assessment of soil organic carbon (SOC) stocks are considerably more complex, particularly in mountainous regions with small-scale landscape variations. Recent global studies have examined SOC stocks (FAO 2018; FAO & ITPS 2019; Poggio et al. 2021). However, regional soil organic carbon modeling is becoming increasingly important due to the limitations of global models in capturing small-scale landscape complexities (Yigini & Panagos 2014; Kotzé & Van Tol 2023; Rota et al. 2024). Developing tailored strategies that address the specific characteristics of small-scale landscapes is therefore needed (Zhang et al. 2023). Regional approaches are vital for informing decisions related to agricultural land-use conversions and supporting climate neutrality efforts. These approaches are essential for carbon conservation, carbon sequestration, and initiatives such as carbon farming. The 'Carbon Inventory South Tyrol' (CIS) project aims to assist the European Union's objectives within the agricultural sector at a regional level. The primary goal is to address the knowledge gaps in quantifying the agricultural soil organic carbon (SOC) stock within the Italian province of South Tyrol. SOC stock is estimated using a soil organic carbon mapping (SOCM) approach. The initial step involves sourcing completed and ongoing soil studies from relevant literature specific to the study area. The subsequent sections will briefly report on the process and preliminary results of collecting soil data from the literature.

Methodology

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This study examined the agricultural regions in South Tyrol, which is the northernmost province of Italy. South Tyrol encompasses an area of 7,400 km^2, with 37 % designated for agricultural use. The agricultural land is generally categorized as follows:

59 % pastures, 27 % hay meadows, 8 % orchards, 3 % vineyards, and 3 % arable land. Notably, 94,000 hectares are classified as intensively utilized agricultural areas (Schönafinger et al. 2024).

As part of the CIS project, which aims to assess SOC stocks using machine learning methodologies for SOCM, the process of generating input data involved acquiring existing soil information from literature sources, which have been gathered from completed and ongoing projects primarily within the boundaries of South Tyrol. To achieve this objective, institutions that have conducted soil surveys were contacted to provide their data. The collected datasets were standardized to create a comprehensive database containing all available soil information. Emphasis was placed on acquiring data concerning SOC content, as well as physical measurements necessary for modeling SOC stock, such as bulk density and coarse fragments. Furthermore, it has been essential that the soil data are georeferenced to facilitate the interpolation of empirical soil data across agricultural areas in South Tyrol.

In addition to the digital collection of georeferenced soil data, Martin Thalheimer from the Institute for Fruit and Viticulture at Research Centre Laimburg has curated an extensive literature collection on soil information for South Tyrol. The collection includes significant contributions such as Avanzini et al. (2007), Biologisches Landeslabor (1986), Fischer & Wetzel (1996), Gruber et al. (2019), Klotzner (1938), Magazzini (2001), Mair (2010), Minerbi (2003), Nitsch (2016), Peer (1969), Porro et al. (2018), Sartori (1978), Schröder (2010), Staffler et al. (2003), and Wenzel et al. (1996). These studies and reports will be used as additional data source and will be digitized when opportunities and needs arise.

Intermediary Results

An extensive collection of soil data has been compiled from literature, resulting in over 34,000 records from various sources (Table 1). In South Tyrol's agricultural regions, the dataset covers 19,203 locations (Figure 1), with 97 % of these records containing information on SOC content.

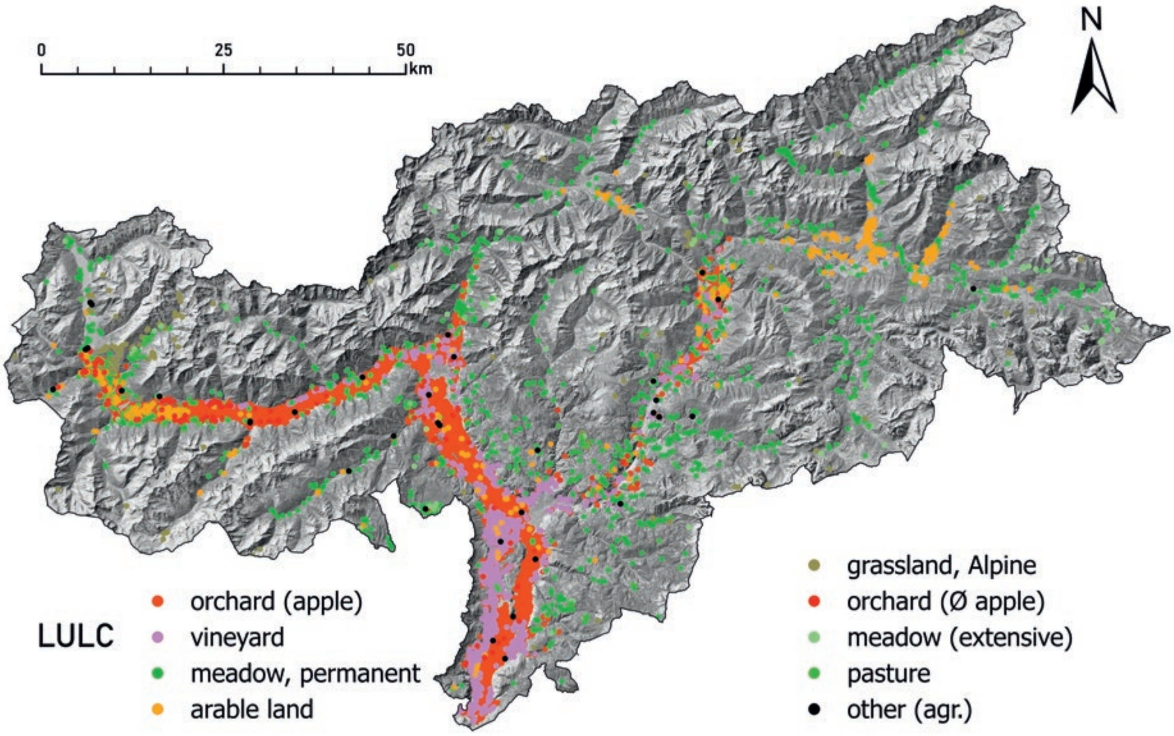

Figure 1: Soil data point distribution on South Tyrol's agricultural land classified by land-use/land-cover (LULC) based on Autonome Provinz Bozen (2021).

Table 1: A comprehensive overview of studies concerning soil properties, including the measurement of soil organic carbon (SOC) in South Tyrol.

ID	Sample period	Data count	Land use	Reference
1	2006–2016	28,964	arable land, (forests), fruit orchards, grassland, vineyards	(Genova et al. 2022)
2	2002–2005	1,033	forests, grassland	(Tasser 2023)
3	1997–2019	747	arable land, grassland	(Burchia 2021)
4	2023–2025	635	fruit orchards, grassland	(INNONährstoffe 2024)
5	2023	504	vineyards	(BioViSo 2025)
6	1998–2002	491	fruit orchards, grassland	(Stimpfl et al. 2006a, 2006b)
7	2019–2023	460	arable land, forests, fruit orchards, grassland, riparian areas, settlement, vineyards, wetland	(Hilpold et al. 2023)
8	1997	403	forests, grassland	(Tasser et al. 2001)
9	2014–2015	326	forests, grassland, vineyards	(Geitner et al. 2017)
10	2011	153	larch meadows	(Nagler et al. 2015)
11	2015	107	forests, fruit orchards, grassland	(LT(S)ER Matsch 2023)
12	2009–2018	103	forests, fruit orchards, grassland, vineyards	(Panagos et al. 2022, 2012; ESDAC et al. 2025)
13	2010–2011	91	grassland	(Niedrist 2023)
14	2010–2016	70	grassland	(Pasolli et al. 2014)
15	2022	56	glacier forefield	(Ramskogler et al. 2023)
16	2010	52	grassland, forests, wetland	(Niedrist et al. 2011)
17	2022	10	fruit orchards	(SCOOP 2025)
18		10	arable land, grassland	(Batjes et al. 2019)
19	2008	6	grassland	(Meyer et al. 2012)
20	2023	3	vineyards	(Callesen et al. 2023)

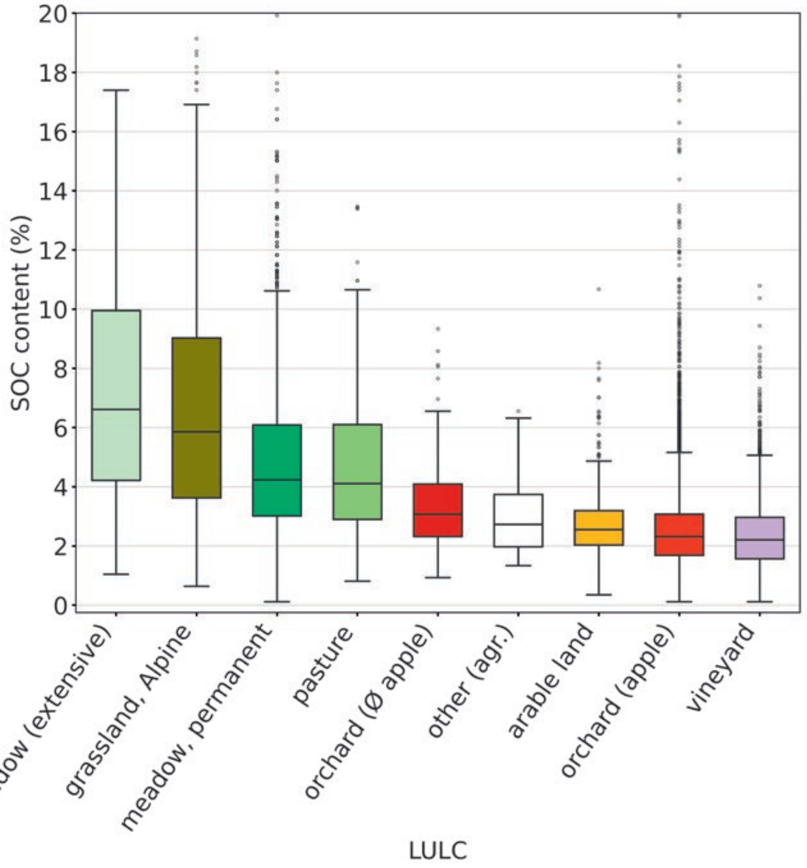

Figure 2: Soil organic carbon (SOC) content variations in the collected literature data classified by agricultural land-use/land-cover (LULC) types based on Autonome Provinz Bozen (2021).

The distribution of soil data points is uneven throughout the study area, primarily located at valley bottoms and largely concentrated in apple orchards, followed by vineyards and permanent meadows.

Based on the data presented (Figure 2), Alpine grasslands (7.38 % ± 0.38) and extensively used meadows (7.18 % ± 0.27) have the highest amount of SOC on average. In contrast, arable land (2.78 % ± 0.05), apple orchards (2.52 % ± 0.01), and vineyards (2.41 % ± 0.02) contain the lowest levels of SOC.

Discussion and directions for future research

The evaluation of data has revealed notable gaps in spatial coverage, particularly the lack of surveys in remote areas such as Alpine grasslands. In contrast, apple orchards, vineyards, and permanent meadows have extensive soil data coverage. Furthermore, there is an insufficiency in the coverage of physical parameters, with only a few soil surveys addressing bulk density and coarse fragments. To address these gaps, an additional field survey has been initiated, which will commence in late summer and autumn of 2024 and conclude in spring 2025.

The objective of this project is to develop a SOC stock map for all agricultural areas in South Tyrol. Moreover, carbon flux has been measured for apple orchards and meadows, and it is currently being monitored for pastures and vineyards. These measurements will be utilized to validate SOC stocks in their stability and to identify potential differences in agricultural land use and land cover (LULC) behavior, determining whether certain LULC types function as carbon sinks or sources.

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Giulia Tomasi[1], Alessio Bertolli[1], Filippo Prosser[1], Costanza Geppert[2], Lorenzo Marini[2]

Alpine flora at the extremes: the distribution of plants vascular plants and bryophytes mountain peaks in Trentino, Italy

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Keywords: flora and bryophytes of Trentino, species migration, upper altitudinal limit, anthropogenic climate warming

Introduction

The Alps are among the European regions with the highest biodiversity; of the approximately 4,500 plant species (Aeschimann et al. 2004), 2,563 are spontaneous or naturalized species found in the province of Trento, and around 1,000 are alpine orophytes (Prosser et al. 2019). The numerous endemisms, 46 Italian exclusive endemisms that also concern Trentino (Bertolli et al. 2024), demonstrate the geological and climatic complexity that has caused isolation and adaptation phenomena to a diversified environment. In the Alps, the climate has warmed by about 1.8°C since 1880, almost double the global average (Zampieri et al. 2021). Climate models are particularly pessimistic for the southern Alps, where, in the worst-case scenario, an increase of more than 4°C is expected by the end of this century compared to the period 1981–2010 (Kotlarski et al. 2022). The evidence of a consequent enrichment of the summit vascular flora in the Alps has already been presented many years ago (Braun-Blanquet 1955). More recently, numerous medium- and long-term studies have confirmed that climate change is causing an altitudinal expansion of species, particularly in the summit areas of the Alps (Lamprecht et al. 2018). Prosser (et al. 2023) suggested that this phenomenon could be particularly evident in the south-eastern Alps.

Materials and Methods

The botanical section of the Fondazione Museo Civico di Rovereto, in collaboration with the DAFNAE Department of the University of Padua, began a study of summits above 2,700 meters above sea level in 2022–2023, sampling 27 representative peaks from different geographical areas and the main geological substrates of the province of Trento. The peaks are located between 2,745 and 3,757 meters in altitude in the Ortles-Cevedale Chain, Fassa and Gardena Dolomites, Adamello-Presanella Group, Pale di San Martino Group and Brenta Dolomites, all within protected areas and/or Nature Parks. The selection of the peaks to be studied took into account the following criteria: elevation (> 2700 m), location (as homogeneous as possible distribution across various mountain ranges), substrate (representative samples of various rock substrates), exposure (preferably south or east-facing ascent paths/tracks), and accessibility to the summit (peaks requiring high-level mountaineering skills were excluded from the study). Field data collection took place during the 2022 and 2023 growing seasons and resulted in the recording of 7,900 geo-referenced data points related to vascular plants and bryophytes. The survey followed a standardized protocol, divided into three sampling phases:

- Ascent sampling: In the last 200 meters below the summit, a transect was performed every 50 meters of elevation gain, recording the species list of both vascular plants and bryophytes visible along the main trail or access track (4 transects in total);

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- Summit area: A complete survey of the flora within a 20-meter radius from the summit cross (most of the summits had a cross or a marker; in the absence of one, the highest point was considered as the summit);
- Descent sampling: Along the main path, the first three populations of each species of vascular plants identified were mapped and geo-referenced up to 200 meters below the summit. For each population, information on size and reproductive status was collected.

Results

The 7,900 geo-referenced data points documented the presence of 295 vascular plant taxa and 161 species of bryophytes. Among these, 138 vascular plant and 72 bryophyte species were recorded above 3,000 meters. The comparison of the vascular plants recorded in this study with the whole flora of Trentino published by Prosser et al. (2019) showed that the summit flora has more orophytes and boreal species and less Eurasian and Mediterranean species. Regarding the life form spectrum, compared to the overall provincial flora, the summit flora shows more hemicryptophytes and chamaephytes, while geophytes and therophytes are less frequent (Figure 1).

With increasing elevation, the number of species decreased for both substrate types. The total number of species associated with sedimentary rocks was lower than the number of species associated with silicate (Figure 1). Interestingly, there were no limestone peaks without plant species even at the highest elevations, indicating that for several species there is no space for further upward expansions.

The study also established the maximum altitudinal record in the province of Trento for vascular plants at 3,607 meters above sea level (*Poa laxa* Haenke subsp. *laxa* on Punta Taviela) and for bryophytes at 3,757 meters (*Grimmia triformis* Carestia & De Not. on Zufallspitze/Cevedale). Compared to the known maximum limits for species in Trentino (Prosser et al. 2019), 229 taxa showed a higher altitude limit. In some cases, the elevation increase was over 500 m, such as for *Gymnocarpium dryopteris* (L.) Newman on Forcola, recorded at 3,295 meters (+625 m). We also observed a single individual of *Larix decidua* Mill. at 3,152 m on Lobbia Alta, which represents the maximum elevation for the entire species' range (Prosser et al. 2023). These records are partly related to climate change but also to incomplete records in the past. An analysis of the maximum elevation recorded for each species helped highlighting the preferred ascent paths of the species through morphological analysis in GIS. For the highest records, we observed an average exposure of the slope of c. 178°, and an average slope of c. 34°.

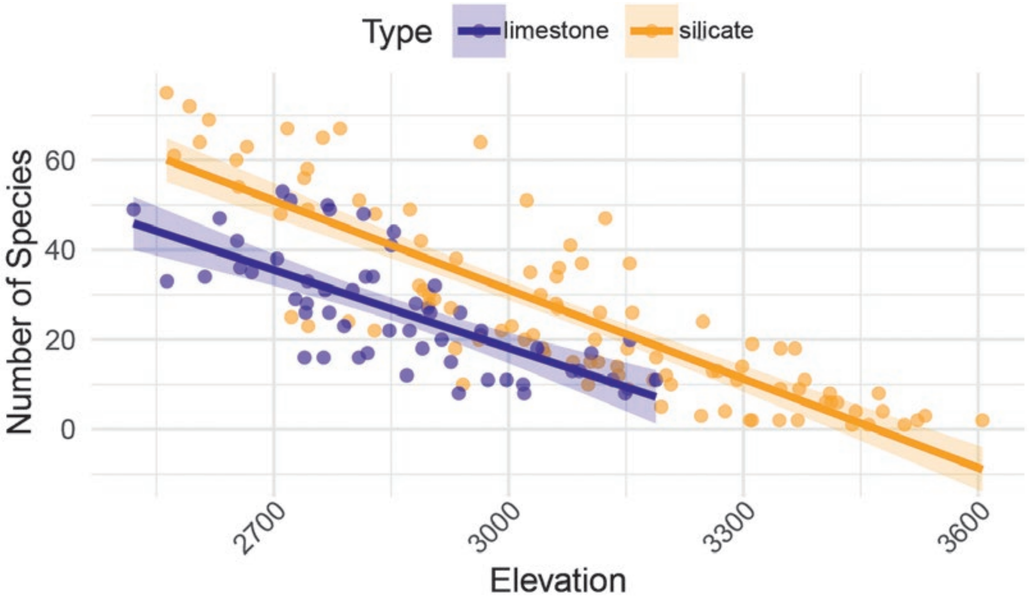

Figure 1: Effect of bedrock and elevation on plant species richness observed in the different elevation bands.

Discussion

The results show a clear decrease in species richness as one moves toward the summits, confirming the strong relationship between species distribution and temperature in mountain ecosystems (Vittoz et al. 2010). However, the rate of colonization of these areas by species characteristic of lower elevation belts has accelerated (Steinbauer et al. 2018), and similar trends were also evident in our case study. The rise in temperatures and the reduction of snow cover are favoring the altitudinal migration of generalist species. In contrast, specialist species at higher elevations are increasingly close to their physiological limits. The differences observed between limestone and siliceous substrates indicate that the availability of potential habitats for species migration is not uniform, with siliceous peaks still offering available empty niches compared to the limestone peaks. The chorological analysis revealed a predominance of orophytes, alpine and arctic-alpine endemics, with a clear differentiation between peaks on siliceous and limestone substrates. Limestone species showed greater altitudinal limitation compared to species from silicate bedrock, with a tendency for habitat saturation at higher elevations. Species with higher thermophilic and nitrophilic indices and a lower moisture index are expected to benefit from the predicted decrease in water availability, favoring their upward migration. Since the study was conducted systematically using a standardized protocol, it provides a solid foundation for advancing our knowledge of alpine flora dynamics in Italy. These semi-permanent plots will be essential for future monitoring aimed at investigating species range dynamics in response to climate warming. High-mountain ecosystems, and summits in particular, represent natural study sites that are easy to relocate, allowing for the collection of reliable time series data.

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6. Short abstracts

Long-term study of heavy metal and nitrogen concentrations in moss species *Hylocomium splendens* in South Tyrol

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Bryophytes are a frequently used bioindicator. Due to their lack of roots and a pronounced cuticle or epidermis, they absorb macro and microelements through their entire surface. Furthermore, they have the ability to accumulate not only nutrients, but also heavy metals in their tissue. One known bioindicator species is *Hylocomium splendens*, a common moss found in South Tyrolian coniferous forests.

This species is at the center of an international, long-term survey, regarding atmospheric pollutant deposition. This study has been conducted every five years since 1990 in many European and Central Asian and American countries as part of the European project "European surveys of heavy metal accumulation in mosses".

Since 1995, the Biological Laboratory of the Agency for Environment and Climate Protection has contributed to this survey. Every five years mosses from twenty sampling sites in South Tyrol are analyzed for various pollutant content. The collected moss samples of *Hylocomium splendens* are analyzed for the concentrations of the following pollutants: arsenic, lead, cadmium, chromium, iron, copper, nickel, mercury, vanadium, zinc, and nitrogen. During the monitoring period of twenty years, different trends of measured concentrations were observed. One example is the detected decreasing trend in lead concentration in the moss tissue since the introduction of lead-free fuel.

Also interesting is a comparison with the results of other countries participating in this project, observing different hotspots of heavy metals in highly industrialized countries. In future, microplastics will also be analyzed in some moss samples of the monitoring network.

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Assessing the impact of habitat and landscape heterogeneity on mountain bird communities

Matteo Anderle[1], Mattia Brambilla[2,3], Andreas Hilpold[1], Chiara Paniccia[1], Ulrike Tappeiner[1,4], Erich Tasser[1], Julia Seeber[1,4]
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The heterogeneity of Alps is the result of abiotic and biotic processes that have taken place over millions of years and the influence of humans since they first settled in the area. These landscapes have been strongly influenced by human activities, in particular the processes of urbanization, intensification of agriculture in the valleys, and the abandonment at high elevations. The Alps are a biodiversity hotspot, with a great diversity of endemic species adapted to extreme conditions. This biodiversity is currently under threat. Birds are sensitive to global change, mainly due to habitat loss and degradation. However, they are a crucial component of ecosystems and serve as bioindicators of overall biodiversity. Understanding how current global change affects birds is essential for identifying the factors that determine their distribution, knowledge that is essential for effective conservation strategies.

The long-term project "Biodiversity Monitoring South Tyrol" analyzed bird communities along land-use and elevational gradients within South Tyrol. Ecological models integrating topographic, climatic, landscape configuration/composition, and habitat heterogeneity variables were used to identify the main drivers of diversities of bird communities.

The results showed that habitat heterogeneity is crucial for maintaining rich and diverse bird communities in agricultural and anthropogenic landscapes. To mitigate the effects of land-use change, it is necessary to promote a complex and heterogeneous landscape, including semi-natural habitats, and a mosaic of different land-use types. In particular, the importance of maintaining the heterogeneity of cultivated areas along valleys and the continuity of forest cover and reducing forest fragmentation was highlighted. The research also confirmed the key role of extensive grasslands and wetlands as key habitats for bird conservation in the Alps.

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Introducing „naturamonta“: a new scientific journal dedicated to biodiversity and related research in the EUREGIO Tyrol, South Tyrol, Trentino

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A regionally focused scientific journal has been lacking in Tyrol since the last issue of “Berichte des naturwissenschaftlich-medizinischen Vereins Innsbruck” in 2014. This journal was popular among researchers and students at the Faculty of Biology at the University of Innsbruck, as well as other scientists in Tyrol and neighboring regions.

To fill this gap, we decided to reintroduce a platform for researchers in the EUREGIO to publish their findings, but include some updates to meet modern standards. Our goal is to highlight regional research that might be overlooked internationally and increase the visibility of published articles.

The result is a new, up to date journal focusing on biodiversity research and related scientific disciplines in the EUREGIO and other alpine regions and connected habitats. We would like to lay out our approach to create such a journal and proudly present the results of this process: “naturamonta”!

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The City Nature Challenge in Innsbruck – exploring the potential of Citizen Science initiatives to strengthen regional biodiversity datasets in museums

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Citizen science initiatives are gaining traction worldwide and are widely regarded as a means to support scientific research by engaging a larger number of citizens. To evaluate the potential of such initiatives in increasing public awareness of biodiversity and supplementing museum data collections, the Natural History Collection of the Tyrolean State Museums has been organizing regional activities for the City Nature Challenge since 2022. In our presentation, we discuss the results and aim to compare various methods used to motivate public participation during these events. Additionally, a survey among participants examined the sustainability of these one-time events in raising awareness and attention towards biodiversity. Our findings will be used to explore how we can more effectively and sustainably engage the public in future biodiversity studies.

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Genetic variability of the chestnut blight fungus *Cryphonectria parasitica* in different populations of northern Italy

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Cryphonectria parasitica, causing chestnut blight, is one of the most important pathogens of sweet chestnut trees (*Castanea sativa*). Since its unintentional introduction to Italy in the 1930s, the invasive fungal species has spread to all chestnut growing areas, where it has been causing considerable damage to chestnut trees. One of the possibilities to control the disease relies on the natural and human-mediated spread of hypovirulent strains of *C. parasitica*, which carry a mycovirus that reduces the virulence of the fungus. The transmission of the mycovirus *Cryphonectria hypovirus* 1 depends on hyphal anastomosis among vegetatively compatible fungal individuals, a feature which is genetically determined and governed by at least six genetic loci. Consequently, knowledge about the genetic variability of the fungal population can help adapting more effective disease management strategies. By analyzing different molecular markers, a high genetic variability was found for both, the fungal and the mycoviral populations in South Tyrol. The investigation was extended to populations of *C. parasitica* and its hypovirus from Lake Garda and the Friuli Venezia Giulia region in northern Italy. In the presentation, population genetic data will be confronted to reconstruct the spread of the fungus and the mycovirus in the investigated regions, with the final goal to improve the knowledge and control of the disease.

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High temperature thresholds for membranes, proteins, photosystem II, and whole leaf tissues in different mountain species

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Mountain plants can be exposed to high temperatures; thereby the extent of natural heat stress varies greatly between species depending on their stature and growing site. Increased intensity and duration of heat waves due to global climate change may push plants closer to their physiological limits, depending on their ability to tolerate and adapt to heat. Heat damage occurs at the molecular level and is associated with increased fluidity of membrane lipids, lipid peroxidation, and protein degradation and aggregation, all of which affect the integrity of cellular structures, including organelles, cytoskeleton, and membrane functions. However, the sequence of events leading to heat damage are poorly understood. Furthermore, measuring thermal tolerance is often limited by the methods used. To better understand the development of heat-induced damage in leaves, we used four methods to determine high temperature thresholds, at which 1) integrity of whole leaf tissues, 2) functionality of PSII, 3) membrane stability 4) and protein stability are lost. We selected six mountain species from different ecological niches that are adapted to different microclimatic conditions and are likely to differ in their heat tolerance and heat damage dynamics: *Dryas octopetala*, *Alchemilla alpina* agg.*,* *Rhododendron ferrugineum*, *Vaccinium vitis-idaea, Kalmia procumbens,* and *Ranunculus glacialis*. In line with the typical habitat preference, we observe different high temperature thresholds, but also differences in the heat damage dynamics and temperature ranges. We present a new method for measuring heat tolerance – a key trait in the face of ongoing climate change – that is reliable, easy and fast to conduct and minimally destructive.

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Alpine flora at the extremes: the distribution of plants on mountain peaks

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High elevation areas typically experience less exposure to land use changes and human disturbances. Nevertheless, even the most remote regions on Earth are undergoing substantial alterations due to anthropogenic climate warming. While it is well-established that climate change augments species richness at high elevations, there is a paucity of studies investigating the distribution of alpine flora on the highest peaks. Examining species through the lens of functional traits enhances our understanding of ecosystem functionality, plant composition, ecological processes, and future ecological predictions. In this study, we sampled the highest alpine summits in the province of Trento. The species identified were characterized using ecological and morphological functional traits. Early snowmelt and an extended growing season are predicted to facilitate the upward migration of generalist species, characterized by increased seed size, extended vegetative cycles, and different dissemination and dispersal mechanisms. The comparison between the highest occurrences observed with the historical thermal niche of alpine species suggested that the speed of upward migration might be much faster than expected from previous studies. We found a strong contrast between volcanic and calcareous mountains. On calcareous mountains, the species-elevation relationship was truncated towards the highest elevations, indicating that several species have already reached the highest elevation areas available. On silicate mountains, on the other hand, several peaks still had empty niches available for future migrations. The analysis of species traits indicated that competitive strategies will gain prominence over the currently prevailing ruderal and stress-tolerant strategies. Above the treeline, the local distribution of alpine species largely depends on topography (microclimate), and the effects of climate warming are expected to be mediated by small-scale local conditions.

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Biodiversa+ Habitat Pilot: Finding a shared method for mapping and monitoring grasslands and wetlands using Remote Sensing data

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Biodiversa+ is a partnership co-developed by the European Commission to support the biodiversity goals and increase harmonization of biodiversity data handling and research methods. The Province of Bolzano is an active partner of Biodiversa+ together with 82 other partners, from 41 countries. For harmonizing the monitoring of biodiversity, Biodiversa+ has launched a series of pilot studies. Each pilot focuses on distinct aspects of biodiversity monitoring and includes several countries collaborating to test and develop methods for long-term transnational monitoring. The Province of Bolzano, represented by Eurac research, is one of 11 active partners in the Habitat pilot which aims to assess methods for mapping and quality monitoring of grassland and wetland habitats using remote sensing (RS) data.

The Habitat pilot is currently concluding its first project module which consisted of (i) identifying synergies between the pilot and other existent projects and (ii) reviewing the partners' current practices and prior experiences of using RS-based and field-based

methods for mapping and monitoring natural areas. During the review, the partners gathered information on over 40 projects and methods for habitat mapping and monitoring, highlighting aspects such as used data sources, spatial coverage, identified strengths and weaknesses, etc. for each project and method. Subsequently, the methods best aligning with the scope of the Habitat Pilot, i.e., to find harmonized methods that could be applied across the continent, were discussed during a workshop in Bolzano in June 2024. After the discussions, a joint decision was made on which methods should be tested in field sites of the pilot partners.

In the following project modules, until the end of 2025, the pilot partners will test the selected mapping and monitoring methods in grassland and wetland sites. Finally, a report on the results from the method implementation and on the outcomes of the pilot study will be produced.

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Climate-driven shifts in the population dynamics of the invasive tiger mosquito (*Aedes albopictus*) in the European Alpine region

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The recent global expansion of *Aedes albopictus* across tropical and temperate regions is an excellent example of the mobility and adaptability of invasive species. While climate change is not the sole factor driving the increase and spread of *Ae. albopictus*, it may contribute to creating more favorable conditions for the species by causing milder winters. As global warming continues to make the climate of mountain areas milder, understanding *Ae. albopictus'* potential for range and seasonality expansion in the Alpine area is crucial, as it could affect native species and ecosystems and lead to the introduction and propagation of mosquito-borne diseases in regions previously free from such threats.

Our objective is to study the impact of climate change on the distribution and seasonality of *Ae. albopictus* for the periods 2040-2050 and 2070-2080. Using the European Alpine area as a case study, we utilize entomological data collected for public health surveillance together with temperature and precipitation datasets from regional climate model simulations (9 km × 9 km) to train a machine learning mosquito population model under different climate emission scenarios.

Our results reveal the joint influence of temperature and precipitation on *Ae. albopictus* distribution and seasonality, indicating a shift in the species' range towards higher altitudes and a lengthening of the suitable climatic conditions. Therefore, changing climate patterns and shifting habitat conditions have the potential to contribute significantly to the future geographic expansion of the tropical and invasive *Ae. albopictus* in Alpine areas.

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Wolf depredation on livestock in Trentino: an analysis of dynamics and prevention strategies

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Over the past century, wolves have made a remarkable comeback in the Eastern Italian Alps, forming over 30 packs in under a decade. In Trentino, this return has sparked significant political and social conflicts and caused tangible damage to livestock. However, no study has yet assessed the impact of wolves on the livestock sector or the effectiveness of prevention measures. Our study focused on wolf depredation dynamics on livestock in Trento province, analyzing all confirmed cases from 2013 to 2022. We examined spatio-temporal trends and hotspots of wolf attacks, identified recurring patterns concerning livestock type and management, and evaluated the presence and effectiveness of protective measures at depredation sites. From 2013 to 2022, Trento province recorded 576 wolf depredations, affecting a total of 2256 livestock. Depredation incidents mirrored the growth of the wolf population, increasing in frequency and geographic spread over time. Most attacks occurred in August and at night. Sheep and goats were most affected (64 %), followed by cattle (26 %), with young cattle under 15 months old being the primary targets (67 % of cattle preyed upon). Sheep, goats, and donkeys were the most vulnerable types of livestock, given their selection by wolves, whereas cattle were least vulnerable. Spatial analysis identified the areas and pastures most impacted by chronic and severe depredations during the study period (2013-2022) and the recent peak period of concern (2020-2022). The hardest-hit areas between 2020 and 2022 included Lessinia, Baldo, Bondone, and Primiero. Thirty specific pastures (malghe) experienced intense wolf depredations, predominantly affecting unprotected livestock (81 % of attacks). Our findings highlight the complexities of wolf-livestock interactions at a local scale, offering insights for enhancing mitigation strategies and prioritizing interventions in high-risk areas.

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Diversity of stink bugs and their egg parasitoids in South Tyrol

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In South Tyrol, the presence of stink bugs has increased in recent years, posing a threat for the productivity of apple orchards. The invasive species *Halyomorpha halys* is now established in the main valleys of the province. An extensive two-year survey across 27 sites was carried out to explore the distribution and abundance of stink bug species and their egg parasitoids. Surveyed sites were located throughout the province in apple orchards, forest edges, and urban areas, spanning three altitude ranges from 200 to 1000 m a.s.l.. The sampled stink bugs were also associated with their host plants. The study detected a total of 25 stink bug species belonging to three families, including mainly phytophagous and a single predatory species. The relative abundance of stink bugs was significantly influenced by habitat type and altitude. The highest richness was found in urban areas, followed by forests and orchards, while the greatest number of individuals was recorded at the intermediate altitude range (501–800 m a.s.l.). Host plants played a crucial role in the distribution of stink bugs and their parasitoids. For instance, *Pentatoma rufipes* was prevalent in forest rims, associated with plant species in the families Betulaceae and Fagaceae, whereas *H. halys* and *Palomena prasina* were

detected on Cornaceae and Oleaceae, often cultivated as ornamentals and in hedges adjacent to orchards. The results revealed a complex network of parasitoid-host interactions, with 12 parasitoid species emerging from stink bug egg masses collected in the field. These included scelionids, eupelmids, pteromalids and eulophids, indicating a wealthy community that contributes in the regulation of stink bug populations. Parasitization rates varied significantly between habitats and stink bug species, reaching nearly 40 % of *H. halys* eggs in urban areas. These results can usefully contribute to improving biological control strategies to manage stink bug populations within agricultural ecosystems.

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Biodiversa+: a European Biodiversity Partnership for a transnational network of harmonized biodiversity monitoring schemes

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Biodiversity is in decline, and reversing this trend requires coordinated, large-scale interventions. To design effective measures, robust monitoring systems are essential for delivering reliable data. Independent monitoring methods have led to various unconnected databases and often non-comparable data. Thus, there is an urgent need to standardize data and harmonize monitoring methods to identify knowledge gaps, develop models and establishing trends at European and global scale, providing policy- and decision-makers with the tools for informed, significant decisions.

We present the progress of Biodiversa+, the European partnership for biodiversity, in establishing a coordinated biodiversity monitoring network that applies standardized methods and creates data flows into centralized international databases. The partnership comprises research institutes, environmental protection agencies, and environmental ministries from several European and non-European countries. Through participatory workshops, surveys, co-designed activities, synergies with other European initiatives, and piloting transnational monitoring initiatives, the partnership addresses various aspects of biodiversity monitoring at a pan-European scale to improve collaborations and produce reports on shared monitoring priorities, guidelines for harmonizing methods, protocols, and data interoperability, exploit of new technologies and citizen science, and fostering of data for research and policy. Additionally, the partnership designs the governance model for national biodiversity monitoring coordination centers to integrate with a European counterpart.

By emphasizing collaboration, standardization, and innovation, Biodiversa+ aspires to enhance the effectiveness of biodiversity monitoring across Europe and beyond, producing outputs that contribute to achieving the goals of the Biodiversity Strategy 2030, the Kunming-Montreal Global Biodiversity Framework, and other European and global initiatives.

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Alien species in Lake Garda

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There is a large consensus today that invasive alien species (IAS) are one of the most important direct drivers of biodiversity loss and change in ecosystem services, along with habitat change, climate change, overexploitation of species and pollution.

Lake Garda, the largest Italian lake, has been suffering from the introduction of several alien species (AS) during the last decades and can now be considered one of the main European freshwater hotspots of xenodiversity. To date, 45 species of alien fish, invertebrates, macrophytes and reptiles have been recorded in Lake Garda, some of which being IAS: *Lagarosiphon major* (Ridley) Moss, *Corbicula fluminea* (O. F. Müller, 1774), *Corbicula fluminalis* (Müller, 1774), *Corbicula largillierti* (Philippi, 1844), *Corbicula leana* Prime, 1867, *Dikerogammarus villosus* (Sowinsky, 1894), *Dreissena polymorpha* (Pallas, 51771), and *Dreissena bugensis* Andrusov, 1897. The latter was observed for the first time in 2022 and is now rapidly expanding in littoral, sublittoral and profundal areas of the lake.

Eight species are included in the Union list (Regulation EU No 1143/2014): *Lepomis gibbosus* (Linnaeus, 1758), *Pseudorasbora parva* (Schlegel, 1842), *Ameiurus melas* (Rafinesque, 1820), *Trachemys scripta* (Schoepff, 1792), *Faxonius limosus* (Rafinesque, 1817), *Procambarus clarkii* (Girard, 1852), *Elodea nuttallii* (Planch.) H. St. John, and *Lagarosiphon major*.

For some IAS, Lake Garda represented the first point of introduction in Italy, i.e., *Dreissena polymorpha*, *D. bugensis, Dikerogammarus villosus, Corbicula fluminalis,* and *C. largilliertii*. The lake therefore represents a significant entry point for first arrival and following dispersal of AS and IAS, mainly driven by recreational boating and aquatic sports. As eradication measures are unfeasible, the adoption of measures for preventing further unintentional biological invasions is the sole way to address the problem. Guidelines for the inspection, the extensive cleaning and prolonged drying of boat hulls should be adopted.

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Does global change make high-elevation plant communities of the European Alps richer but less unique?

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Alpine plant communities are highly sensitive to climate warming. Recent studies have shown an increase in species diversity, driven by the establishment of upwards migrating species from lower elevations. This not only alters the species composition of the communities, but also the interspecific interactions. Consequently, an increase in competition is to be expected as the communities become denser, which might eventually result in the extinction of uncompetitive cold-hardy species. Here, we present results of two research sites in the region Trentino-South Tyrol (Italy) included in the vegetation monitoring program GLORIA (Global Observation Research Initiative in Alpine Environments). Each of the research sites comprises four summits along an elevation gradient from the treeline ecotone to the subnival zone. Since 2001 and 2003, plant species diversity and cover have been systematically recorded every 5-7 years in accordance with the GLORIA standardized protocol. This sequence of observations, spanning over 20 years, allows us to investigate whether the species richness in alpine vegetation continues to increase or whether it has reached a point of stabilization due to an increased extinction rate of cold-hardy species. The most recent resurvey from the Dolomites (Southern Alps) in 2022 revealed a continued marked increase in species richness on the highest summit in the subnival belt, whereas this trend had already stagnated in lower summits. Furthermore, species numbers and trends differed between the different aspects of a summit. In particular, the highest increase in species numbers was observed on the southern and eastern aspects of the highest summits. This suggests that species enrichment is slowed down by the colder environmental conditions on the northern and western aspects. The trends in the second study site in the Texel Group (Central Alps) will be presented based on data surveyed in summer 2024.

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Effects of global warming on the alpine vegetation of four peaks in the Texel Group, South Tyrol, as part of the GLORIA project

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Climate change has a particularly strong impact on alpine vegetation, its distribution and its phenology, as these ecosystems are determined by cold temperatures. Global warming has triggered an increase in species richness at higher elevations, due to upwards migration of less cold-tolerant species. However, this is predicted to set local cryophilic species under an extinction risk, due to an increase of competition. In order to track this trend, the GLORIA monitoring program (Global Observation Research Initiative in Alpine Environments) operates permanent observation plots in 130 study areas worldwide. The study presented here focuses on the GLORIA study area Texel Group (South Tyrol, Central Alps). The study area consists of four monitored summits, ranging from the subalpine/alpine ecotone to the nival elevation belts. In each summit, four permanent plots and eight sections of the summit area were monitored since 2003, following the standardized protocol of GLORIA. The soil temperature is also recorded. Recent comparisons of the monitoring data from 2003, 2011 and 2017 showed that the species number on the three lower summits increased significantly, mostly due to new occurrences of thermophilic species, as generally observed in most European mountain ranges. Additionally, loss of cold-hardy species was observed, particularly in the two lowest summits. The next monitoring cycle in summer 2024 will result in a data-series of more than twenty years of vegetation and temperature monitoring. With this data, we test here whether the species richness continues to increase, or the alpine vegetation starts paying its extinction debt in form of significant losses of cold-hardy species.

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Developing a standardized monitoring scheme of the I Annex Bird Directive species breeding in South Tyrol: methods and first results

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Rigorously standardized monitoring schemes are crucial to obtain reliable information on populations, which is essential to properly inform management and conservation practices. Bird species listed in the I Annex of the Bird Directive (2009/147/EC) are a high priority for conservation, and 26 of them regularly breed in South Tyrol. In this region, for many of these species we relied on scarce or incomplete information especially about population sizes and trends. To fill these knowledge gaps, we developed a standardized monitoring scheme, selecting survey methods with the aims of

i) maximizing the amount of collected information in relation to the sampling effort, and ii) allowing to account for detection probability (repeated surveys). The first two field seasons (years 2023 and 2024) already allowed to strongly improve the information available for several I Annex bird species and to identify many sampling areas, laying the groundwork for the long-term monitoring of the target species.

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Factors influencing intraspecific variation in wing morphology in high-elevation specialist birds

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The morphology of bird wings can vary at the intraspecific level according to a variety of factors including sex, age, migration habits and habitat characteristics. The relationship between wing morphology and ecological factors such as, e.g., habitat availability and vegetation structure has been scarcely investigated and is still poorly understood. Also, the influence of elevation on wing morphology is still unclear. Mountain areas represent an ideal study system to investigate such relationships, because abiotic and biotic factors strongly vary across short distances due to the steep elevational gradient. We investigated the intraspecific variation in wing morphology (wing size and shape) in two high-elevation specialist birds, the water pipit *Anthus spinoletta* and the white-winged snowfinch *Montifringilla nivalis*, considering a wide area in the central-eastern Italian Alps and accounting for sexual dimorphism. Wing size and shape indexes were derived from measures of the primary feathers of birds captured and ringed at their breeding sites. For both species, we found significant effects of environmental and topographic/geographic predictors on the considered wing traits. Elevation contributed to shape wing morphology in both species, but showed a clear effect only in the snowfinch. Part of the variability in wing traits remained unexplained, possibly also due to within-population differences in migration strategy among individuals.

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Morphological and DNA metabarcoding approaches to identify reliable metrics for the assessment of trout farming-related effects on biological water quality in Alpine rivers

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Trentino Province is one of the most important producers of salmonids in Italy, with about 60 farms, mainly rearing rainbow trout (*Onchorhynchus mykiss*).
Fish farming can affect the quality of receiving watercourses through nutrients, organic matter, and suspended solids enrichment as well as through the release of drugs and chemicals. The impact of aquaculture practices on watercourses is determined by the farm size, the volume of water diverted and the self-purification capacity of the receiving watercourse. Local impacts can be observed, extended to about a kilometer downstream, but effects can occur at higher space scales (regional scale).

The Filiera ASTRO's Project "Competitività e Sostenibilità dell'Acquacoltura di Montagna" founded by "Piano Nazionale Complementare – PNC" (MASAF – Ministero dell'agricoltura, della sovranità alimentare e delle foreste) aims to improve the sustainability and economic value of mountain aquaculture.
Within this framework, the quality of receiving watercourses of trout farms' effluent will be studied over a sampling period of three years with the following goals: 1. assess specific aquaculture impacts on freshwater biodiversity; 2. evaluate innovative analysis methods for biological communities; 3. identify the best analysis tool to assess the impact of aquaculture; 4. assess efficacy of mitigation measures.
Biological monitoring of macroinvertebrate and periphyton communities (with a focus on diatoms) will be carried out in water courses upstream and downstream of trout farms' effluents via both morphological and molecular (environmental DNA – eDNA) approaches.
Specific aquaculture impacts and efficacy of mitigation measures (e.g., filters, settling basins) will be assessed by applying both established and candidate water quality metrics. The latter will be used to obtain or confirm environmental certification of good practice, thus providing a cost-effective and reliable tool for better management of sustainable aquaculture.

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Unraveling the biology of the invasive apricot aphid (*Myzus mumecola*)

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Italy, 2016: an aphid species is found in apricot orchards that does not belong to any of the pests previously identified on this important fruit crop. As part of many invasive insects, concern arose over its threat towards local ecosystems and economy. Identified as *Myzus mumecola* (Hemiptera: Aphididae), an aphid native to Eastern Asia, it rapidly invaded neighboring countries like France, Germany, Serbia, Hungary, and Czech Republic, causing damages to leaves and shoots of the plant. With Italy being the highest producer of apricots in Europe and South Tyrol providing its well-known "Vinschger" variety, there is a strong need to explore the life and behavior of this unknown pest. Initial morphological and phylogenetic characterizations of the insect were carried out to confirm the correct pest identification. Moreover, we performed laboratory trials to study the life cycle of this pest species. Feeding behavioral tests and a molecular plant DNA analysis through an Oxford Nanopore metabarcoding approach were carried out to determine the summer hosts and potential alternative hosts of the pest. Finally, the endosymbiont community was explored to understand their potential role for the life cycle of this aphid. Here we present our first results about the ecology of this emerging pest species and its potential secondary source of food.

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Airborne pollen biodiversity: changes in 30 years of data at San Michele all'Adige (North Italy)

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The analysis of airborne pollen allows to characterize an important component of bioaerosol; the pollen spectrum reflects the structure of vegetation and changes in plant composition and flowering phenology. This study reports the retrospective analysis (1989-2018) of the pollen data collected in San Michele a. A. at the FEM Research and Innovation Centre.

Airborne pollen was collected using a volumetric Hirst-type aerobiological sampler, and the daily concentration of airborne pollen (P^*m^{-3}) was calculated over a 30-year period. The sampling and analysis of airborne pollen have been performed in accordance with the UNI EN 16868:2019 procedure. The main pollen season (MPS) descriptors were calculated for a total of 24 taxa and analyzed to detect the significative changes.

The results show: (i) a significant increase in annual pollen integral especially for arboreal pollen (AP; +155 %); (ii) a significantly earlier start of the main pollen seasons for 6 out of 24 taxa considered, mostly herbaceous; (iii) the spread of invasive species.

The analysis highlights that the changes (i) and (ii) are related to climate change with increased temperatures and milder winter conditions in the study area (Cristofolini et al. 2024 https://doi.org/10.1007/s10113-024-02223-6).

Through the modifications of the pollen spectrum, it is also possible to describe the arrival of invasive taxa such as *Ambrosia artemisiifolia* and the spread of the invasive species *A. annua* and *A. verlotiorum*, which are causing a considerable increase in pollen concentration in the late pollen season in recent years (Cristofori et al. 2020 https://doi.org/10.1007/s10453-020-09663-7).

The analysis of the pollen component of the bioaerosol on the one hand contains important information for the biodiversity of the air environment and as a proxy for vegetation biodiversity, on the other hand it has important implications for human health considering that airborne pollen is often a cause of allergy.

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AtlasFloraAlpina – towards a first online flora atlas for the entire Alpine arc

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The Alps are among the floristically longest and best-studied mountain ranges in the world. Knowledge of the distribution areas of the individual alpine vascular plant taxa was already relatively extensive at an early stage, but it was only the systematic territorial inventory of the flora according to the standards of the floristic mapping of Central Europe that provided the basis for a detailed and comprehensive representation of these areas. A first approach to depicting the entire Alpine flora in distribution maps was provided by the "Flora Alpina" (Aeschimann et a. 2004), albeit only at the level of administrative units (province, region). Since then, there have been no more such integrative attempts.

Ongoing progress in the collection, storage, management and presentation of floristic data in the Alps would currently make it possible to produce very detailed distribution maps – at least at the level of grid cells ("quadrants" = ca. 6.3 x 5.5 km) – of the entire Alpine region, which can be regularly updated and made more easily accessible through the Internet.

This is where the present project comes in: an online atlas project, run by an international consortium of members from across the Alps, offers the opportunity to enhance and promote floristic knowledge of the Alps. The project will bring together information on the distribution of species from all partner institutions in the consortium, create grid maps that will be published on a dedicated website and update these maps regularly.

The project also strives to promote the inter-regional exchange of knowledge, including on taxonomic issues (especially the problem of different species concepts depending on region and country!) through its own working groups, to ensure data maintenance and control and thus to stand out from globally managed platforms.

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Phylogenetic remarks on hexaploid varicoloured fescues in the Southern Alps

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The knowledge of phylogenetic relations within the varicoloured fescues (*Festuca varia*-group, *Festuca* sect. *Eskia*), which is widespread throughout the European and Western Asian mountain ranges, is rather limited.

In addition to the diploid *Festuca acuminata*, two hexaploid taxa (*F. scabriculmis* subsp. *luedii* and subsp. *handel-mazzettii*) occur in the Southern Alps, whose morphology suggests relationships to each other and to the Western Alpine *F. scabriculmis* subsp. *scabriculmis*.

They were the target of a molecular genetic exploration, which included not only the common nuclear (ITS) and plastid markers (trn L-F) but also other markers already tested on the genus *Festuca* (especially microsatellite loci). This required extensive methodological preparatory work, which ultimately led to a selection of 9 primer pairs already tested on *Festuca* or *Lolium*. 7 of these provided amplicons whose sequences have now been subjected to an initial evaluation.

We now present the first results: Accordingly, subsp. *luedii* and subsp. *handel-mazzettii* are largely homogeneous, even in their relict areas in the Southern marginal Alps. *F. acuminata* is involved in all of them.

The taxonomic concept already presented is consistent with these findings. Further investigations must primarily clarify the relationship to the Western Alpine subsp. *scabriculmis*, and the large gap between the two sub-areas of subsp. *luedii* also requires a conclusive explanation. *F. acuminata* itself has a highly fragmented area, and differences between populations in the sub-areas are expected; for the time being, only accessions from the central Southern Alps could be considered in this study. Whether the far northern outposts of subsp. *luedii* (Maloja Pass) and subsp. *handel-mazzettii* (Penser Joch) show remarkable genetic divergences will also be of special interest.

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Impact of land management and elevation on composition and structure of alpine flower-visiting arthropod communities

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Decline in arthropod biodiversity, as well as flower-visiting arthropods, due to human activities and changing in land use is acknowledged for many ecosystems, including those in the Alps. Here, seminatural habitats, as meadows and pastures, host a high arthropod biodiversity, but little is known about their ecology and how they are impacted by land use types.

This two-year study (2021-2022) aims to investigate how the different type of land use affects the composition, abundance, and diversity of flower-visitor arthropod communities in mountain environments. The study was conducted selecting 14 sampling sites located along the Martello valley (Stelvio National Park, Eastern Italian Alps) diversified both for type of land use (apple orchards, hay-meadows, pastures, high-altitude grasslands) and for altitude (900-2700 m a.s.l.). Four plant families diversified for flower morphology (Asteraceae, Fabaceae, Ranunculaceae, Rosaceae) were selected for sampling flower-visiting arthropods. Multivariate analysis was performed to assess the influence of environmental parameters (elevation, plant family, land use) both on abundance of all flower-visitors and species diversity. Results highlighted that diversity and abundance of wild Apoidea decreases with increasing elevation, being replaced by Syrphidae and other Diptera Brachycera. Arthropods abundance is affected differently by the type of land use: Brachycera, Hymenoptera wasps, and Hemiptera are associated with orchards and hay meadows, while wild Apoidea and Coleoptera are favored within pastures and high-altitude grasslands. Finally, we observed a high abundance of Coleoptera and Thysanoptera as flower visitors in environments located above the treeline, suggesting that pollination may be performed by more, or different, taxa than those commonly studied. These results could give fundamental knowledge for conservation management organizations to maintain and promote a high biodiversity in plant and arthropods communities.

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Remarkable bryophyte discoveries in the area of the "Alter See" natural monument in the Lienz Dolomites (East Tyrol, Austria)

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In the course of field surveys in 2024, 80 bryophyte species, including rare species such as *Crossocalyx hellerianus, Warnstorfia fluitans, and Buxbaumia viridis,* which is listed in Annex II of the Habitats Directive, were recorded in the area of the "Alter See" natural monument. The recent data on *B. viridis* in East Tyrol is sparse (Schröck et al., 2015). *C. hellerianus* is new to East Tyrol (Köckinger 2017). The high-quality habitats in the "Alter See" area, mainly mixed forests with their rich occurrence of deadwood, are also noteworthy.

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Integrating genetic diversity into biodiversity conservation (Keynote)

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Human exploitation of nature poses a major threat to biodiversity, through factors such as land use and climate change, as well as pollution and overexploitation or the spread of invasive species. This loss manifests itself at all three levels of biodiversity, species and ecosystem diversity, as well as at the most fundamental level, genetic diversity within species. It's estimated that more than 6 % of the genetic diversity found in wild populations has been lost since the industrial revolution. This decline has significant consequences, it reduces the ability of species to adapt to changing environments and new diseases, and hence general reduces the adaptive potential. This loss also threatens human well-being by weakening ecosystem stability as well as ecosystems services and generally the nature's contributions to people. In the past, efforts to maintain and conserve genetic diversity were neglected due to technical limitations, with the genomic revolution this has change. The Swiss biodiversity action plan already stated in 2012, that genetic diversity should be monitored, but only with the 2022 Kunming-Montreal Global Biodiversity Framework (GBF), concerted efforts have been made to incorporate within-species genetic diversity into international monitoring projects and conservation initiatives, but still using proxy-based estimator of genetic diversity. To date, there has been little systematic monitoring of genetic diversity at the national level, the scale at which most biodiversity conservation is funded. Therefore, capacity, knowledge and experience need to be built up first. Therefore, we initiated in 2019 a feasibility study followed by a pilot study in 2020 on how genetic diversity can be monitored using a genomic-based approaches, with the aim of assessing genetic diversity indicators, thereby gaining the practical experience necessary for setting up a monitoring programme. For the pilot study we selected five focal animal and plant species based on multiple criteria, including their occurrence in habitats of national importance or in anthropogenically modified landscapes. We developed a tailored sampling strategy to monitor genetic diversity, based on which we sampled >1,200 individuals across all biogeographic regions in Switzerland. For each species, we *de novo* assembled its reference genome and re-sequenced the whole genome of all sampled individuals. Further, a museomics approach was used to travel up to 200 years back in time to retrospectively assess temporal changes in genetic diversity for two species. The data from our pilot study allow detailed conservation-relevant analyses of not only the current and historic spatial distribution of genetic diversity, but also of other genetic indicators such as genetic connectivity, inbreeding (F_{ROH}), adaptive genetic variation, and estimates of effective population size (N_e). With the experience gained, we are creating a framework for monitoring genetic diversity that can serve as an example for other international initiatives.

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Trait space occupancy of ants, butterflies, carabid beetles, grasshoppers, and vascular plants along elevation in Val Mazia – Matschertal

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Understanding how species assemble into communities has been a major focus of ecological research, traditionally analyzed through simple indicators like species richness and Shannon diversity for alpha diversity and more complex indices for beta diversity components such as turnover and nestedness.

Recently, a multidimensional approach, the hypervolume concept, has been revised to allow characterization of communities using distance metrics and kernel density estimates. The concept was applied to understand functional niche space, predict ecological strategy losses, and study ecosystem stability. Comparing hypervolumes can help to reveal spatial variations in species assemblages across different elevations.

In our Long-Term Socio-Ecological Research (LTSER) site, Matschertal/Val di Mazia, we studied an elevational gradient from 1000 to 2500 m a.s.l., collecting data on arthropods and plants. Despite challenges in obtaining trait information for some species, we analyzed four distinct traits for each species group at four elevational steps using the hypervolume concept.

Our study aims to advance understanding of how elevation influences species trait space and to shed light on ecological processes in mountainous landscapes. These findings have significant implications for predicting species responses to climate change and informing conservation strategies in mountain ecosystems.

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Cold-adapted species in the warming Alps: who will survive?

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Ice-related landforms (e.g., glaciers and rock glaciers) are protected in the Natura2000 network (habitat code: 8340), and there is a growing literature suggesting their potential role as warm-stage refugia in the current interglacial period; but, to date, this finding is supported only by studies performed at limited geographic scale.
During the last 20 years of surveys performed along the entire Italian alpine arch, we collected data on vascular plants, ground beetles (Coleoptera: Carabidae) and spiders (Arachnida: Araneae) on ca. 700 sampling points located on different ice-related landforms (glacier forelands, glaciers, and rock glaciers).
The obtained dataset has been analyzed through spatially explicit models (e.g., GAMs) in order to test the relationships between the recorded species (363 vascular plant species, 52 ground beetles, 98 spiders) and the relative landforms.
All the considered taxonomic groups showed a high percentage of species negatively linked to elevation, having none or negative relationship with ice-related landforms (these species will be "winners" in a climate change scenario, because they will probably benefit from warmer temperatures) and of species without a clear response pattern to environmental predictors, "neutral". Overall, 17 of the recorded species resulted associated to ice-related landforms. Plants and spiders experienced the highest percentage of cold-adapted species that are linked to sites at high elevation but do not show the ability to live on ice-related landforms ("losers" in a period of glacier shrinkage). On the other hand, all the taxa also include a low percentage of "losers" found also in ice-related landforms (e.g., debris-covered glaciers, rock glaciers) acting as refugia due to their peculiar thermal profile. Understanding the fate of high-altitude species in relation to the reduction of cryosphere is mandatory for the development, for instance, of a Euregio Glacial Biodiversity Monitoring Program.

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Insect community simplification across land-use and elevational gradients deliver conservation insights from South Tyrol

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In Europe, agricultural intensification and land-use change are causing a widespread decline in insect diversity, which requires an impact assessment of land-use practices. Furthermore, climate change is expected to pose an additional threat in altering the climatic niches, community compositions and trophic interactions. Butterflies and orthopterans are considered important ecological indicators, especially in grasslands, where human intervention is the main cause of both their demise and conservation. In this study, conducted within the framework of the Biodiversity Monitoring South Tyrol, 214 butterfly and orthopteran communities were compared across seven dominant land-use types in the mountainous region of South Tyrol, Italy. These land-use types, which extend from lowlands to alpine grasslands (214-2455 m a.s.l.), include meadows and pastures of varying land-use intensity as well as vineyards, arable land, apple orchards and settlements. For both butterflies and orthopterans, we found that high nature value (HNV) grasslands support high species diversity, with species numbers ranging from double to one-third more than in non-subsidized sites. Furthermore, these grasslands host more specialized and threatened communities than all other land-use types. Community compositions varied across land-use types and were influenced by plant-based indicator values reflecting site management. The climatic environment exerted a significant influence on community composition, yet its overall impact on biodiversity scores (especially for butterflies) was less pronounced than that of land use type and intensity. These findings reinforce the efficacy of regional agri-environmental measures and the European conservation strategy, which aims to preserve HNV grasslands.

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Cryptic evolution and diversification of the agmatoploid-polyploid species complex *Luzula* sect. *Luzula* (Juncaceae) in the Eastern Alps

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The diversification of flowering plants has been accompanied by changes in the number and structure of chromosomes. While the evolutionary consequences of chromosome duplication (polyploidy) are well documented, much less is known about the effects of chromosome fragmentation (agmatoploidy). *Luzula* (Juncaceae) is a genus with common incidence of both phenomena, leading to a variety of cytotypes. The most taxonomically intricate group within the genus is *Luzula* sect. *Luzula*, of which eight species with six karyotypes, including di-, tetra- and hexaploids, have been reported for the Eastern Alps. However, due to weak morphological differentiation among taxa, their distributions and phylogenetic relationships are insufficiently known. By using an integrated approach employing extensive vegetation surveys, relative genome size estimations, chromosome counts, RAD- and plastome sequencing, we aim at disentangling the evolutionary history and ecological niche segregation within this species complex. Combining a variety of different methods allows us to reconstruct phylogenetic relationships among species as well as unravel the roles of chromosome duplication and fragmentation for speciation and ecological divergence in *Luzula*. During the talk we will present preliminary results of ecological and genomic data. Our findings include common co-occurrence of cytotypes at the same locality and a varying degree of ecological and genetic differentiation among species. Phylogenetic analyses provided evidence for at least two independent chromosome fragmentation events and identified tetraploid taxa as allopolyploids formed through hybridization between different diploid species. Together, our results contribute to understanding the complex processes shaping the evolution of polyploid-agmatoploid groups such as the genus *Luzula*.

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Five years of Biodiversity Monitoring South Tyrol – report on the first monitoring cycle

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2019 was the starting point of an ambitious long-term project in South Tyrol: The Biodiversity Monitoring South Tyrol has been set up with the goal of understanding in detail how biodiversity is distributed over the territory and across the different local habitat types, and to map the changes of the biodiversity over the long term. For this aim, 320 terrestrial and 120 running water sites of various habitat types and typologies are investigated in cycles of five years. Next to the monitoring activities, promoting biodiversity research in South Tyrol and raising awareness for this topic are at the core of the long-term project. The expertise and the results are made available to politicians and stakeholders to support activities that promote biodiversity in the region, for a biodiversity-friendly future of the province.

The first monitoring cycle of five years has been concluded and the results are presented in a comprehensive report. While it is still too early to analyze biodiversity trends due to the short period of time, we are able to evaluate the importance of single habitat types for the conservation of the investigated taxonomic groups. The presentation provides an insight into the 5-year report and outlines what further activities have been carried in the initial phase of the monitoring program.

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Species distribution modeling for farmland birds in South Tyrol using remote sensing data

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Farmland biodiversity is rapidly declining due to intensification of management practices. Birds are important ecological indicators and can play a key role in evaluating farmland landscapes. Thus, assessing bird habitats requirements is crucial to better understand their ecological patterns of these ecosystems.

This study models the habitat preferences of six farmland bird species across South Tyrol: *Alauda arvensis, Emberiza citrinella, Lanius collurio, Passer montanus, Saxicola rubetra,* and *Sturnus vulgaris*. Using remotely sensed environmental features, we aim to evaluate the conservation status of these species within the Central Alps.

Our data included breeding bird occurrences from 2017-2023 from the Museum of Nature South Tyrol and Eurac Research. We also acquired spatial information on elevation, climate, land-use, and high-resolution satellite data to derive the timing and frequency of mowing events. We used Ensemble Species Distribution Models to explore the relationship between environmental features and bird occurrences. Models were computed using five algorithms: Generalized Linear Models, Generalized Additive Models, Gradient Boosting Models, Random Forest, and Maxent. Mean, weighted mean, and median probabilities for models with a True Skill Statistic value higher than 0.7 were calculated to obtain final predictions.

We derived presence probability maps and variable importance statistics for the six bird species. Predictions were evaluated by expert ornithologists and captured species-specific patterns. Overall, *Saxicola rubetra* showed a low distribution with mean values only up to 0.78. *Lanius collurio* preferred transition zones including landscape features like hedgerows, while *Alauda arvensis* stuck to open grasslands. Mowing was a significant predictor, improving the quality of models, i.e., high herb is important for nest and chick survival.

Our insights can support biodiversity conservation and identify critical areas for farmland bird species.

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Genomic insights into evolution and refugial dynamics of endemic vascular plants in the Southeastern Limestone Alps

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Mountain ranges like the European Alps are rich in endemic species, with patterns of endemism offering insights into the historical processes shaping mountain biodiversity. This study examines six vascular plant species endemic to the Southeastern Limestone Alps (SELA) — *Achillea oxyloba*, *Androsace hausmannii*, *Physoplexis comosa*, *Phyteuma sieberi*, *Potentilla nitida*, and *Sesleriella sphaerocephala* — to investigate late Pleistocene range and diversification dynamics. To do so, we generated genomic data from hundreds of individuals across their current distribution ranges. Using a combination of exploratory analyses and explicit demographic modeling, we unraveled patterns of spatiotemporal diversification in the SELA and assessed the likelihood of various evolutionary scenarios. Our findings illuminate the evolutionary history of iconic SELA mountain chains, such as the Dolomites, and aim to provide genomic evidence to inform future, evidence based conservation strategies.

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Glacial legacies: Refugial dynamics of the endemic bush cricket *Anonconotus italoaustriacus*

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Temperate mountain ranges such as the European Alps are home to a large number of endemic species. However, the evolutionary processes underlying patterns of endemism in the Alps remain poorly understood, especially for Alpine arthropods. This research focuses on the bush-cricket species *Anonconotus italoaustriacus*, which is endemic to the Southern Limestone Alps (SLA) and the Eastern Central Alps. The study uses genomic data to investigate the species' diversification and refugial dynamics, comparing two non-exclusive evolutionary hypotheses to explain its extant distribution. We find that *A. italoaustriacus* did not recolonize the Alps from the southern margin of the SLA, but from refugia on the eastern or southeastern margin of the Alps. All known populations in the interior of the Alps originate from these eastern refugia, suggesting a dynamic spatiotemporal history including rapid range expansions. The age of interior populations coincides with either the last glacial maximum or the postglacial period (~32-5 ka), which is likely the result of allopatric isolation facilitated by large glacial advances and the subsequent postglacial expansion of forests. A geographically isolated population from the southernmost Dolomites was resolved as phylogenetic sisters to all other lineages, which separated before the last interglacial period (~220 ka). Our results contribute to a deeper understanding of Alpine biogeography and have important implications for the conservation and management of *A. italoaustriacus* that might be applicable to other endemic species in this area.

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Is better living upward or downward? Spatial segregation of water shrews *Neomys fodiens* and *Neomys milleri* in South Tyrol

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Two species of water shrews occur in South Tyrol: Miller's water shrew (*Neomys milleri*) and Eurasian water shrew (*Neomys fodiens*). Their dependence on water sources, wetlands, and rivers makes them susceptible to land use changes or degradation and water pollution. In South Tyrol, both species have been declining in recent decades due to the exploitation of wetland habitats. Based on their distributions and habitat requirements, potential competitive exclusion between the two water shrew species was investigated. Occurrence data have been collected in the database of the Museum of Nature South Tyrol since 1995. Data from 61 sites with *Neomys milleri* (49 individuals) and *N. fodiens* occurrences (27 individuals) were analyzed in relation to topographic and climatic parameters, and habitat characteristics.

While the Eurasian water shrew is exclusively detected in sites above 1,000 m a.s.l., more than 2/3 of the Miller's water shrew records occurred at elevations up to 1,000 m. *N. fodiens* prefers locations with lower temperatures and higher precipitation values, whereas the opposite is true for *N. milleri*. The Eurasian water shrew has been detected on the proximity of large and small watercourses, Miller's water shrew is characterized by greater ecological plasticity and its sites were mostly located at a larger distance from fast running waters. The species was detected in riparian vegetation of streams and standing waters. In intensive agricultural areas, it also inhabits small ditches.

The two species seem to occupy a different ecological niche, competitive phenomena between them as a cause for the existing distribution gaps therefore seem unlikely.

For the conservation of the two threatened shrew species, maintaining freshwater quality and structurally rich riverbanks is crucial for *Neomys fodiens*, while the preservation of small protected wetlands and the connection and maintenance of ditches in valley bottoms is essential for the conservation of *N. milleri*.

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Chironomid microbiome: new insights for cold adapted species from DNA metabarcoding analysis

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Diptera Chironomidae are the most frequent and abundant insect taxon in Alpine headwaters. In the last two decades we accumulated a lot of knowledge on their autecology, specifically on kryal species nowadays at real risk of extinction due to climate change in the Alps. Among the others, several species of *Diamesa* genus, surviving extreme conditions for life, including poor food availability in the eukryal and kryal habitats. Starting from the results of a gut content analysis carried out under the microscope, we investigated the gut microbial structure of *Diamesa* and few other cold-adapted Chironomidae larvae via metabarcoding 16S rRNA. In all, 34 larvae were analyzed, collected in three glacial sites, in Trentino: the two glacial streams Amola and Mandrone and the proglacial pond Agola. Additionally, we analyzed 14 samples collected in abiotic matrices (ice melt water, soil, sediments, etc.). Diversity and differences between habitat and species and among species were analyzed by Shannon and Chao-1 indices, Cluster Analysis, Principal Coordinates Analysis and Heat Tree Analysis. New insights were provided on which bacteria ingested from the environment can be configured as 'food' and which, among those present in the gut, can be considered the stable, resident metabolic ‘chefs’ of the host animal, allowing glacial species to feed on hard-to-digest or nutrient-poor foods available in eu- and kryal habitats. A first list of bacteria with potential physiological functions was produced, including: the Proteobacteria *Massilia, Serratia, Pseudomonas, Providencia, Undibacterium, Janthinobacterium* and *Iodobacter*; the Bacteroidota *Flavobacterium*; the Actinobacteriota *Arthorbacter.*

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Research on CLIMATE and ECOLOGY at the MUSE-Science Museum of Trento

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CLIMATE and ECOLOGY is the scientific area of the muse that is concerned with analysing the effects of climate change on aquatic and terrestrial ecosystems, with a focus on high-altitude alpine ecosystems. Specifically, it studies the physical evolution of alpine glaciers, plant and animal ecology in periglacial and high-altitude areas, the adaptive biology of species indicative of climate change, and in general the evolutionary dynamics (including extinction dynamics) in the past and present, predominantly in mountain environments. Field monitoring and analysis of museum collections are the primary sources of data, with particular reference to target groups such as arthropods and birds. Alpine glaciology, climate and quaternary dynamics; Biodiversity and climate change; Ecosystem Services are the three main research lines, accounting a dozens of national and international projects with a strong multidisciplinary connotation. Recent findings and future research trends will be presented with a focus on global warming, glacier retreating, biodiversity changes and human-nature relationships.

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Monitoring invertebrates included in the Habitats Directive in South Tyrol: First results and future strategies

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The Birds Directive (1979) and the Habitats Directive (1992) regulate species and habitat protection in all EU Member States. Every six years, the Member States, as well as their autonomous regions and provinces, must report on the conservation status of these species and habitats. The fifth Habitats Directive report is planned for 2025 and requires detailed data on distribution ranges, population trends, and conservation measures for species listed in Annexes II, IV and V.

In this context, the “Species Monitoring” project was initiated in 2023, bringing together various regional partners such as the University of Bolzano, Museum of Nature South Tyrol (Bolzano), Eurac Research, and the Nature Office of the Autonomous Province of Bolzano, which is acting as project coordinator. The primary aim of this project is to monitor and update the distributions of species listed in the two directives, thereby preserving South Tyrol’s natural heritage.

This presentation will outline the initial results of the project, focusing on invertebrate species listed in the Habitats Directive. We will describe the steps taken to assess the current state of knowledge and update the distribution data of these species. Additionally, we will discuss the initial steps towards the development of a long-term monitoring strategy for invertebrate species, prioritizing each species according to its conservation needs.

The invertebrate species of interest currently known in the South Tyrol region include the butterflies *Euphydryas aurinia, Phengaris arion*, and *Parnassius apollo*; the moth

Euplagia quadripunctaria; the dragonfly *Leucorrhinia pectoralis*; the beetles *Osmoderma eremita*, *Lucanus cervus* and *Cerambyx cerdo*. But also the mollusks *Helix pomatia*, listed in Annex V, and the four *Vertigo* species included in the Habitats Directive, with *V. geyeri* and *V. genesii* being unique to South Tyrol for Italy, which underlines the importance of the region's responsibility for their conservation.

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Evolution and range formation of the threatened steppe plant *Astragalus exscapus* and its relatives

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The Eurasian steppes are among the largest and most threatened biomes on Earth. During cold periods of the Pleistocene, the zonal Eurasian steppes had a much larger extent as compared to interglacial periods like today. The rare, threatened and disjunctly distributed northwestern African and European members of *Astragalus* sect. Caprini constitute an ideal model for gaining insights into the evolutionary dynamics of steppe biota. We reconstructed the interspecific spatiotemporal diversification of the latter and the intraspecific evolutionary history and past population dynamics of *A. exscapus* based on a combination of RADseq data, single gene markers, genome size measurements and multivariate morphometrics. We outline an evolutionary scenario in which the group originated in the Irano-Turanian region and started to diversify shortly after the Mid-Pleistocene-Transition. While lineages occurring in (sub-)mediterranean mountain ranges diverged early, lineages occurring in northern lowland steppes like *A. exscapus* are much younger. Within *A. exscapus,* populations from the Apennines diverged early while the inner-Alpine dry valleys including the Vinschgau/Val Venosta in South Tyrol were colonized later by small fractions of Pannonian populations. Furthermore*, A. exscapus* has experienced unexpected and complex population dynamics in the past and is much more range-restricted than previously assumed, which has direct implications for the future conservation and protection status of this threatened and declining species.

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A survey of larval parasitoids of *Drosophila suzukii* (Matsumura) (Diptera: Drosophilidae) in semi-natural habitats and ecotones in South Tyrol

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Drosophila suzukii is an invasive pest present in South Tyrol since 2010. It is very polyphagous and infests wild and ornamental species, cultivated stone and soft fruits and susceptible grape varieties. The pest control is challenging especially in mountain environments with the proximity of crops to natural forest environments. In the pest native area, *D. suzukii* populations are attacked by a complex of parasitoid wasps belonging to the Hymenoptera genus *Ichneumon*, in particular by sympatric larval parasitoid species as *Leptopilina japonica* Novkovic & Kimura and *Ganaspis* cf. *brasiliensis* (Ihering) (Hymenoptera, Figitidae). The local natural enemy community in the invaded area mostly consists of generalist pupal parasitoids unable to control the pest efficiently.

In Italy, a propagative biocontrol program started in 2021 with the release of the exotic parasitoid *Ganaspis brasiliensis,* originated from Japan, at selected sites to force the introduction of the most species-specific parasitoid lineage of *Drosophila suzukii* in the invaded areas.
A monitoring of the presence of larval parasitoids was carried out before and after the releases to assess the presence of autochthonous and adventitious species of larval parasitoids. Here we report on the results of the survey carried out in South Tyrol at different altitudes.
The survey showed the presence of different communities of parasitoids species and generally a prevalence of the species *Leptopilina japonica,* probably accidentally introduced. It was found that the released species *Ganaspis brasiliensis* was not present prior to the releases.
Monitoring will be extended over the next five years to assess the increase in the presence of allochthonous species and the level of parasitization levels in ecotones and natural environments. It should give an insight into the potential of classic biological control in terms of effectiveness in promoting a balance between the invasive pest, endemic generalist, and exotic specialist parasitoids.

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A bibliometric analysis to discuss taxonomic bias in studies of Italian fauna

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Italy is renowned as the most biodiverse country in Europe, with hotspots of species richness and endemism spanning from mountainous regions to islands. The “Checklist of Italian Fauna” published by Minelli et al. in 1995 laid a crucial foundation to list the diversity of the kingdom Animalia. However, the trajectory of biodiversity research in Italy over the past three decades remains unclear. For instance, insect taxa may be underrepresented in conservation biology research, overshadowed by more charismatic vertebrate species, bias that is then transposed to practical conservation actions and on the perception of the wider public of extinctions within this diverse animal taxon.
Here we present a preliminary study to create a comprehensive and unbiased summary of Italian biodiversity research since 1995. Using the ROSES (RepOrting standards for Systematic Evidence Syntheses) protocol to search several databases of primary literature online including Web of Science and Scopus, grey literature and doctoral theses, we have conducted a bibliographic analysis of studies on Italian fauna. Our research aims to identify potential taxonomic and geographical biases in the literature and across administrative regions of Italy, highlighting how invertebrate taxa have been treated in comparison to vertebrate taxa in major fields of ecological research. The results will offer valuable insights to support balanced conservation planning, guide future research directions and share major findings with policymakers and the wider public, ensuring a mindful allocation of resources to preserve Italy’s rich biodiversity.

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DNA barcoding of minor fish fauna in South Tyrol

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The fish fauna of South Tyrol nowadays numbers at least 35 species mostly defined on morphological basis. The majority of originally occurring fish were presumably native to the northern Adriatic catchment, as the alpine divide is considered an absolute migratory barrier for fish. However, in the past fish from north of the Alps have been repeatedly introduced in South Tyrol. In recent years, several genetic studies have been conducted on fish species of angling interest, such as marble trout, barbel, grayling, and pike. On the other hand, among the so called "minor fish fauna" only a few native species of conservation relevance have been analyzed.
The aim of the project is to clarify, through genetic analysis, which species of the minor fish fauna are occurring in South Tyrol. In fact, proper taxonomic identification is essential to distinguish native from allochthonous species and to recognize any threatened populations deserving protection. In the case of allochthonous species it is important to know and understand the history of their introduction and spread. All this information is essential for the appropriate protection and management of fish fauna. A total of about 500 genetic samples representative of different populations from 10 fish genera: *Alburnus, Carassius, Cobitis, Gambusia, Gasterosteus, Padogobius, Rutilus, Sabanejewia, Scardinius*, and *Squalius* were planned to be analyzed with the molecular marker COI. Fish sampled by electrofishing were weighed, measured, photographed, and before their release into the wild, a fragment of anal fin was taken for genetic analysis. The project is funded by the Research Fund of the Betrieb Landesmuseen.

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The freshwater jellyfish *Craspedacusta sowerbii* species complex (Cnidaria, Olindiidae) in Italy: distribution and genetic lineages

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Olindiid freshwater jellyfishes of the genus *Craspedacusta* Lankester, 1880 are native to eastern Asia; however, some species of the genus have been introduced worldwide and are nowadays present in all continents except Antarctica. Due to the morphological plasticity of the medusa stages, there is no consensus regarding the taxonomy within the genus *Craspedacusta*. The species *C. sowerbii* Lankester, 1880 was first recorded in Italy in 1946, and until 2017, sightings of the jellyfish *Craspedacusta* were reported for 40 water bodies. This study provides new insights into the occurrence of *Craspedacusta* across the Italian peninsula, Sardinia, and Sicily. Here, we report 21 new observations of this non-native taxon, of which eighteen refer to medusae sightings, two to environmental DNA sequencing, and one to the finding of polyps. Additionally, we investigate the molecular diversity of collected *Craspedacusta* specimens, using a Bayesian analysis of sequences of the mitochondrial gene encoding for Cytochrome c Oxidase Subunit I (mtDNA COI). Our molecular analysis shows the presence of two distinctive genetic lineages: (i) a group that comprises sequences obtained from populations ranging from central to northern Italy (clade "C1"); (ii) a group that comprises three populations from northern Italy – i.e., those from the Lake Levico, the Lake Santo of Monte Terlago, and the Lake Endine – and the single known Sicilian population (clade "C2"). Phylogenetic analysis showed that both clades were found in nearby Trentino-South Tyrol sites. Clade "C1" was detected in Lake Garda and Large Lake Monticolo, which are located 37 and 45 km away from Lake Levico, respectively, and in which instead clade "C2" was found. Furthermore, clade "C2" was also found in Lake Santo of Monte Terlago, which is located about 34 km away from Lake Garda. Outside their native home range, *Craspedacusta* population are mostly unisexual. However, here we report additional findings of the second currently known case in Italy of a population including both sexes in Lake Santo of Monte Terlago.

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The MonitAnt project: towards a European standardized protocol for red wood ants monitoring

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Formica rufa species-group (red wood ants – RWA) are Holarctic ants, dominant in coniferous and grassland environments, where they act as umbrella and keystone species, providing ecosystem functions of undeniable importance. Since local declines have been reported across Europe, recent concerns for RWA conservation have arisen with the need of an international standardized monitoring protocol.

Because population trends and conservation status of RWA across Europe is not assessed, the MonitAnt project (Biodiversa+ BiodivMon call) aims to both define and test a monitoring protocol for RWA on local and continental scale. With the validation of this protocol, basic ecological research questions are to be addressed to better understand the ecology of this interesting ant group from many different perspectives.

South Tyrol (northern Italy) has half of its surface covered by forests, mainly dominated by coniferous species, as well as a heterogeneous climate and a pronounced orography. These wide range of environments suitable for RWA species are hosting seven out of the thirteen European species. This high diversity of cooccurring RWA species, provides an opportunity to investigate interactions and cooccurrence as well as niches modelling and biotic interactions studies.

With the aim of providing new insights for monitoring and conservation purposes, this PhD thesis will provide information concerning the distribution of *Formica* ants in South Tyrol, also investigating the ecological preferences, phenotype plasticity and the realized niches covered by each species.

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A long-term perspective on hypolimnetic dissolved oxygen and surface CO_2? Case study mountain Lake Tovel

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Climate warming impacts biogeochemical cycles in lakes. A decrease in hypolimnetic dissolved oxygen (DO) is a commonly seen effect of climate warming. Furthermore, lakes are emitters of CO_2. Capitalizing on long-term monthly data (1995–2022) of oligotrophic Lake Tovel, (Italy), a deep mountain lake, we analyzed temporal patterns and driving factors of hypolimnetic DO and surface CO_2 and surface CO_2 fluxes. In oligotrophic Lake Tovel, annual mean DO (% saturation) has increased from near anoxia to > 20 % in the bottom layer (35–39 m) from 2010 onwards. We suggest that Lake Tovel's shift from meromixis to dimixis was driven by climate warming (i.e., increasing air temperature 0.6°C/decade) that delayed ice-in and increased autumn mixing. How did this ecosystem shift impact the lake's CO_2 emissions? Since sensors for CO_2 are not deployed at Lake Tovel, we applied geochemical relationships and the thin boundary layer approach to calculate surface CO_2 concentrations and flux. The air-water CO_2 flux ($\mu mol\ CO_2\ m^{-2}\ d^{-1}$) showed a period of lowest (mean 1995–2010: 6.4 ± 0.7), highest (mean 2011–2017: 35.7 ± 2.1), and intermediate emissions (mean 2018–2022: 19.3 ± 4.7) and these patterns were mirrored by surface CO_2 concentrations. The recent decline in surface CO_2 concentrations from the year 2018 onwards was attributed to increased stratification that offset lake autumn mixing and thus led to the observed decline. The overlap between temporal trend patterns of hypolimnetic DO and surface CO_2 and regression results indicated that surface CO_2 concentrations of Lake Tovel were positively influenced by internal (lake autumn mixing) and external (loading of allochthonous carbon) factors. These results help us to better understand biogeochemical cycles in mountain lakes in a changing climate.

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Evaluating the impact of grassland management on wild bee communities along an elevational gradient

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Wild bees are classified as central place foragers, relying on several habitat characteristics in close proximity to their nesting sites. Consequently, they exhibit strong responses to land-use and climate change. Particularly, increasing land-use intensity in grasslands has been documented to negatively affect wild bee communities. However, most research was conducted in lowlands, neglecting mountain regions. These regions are characterized by challenging abiotic conditions, potentially interacting with land-use intensity when shaping wild bee communities. Investigating potential additive or interactive effects is essential for the development of targeted conservation strategies. In this study, we surveyed 30 grasslands sites characterized by increasing land-use intensity and distributed along an elevational gradient ranging from 750 to 2100 m a.s.l. To prevent the isolation effects of grassland patches, a minimum of 20 % grassland cover within a 500 m radius around each survey site was ensured. Surveys were conducted over two consecutive years using time and area standardized transect walks and yellow, white and blue pan traps. In the first study year a total of 1221 individuals of approximately 130 species were assessed. Preliminary analysis considered flower richness as a proxy for land-use intensity. Results indicated that both wild bee

species richness and abundance decreased with decreasing flower richness and increasing elevation. When addressing additive effects of flower richness and elevation, both factors significantly affected wild bee species richness. This suggests that increased flower richness positively affects wild bee species richness along the entire elevational gradient, even at higher elevations where abiotic conditions act as a limiting factor. Further analysis will incorporate functional traits to better predict wild bee responses to land-use intensity and elevation.

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Extensive management practices and natural structural elements enhance bat conservation in mountain agricultural landscapes

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Changes in agricultural practices have been recognized as a significant driver of biodiversity loss worldwide. Bats are facing a global decline primarily due to habitat loss and agricultural intensification. In Italy, the International Union for the Conservation of Nature reports that 33 % of bat species are threatened by agriculture expansion. This study investigates the impact of natural structural elements and agricultural intensity variables on bat diversity.

We selected 47 sites in open agricultural areas, considering pastures, hay meadows, dry grasslands, and annual crops. The total area of natural structural elements (e.g., hedgerows, trees), a management intensity index, the presence of manure hills, a grazing pressure index, and the number of cutting events in hay meadows were selected as the most important variables to explain agricultural intensification in mountain environments (South Tyrol, Northern Italy). We used generalized linear mixed models to analyze the acoustic activity of bats divided into guilds in relation to agriculture-related variables and landscape features such as distance to water sources, buildings, roads, and forest types. Overall, the results revealed that natural structural elements and water sources positively influenced the presence of short-range echolocators and low foragers, playing a key role for bats in agricultural areas. Grazing and mowing practices showed mixed impacts on bat diversity, while the presence of manure hills displayed a negative correlation with most bat species. This study underscores the need for nuanced approaches to agricultural management that consider the complex effects on bat species diversity. It highlights the importance of maintaining natural structural elements and implementing extensive grazing and mowing practices. The findings contribute to a holistic understanding of how agricultural practices and natural structural elements can support or compromise bats in agricultural landscapes.

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The new MUSE biotope: ecological survey for the study of aquatic biodiversity

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The MUSE biotope is an ecosystem that mimics the wetland areas of the Trentino lowlands, located in an urban context. In 2023, we conducted a monitoring campaign, consisting of four seasonal samplings (February, April, July, and October). The analysis included the study of zoobenthos, phytoplankton, zooplankton, benthic diatoms, and other algae. Additionally, we quantified primary production (assessed via chlorophyll a), dissolved organic carbon, suspended solids, seston, biomass, CPOM, FPOM, and chemical compositions (heavy metals, nutrients, main anions and cations). We investigated which taxa colonize this type of habitat, with a focus on the presence of species of conservation significance. The key parameters for defining the trophic level, such as nitrogen and phosphorus, showed generally low concentrations, with an increase in nitrogen during the summer and autumn months. Chlorophyll a values indicated high primary production, especially in summer and autumn, with the highest levels of photosynthetic pigments recorded in July. The high electrical conductivity indicated a significant concentration of dissolved salts. Dissolved oxygen indicated a highly productive environment, with seasonal variations typical of eutrophic lakes. Chemical analyses detected heavy metal values within legal limits, without significant criticalities. The observation of benthic and planktonic fauna and flora allowed the compilation of taxa lists useful for study, naturalistic conservation, and educational activities related to Citizen Science. In conclusion, the monitored lacustrine ecosystem presents chemical and biological characteristics indicative of a eutrophic environment, with an increase in nutrients during the warmer months; it nevertheless remains a suitable habitat for hosting high biodiversity, similar to that typical of valley floor wetlands.

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Drivers and patterns of arthropod colonization of recently deglaciated terrains in the Dolomites (North-eastern Italian Alps)

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Glacier disappearing is affecting the distribution of cold-adapted ground-dwelling arthropod species along the glacier forelands of the Alps, but no studies compared the glaciers of the Dolomites (Italian Alps). Thus, we compared the datasets obtained investigating the communities of ground beetles (Coleoptera: Carabidae) and spiders (Arachnida: Araneae) of three glacier forelands belonging to vanishing glaciers located in the Dolomites: Fradusta (1.94 ha; Pale di San Martino Dolomites), Agola (17 ha; Brenta Dolomites) and Sorapiss (19 ha; Ampezzo Dolomites). The species and functional composition of the carabid and spider communities of the glacier forelands were investigated by correlating species distribution with the following predictors: Age of Deglaciation, Soil Temperature (SoilT), Normalized Difference Vegetation Index (NDVI) and Topographic Position Index (TPI). The carabid and spider communities show different colonization patterns in relation to the glacier foreland along which they were sampled: species common to the three proglacial forelands were sampled at different stages of the ecological succession. Along Agola and Sorapiss forelands the sites deglaciated by less of 65 years are characterized by high species turnover with cold-adapted species quickly substituted with more temperature tolerant species, while those of the Fradusta foreland are characterized by a greater persistence of cold-adapted species from the glacier front to sites deglaciated since more of 100 years. The analysis of functional traits showed that the variables Age of Deglaciation, NDVI and SoilT are positively correlated with the functional richness of the carabid and spider communities. The comparison showed that Fradusta glacier foreland is acting more efficiently as refuge area for cold-adapted species respect to Agola and Sorapiss glacier forelands despite the very small size of the glacier.

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Impact of land-use intensity on spider communities: A study on the taxonomic resolution effect

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Soil is the basis of life for plants, animals and humans, yet soil and its inhabitants are generally undervalued: pollution, soil sealing, deforestation and land use intensification continue to increase, with negative impacts on soil biodiversity. It is a very diverse habitat, much more than a substrate for growing plants, but a place where many processes take place that control a wide range of ecosystem services and functions.

Spiders are considered important for soil biodiversity. They are a well-studied group and have traits that make them valuable bioindicators, in addition to being highly diverse and playing key roles in ecosystem functions; spiders' rapid reproductive cycles and high mobility make them useful for detecting early changes.

We present a study on spider communities of 73 agricultural sites sampled between 2019 and 2021 as part of the Biodiversity Monitoring South Tyrol (BMS), including apple orchards, arable fields, vineyards, semi-intensively used meadows, extensively used meadows, and pastures. We installed two pitfall traps on each site twice a year (spring and autumn) for a total of two weeks. Ground-dwelling arthropods were sorted and identified to family level where possible, and adult spiders to species level. Our aim was to assess the effect of land use type and intensity on soil biodiversity, represented by spiders, and test at which taxonomic level (family, genus, species) the effect of land use intensification can be well detected.

We found significant differences in community composition between land use types at all three taxonomic levels, but the best discrimination was at the species level. Diversity measures showed that vineyards and extensively managed grasslands had the highest spider richness and diversity, while intensive management sites (intensively used hay meadows, apple orchards and arable fields) resulted in low richness and diversity.

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Functional diversity of alpine dragonfly communities: The interplay between thermal adaptations and habitat requirements

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Organisms inhabiting alpine environments need to withstand low and often fluctuating temperatures. As active predators, dragonflies rely on flight to capture prey, reproduce and disperse. To maintain optimal body temperature, which is necessary for sustained flight, they need to thermoregulate effectively. Additionally, their reproduction

is tied to a specific water body. Thus, they also need to adapt to the local conditions of their reproductive site. Climate change, coupled with increasing demands from tourism, agriculture, and energy production, is straining hydric resources. This has led to the construction of artificial water bodies across all altitudes, which represent novel habitats for dragonflies. However, adapting to artificial habitats may conflict with adaptations to low temperatures. We investigate the functional diversity of dragon- and damselfly communities in artificial and natural habitats along an altitudinal gradient from 230 to 2450 m in South Tyrol, Italy. Specifically, we investigated traits linked to thermoregulation (body size and color), to larval development (developmental time) and to habitat preference (species temperature optimum and habitat breadth). We found that temperature significantly affected body size and color for dragonflies but not for damselflies. Dragonfly communities occurring on natural sites tracked varying temperatures in their habitat preferences while those on artificial sites were not affected. Damselflies exhibited similar responses in habitat preference traits across both habitat types.
The reported responses of dragonflies align with established ecological theories like Bergman's rule and the thermal melanism hypothesis and these apply to both natural and artificial habitats, even though the latter was comprised primarily of warm adapted generalists. Damselflies followed no clear pattern in thermoregulation traits, possibly they remain limited in their adult body size by shorter larval development time.

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Population genomics and invasion history of a Nearctic leafhopper in Europe *Scaphoideus titanus*

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The American grapevine leafhopper, *Scaphoideus titanus* (Hemiptera: Cicadellidae), is the primary vector of Flavescence dorée phytoplasma, the causal agent of the only epidemic grapevine yellows in Europe and therefore classified as a quarantine pest in the EU. Flavescence dorée causes significant economic losses to grape growers. *S. titanus* is native to the United States and North America and was introduced before the 1950s in France. Subsequently, *S. titanus* invaded 15 European countries from Portugal to Romania, from Czech Republic to Italy. Considering its limited dispersal capabilities, its widespread dissemination across Europe was explained by long distance propagation of *S. titanus* eggs on wood canes produced in grapevine nurseries. Bayesian inferences applied to the comparison of *S. titanus* homogenous population genetic structures in Europe suggested that this species arrived in Europe through a single introduction. Population genetic studies were performed using markers of limited resolution preventing from tracing the invasion dynamics of *S. titanus* in Europe. Therefore, the genome of *S. titanus* is currently being sequenced within the BGE project. The goal of our study is to investigate the population genomic structure of *S. titanus* in Europe, 70 years after the first record of the species. To this end, we sequenced several populations from both western and eastern European countries and investigated the gene flow among these populations. With this information we will investigate the main invasion pathways of *S. titanus* across Europe and thus helping to develop strategies to monitor and limit the spread of *S. titanus* in European vineyards.

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The nematode community of the spruce bark beetle in South Tyrol

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The spruce bark beetle *Ips typographus* (L.) is a major forest pest in Europe leading to significant economic losses and ecological disturbances each year. Rising temperatures and prolonged dry periods put its host, the Norway Spruce *Picea abies*, under stress allowing the beetles to attack healthy trees and proliferate rapidly. The storm Vaia in 2018 and heavy snowfalls and droughts in the following years led to a massive and on-going bark beetle outbreak in South Tyrol. Natural antagonists that co-occur with the beetle might be a new way to control the beetle population. A variety of organisms are associated with the spruce bark beetle, but some of them, like nematodes, are understudied. In our current project, we study the nematode community of *I. typographus* by performing metabarcoding of whole beetles and single tissues. The beetles are collected at different locations and altitudes across South Tyrol. Thus, we can determine which nematode species are living on and within the beetle and identify potential antagonists and symbionts. In addition, we analyze the influence of altitude and location on the composition of the nematode community. Moreover, we compare our results with studies from other places in Europe to see how similar or variable the nematode community of *I. typographus* is on a larger spatial scale. A deeper understanding of the associated nematodes of *I. typographus* will show if there is a species suitable for spruce bark beetle control.

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Orthopterological highlights from the Biodiversity Monitoring South Tyrol

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The long-term project Biodiversity Monitoring South Tyrol started in 2019, led by Eurac Research, in collaboration with the Museum of Nature South Tyrol and the Autonomous Province of Bolzano/Bozen. It aims at gaining insights into the actual state of biodiversity and to observe the future response to environmental and land use changes.

One of the studied groups are grasshoppers (i.e., Orthoptera) and mantids, which are looked for at all monitoring sites. As part of the project, 320 locations at an altitude between 220 and 3060 meters are studied repeatedly. It is conducted on a quinquennial basis with 64 sites surveyed each year. For grasshoppers and mantids one survey per site is carried out at the end of the summer. Each survey uses a combination of walking transects (14°m) and a comprehensive search within a 100°m^2 area. The survey area is extended in forests to a 1000°m^2 plot and in settlements and lakes to a 50°m walking transect. In addition, data from other survey methods is used to validate and complete the community data (e.g., data collected with pitfall traps).

At the end of the first cycle, which ended in 2023, some fascinating records have been made. Two new sites of occurrence for the endemic bush cricket species *Anonconotus italoastriacus* were located. *Pezotettix giornae, Euchorthippus declivus, Bicolorana bicolor* were recorded for the first time in the province of Bolzano/Bozen. Additional interesting findings and confirmations were made for the rare and endangered species *Conocephalus dorsalis, Leptophyes punctatissima, Pseudochorthippus montanus, Omocestus petraeus, Stenobothrus nigromaculatus,* and *Aeropedellus variegatus*.

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On the composition of the apple's Sooty Blotchs pathobiome

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Fungal agents of the Sooty Blotch (SB) complex live on the outer waxy layer of apple peels. Although the representatives of the SB complex are generally not classic pathogens on apples, subsequent to their mycelial growth, symptoms appear as blemishes and smudges on the surface of apples, hindering the commercialization of fresh fruits. Currently, forecasting models are inadequate to reliably predict the development of SB symptoms due to SB's heterogeneous composition in different growing areas. Furthermore, it is unknown whether infections can be affected by biotic factors, such as interactions with the microbial species of the apple's microbiome. This study aims to reveal whether SB fungi change the composition of the apple microbiome, if certain compositions of the apple microbiome favor or hinder SB growth and if so, which bacteria or fungi within the microbiome actively antagonize SB growth. To answer these questions, two experiments are envisaged. The first experiment, metabarcoding of the apple pathobiome, by applying next generation sequencing technologies (Oxford Nanopore technology and Illumina sequencing) with organism barcoding shall extract, identify and compare the fungal and bacterial species present in the microbiomes of healthy and infected apples. The second experiment focuses on the inhibition of putative antagonistic microbe species identified from the microbiome of healthy apples with SB fungi by co-culturing. Thus, identification of the SB complex composition is essential for a better understanding of symptom expression and might contribute to the development of targeted and environmentally friendly management strategies.

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Monitoring of the Alpine Salamander, *Salamandra atra*, in Trentino: a double observer approach

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Wild population monitoring plays a pivotal role in evaluating the conservation status of a species. However, information on *Salamandra atra* is limited due to its unique morphological and ecological characteristics. The salamander's black coloration prevents the application of the Capture-Mark-Recapture approach, one of the most robust and reliable methods for estimating abundance, without invasive marking techniques and substantial sampling effort. Furthermore, this species often inhabits remote high-altitude areas and is primarily active during the night and after rain. To address these challenges, in 2019, MUSE and the Paneveggio-Pale di San Martino National Park initiated a research program with the following objectives: i) identifying potential monitoring sites, ii) estimating population abundance and density using a less-effort and non-stressful technique, iii) verifying the new method reliability, iv) assessing the fine-scale ecological requirements of the alpine salamander. To evaluate the suitability of potential monitoring sites, we employed a scoring system based on environmental suitability, cost-effectiveness, and security. To understand ecological requirements, we assessed the relative importance of various environmental and topographical variables. For population abundance estimation, we employed a dependent double-observer approach based on multinomial N-mixture models. This method, applied under appropriate weather conditions, proved to be a cost-effective technique providing reliable demographic estimates while minimizing potential stress on animals. Key fine-scale ecological factors positively correlated with salamander abundance included terrain ruggedness and canopy cover, both related to shelter availability and soil moisture retention. Implementing this monitoring protocol will significantly enhance our understanding of Alpine salamander distribution and abundance, thereby improving our evaluation of alpine salamander conservation status.

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The landscape of fear in cow farms: breeding barn swallows reduce housefly activity in cattle sheds

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The global decline of insects is strongly affecting the population trends of aerial insectivorous birds. Cattle farms represent crucial breeding sites for the barn swallow *Hirundo rustica*, providing high availability of insect prey and potential nesting sites. To assess whether swallow occurrence and number of breeding pairs inside cattle sheds affect the activity rates of a common pest fly, *Musca domestica*, we investigated 9 dairy cow farms in Non valley (Trentino, NE Italy), occupied or not by breeding swallows. From April to August 2022, we collected weekly data on the activity rate of flies by counting fecal and regurgitation spots deposited on 8 white index cards inside each cattle shed. Simultaneously we recorded the number of active swallow nests. Using generalized linear mixed models, we modelled the factors affecting the activity rate of flies on a weekly basis, with spot card and farm as nested random effects, to account for card and farm potential effects. Through model selection, we assessed the effect of the number of cows and temperature in interaction with either swallow occurrence or number of active nests. We found that the activity rate of flies strongly increased with temperature, but swallow occurrence consistently reduced such an increase. Moreover, at higher numbers of swallow nests, the positive relationship between fly activity and temperature was much weaker. We demonstrated the role of barn swallows as providers of ecosystem services, by acting as effective biological control agents on flying insects in livestock farms.

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Crowded mountains: large-scale and long-term responses of mammals to human outdoor activity in mountainous areas

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Many European large mammals have increased their distribution and abundance following land abandonment with consequent decrease in agricultural activities and re-expansion of forests. At the same time, natural and protected areas (PAs) are increasingly being visited for outdoor recreation, raising new challenges for the harmonization of wildlife conservation and recreational ecosystem services. In 2020 we systematically sampled with camera-traps 4 mountainous protected areas and surrounding zones and assessed the responses of 16 species of mammals to outdoor activity during diurnal, crepuscular and nocturnal hours. We evaluated responses both at community and species levels using Generalized Additive Mixed Models. In one of these areas (Adamello-Brenta natural park in Trentino, north-east Italy) that we monitored systematically since 2015, we could estimate long-term trends in occupancy and trap rate, as well as the behavioral responses of mammals to intense and growing human frequentation.

We found that responses of mammals to human activity were mediated by body mass, with smaller species being generally more nocturnal and showing an increase in site use at more disturbed sites. Larger species tended to be more diurnal where exposed to low levels of human activity and they markedly decreased diurnal and crepuscular site use where outdoor recreation was more intense. In the study area monitored since 2015, we found that even though outdoor recreation increased, mammals' occupancy was stable or even on the rise. Our results give grounds for optimism for the conservation of mammals in areas with intense human frequentation, but at the same time highlight marked behavioral changes in response to human activities even within PAs. Increased nocturnality in the whole community and spatio-temporal avoidance of humans by large species can imply physiological costs that might affect population trends on a longer time frame and altered inter-specific interaction.

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Large-scale passive acoustic monitoring of birds in an Alpine ecosystem

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There is a growing need for cost-effective, scalable ecological monitoring techniques in the face of global biodiversity loss. Thus, passive acoustic monitoring and automated identification are increasingly used in ecological research to assess bird diversity, yet achieving meaningful results remains challenging. However, the large-scale implementation of acoustic devices still needs to be improved.

In 2024, we implemented a passive acoustic bird monitoring within the Biodiversity Monitoring South Tyrol, a long-term project analyzing bird communities within a mountainous region characterized by heterogeneous ecological patterns. We deployed AudioMoth v.1.2.0 devices at 68 sites, categorized by main habitat within the region, to record bird communities throughout the whole breeding season. To process the collected data, we used the bird song recognition software BirdNet Analyzer 2.4 and for batch processing Raven Pro 1.6.5. We focused on bird species richness and analyzed the soundscape using different eco-acoustic indices.

A richer bird community and a more diverse soundscape, strongly correlated with heterogeneous landscapes. BirdNet accurately identified most bird species, though ornithological specialists' verification remains necessary. Identifications with low confidence scores, provided by BirdNet to indicate the probability of correct detection, are particularly error prone. Establishing species-specific confidence thresholds can significantly enhance automated identification accuracy. To further improve and generalize this approach, extensive projects in different regions are necessary.

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Advancing biomonitoring through automated image and sound recognition: two European pilot studies

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Biodiversity is declining globally, yet evidence remains biassed to most studied regions and easy to monitor species groups. To expand and increase the resolution of biodiversity monitoring automated monitoring schemes are crucial.

As proof, two pilot studies involving several EU countries have been developed within the European Biodiversity Partnership Biodiversa+: The Automated Biodiversity Monitoring Stations (ABMS) and the Invasive Alien Species (IAS) pilot. These projects aim to establish a harmonized scalable monitoring scheme at EU level using sound and image identification. ABMS focuses on birds, bats, and nocturnal insects while IAS on invasive moth and plant species.

The center piece for image identification is the UKCEH's automated insect monitoring trap (AMI trap). This camera trap uses UV and white light to lure nocturnal insects onto a screen. Each time an insect moves in front of the camera, an image is captured, cropped, and analyzed with models developed by Aarhus University. The device is promising and versatile, although image quality and algorithms could be improved.

TheAiLab's CamAlien is a high-speed camera system that is mounted on a car and captures high-quality images of roadside vegetation while driving. Using an algorithm based on PlantNet and focusing on invasive species, plants from the images are identified to species level. Each image's location coordinates are saved so that distribution maps can be created. The system works smoothly and requires little effort from the operators.

For automatic sound detection, Wildlife Acoustics Song Meter Mini 2 and Mini Bat 2 recording devices are used to record bird and bat sounds. The bird song recognition software BirdNet Analyzer 2.4 is used to identify the species, while bats are identified by experts. The devices can remain in the field for weeks, drastically increasing species detection. Together, these three techniques can facilitate and greatly expand biodiversity monitoring.

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A DNA barcode library of Austrian Geometridae (Lepidoptera) reveals high potential for DNA-based species identification

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Situated in the Eastern section of the European Alps, Austria encompasses a great diversity of different habitat types, ranging from alpine to lowland Pannonian ecosystems, and a correspondingly high level of species diversity, some of which has been addressed in various DNA barcoding projects. Here, we report a DNA barcode library of all the 476 species of Geometridae (Lepidoptera) that have been recorded in Austria. As far as possible, species were sampled from different Austrian regions in order to capture intraspecific genetic variation. In total, 2500 DNA barcode sequences, representing 438 species, were generated in this study. For complete coverage of Austrian geometrid species in the subsequent analyses, the dataset was supplemented with DNA barcodes from specimens of non-Austrian origin. A total of 464 out of 476 species (97 %) that can be identified by their COI sequence. Species delimitation by the BIN method yielded 510 molecular operational taxonomic units. Congruency of BIN and with morphospecies assignments was reasonably high (85 % of morphospecies in unique partitions). The study furthermore identified taxonomically relevant cases of morphospecies splitting and sharing in the molecular partitions. We conclude that DNA barcoding and sequence analysis revealed a high potential for accurate DNA-based identification of the Austrian Geometridae species.

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Carbon Inventory South Tyrol – quantification of soil organic carbon (SOC) stocks and assessment of their stability for agricultural areas of South Tyrol, Italy

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The European Union (EU) is aiming to achieve climate neutrality by 2050, which is legally binding for all member states, in line with the Paris Agreement and the European Green Deal. The Land Use, Land-Use Change and Forestry (LULUCF) sector, which includes agriculture, has agreed to an even more ambitious target of climate neutrality by 2035. The project 'Carbon Inventory South Tyrol' (CIS) aims to contribute to the EU targe of achieving climate neutrality in the agricultural sector. The main objective is to fill knowledge gaps in quantifying the carbon budget of the Italian province of South Tyrol, which can be essentially divided into carbon bound in biomass and carbon present in the soil (SOC). While carbon in biomass is relatively easy to estimate or plays only a minor role for some land uses, such as grasslands, the quantification and assessment of SOC stocks is more complex, especially in mountainous areas with differences even at small scales.

Our study uses a machine learning approach to predict the spatial distribution of SOC stocks in agricultural areas, based on empirical data combined with spatial covariances (land use, topography, geology, climate, etc.) to consider the complexity of the landscape. In addition, to determine the stability of these carbon stocks (sink/source), data from CO_2-flux measurements (based on the Eddy Covariance method) are used. Thanks to several studies in South Tyrol, SOC contents and CO_2-exchange between soil and atmosphere are already measured at selected sites. CIS will build on these empirical data, by combining them into a homogenized database and by filling the most important data gaps through a field survey in summer/autumn 2024. Currently, more than 17,500 data points have been provided and we are in the process of preparing the field survey. The first preliminary results are expected by the end of 2024.

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A few more tiny steps towards a better understanding of the flora of the Euregio region

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Fostered by the widespread use of molecular tools and their combination with traditional methodology ("integrative taxonomy"), recent years have seen a big leap forward in the knowledge of the taxonomy of the Alpine flora. In my talk, I will present a few – published and unpublished – studies, which have contributed towards a better understanding of the evolution and taxonomy of the rich flora of Euregio region. Further, I aim to draw the attention to remaining "taxonomic nightmares", which are still waiting for a satisfactory solution.

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Rivers run through it – exploring aquatic macrobenthos diversity in the Vinschgau/Venosta valley

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Aquatic biodiversity is declining rapidly on a global scale, yet the precise factors influencing high or low biodiversity in lotic ecosystems remain poorly understood. Given the anticipated impacts of climate change on glacier mass and water availability, it is crucial to establish a baseline understanding of current riverine biodiversity. This study aims to investigate the determinants of riverine macroinvertebrate presence, abundance, and community composition in Vinschgau/Venosta.

Vinschgau/Venosta is an inner alpine dry valley characterized by low precipitation and significant reliance on glacier melt. There, we surveyed 24 sites, ranging in altitude from 800 to 2600 meters above sea level between 2021 and 2023. At each site, we measured various abiotic parameters, including water chemistry and nutrient levels, as well as physical stability indices of the channels. Additionally, we assessed the impact of land-use cover on biodiversity. The collected macroinvertebrate fauna was identified to the highest possible taxonomic resolution in the laboratory.

Our analyses provide a comprehensive overview of the valley's aquatic biodiversity, establishing a crucial reference point for future studies on climate and human impacts such as ongoing construction of hydro power plants and water extraction. We calculated diversity indices such as Taxa richness and Shannon index and identified potential environmental predictors of biodiversity. Furthermore, by sampling different microhabitats, we assessed the effectiveness of different substrates in capturing species richness, finding the highest diversity in large mineral sediments (rocks, pebbles between 25-250 mm).

This study offers valuable insights into the environmental drivers of lotic macroinvertebrate diversity in alpine river systems and underscores the importance of ongoing monitoring in the face of climate change and especially the enhanced/increasing glacier melts in the Vinschgau/Venosta Valley.

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Soil biodiversity in protected, near-natural forests

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Soil biodiversity is immense and includes a large taxonomic diversity of organisms, many of which are still unknown. The main limitations in the study of soil organisms are their physical inaccessibility, partly due to the complex spatial structure of the soil matrix, and a lack of taxonomic knowledge. There is a huge need for more data on soil biodiversity, particularly covering all taxa from microbes to invertebrates, which is currently largely lacking.

As part of the Biodiversa+ partnership, we are coordinating a pilot study on soil biodiversity to pave the way for transnational soil biodiversity monitoring. We are assessing the diversity of soil microbes and invertebrates at forest sites in ten countries in and around Europe. We are using pitfall traps, soil cores and eDNA samples to (1) get an overview of diversity in different forest types and (2) compare traditional morphological species identification with results from eDNA analyses. Here we present the results of the first sampling effort in 2023, showing that traditional and molecular methods differ in diversity patterns and taxonomic resolution.

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Grasslands4Biodiversity (G4B) – How can we protect biodiversity-rich grasslands in the Central Alps?

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Semi-natural grasslands are some of the most biodiverse habitats in Europe and play a special role in the mountainous landscape of the Central Alps. However, many show a decrease in biodiversity due to increasingly intensive use or abandonment. The Biodiversa+ project G4B investigates the underlying natural conditions and management practices that affect grassland plant diversity in the Alps and Carpathians.

In Tyrol, South Tyrol, and surrounding areas, we collected over five thousand spatially explicit botanical records, primarily using the Braun-Blanquet method. Topographical and climate data as well as land-use information provided by farmers and stakeholders through questionnaires and interviews is then correlated with the diversity records.

An initial evaluation reveals a strong influence of management practices on plant species diversity. Non-fertilized hay meadows, which are cut every two years, host an average of 40 species. A slightly lower species count is found in agroforestry systems. However, the number of species drops significantly with increased mowing frequency and fertilization, averaging 18 species.

This insight into the connection between management practices and plant diversity will provide stakeholders with valuable guidelines to create and implement grassland management strategies that benefit biodiversity.

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Peatlands in Trentino: an overview based on surveys covering 224 hectares conducted since 2011

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BioMonitoring Team, Tre Ville (I)

Peatlands are wetland habitats of exceptional natural value at our latitude as they are much less widespread than in the temperate-boreal zone. In Italy, peatlands are more frequently found in the Alps, and in Trentino they represent about 0.1 % of the entire surface area (approximately 600 hectares). With the aim of assessing the conservation status, I began a series of surveys of peatlands since 2011, which involved sampling plants and bryophytes and measuring fundamental ecological variables such as the chemical and physical characteristics of groundwater and the depth of the peat to estimate the volume of peatlands and the carbon stock. Using this approach over the years, as many as 147 peatlands have been surveyed, corresponding to 224 hectares. Most of the sites were located between 1500 and 2400 m asl, almost all on siliceous substrates, although there were some calcareous peatlands. The surveys have revealed a remarkable diversity of floristic species, many of which are listed as endangered. Notable findings include the identification of *Sphagnum subfulvum*, a species new to Italy in 2012, and new locations for rare species such as *Paludella squarrosa* and the liverwort *Calypogeia sphagnicola*. A number of threats were also identified, the most common of which were overgrazing and trampling, eutrophication, hydrological disturbance, and accelerated succession triggered by the cessation of management. For the first time in Trentino, the depth of the peat has been estimated (on average just over 1 meter, but with peaks of over 5 meters), and thus the amount of stored carbon has been calculated (about 0.4 million tons). These findings highlight the significant ecological value of peatlands and underscore the importance of their conservation.

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South Tyrol's bat guardians: Citizen science for Barbastelle bat conservation in settlements

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The Western Barbastelle bat (*Barbastella barbastellus*), a species reliant on mature or semi-natural forests, is listed in the Annexes II and IV of the EU Habitats Directive and classified as Near Threatened in the IUCN Red List. This status underscores the need for enhanced research and long-term monitoring to support populations of this species. Understanding their roosting preferences and behavior is essential, especially regarding maternity roosts, which are typically found under bark or in tree crevices. However, in South Tyrol, Barbastelle bats have been observed roosting behind window blinds of houses (18 occurrences reported in the last decade), while solid data on tree roosts remains lacking.

Our study aims to gather reliable data on the status of Barbastelle maternity roosts in settlements by employing a combination of monitoring techniques. Maintaining contact with homeowners of known colonies is essential for protection. As the animals have several roosts that they use alternately, known as roost-switching, it is important to monitor the current situation. By using data from large-scale acoustic monitoring in South Tyrol, we identify distribution gaps and specifically search for maternity roosts in areas where colonies are expected but have not yet been detected. For this purpose, we leverage local newspapers, websites, and public events to search colonies and raise public awareness.

Our project highlights the value of combining survey techniques to identify and monitor Barbastelle bat maternity roosts. Knowledge transfer from monitoring enables citizens to become guardians of bat colonies and take protective measures. Close collaboration between scientists and citizens is crucial for conservation. Species roosting in buildings are particularly impacted by human activities, such as facade renovations. Our approach also allows for further research, like collecting droppings with the help of homeowners to study diet and identify important hunting habitats.

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Soil fauna on mountaintops: first results from the GLORIA extended samplings in South Tyrol

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For decades, the GLORIA program has been studying how plant communities living on mountaintops are changing around the world. It has therefore become a standard method for assessing plants on mountains. In 2020, an additional module was introduced to study the soil fauna on GLORIA mountaintops. So far, it has only been used twice: first in the Gesäuse National Park in Styria (Austria), and then in South Tyrol (Italy).

In South Tyrol there are two GLORIA target regions: (1) the Dolomites and (2) the Texel Group. Each target region consists of four isolated mountain peaks at four different elevations (e.g. in the Dolomites from 2199 to 2893 m a.s.l.). Five meters below each summit, we installed four pitfall traps in each of the four cardinal directions (i.e. 16 traps in total), which remained active for two weeks. Additionally, we also conducted suction sampling for small invertebrates living in the ground vegetation.

First results reveal major differences between the soil fauna communities of the four peaks. The mean abundance (as activity density) decreases linearly with increasing elevation (from 35 to 10 caught soil invertebrates). Coleoptera were the most dominant taxa always exceeding 30 % of the entire community; even 60 % on the highest peak. Other dominating groups change with elevation: e.g. Formicidae at 2199 m (<25 %), Opiliones at 2730 m (~18 %), and Araneae at 2890 m (~15 %). Further, no Isopoda was present at the two higher peaks.

Preliminary insights into the composition of the soil fauna revealed highly diverse soil fauna communities, also in the high alpine sites. Certain groups such as Diplopoda and Opiliones were found up to 2900 m, showing that the soil fauna is also active in the high alpine zone. We expect new insight into alpine soil fauna as such remote peaks have not been sampled before.

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Do dissolved heavy metals enter the food webs of Alpine streams?

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The Euregio project “ROCK-ME: Geochemical response of Alpine Rock Glaciers to global warming” (IPN 159, 2022-2025) investigates the origin, export, and ecological effects of trace elements in Alpine river networks influenced by permafrost (i.e., rock glacier) thawing and glacier retreat. Permafrost degradation and glacier recession can cause elevate export of solutes, including heavy metals, into Alpine headwaters while the contribution from groundwater is usually negligible. However, the ecological effects remain understudied. We assessed if and how the enrichment in trace element observed in high altitude Alpine streams causes biomagnification processes in the aquatic organisms by characterizing the food webs of different stream types (i.e., fed by intact and relict rock glaciers, and reference spring draining an area without periglacial landforms/glaciers/permafrost) using δ13C and δ15N isotopic ratios analysis, and measuring the content of trace elements in each component of the food web. The investigation was conducted in late summer 2022 in two catchments in South Tyrol: Lazaun in Schnalstal/Senales Valley and Madritsch/Madriccio in Martell/Martello Valley. The analyzed matrices were: coarse and fine particulate organic matter (CPOM and FPOM), epilithic biofilms, bryophytes, and benthic invertebrates of different taxa characterized and grouped by feeding habit (omnivore, carnivore, herbivore, detritivore). The same trace elements were measured in the water of each stream type. As expected, most of the biomagnification occurred in streams originating from intact rock glaciers. However, due to the paucity of predators in the benthic community and hence in the food web, biomagnification was more pronounced (up to 11 times the content in the basal sources) for the first levels of the food web. Comparable or higher levels of bioaccumulation in the second food web level occurred only in two of the studied streams.

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Disentangling evolutionary relationships within *Euphorbia angulata* (Euphorbiaceae)

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Euphorbia angulata (Euphorbiaceae) is a disjunctly distributed species, having its main distribution in central, eastern and south-eastern Europe, and smaller range in the north-western Iberian Peninsula and adjacent western France. It grows in light forests, in forest margins, nutrient poor meadows and heaths. Using relative genome size estimation we inferred three ploidy levels within the species. Whereas the diploids are restricted to the easternmost distribution area (Carpathians and eastward), the tetraploids are most widespread, and the hexaploids can only be found in the central part of the Balkan Peninsula, where they mostly grow over serpentine. We will use RAD sequencing to explore the origin of polyploids and disentangle the demographic history of conspicuously disjunctly distributed tetraploid populations, which could be a result of a complex history of range contractions and dispersals during the Pleistocene glacial cycles (vicariance), or colonization of western Europe from the main distribution area via long-distance dispersal. Using multivariate morphometrics we will investigate morphological differentiation among different ploidy levels as well as the main phylogenetic lineages. Our comprehensive analyses will provide new insights into the evolutionary history of *Euphorbia angulata*, contributing to our overall understanding of European plant biogeography during the Quaternary.

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Caddisflies (Trichoptera) diversity in South Tyrol: From historical records to new findings

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Caddisflies (Trichoptera) are an order of insects with aquatic larvae and terrestrial adults that are good indicators of water quality. Here we focus on the diversity of both adult and larval Trichoptera in the province of Bolzano/Bozen, Italy, including historical and recent records. A literature review documented 106 species in South Tyrol, including 22 alpine endemics, in 26 published works by 36 authors. The first records of caddisflies in the province were made by McLachlan in 1874, who reported the presence of seven species. After Christandl-Peskoller and Janetschek's faunistic fieldwork in the Central Eastern Alps in 1976, most studies have been based on literature or sporadic collections, and no further structured monitoring of adult Trichoptera has been carried out in South Tyrol for almost 50 years.

In 2023, adult caddisflies were collected monthly from May to October at six sites at different altitudes (200-1200 m a.s.l.) across the province, which were also investigated within the aquatic Biodiversity Monitoring South Tyrol (BMS) program. Light traps, placed near streams, were used to attract the insects at night. This effort resulted in the collection of 5800 specimens, representing 52 species. In particular, 14 species were recorded for the first time in South Tyrol, and another 14 previously poorly documented species were identified. Comparisons were made between these adult specimens and larvae identified during previous BMS monitoring.

The results underline the importance of adult identification for a comprehensive biodiversity knowledge, as larval stages do not always allow species-level recognition. This study provides updated data on the distribution, life cycles and diversity of Trichoptera in South Tyrol, including rivers at different altitudes, from montane to lowland streams. It also highlights the need for ongoing monitoring in specific and sensitive habitats, such as springs and wetlands, to better understand and conserve local biodiversity.

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Rock glaciers as climate refuge: Preserving aquatic biodiversity in the face of glacier loss in the Eastern Italian Alps

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Glacier loss due to climate change is affecting the alpine hydrological dynamics as well as aquatic biodiversity. Mountain permafrost – especially rock glaciers, which are creeping rocky debris containing permafrost ice – is becoming increasingly significant. Streams originating from rock glaciers, known as "icy seeps," may serve as crucial, future refuges for cold-adapted organisms by maintaining cold waters even as climates warm.

Our study, conducted in late summer 2021, investigated biotic and abiotic parameters of icy seeps, glacier springs, and non-glacial springs (spring brooks) across five catchments in Vinschgau Valley/Val Venosta, in the Eastern Italian Alps. We assessed discharge, turbidity, water chemistry (including major ions and trace elements), stable water isotopes (δ18O, δ2H), and aquatic macroinvertebrate communities across these spring types. Icy seeps exhibited intermediate meltwater contributions to runoff, reflecting an environment with very cold water temperatures (< 1.5 °C) enriched in trace elements, similar to glacier springs. The macroinvertebrate community composition in icy seeps was strongly related to chemical harshness gradients, primarily driven by trace element levels. Icy seeps with lower concentrations of trace elements hosted communities similar to those in spring brooks. Notably, icy seeps with harshest water chemistry, especially high in nickel, and higher meltwater contributions, harbored among other species, *Diamesa steinboecki*, which are currently in decline due to glacier loss.

Our findings highlight the high conservation value of icy seeps and their ecological significance. These habitats, are essential under the increasing threat of warming and drying in alpine regions. Icy seeps may become increasingly important aquatic biodiversity refuge for cold-adapted, alpine species. Protecting these habitats is crucial as they provide cool environments for species at risk of extinction due to climate change.

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Analysis and conservation of natural and semi-natural habitats in South Tyrol (LEST Project)

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The project "Habitats South-Tyrol" (LEST) documents and evaluates the ecological status of natural and semi-natural habitats in South Tyrol aiming to analyze vegetation diversity at the landscape scale and to support conservation efforts. The study includes grasslands, mires, scrublands and freshwater habitats. Pre-mapping incorporates satellite imagery and previous studies to identify survey areas systematically. A bibliographic study on mires from the 1970s to the present aids in understanding ecological trends and establishing a foundation for future monitoring. Data are gathered and spatially contextualized, complemented by photo-identification of wetlands via remote sensing and previous surveys. Preliminary findings show significant habitat quality and biodiversity variability, with differences in species richness and composition influenced by altitude, soil type, and land-use history. Key environmental gradients affecting vegetation dynamics and habitat stability are identified. These results highlight the need for continuous monitoring and adaptive management to address climate change and human activity challenges. The data will inform conservation policies and practices to protect vulnerable habitats and their species, enhancing our understanding of South Tyrol's biodiversity and ecological processes.

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Tiny but mighty – Pollen of South Tyrol

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Up to 20 % of the South Tyrolean population is affected by pollen allergy. The pollen information service (PIS) is provided by the Biological Laboratory of the Agency of Environment and Climate protection. Besides publishing weekly pollen reports, producing pollen calendars for the region and providing a pollen forecast, the PIS is involved in other projects of this research-field. One of them is a study which focused on pollen concentrations in alpine valleys of South Tyrol. Therefore, the pollen concentrations of two alpine stations in Prettau and Grub (both located above an altitude of 1400 m) were measured during the period from 2019-2021. Results showed that the Seasonal Pollen Index (SPI) of the alpine stations was lower compared to the SPI of the nearby surveyed stations located at lower altitude in the main valleys. This could be due to the absence of pollen sources at a certain altitude and to a shorter vegetation period at alpine locations. Nevertheless, the phenomenon of long-distance transport of pollen by strong winds could also have impacted the concentration and species spectrum of pollen measured in these stations. Similar difference in pollen load correlated to the altitude had been found focusing on the pollen of only one species: the invasive *Ambrosia artemisiifolia*. In cooperation with a working group, the mean daily concentrations of *Ambrosia* pollen of five regions in Northern Italy were evaluated for the period 2000-2023. The results showed that in the stations at higher altitude, the pollen concentration of *Ambrosia* was lower than in the stations located at lower altitude. Additionally, a significantly decreasing trend was observed in the stations of the lowlands around Milano. This finding can be linked to the accidental import of an invasive leaf-beetle species, *Ophraella communa*, which reduced the *Ambrosia* population because it feeds preferably on these plants.

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The air as a means to assess plant biodiversity in Alpine environments

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Alpine environments are particularly susceptible to the impacts of global change with climate warming causing significant shifts in plant communities. Many plants reproduce by dispersing pollen and spores through the air, each with unique micromorphological traits specific to their species. We aim to explore the air as an innovative substrate for plant biodiversity monitoring in alpine environments.

Air deposition samples from four alpine sites in Trentino: Rifugio Larcher al Cevedale, Rifugio Rosetta, Rifugio Val di Fumo and Rifugio Altissimo are used both for traditional microscopic analysis of plant propagules, and the analysis of environmental DNA (eDNA). By adopting DNA metabarcoding methodology, higher taxonomic resolution of airborne plant biodiversity in the bioaerosol can be achieved than with current standards. Additionally, vegetation and floristic data were acquired at various scales from the receptor site to interpret the origins of plant bioaerosols.

At Rifugio Larcher, for example, 21 pollen taxa were identified with the optical microscope at a magnification of 400 x in 2023. 84 % of the total pollen recorded were of herbaceous and 16 % of woody plants. In five plots (total area 20 m^2), a total of 46 vascular plant taxa were recorded. Ten species identified in the vegetation analysis were absent in the air sample. Conversely, the air samples contained pollen from 13 taxa originating outside the local area. In parallel, a protocol for eDNA extraction and amplification has been developed, as well as a customized reference database targeting the ITS1 and ITS2 regions for identifying pollen.

In the open alpine environment airborne pollen generally mirrors the local flora. Nonetheless, a portion of the biodiversity originates from distant or lower-altitude sources. Preliminary results from the molecular analysis of the air samples validated with vegetation data indicate that eDNA can be a powerful tool to assess plant biodiversity.

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Distribution of polyploid plants in the Eastern Alps: a preliminary report

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Polyploidy, the possession of more than two chromosome sets, is a key feature of plant biodiversity. A recent comprehensive analysis of global chromosome count data has shown that the frequency of polyploids increases with latitude. Much less is known about ploidy variation and distribution in mountain areas. In temperate mountain ranges the frequency of polyploids may rise towards high-elevation habitats (due to, for instance, their higher stress tolerance) and with increasing distance from glacial refugia (due to better colonizing abilities). Employing flow cytometry, we established ploidy levels of a flora-wide sampling of several ten thousand individuals of angiosperms from 101 elevational transects in the Eastern Alps – of which 36 are situated in Tyrol, South Tyrol and Trentino – and spanning from 550 m below timberline to 550 m above it. Generalized linear mixed effects models were used to analyze whether there is a generic pattern of increasing polyploid frequency with increasing elevation and/or distance from the closest Pleistocene refugium. This project represents an unprecedentedly broad empirical test at the landscape level of the long-standing hypothesis of a positive association between genome duplication and spatio-temporal environmental variation. I will present the project and some recent results on the distribution of polyploids along the elevational gradient. Preliminary results on the distribution of cytotypes of mixed ploidy taxa in the Euregio will also be presented.

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