

Report from the  
**Master Summer School**  
**“Biodiversity Monitoring”,**  
**Preda, Parc Ela, Switzerland, 10–20 August 2020**



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## Cover photo

The highest permanent plot C09 at around 2,600 m a.s.l. close to Lai Negr (Photo: J. Dengler).

## Disclaimer

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## Preface

*Jürgen Dengler & Jamyra Gehler*

The Master Summer School “Biodiversity Monitoring” was planned as a joint international class for Master students in Environment and Natural Resources of the Zurich University of Applied Sciences in Wädenswil, Switzerland, and the Master programs of the Faculty of Biology of the University of Warsaw, Poland. Both students and teachers are from both universities. It should be conducted alternatingly in Parc Ela, a regional nature park in Grisons, Switzerland, and in and around the Białowieża National Park in Eastern Poland. After planning at both universities, it was conducted for the first time in summer 2019 in Preda, Parc Ela, Switzerland (Dengler 2020a, 2020b). In that year, we had both teachers and students from both countries.

Unfortunately, the first scheduled conductance in Poland in summer 2020 had to be cancelled due to the Corona pandemic. Instead, the Master Summer School was possible only with Swiss students and teachers in Switzerland again. It took place from 10 to 20 August 2020 in the Sonnenhof in Preda, Grisons, with 11 students and seven teachers, all from Switzerland, except one Chinese Postdoc. Luckily, the latter “forced” us to communicate in English despite the lacking Polish participation.

The main topics of the Summer School are how to sample and monitor biodiversity in a standardised manner. This is demonstrated for a range of different taxonomic groups with contrasting properties to provide the students with a broad set of skills and to allow multi-taxon studies that are highly interesting scientifically (Allan et al. 2014; Zulka et al. 2014). Since one of the aims is “monitoring”, we had already in 2019 installed a transect of 11 permanent plots for studying four taxonomic groups (vascular plants, fungi, orthoptera, small mammals), permanently marked them and equipped them with temperature logger, which record soil and air temperature around the year. Apart from acquiring knowledge on species determination and standardised biodiversity sampling, the Summer School also provides deeper insights into modern statistical analyses of such data and how to write up the results in the style of a scientific paper.

The first part of the Summer School was dedicated to the reconnaissance of the habitats in the surrounding and joint resampling of two taxonomic groups (vascular plants, small mammals) in some plots on the transect. The other two groups (fungi, orthoptera) could not be studied in 2020 as the Polish colleagues responsible for them could not participate. Additionally, six new permanent plots could be installed on the calcareous side of the valley, the Val Zvretta. In the second part of the Summer School, the students conducted in small groups three projects on the following topics:

- Small mammal communities around Preda
- Resampling vascular plant vegetation in the 13 transect plots after 1 yr
- Biodiversity patterns of vascular plants in comparison of the two sides of the Albula valley with contrasting bedrock

This Reader mainly comprises the scientific reports from the three student research projects, accompanied by details on the permanent plots and a complete list of species recorded during the

Summer Schools 2019 and 2020. It closes with some photographic impressions, compiled by Tom Bischof – many thanks to him! It thus provides the participants with the product of their efforts, the teachers with baseline material for the next conductance and the conservation authorities of the canton and the Parc Ela and other partners with a documentation of the findings and thus complements the reports from the first year (Dengler 2020a, 2020b).

Enjoy reading!

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## The permanent plots

*Jürgen Dengler & Jamyra Gehler*

The sampling transect was established in a way that it matches the sampling strategy of two international plant biodiversity sampling initiatives: On the one hand, the plots correspond to the EDGG multi-scale “biodiversity plots” of EDGG (Dengler et al. 2016), and the non-forest plots among them are contributed to the GrassPlot database (Dengler et al. 2018, 2020). On the other hand, the plots combined with some additional co-occurrence plots sampled by I. Dembicz and J. Dengler are part of the DarkDivNet (Pärtel et al. 2019) as site D095 (see <https://www.botany.ut.ee/macroecology/en/darkdivnet>). In Preda, we established 13 permanent plots of 100 m<sup>2</sup>, 11 of them along an elevational transect from Naz through the (mostly acidic) Val Mulix to the Lai Negr, placed in near-natural vegetation every approx. 100 m of elevation between 1750 and 2650 m a.s.l. (plots C01–C09 and N1C). At approx. 2050 m a.s.l., in addition to plot N1C in near-natural forest we established a second plot A1C in secondary grassland nearby, following the DarkDivNet protocol. Additionally, we established two permanent plots in the alluvial plain of the Albula river near the Sonnenhof, one in open vegetation (C10) and one in forested vegetation (C11). In 2020, we established six additional permanent plots on the limestone side, in Val Zavretta, between 1840 and 2440 m a.s.l. (plots L01–L06). The 19 permanent plots have been georeferenced with a differential-GPS, marked in two corners with coloured wooden poles and additionally with magnets buried in the soil to allow precise relocation in future sampling campaigns (note that wooden poles are missing in some plots in Val Zavretta). Moreover, each of the 13 permanent plots installed in 2019 was equipped with a pair of temperature loggers, one 10 cm below soil surface and one 10 cm above to record during the next years the actual temperature in 30-min intervals. Following, the protocol of Dengler et al. (2016), in each of all 19 100-m<sup>2</sup> plots and two nested subseries in two opposite corners of 0.0001, 0.001, 0.01, 0.1, 1 and 10 m<sup>2</sup> vascular plant species composition was recorded. In the 10-m<sup>2</sup> plots additionally coverage of each species in % was estimated and some simple structural and environmental variables recorded. While in 2019, in (most of) the 13 permanent plots, also small mammals, orthoptera and fungi were recorded, in 2020 only small mammal sampling could be repeated and only in the lower six plots of the transect. Moreover, following Pärtel et al. (2019), for A1C and N1C, a mixed soil sample for additional metagenomic assessment in the DarkDivNet project was taken.

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## **Reports from student projects**

The participants of the Summer School have carried out three research projects in small teams of 3–4 students. These reports were prepared in the style of a scientific paper. Please note that the three presented projects are published as submitted by the students, except minor adjustments in the layout. The responsibility for the content solely rests with the authors.

# Small mammal and biodiversity monitoring in Val Mulix 2020

*Svenja Crottogini, Ninetta Graf, Tom Bischof, Hanna Schreiber*

## Abstract

Small mammals play an important role in many ecosystems. As they live very secretly it is quite challenging to study them. One method in small mammal monitoring is the camera trap. In this study the newly developed MammaliaBox, a camera trap that is installed inside a box with tunnels attached to it, was used to monitor small terrestrial mammals in the Val Mulix (canton of Grison, Switzerland). The aim of the study was to find a relationship between the prevailing habitat structure at the trap sites and the occurrence of certain small mammal species. Additionally, the biodiversity of the small mammals in the Val Mulix was investigated.

During the five days that the 11 camera traps were installed across the Val Mulix, they were visited 183 times by 7 different small mammal species. A lot of the species that we expected to find due to the habitat structure at the sites could be identified. The most abundant species was *Myodes glareolus*. For almost all the species we did not find a significant effect of habitat structures on the occurrence of the individual species. The *Myodes glareolus* was the only species that had a high enough occurrence to make an assumption. The diversity of small mammals was assessed for each trap and for the whole Val Mulix area. On average the traps recorded only 2 different species. Shannon diversity was overall very low. The calculated alpha-diversity of the traps was on average 0.44. Gamma-diversity for the Val Mulix area was 1.09. The overall species richness and diversity was similar to the study conducted in 2019 in the same area.

## Introduction

In most ecosystems, small mammals have an important role as herbivores, seed consumers and prey for predators (Mc Cleery et al. 2014). In addition, they can be strong indicators of overall ecosystem health (Keesing 2000, Manson et al. 2001, Monadjem and Perrin 2003, Avenant and Cavallini 2007). The small mammals of the alpine stage have only rarely been studied (Schade et al. 2011). There is a lack of data on population biology, on the role of ecosystems, and on interactions with vegetation (Marchesi et al. 2014). There are also hardly any studies on the Eulipotyphla of the alpine stage (ibid.). In order to gain such information about different species, it is a common practice to live-capture small mammals in box traps (Mc Cleery et al. 2014). With live-trapping methods, detailed information about the captured individuals (i.e. species, sex and numbers) can be obtained. However, there are certain restrictions regarding the use of live box traps for small mammal research (ibid.). Studies using live traps usually need to be approved by animal ethics authorities for animal welfare concerns (Chiron et al. 2018). Livetraps are designed to capture only one animal per night and the physical capture has the significant disadvantage of trapping it for several hours, with the potential to stress the animal and disrupt its normal activities (De Bondi et al. 2020, Mc Cleery et al. 2014). Apart from being cost and labour intensive, live-trapping methods can also be very time consuming (Chiron et al. 2018). Traps need to be checked very frequently, usually at 12-h intervals, to ensure the well-being of the animals captured



(ibid.). For some taxa such as Eulipotyphla, intervals may have to be much shorter because the food provided in traps cannot meet the energetic needs over a long period (Chiron et al. 2018).

Another, less invasive technique for sampling a variety of terrestrial mammals is the camera trap (De Bondi et al. 2020). This method has the advantage that it does not need to physically detain the animal (ibid.). It is also a cost-effective and easily reproducible method to study and monitor ground-dwelling terrestrial mammals (O'Connell et al. 2011). The use of camera traps for wildlife monitoring and studies has significantly increased in the last decade (Burton et al. 2015, O'Connell et al. 2011). However, few studies have used this method to systematically survey small, terrestrial mammal populations (De Bondi et al. 2020). Due to the sensitivity of the passive-infrared sensor that triggers these devices, camera traps often are unable to detect small and rather fast-moving species (Meek et al. 2014, Kolowski and Forrester 2017). To solve this issue, a so called "MammaliaBox" has been developed by the ZHAW (Aegerter, 2019) to capture photos of small mammals. It combines tracking tunnels with a regular camera trap. In this research project we will monitor small terrestrial mammals in the Val Mulix, Switzerland, using such a Mammali-aBox. We will analyse the relationship between the occurrence of different small mammal species and the prevailing habitat structures as well as investigate their biodiversity. The following three research questions will be answered in this study: (1) Can we determine the small mammal species that we expect based on the different habitat structures at the selected sites? (2) Which habitat structures explain the occurrence of the detected small mammal species? (3) What is the biodiversity of small mammals in the Val Mulix?

## Methods

### Study site

The study was conducted in the lower part and at mid altitude of the Val Mulix in the Swiss alps (Figure 1). The area includes the surroundings of solitary buildings in Naz close to the village Pre-da, the adjacent floodplains, subalpine forests and alpine dwarf shrub habitats above the tree line. It starts at 1750 m and reaches up to 2250 m altitude. The area covers about 6 km<sup>2</sup> and contains all the typical habitats of the region.

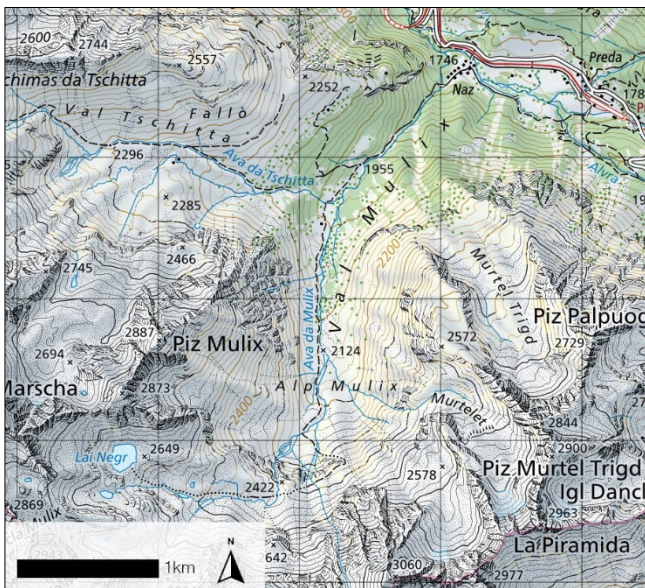


Fig. 1. The study area of Val Mulix in the central Swiss alps (geo.admin).

### MammaliaBox

In total 11 MammaliaBoxes were placed in different places across the study area for about five days. The MammaliaBox was invented to photo-trap small mammals using a wooden box, two tunnels, a scent board and a wildlife camera (Figure 2). Dog food and peanut butter was rubbed on the scent board to attract the small mammals but without feeding them, so that the individual animals do not stay in the box for too long and thereby prevent others from entering. After installing the camera, the boxes M01-M06 were placed on the same spot as last year (Hoppler et al. 2020, Figure 4). The cameras R01-R05 were placed in different habitats surrounding the group house "Sonnenhof" (Figure 5). In order to maximize the likelihood of small mammals to enter the boxes, they were placed close to structures that the animals use for orientation and therefore frequently pass. To prevent the box to heat up during the day, the boxes were covered with soil and vegetation (Figure 3).



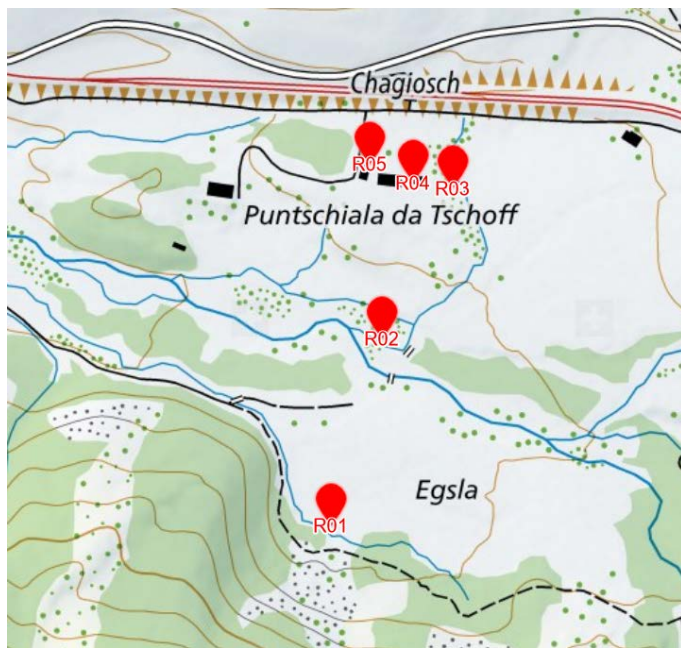
**Fig. 2.** Inside of a MammaliaBox with tracks of activity after recording for five days (Photo: Svenja Crottogini)



**Fig. 3.** Situated and covered MammaliaBox on the trapping site R05 (Photo: Tom Bischof)



**Fig. 4.** Positions of the camera traps M01-M06 in Val Mulix (geo.admin)



**Fig. 5.** Positions of the camera traps R01-R05 around the Sonnenhof in Preda (geo.admin)

## Field sampling

### *Analysis of the camera pictures*

All pictures of all 11 camera traps were classified into so called events. The following rules were applied for this classification:

1. The minimal duration of an event is 1 second.

2. An event lasts from the first picture that is triggered by an individual to the last one on which it is visible.
3. If a new animal shows up, which can be distinguished from the one before based on species or other physical characters, a new event must be recorded.
4. To prevent double counting of the same individual, which just left the box and came back in, a buffer of 5 min is used. This means that a new event can only be created if the next appearance is more than 5 min apart or if the next individual can be distinguished based on species or other physical characteristics. If the next appearance is less than 5 min apart and is the same species, it still counts to the event before.
5. If during an event another individual of the same species appears, it will be included in the same event until all the individuals have left.

For each event the following information was recorded: Event ID, trap ID, start date, start time, end time, total time in the box, the species and the number of individuals. Species determination was done with the use of the determination key by Reifler-Bächtiger & Stephani (2019, ZHAW unpublished) based on physical characteristics. If possible, the individuals were identified to the species level, if not to the genus level or considered as not identifiable.

#### *Determination of expected species*

To determine the small mammal species we would expect on the different camera sites based on the habitat structures, a habitat type (“forest”, “building”, “wetland”, “dwarfshrub”) was assigned to each camera. The lists of expected species for each habitat (Table 1) are based on the habitat preference of different small mammal species and on the evidence of occurrence in the Preda region (Müller et al. 2010, Canalis 2012, Hoppler et al. 2020).

**Table 1:** List of expected species and habitat type for each camera trap

Camera trap	Habitat type	Expected species
<b>M01</b>	Forest	Apodemus sp., Mustela erminea, Myodes glareolus, Sorex alpinus, Sorex minutus, Sorex sp.
<b>M02</b>	Forest	Apodemus sp., Mustela erminea, Myodes glareolus, Sorex alpinus, Sorex minutus, Sorex sp.
<b>M03</b>	Forest	Apodemus sp., Mustela erminea, Myodes glareolus, Sorex alpinus, Sorex minutus, Sorex sp.
<b>M04</b>	Forest	Apodemus sp., Mustela erminea, Myodes glareolus, Sorex alpinus, Sorex minutus, Sorex sp.
<b>M05</b>	Dwarfshrub	Apodemus sp., Chionomys nivalis, Mustela erminea, Mustela nivalis, Myodes glareolus, Sorex alpinus
<b>M06</b>	Dwarfshrub	Apodemus sp., Chionomys nivalis, Mustela erminea, Mustela nivalis, Myodes glareolus, Sorex alpinus
<b>R01</b>	Wetland	Microtus arvalis, Mustela erminea, Neomys sp., Sorex sp., Sorex alpinus, Sorex minutus
<b>R02</b>	Wetland	Microtus arvalis, Mustela erminea, Neomys sp., Sorex sp., Sorex alpinus, Sorex minutus



<b>R03</b>	Forest	Apodemus sp., Microtus arvalis, Mustela erminea, Myodes glareolus, Sorex minutus, Sorex sp.
<b>R04</b>	Building	Apodemus sp., Crocidura sp., Microtus sp., Mustela nivalis, Sorex sp.
<b>R05</b>	Building	Apodemus sp., Crocidura sp., Microtus sp., Mustela nivalis, Sorex sp.

### Habitat type “wetland”

In the habitat type “wetland” we placed two camera traps (R01 and R02). The traps were both placed in the alluvial plane close to the house “Sonnehof” and were situated right next to the running water (Figure 6). The habitat around the traps was characterized by rocks, some gravel and tree species like *Pinus cembra* and *Picea abies*, covering about 40% of the plot. While around trap R01 the vegetation was dominated by species like *Vaccinium uliginosum* and *Vaccinium myrtillus*, around the trap R02 the species *Calamagrostis villosa* and *Adenostyles alliariae* were mainly present.



**Fig. 6.** Habitat type “wetland” showing the camera trap R02 (Photo: Tom Bischof)

### Habitat type “building”

In the habitat type “building” we placed two camera traps (R04 and R05). Both traps were placed outside right next to a building standing close by the group house “Sonnenhof”. Trap R04 was placed next to a meadow dominated by plant species like *Epilobium angustifolium* and *Dactylis glomerata* (Figure 7), while trap R05 was in a habitat covered by a few trees and plant species like *Rubus idaeus* and *Calamagrostis villosa* covering the ground.



Fig. 7. Habitat type "building" with a shed next to the house "Sonnenhof" where trap R04 was set (Photo: Tom Bischof)

### Habitat type "forest"

In the habitat type "forest" we placed five camera traps (Figure 8). Trap R03 was placed in a new spot close to the group house "Sonnenhof". We situated the trap right next to a fallen tree, adjoining a pasture consisting of plant species like *Calamagrostis villosa*, *Urtica dioica* and *Vaccinium vitis-idaea*. The traps M01 - M04 were placed within the given plots and in the same spot as the year before. Therefore, the species list for this habitat type was mainly based on the identified species from last year's group combined with the findings from Müller et al. (2010). Apart from trees, this habitat type is characterized by dead wood, a few rocks and different herbaceous plant species.



Fig. 8. Habitat type "forest" where the camera trap M04 was placed (Photo: Tom Bischof)

### Habitat type "dwarfshrub"

In the habitat type "dwarfshrub" we placed two camera traps (M05 and M06). Like the traps in the habitat type "forest", both traps M05 and M06 were placed within the same plot as the year before. This habitat above the tree line is characterized by dominant species of shrubs such as *Rhododendron ferrugineum*, *Vaccinium vitis-idaea* and *Juniperus communis*. The ground is very rocky and shows a varying degree of crevices in which small mammals could hide (Figure 9).





**Fig. 9.** Habitat type "dwarfshrub" on the camera site M06 with the covered camera trap (Photo: Tom Bischof)

#### *Variables for statistical analysis of the habitat structure*

The statistical analysis of the habitat structure was only done for those species, which occurred in three or more different traps. Therefore, the analysis includes *Myodes glareolus*, *Sorex sp.* and *Apodemus sp.* For each species there were two different approaches: once with presence/absence as the dependant variable and once with the animals counts per trap (Table 2).

**Table 1:** The dependent variables used in the statistical analysis including three species, each with presence/absence and animal counts per trap.

<b>Name</b>	<b>Description</b>	<b>Unit []</b>
<b>myodes_pres</b>	Presence or absence of <i>Myodes glareolus</i> in the traps	1/0
<b>sorex_sp_pres</b>	Presence or absence of <i>Sorex sp.</i> in the traps	1/0
<b>apodemus_pres</b>	Presence or absence of <i>Apodemus sp.</i> in the traps	1/0
<b>myodes_count</b>	Number of visits by <i>Myodes glareolus</i> in the traps	cardinal numbers
<b>sorex_sp_count</b>	Number of visits by <i>Sorex sp.</i> in the traps	cardinal numbers
<b>apodemus_count</b>	Number of visits by <i>Apodemus sp.</i> in the traps	cardinal numbers

The independent variables listed in Table 3 were chosen based on the habitat requirements of the different small mammals (Müller et al. 2010, Canalis 2012). Except the variable "distance to water", all the independent variables were measured inside the 10x10 m plot also used in the vegetation analysis.

**Table 2:** The independent variables used in the statistical analysis of the habitat structure.

Name	Description	Unit []
<b>max_microrelief</b>	Max. microrelief measured from the highest point in the plot	cm
<b>mean_soil_depth</b>	Mean soil depth of five samples inside the plot	cm
<b>rocks</b>	The percentage of rocks inside the plots with a size > 63mm	%
<b>dead_wood</b>	The percentage of dead wood inside the plot	%
<b>shrubbery</b>	Shrub layer cover including shrubbery with a height of 0.5 - 5m	%
<b>distance_water</b>	Distance to nearest water source around the trap	m
<b>tree</b>	The tree layer cover including trees with a height of > 5m	%
<b>herb_layer</b>	Herb layer cover inside the plot	%
<b>building</b>	The percentage of building in the plot	%

## Statistical analyses

### *Habitat structure*

For the analysis of the different independent variables a Generalized Linear Model (GLM) (R Core Team, 2020) was used with both a binominal distribution for the presence/absence model and a poisson distribution for the counts model.

For ecological reasons, one of the correlating variables “water” and “distance to water” (Kendalls Tau > | 0.7 |) was removed from the analysis (Figure 13). The remaining independent variables for the model, which are listed in Table 3, were scaled. For each of the three species the following steps were done: An automatic model selection using the dredge-function (Barton, 2020) was conducted. Models, which showed an dAIC > 2, were kept to be used in a model averaging. After a refit of the independent variables for the GLM, the result then shows the final models.

### *Evaluation of small mammal diversity*

#### Richness

The richness of species was recorded in compiled species lists. The lists were made for each of the 11 traps separately to represent the richness of each habitat. Later they were combined into one list for the Val Mulix area. In some instances, the exact species of individuals of the genus *Apodemus*, *Sorex* or *Pitymys* could not be determined. In these cases, all observations of the unspecified species of each genus was counted as one species.

#### Alpha and Gamma Diversity

To determine the alpha diversity, the Shannon diversity index (H) was calculated for all the 11 sub-communities at each trap site (Figure 10). This was done with the species list of each trap containing the number of species as well as the relative abundance of each species. Shannon diversity index was calculated using the R package “vegan” (Oksanen et al., 2019). To determine the total diversity on a landscape level, the gamma diversity was calculated with a combined list of species and relative abundance of all 11 traps.

$$H' = - \sum_{i=1}^R p_i \ln p_i$$

**Fig. 10.** Formula to calculate the Shannon Diversity Index

### Pooling our data with data from 2019

The same method for calculating the diversity for the Val Mulix was applied on older data from a study conducted in the previous year. The gamma diversity of the two studies were compared to evaluate the success of this year's survey. Subsequently the list from 2019 was pooled with the new data to determine the change in diversity over a two-year time span using the same method.

## Results

### Expected and identified species

In Table 4 the detected species in each camera trap and their assigned habitat type are listed. Below, the findings in each habitat type are compared to the expected species list.

**Table 3:** List of detected species in each camera trap with the assigned habitat type.

Camera trap	Habitat type	Detected species
M01	Forest	<i>Myodes glareolus</i> , <i>Sorex sp.</i>
M02	Forest	Nid*
M03	Forest	<i>Apodemus sp.</i> , <i>Myodes glareolus</i>
M04	Forest	<i>Apodemus sp.</i> , <i>Myodes glareolus</i>
M05	Dwarfshrub	<i>Chionomys nivalis</i> , <i>Myodes glareolus</i>
M06	Dwarfshrub	<i>Apodemus sp.</i>
R01	Wetland	<i>Myodes glareolus</i> , <i>Sorex sp.</i> , <i>Sorex alpinus</i>
R02	Wetland	<i>Apodemus sp.</i> , <i>Sorex sp.</i> , <i>Sorex minutus</i>
R03	Forest	<i>Apodemus sp.</i> , <i>Myodes glareolus</i>
R04	Building	<i>Apodemus sp.</i> , <i>Pitymys sp.</i> , <i>Sorex sp.</i>
R05	Building	<i>Apodemus sp.</i> , <i>Myodes glareolus</i>

\*Nid: not identified

#### Wetland

Three species from our expected species list could be identified in the traps: *Sorex alpinus*, *Sorex minutus* and *Sorex sp.* In both traps, we could detect the species *Apodemus sp.*, which was not on our expected species list. The three expected species *Microtus arvalis*, *Mustela erminea* and *Neomys sp.* could not be detected in the traps.

#### Building

Three of the expected species for this habitat type appeared in the traps: *Apodemus sp.*, *Pitymys sp.* and *Sorex sp.* In trap R05, the species *Myodes glareolus*, which was not on our expected species list, could be identified. The two species *Crocidura sp.* and *Mustela nivalis*, which were both an expected species, did not appear in this habitat type.

#### Forest

Of the six expected species in this habitat, three could be identified (*Myodes glareolus*, *Sorex sp.* and *Apodemus sp.*) and three could not be detected (*Sorex minutus*, *Sorex alpinus*, *Mustela erminea*). In trap

M02, there was one not identified species that we assume to be *Pitymys sp.* This would have been a species occurring that we did not expect.

### *Dwarfshrub*

As expected, in the habitat type "dwarfshrub" we could identify the species *Chionomys nivalis*, *Apodemus sp.* and *Myodes glareolus*. The three other species *Mustela erminea*, *Mustela nivalis* and *Sorex alpinus* could not be identified in the habitat type "dwarfshrub" this year. There were no unexpected species that appeared in those two traps.

## Statistical analysis of the habitat structures

The minimal adequate models of the three different species for presence/absence and animal counts per trap are shown below:

### Presence/absence models

#### *Myodes glareolus*

```
glm(myodes_pres ~ max_microrelief_scaled + mean_soil_depth_scaled + rocks_scaled +
dead_wood_scaled + shrubbery_scaled + distance_water_scaled + tree_scaled + herb_layer_scaled,
data = habitat_data_pres_abs, family = binomial, na.action = "na.fail")
```

#### *Sorex sp.*

```
glm(sorex_sp_pres ~ dead_wood_scaled + tree_scaled + herb_layer_scaled, data =
habitat_data_pres_abs, family = binomial, na.action = "na.fail")
```

#### *Apodemus sp.*

```
glm(apodemus_pres ~ max_microrelief_scaled + mean_soil_depth_scaled + shrubbery_scaled +
distance_water_scaled + tree_scaled + herb_layer_scaled + building_scaled, data =
habitat_data_pres_abs, family = binomial, na.action = "na.fail")
```

### Animal counts per trap

#### *Myodes glareolus*

```
glm(myodes_count ~ max_microrelief_scaled + mean_soil_depth_scaled + rocks_scaled +
distance_water_scaled + tree_scaled + building_scaled, data = habitat_data_pres_abs, family = poisson,
na.action = "na.fail")
```

#### *Sorex sp.*

```
glm(sorex_sp_count ~ herb_layer_scaled + tree_scaled, data = habitat_data_pres_abs, family = poisson,
na.action = "na.fail")
```

#### *Apodemus sp.*

```
glm(apodemus_count ~ max_microrelief_scaled + building_scaled, data = habitat_data_pres_abs, family
= poisson, na.action = "na.fail")
```

The presence/absence models for all the three species are insignificant ( $p \geq 0.999$ ) and therefore it is not possible to make any interpretation of the results (Table 5).

**Table 4:** Results of the GLM analysis of the presence/absence models with three different species.

Predictors	Myodes glareolus				Sorex sp.				Apodemus sp.			
	Log-Odds	std. Error	CI	p	Log-Odds	std. Error	CI	p	Log-Odds	std. Error	CI	p
Intercept	11.73	55254.91	-108285.91 – 108309.36	1.000	-185.68	146735.42	-287781.83 – 287410.47	0.999	51.38	246944.85	-483951.64 – 484054.40	1.000
Max. microrelief	56.05	254080.27	-497932.13 – 498044.22	1.000					3.57	706567.44	-1384843.16 – 1384850.30	1.000
Mean soil depth	10.15	90453.65	-177275.75 – 177296.05	1.000					-67.86	911052.77	-1785698.48 – 1785562.75	1.000
Rocks	-33.67	186724.40	-366006.77 – 365939.43	1.000								
Dead wood	-4.95	97618.85	-191334.38 – 191324.48	1.000	65.69	173362.33	-339718.24 – 339849.62	1.000				
Shrubbery layer	-20.89	130290.22	-255385.04 – 255343.25	1.000					-39.52	227859.75	-446636.42 – 446557.38	1.000
Distance to water	-0.45	153408.54	-300675.65 – 300674.76	1.000					-95.97	883362.15	-1731453.96 – 1731262.03	1.000
Tree layer	21.58	303773.50	-595363.53 – 595406.70	1.000	-179.54	197565.95	-387401.69 – 387042.61	0.999	-98.54	556030.50	-1089898.30 – 1089701.22	1.000
Herb layer	28.99	226124.04	-443166.00 – 443223.97	1.000	-404.25	298108.80	-584686.76 – 583878.25	0.999	-9.26	129074.71	-252991.04 – 252972.52	1.000
Building									130.91	1008087.32	-1975683.93 – 1975945.75	1.000
Observations	11				11				11			
R <sup>2</sup> Tjur	1.000				1.000				1.000			

The results for the animal counts per trap models are only significant ( $p \leq 0.05$ ) for the species *Myodes glareolus* (Table 6). For the *Sorex sp.* and *Apodemus sp.* no interpretation was possible ( $p > 0.05$ ). For the *Myodes glareolus* the max. microrelief, mean soil depth, distance to water and tree layer seem to be very important variables for their habitat, whereas rocks and buildings are avoided.

All the models have more or less the same R<sup>2</sup> value, which is between 0.88 and 1.00. Since this value is very high for such a model, we assume an overfit.

**Table 5:** Results of the GLM analysis of the animal counts per trap models with three different species.

Predictors	Myodes glareolus				Sorex sp.				Apodemus sp.			
	Log-Mean	std. Error	CI	p	Log-Mean	std. Error	CI	p	Log-Mean	std. Error	CI	p
Intercept	-26.62	9.77	-45.78 – -7.47	<b>0.006</b>	-6.73	4.12	-14.81 – 1.36	0.103	0.37	0.28	-0.18 – 0.91	0.187
Max. microrelief	40.21	13.35	14.04 – 66.38	<b>0.003</b>					-0.56	0.40	-1.33 – 0.22	0.158
Mean soil depth	44.26	14.76	15.33 – 73.18	<b>0.003</b>								
Rocks	-28.52	9.45	-47.05 – -9.99	<b>0.003</b>								
Distance to water	40.05	13.27	14.05 – 66.06	<b>0.003</b>								
Tree layer	32.62	10.73	11.59 – 53.65	<b>0.002</b>	-6.63	4.35	-15.16 – 1.90	0.128				
Building	-47.82	15.81	-78.81 – -16.84	<b>0.002</b>					0.43	0.22	0.00 – 0.85	<b>0.049</b>
Herb layer					-12.92	7.71	-28.04 – 2.20	0.094				
Observations	11				11				11			
R <sup>2</sup> Nagelkerke	1.000				0.957				0.882			

### Small mammal diversity

#### Richness

Overall, seven species of small mammals could be detected. The 11 traps captured recognizable images of 0 to 3 different species. On average two species were recorded with each trap. The number of detected species for each of the 11 traps M01-M06 and R01-R05 are shown in Table 7.

**Table 6:** Number of detected species for each trap.

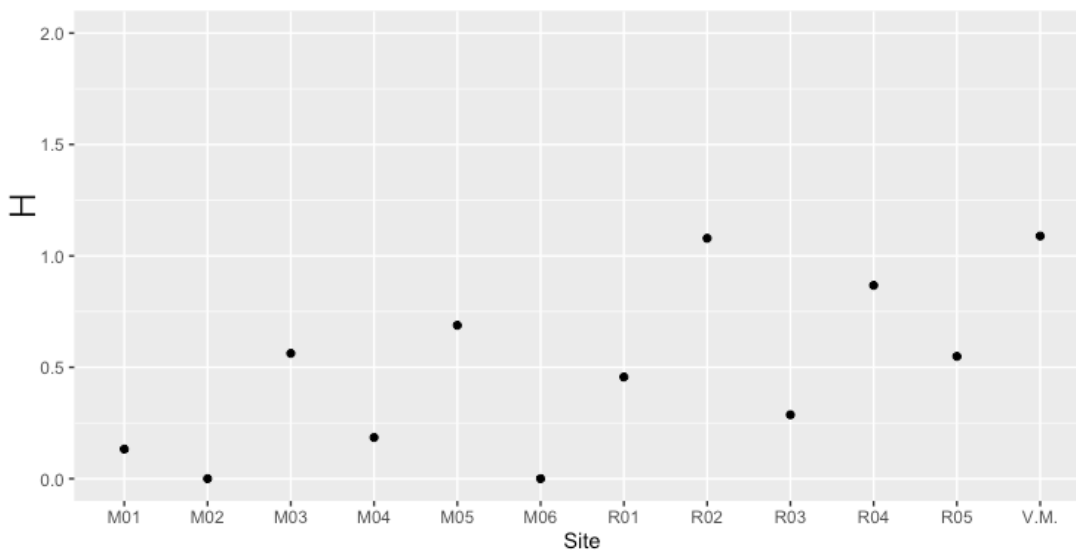
Trap	M01	M02	M03	M04	M05	M06	R01	R02	R03	R04	R05
Number of detected Species	2	0	2	2	2	1	3	3	2	3	2

### Alpha and gamma diversity

**Table 7:** List of detected species and number of individuals used to calculate the Shannon diversity indices.

Species	M01	M02	M03	M04	M05	M06	R01	R02	R03	R04	R05	total
<i>Apodemus sp.</i>	0	0	3	1	0	3	0	2	1	8	5	23
<i>Chionomys nivalis</i>	0	0	0	0	14	0	0	0	0	0	0	14
<i>Myodes glareolus</i>	33	0	1	21	17	0	21	0	11	0	16	120
<i>Pitymys sp.</i>	0	0	0	0	0	0	0	0	0	9	0	9
<i>Sorex alpinus</i>	0	0	0	0	0	0	1	0	0	0	0	1
<i>Sorex minutus</i>	0	0	0	0	0	0	0	2	0	0	0	2
<i>Sorex sp.</i>	1	0	0	0	0	0	2	3	0	1	0	7

A list of detected species and their individual counts per trap are shown in Table 8. This data was then used to calculate the Shannon diversity index for each trapping site and the whole Val Mulix (Figure 11). Similar to the number of detected species, the average alpha-diversity at each site was very low with a Shannon diversity value of 0.44. The diversity value at the trapping site R02 was the highest at 1.08. Trap M02 did not record any species and Trap M06 found only one species. Diversity at both sites was therefore 0.

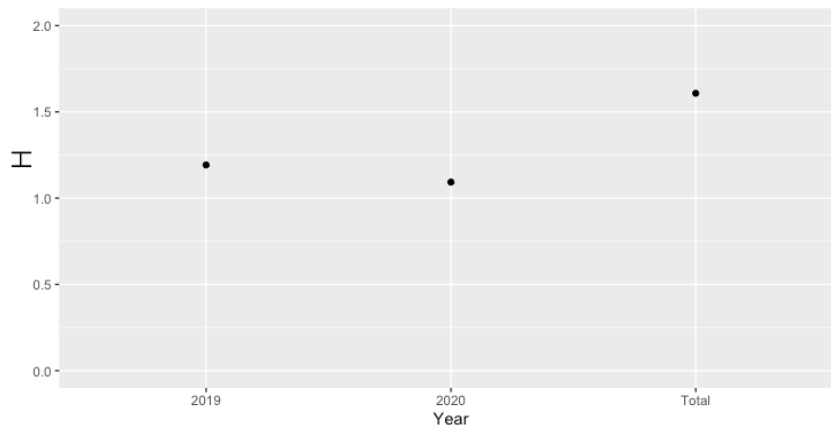


**Fig. 11.** Shannon Index (H) on an alpha diversity level for each trap as well as on the gamma level for the whole study site Val Mulix (V.M.)

Gamma Diversity for the Val Mulix was calculated using the pooled data of our study. The overall Shannon diversity value is 1.09 (Figure 12). The same procedure with data from a study done by Hoppler et al. in 2020 resulted in a similar value of 1.19.

The overall Shannon gamma-diversity for the combined data of Hoppler et al. (2020) and our study is 1.6. It is higher than the gamma diversity found in either of the two years and it represents the result of a repeated monitoring over 6 days in two consecutive years conducted at the same season.





**Fig. 12.** Shannon Index (H) on the gamma level for Val Mulix in 2019, 2020 and for the combined 2-year study.

## Discussion

### Expected and identified species

Several species that we expected to appear in the traps could be identified, such as *Sorex minutus*, *Sorex alpinus* and *Chionomys nivalis*. Other species like *Apodemus sp.* and *Myodes glareolus* were identified in traps where we did not expect them to appear, like in the habitat type “wetland” for example. Running waters and wetlands are not the most typical habitat for those two species, which is why we did not put them on the list of the most expected species for this habitat type. But *Apodemus sp.* and *Myodes glareolus* are both species that occur in various types of habitats (Müller et al. 2010). Close to where we placed the traps R01 and R02, different habitat types such as forest and grassland can be found, which could explain their occurrence in the traps. This finding leads to the conclusion that for future studies investigating the relationship between habitat structure and occurrence of small mammal species, the habitat should be looked at on a larger scale. In this study only an area of 100 m<sup>2</sup> was considered, which might be too small, as the home range of small mammal species can be much larger (Kollars 1995).

There were also species that we expected to appear, but could not be identified in the traps, such as *Mustela erminea*, *Neomys sp.* and *Crociodura sp.* There are different possible reasons why those species did not show in the traps. One reason could be that the duration, how long the traps were outside, was too short. After all, even though at least seven species were present in the larger area, the maximum number of species recorded by one trap was three (Table 7). Other possible reasons are that the species do not actually live in the habitats where we placed the traps or that the species were not curious or courageous enough to enter the traps.

For the habitat types “dwarfshrub” and “forest”, where we could rely on the findings from the year before, our expectations mostly matched our findings. The traps M01-M06 were all placed in habitats that are quite similar in a wide area. In contrast to that, the traps R01-R05 were placed in a spot where the habitat was quite diverse on a small scale. Even though we categorized the habitats into “wetland”, “forest” and “building”, the habitats could be suitable for a various type of species because the vegetation and structures were very different in a small space. Of all habitats, the highest number of species was found in the habitat type “wetland”. This can be explained with the same reasoning, since close to the traps placed in the habitat type “wetland” also structures like meadows, trees and bushes could be found.

A quite noticeable finding was that the species *Myodes glareolus* appeared with no exception in all habitat types. In contrast to this, last year's group had only very few individuals in their traps (5 individuals). This striking difference could be explained by annual population cycles. Many small mammal species are known to have fluctuating population cycles, where their abundance is very high in one year and very low in the next (Korpimäki et al. 2004). This phenomenon might become much more visible in future studies at this study site, which will be able to compare data over several different years.

### Statistical analysis of the habitat structure

As almost all presence/absence and animal counts per trap models were insignificant, we are not able to fully answer the second research question of this study. We can only make assumptions on why we were not able to find significant results. One possible explanation is that the chosen variables simply do not have a detectable effect on the presence or absence of the small mammal species that we trapped. For a similar study it would therefore be advisable to investigate other explanatory variables, like food sources for example. Another reason for the insignificant results could be the small sample size. It would increase the significance massively if there were more camera traps that were evenly distributed across the different habitat types and a much longer trapping time. If in the next few years further data is collected at this study site it might be possible to find significant effects.

As the animal counts per trap models for *Myodes glareolus* were significant, we can partly answer our second research question, at least for this species. This shows that for a highly abundant species it might be better to analyse counts instead of presence/absence when the sample size is small.

The correlation between the two variables "distance to water" and "water" was solved by taking out the variable "water" since all three small mammals used in the statistical analysis are not dependant on a certain amount of water, but only on a water source. Therefore, the variable "distance to water" was chosen over the variable "water", since it's irrelevant how much water is in the area. If e.g. the *Neomys* sp. would have been in the analysis, the amount of water in the area would be an important factor.

The  $R^2$  value in all models show an overfitting. The reason for this overfitting can be the small sample size that was used to calculate the models. There are too many terms for the number of observations that we collected. To avoid an overfit, a much larger sample size is needed or reduce the number of independent variables that we have chosen.

### Richness

Overall, the species richness in the Val Mulix turned out to be rather small. We expect the actual number of species to be higher. The fact that there were some mammals that we could only identify to the genus level could have reduced the species number and could have also had an impact on the abundance data. A solution for this problem would be to add some adhesive tape to the MammaliaBox to collect hair samples that could be genetically analyzed to the subspecies level. Another factor that had an impact on the abundance data is the method we used to classify the events. If an individual left the box for more than five minutes and returned 6 minutes later, it was considered as a new individual, although it could have been the same. This means that we might have overestimated the abundance of the individual species. This issue could also be solved with the genetic analysis. The higher Shannon diversity index that we found when calculating it with the data of this and of last year's monitoring together also supports the theory, that the actual biodiversity might be higher. It will be interesting to

calculate the Shannon diversity index after some years of further data collection. With such a long-term study, also the mentioned population cycles could be better accounted for.

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# Changes in temporal biodiversity indices and species composition in the subalpine Mulix Valley in the Grisons, Switzerland

*Ricarda Ferrari, Isabelle Livebardon, Jonathan Pachlatko & Lea Schubert*

## Abstract

Alpine habitats are extremely important for biodiversity and provide a refuge for many rare and sensitive species. The diversity and composition of the plant community is characterized by a complex interplay of different factors such as temperature, duration of snow cover and the altitude gradient. In our research we considered if changes in species composition or cover can be detected after one year.

Our research area was in Val Mulix, a north-facing Valley in the Swiss Alps, where in 2019 thirteen permanent nested plot series including temperature loggers were installed. We resampled the vascular plants in all permanent plots in 2020. For analyzing changes in species composition, we calculated the species turnover, floristic dissimilarity, biodiversity indices as well as indicator values. Further we compared biodiversity indices and indicator between 2019 and 2020 per plot and computed an ordination and cluster analyze.

The species turnover and the Bray-Curtis Index show a moderate change in species composition. However, the results of direct comparison between biodiversity indices, indicator values and species number reveal no visible changes. The ordination and cluster analyze shows a similar result. The related plots (NW + SE and 2019 + 2020) are close together.

We could not detect any changes in the diversity and composition of vascular plants, but we determined observer differences. Nevertheless, our report can serve as a template for future summer schools and we expect that in few years the long-term biodiversity study can provide changes in the alpine plant community.

## Introduction

The habitats of the Alps are extremely important for the biodiversity of Switzerland but also for the whole of Europe, because they provide a refuge for many rare and sensitive biota. The Federal Office for the Environment (2009) points out that the grassland in the subalpine and alpine locations is about a quarter more species-rich in plants than the grassland in the lowlands. The existing species diversity in the Alps is characterized by a complex interplay of different environmental factors such as temperature or duration of snow cover and the close interaction with the cultural and natural landscape found there. Another potential driving force for the diversity and composition of the plant community in the high mountains is the altitude gradient (Baumann et al., 2016).

In view of the current loss of species, the Alpine regions therefore bear a great responsibility for many target and indicator species that react very sensitively to global climate change. In recent years, an increasing number of studies such as Cannone et al. (2007) or Choler (2018) have been published which

show that the already measurable temperature changes in the Alpine region have an effect on the performance of plants. Vegetation zones are shifting upwards and an increase in the shrub layer is becoming apparent.

The analyses of long-term field data are crucial to assess the quality of biodiversity and to estimate its susceptibility to temperature increases (Theurillat & Guisan, 2001). They are also relevant because effects of changes in biodiversity are only visible with a time lag (Magurran et al., 2010).

This case study should serve to improve quantitative predictions and close existing knowledge gaps about distribution patterns of certain species. Scientific articles such as Cannone et al. (2007), Morrison (2016), Verheyen (2018), Pauli et al. (2003), Theurillat and Guisan (2001) as well as the report of the Federal Office of the Environment (2009) form an important information basis for this report. In addition, recent research reports such as those by Verheyen (2018) or Morrison (2016) increasingly address the issue of observation errors. A topic that also plays an important role for the analysis described here and for this reason is taken up and critically examined in the discussion.

The report was prepared within the Master Summer School "Alpine Biodiversity Monitoring", which took place from August 10th, to August 20th, 2020 in the Parc Ela Nature Park in Grisons, Switzerland and takes up the topic of vegetative biodiversity in the Alpine region and its possible changes.

We focused on following questions:

- Can changes in species composition or cover be detected compared to the vegetation data of 2019?
- If changes are visible, which factors (environment, methodology, bias of the surveyor) might be responsible?

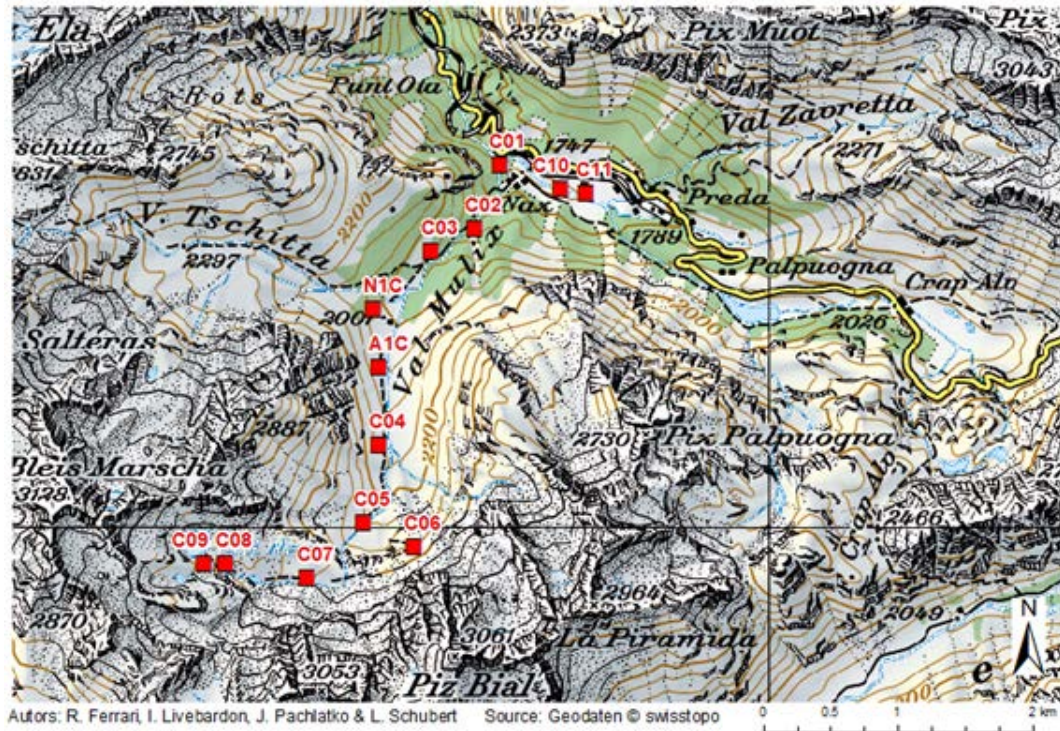
## Methods

### Study site

Our study was conducted in Val Mulix, a north-facing Valley in the Swiss Alps, which can be reached from the village Preda (Figure 1). The whole valley belongs to the regional Parc Ela in the canton of Grison, where biodiversity in general is of high importance.

Val Mulix consists mainly of granodiorite, granite or quartz rocks. Because of the silicate rocks, the soil of the grasslands and forest are mainly alkaline (Schmid & Müller, 2010). The climate around Preda is defined as continental, with a relatively low annual average (711 mm) and an annual temperature of 2°C at the local weather station in Samedan (MeteoSwiss, 2020). Typical is also the daily and sessional contrast of temperature and intense solar radiation.

Between the 10<sup>th</sup> and 16<sup>th</sup> of August 2020 we sampled vascular plants along the valley on thirteen permanent plots, that were installed during the "Biodiversity Monitoring Summer School" in the year 2019 (Figure 1). The plots were systematically placed between 1705 and 2650 meters above sea level, with an altitudinal difference of about 100 meters. The transect thus represents an altitude gradient through different alpine habitats. While subalpine forest communities and extensively used meadows can be found in the lower parts of Val Mulix, lean meadows dominate in the higher areas (Schmid & Müller, 2010).



**Fig. 13.** Study area in Preda, Canton of Grisons CH, with the locations and plot ID's of all permanent plots at the Val Mulix.

The plots C01-C09 and N1C were installed on the transect between Naz and the Lai Negr in near-natural vegetation. A further plot (A1C) was established in approx. 2050 m a.s.l. in a secondary grassland near to the plot N1C. Another two plots (C10 and C11) were installed in the alluvial plain of the Albula river. C10 was situated in open vegetation and C11 in forested vegetation. Further details on each plot can be found in Table 1.



**Table 8.** Overview of all plots of the monitoring, which were incorporated into the analysis and some of their abiotic factors.

Plot	Subplot	Vegetation type	Elevation (m a.s.l.)	Snow cover (d)	Aspect (°)	Inclination (°)	Max. micro-relief (cm)
A1C	NW	subalpine grassland	2027	184	70	26	15
	SE	subalpine grassland	2020	184	100	6	26
C01	NW	subalpine forest	1711	171	334	40	20
	SE	subalpine forest	1707	171	325	4	13
C02	NW	subalpine forest	1810	159	84	29	21
	SE	subalpine forest	1793	159	92	35	33
C03	NW	subalpine forest	1906	119	165	45	21
	SE	subalpine forest	2019	119	173	38	55
C04	NW	subalpine heathland	2096	194	90	26	41
	SE	subalpine heathland	2094	194	90	21	25
C05	NW	subalpine heathland	2211	162	120	30	34
	SE	subalpine heathland	2191	162	108	30	30
C06	NW	alpine grassland	2312	168	355	28	14
	SE	alpine grassland	2308	168	335	33	6,5
C07	NW	alpine grassland	2407	150	180	31	22
	SE	alpine grassland	2401	150	180	36	24
C08	NW	alpine grassland	2533	202	130	29	23
	SE	alpine grassland	2530	202	100	37	60
C09	NW	alpine grassland	2594	183	90	25	30
	SE	alpine grassland	2590	183	90	13	16
C10	NW	floodplain (habitat mosaic)	1713	160	301	10	6
	SE	floodplain (habitat mosaic)	1713	160	270	2	9
C11	NW	floodplain forest	1706	163	210	6	23
	SE	floodplain forest	1705	163	330	5	5
N1C	NW	subalpine forest	1977	175	90	21	36
	SE	subalpine forest	1974	175	90	23	36

### Field sampling

We used the same field sampling methods as described by Dengler et al. (2016). The plots consisted of 100 m<sup>2</sup> squares and the corners were aligned to the NE, SE, SW and NW. We recoded the plants in a nested-plot series of 0.0001, 0.001, 0.01, 0.1, 1.00 and 10 m<sup>2</sup> in the SE- and NW-corner using shoot presence method. For the 10 m<sup>2</sup> square we estimate the cover in percent for each determined species, for different vegetation layers and for other surfaces such as liter and dead wood. Further we measured

the aspect, inclination, max. microrelief, soil depth and ground layer. In the remaining area of the 100 m<sup>2</sup> square we searched for further species, which didn't occur in the 10 m<sup>2</sup> plots.

All plots were equipped with two temperature loggers in 10 cm below and 10 cm above soil. The temperature was recorded in 30 min. intervals over the last year (between August 2019 and August 2020).

### Statistical analysis

The vegetation data was statistically processed with R (Version 4.0.2) and R Studio (Version 1.3.959). To arrange vegetation lists in .csv format we used Excel (Office 365 ProPlus 2020). We calculated then the weighted Landolt indicator values of the vascular plants per plot using *VegeDaz* (WSL, 2019). R- Packages are subsequently written in italics.

#### *Species turnover & Floristic Dissimilarity*

After digitising the data recorded in the field, we merged the vegetation list of 2019 and 2020 and calculated the Bray-Curtis Index (*vegan*) pairwise per plot. Due to high dissimilarities we checked the species lists per plot with regard to their taxonomy. This led to a unified species list, where subspecies were included, spelling mistakes were corrected and outdated spellings were adapted. We repeated the Bray-Curtis calculation for the adjusted list and pointed out in which plant family high varieties occurred.

With the estimated species covers from the 100 m<sup>2</sup> plots of the years 2019 and 2020 we calculated the cover change for each species and plot and computed, how many and which species appeared or disappeared in 2020 compared to 2019 for each plot. Whereas huge number of species appeared and disappeared, we had a deeper look on the determination of plants and found differences in observation and notation. These differences were defined as not observed species, which were actually present (overlooking error), as not correctly identified species (misidentification error) and species which were notated at different taxonomic levels.

Using a presence/absence comparison between 2019 and 2020 we then carried out a *t*-test to assess their significance calculated the species turnover as:

$$\text{Total Turnover} = \frac{\text{Species gained} + \text{Species lost}}{\text{Total species observed in both timepoints}}$$

#### *Days of snow cover*

To calculate how many days each plot lay under snow cover, we used the data from the temperature logger. With the daily averaged air temperatures, between August 2019 and August 2020, we created a diagram for each plot (*ggplot2*), from which the temperature variations could be read. As soon as the temperature curve stabilized, we could assume that the logger was under snow.

#### *Comparison of Diversity-Parameter and Indicator Values*

The following calculations were only carried out with the 10 m<sup>2</sup> plots of the NW- and SW-corners from the nested-plot series; we regarded them as sufficiently independent.

To visualize potential changes in vascular plant structure, we derived the indicator values per plot and calculated the numerical parameters Shannon Index and Pielou's Evenness (*vegan*). Since the number of samples per plot type (vegetation type) is very small, the requirements for a *t*-test are not fulfilled. However, the similarity can be derived from boxplots (*ggpubr*). In addition to the plots by vegetation type, we compared the same parameters for all plots taken together by year. We tested the parametric assumptions for a *t*-test with the Shapiro-Wilk-test and the Levene-test (*base*).

### *Detrended Correspondence Analysis (DCA) & Hierarchical Clustering*

We calculated the ordination of the vegetation data with a DCA (*vegan*), in which we down weighted the rare species and projected a set of five environmental variables passively onto the ordination diagram.

To form a cluster of similar surveys we used the Bray-Curtis Distance table and applied an agglomerative clustering with complete linkage (*stats*). We conducted the visualization of the dendrogram with *dendextend*.

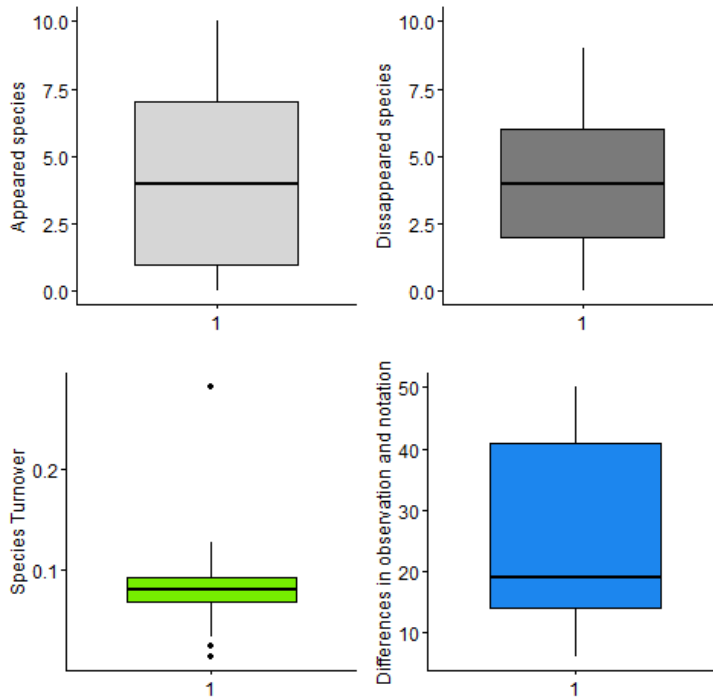
## Results

### Species turnover & Floristic Dissimilarity

Table 2 shows the species turnover and the number of species which bear a difference in observation and notation. The highest species turnover occurred in the plots C01 and the highest differences in observation and notation was found in the plot C05. In figure 2 we can see that the numbers of appeared and disappeared species per plot are very similar. The numbers of differences in observation and notation shows high variability over all plots.

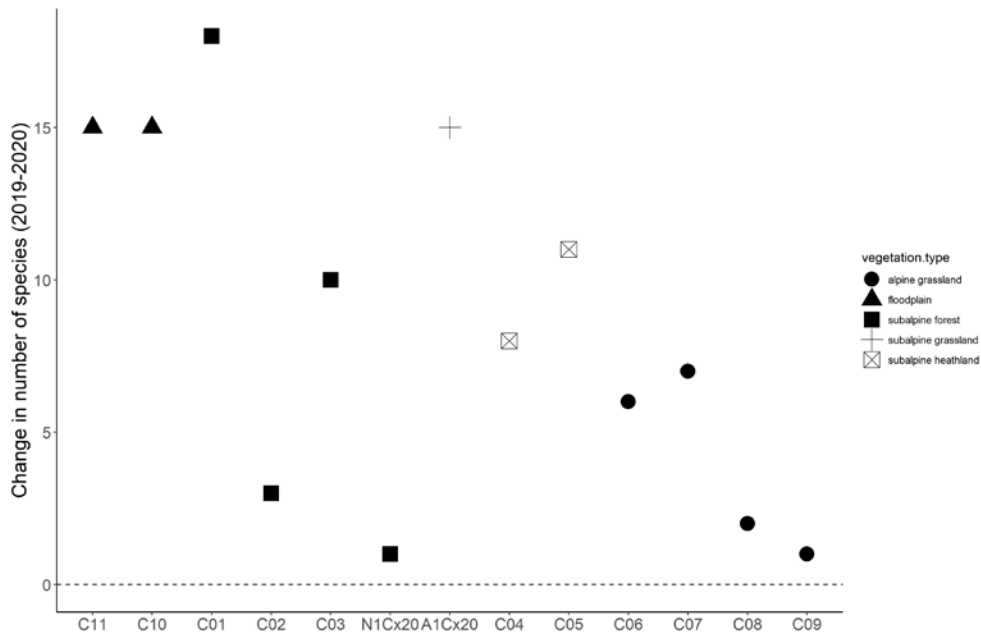
**Table 9.** Number of appeared and disappeared species (corrected list) in the 100 m<sup>2</sup> plots as well as species turnover and differences between 2019 and 2020 in observation and notation per plot.

Plot	C01	C02	C03	C04	C05	C06	C07	C08	C09	C10	C11	A1C	N1C
Appeared species	9	0	8	4	5	4	3	1	0	6	10	7	1
Disappeared species	9	3	2	4	6	2	4	1	1	9	5	8	0
Species Turnover	0.28	0.07	0.13	0.09	0.09	0.07	0.07	0.02	0.02	0.08	0.1	0.09	0.03
Differences in observation and notation	14	6	14	16	50	25	27	19	13	48	41	49	9

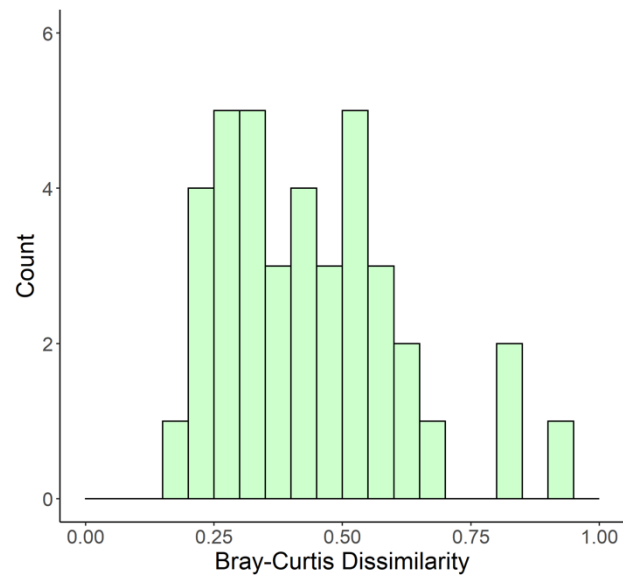


**Fig. 14.** Boxplot of the 100 m<sup>2</sup> plot comparison between 2019 and 2020: Appeared and disappeared species per plot, Species-Turnover and differences in observation and notation. The values are listed in Table 2.

The change in number of species (Sum of appeared and disappeared species per plot) between 2019 and 2020 is with an average of 8 - 9 species per plot highly significant (One Sample *t*-test,  $p < 0.001$ ,  $t = 5.2564$ ) (Figure 3).



**Fig. 15.** Change in number of species (Sum of New and Disappeared Species) in the 100 m<sup>2</sup> plots. On the X-axis the plots are arranged according to altitude, the shape of the point gives information about the vegetation type. The lower-lying floodplain plots show a higher species change. The changes are significant ( $p$ -value =  $< 0.001$ ).

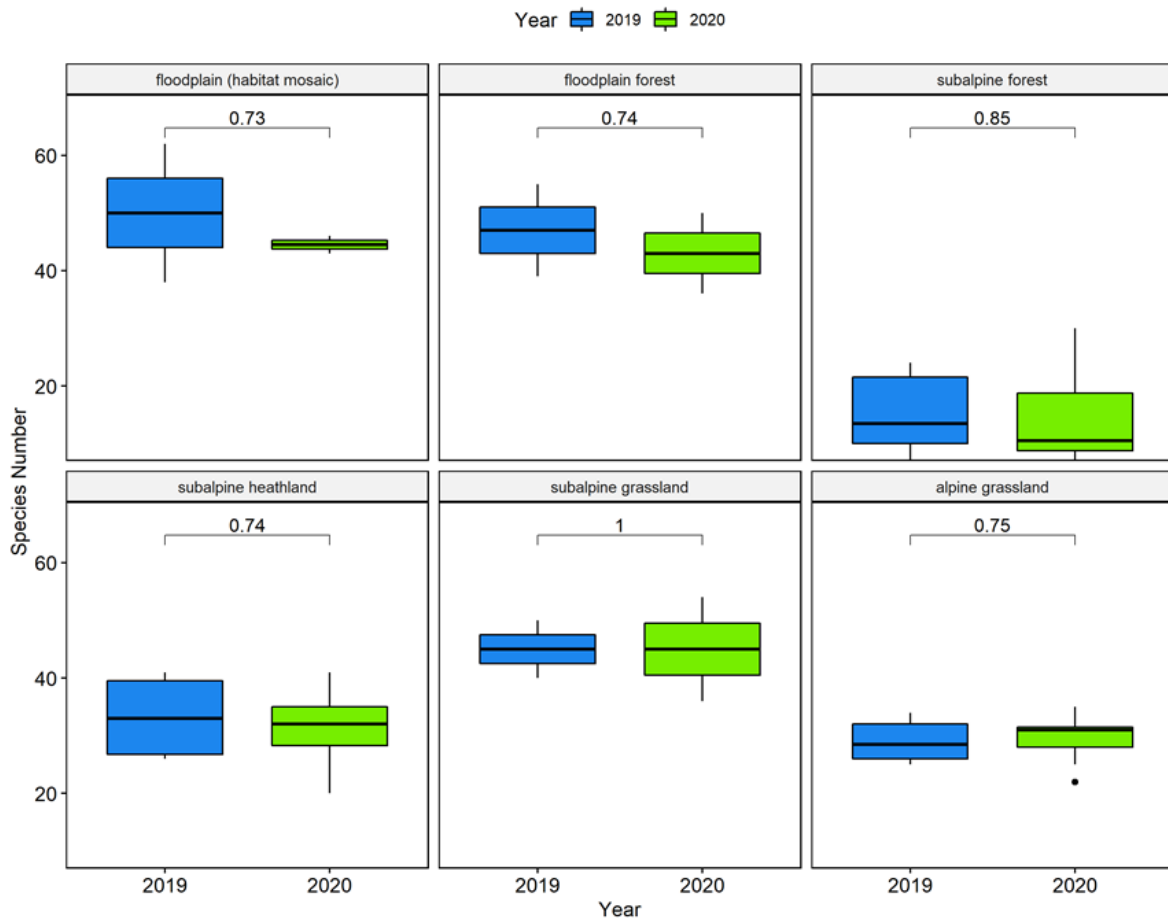


**Fig. 16.** Histogram of the Bray-Curtis Dissimilarity between the plots of 2019 and 2020. Most of the plots show a moderate change in species composition since the last year.

The above results of the 100 m<sup>2</sup> plots can also be found in the Bray-Curtis Dissimilarity of the compared 10 x 10 m<sup>2</sup> plots. The histogram (Figure 4) shows how most of the plots have undergone a moderate change since last year. Three outliers find a Bray-Curtis value close to one, which is a very large change. As we can see in Table 2, there was a considerable species turnover in some cases, which all have been accompanied by an eminent difference in the notation of the taxonomy.

### Comparison of Diversity-Parameter and Indicator Values

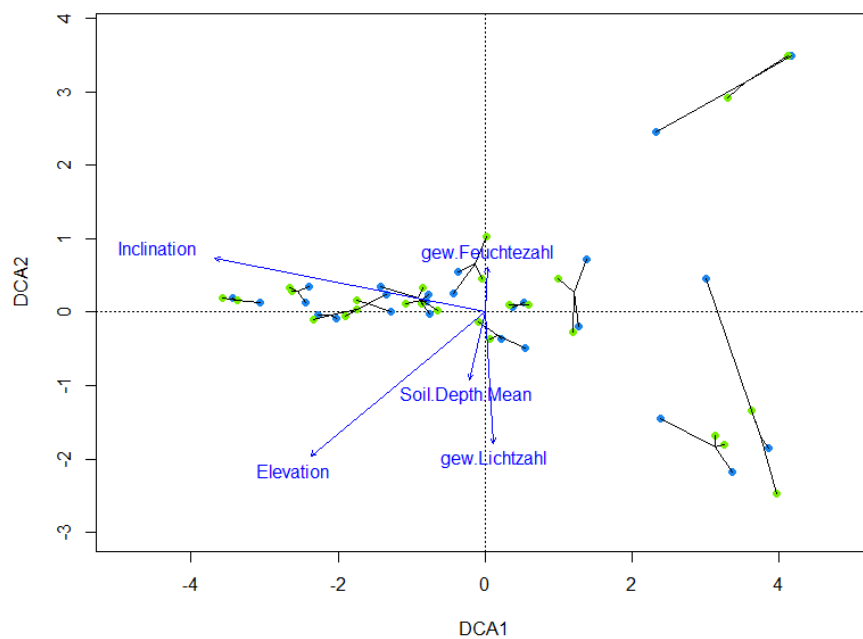
The comparison between all plots from 2019 and 2020 showed no dissimilarities in the biodiversity indices (species number, Shannon and Evenness) and indicator values (Landolt's Weighed Moisture, Light and Nutrient Value). The parametric requirements are met, and the *p*-values vary between 0.39 and 0.96 (i.e. show no significant numerical differences). Additionally, the comparison of the same indices and values per plot type also does not indicate any significant change between 2019 and 2020. The parametric assumptions are not fully met, as the sample size per vegetation type is very small. The similarity is in the most cases visually obvious. Figure 5 shows the comparison of the species number per vegetation type and year.



**Fig. 17.** Number of species per vegetation type and year. The number (p-value of the t-test) is everywhere far above 0.05. Even if the parametric conditions are not given, it is visible how similar the recordings are.

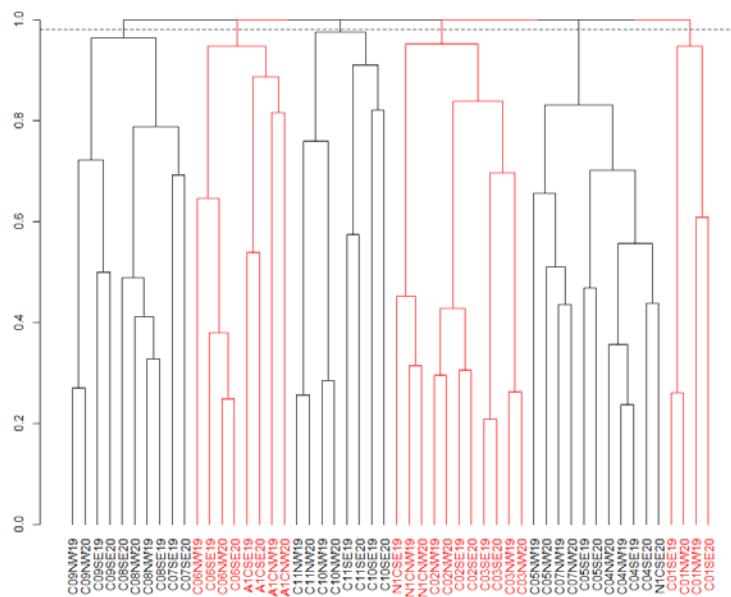
### Detrended Correspondence Analysis (DCA) & Hierarchical Clustering

Axes 1 and 2 in Figure 6 explain most of the variation in species composition with a total inertia of 11.95 % (eigenvalues: 0.87 and 0.69). The gradient length for the first axis is 7.75 SD, which indicates an almost double species change along the gradient. The underlying gradient (negatively related to inclination) thus shows a high ecological significance, resp. explains a maximum of variance. The second axis with a length of 5.96 SD (>4 = there are no common species at the top and bottom), is negatively related to Soil Depth and the Weighted Light Value and positively related to the Weighted Moisture Value.



**Fig. 18.** DCA Ordination of 52 vegetation plots with a total of 392 species. Eigenvalues of the first/second axis: 0.87 and 0.69, gradient length: 7.7 and 6 SD. The position of the plots is shown by points (blue: 2019, green: 2020). Corresponding plots (NW and SE & Year) are connected by a black line. Finally, the correlation of the five environmental parameters with the two ordination axes is visualized via arrows (Abbreviations: gew. Feuchtezahl = Weighted Moisture Values, gew. Lichtzahl = Weighted Light Value).

From the dendrogram of the cluster analysis (Figure 7), six main vegetation types, which are more similar to each other than to the others, can be identified in the 52 included plots. The main types are very similar to the vegetation types addressed in the field. Group 1 (C09, C08, C07SE) builds the alpine grasslands and group 2 (C06, A1C) includes an intermediate stage from alpine to subalpine grassland. Group 3 (C11, C10) contains the alluvial plots, group 4 (N1C, C02, C03) the subalpine forests and group 5 (C05, C04, C07NW) the subalpine heathland). Group 6 (C01) consists of a deviating plot of subalpine forests.



**Fig. 19.** Dendrogram of the Agglomerative Clustering using complete linkage. The six main groups of similar vegetation plots are shown in red and black.

## Discussion

The vegetation analyses on which this work is based served to answer the question whether the vegetative biodiversity in Val Mulix has changed compared to the previous year and which factors could be responsible for this.

With this question, the present study is in line with studies such as those by Markham et al. (1993), Theurillat and Guisan (2001) or Beniston (1994) with the focus on a possible change in Alpine biodiversity and potential effects on the local ecosystems. It provides data that are relevant for research, since high mountain ecosystems are considered particularly vulnerable to climatic changes.

The present study is also important because the vegetation in the Alpine region can be used as a sensitive ecological indicator for the effects of climate change, since abiotic factors, especially climate, dominate over biotic factors. In addition, many high mountain plants are long-lived and slow-growing, which means that climate-related changes in vegetation are more a consequence of ongoing climate changes than of short-term climate fluctuations (Pauli et al., 2003). Within the analysis presented here, no significant changes in species diversity could be detected compared to the previous year. Although the methods used were well suited to answering the questions, an effective quantification of changes in vegetation structure due to climate change also requires, as Pauli et al. (2003) emphasize, a monitoring period longer than one year. The changes in the vegetation, which were nevertheless determined, were attributed to observation errors due to their extent. The problem of observation errors is already widely discussed in the literature. In our analysis we looked at similar types of error as described, by Morrison (2016). In this study, however, they also analyzed if the coverage of species was estimated inaccurately. Due to time constraints, we were unable to address this issue. For further investigation it would certainly be advisable to look at the errors separately.



Regarding the causes for the occurrence of observation errors, Morrison (2016) mention (i) the difficulty to precisely identify a species, (ii) the ecological site conditions such as bad weather or steep topography and (iii) the observers' experience with vegetation analysis. Verheyen et al. (2017) add that images taken by many different people should be interpreted with caution. The most frequent differences in determination between 2019 and 2020 were found in *Asteraceae*, *Poaceae* and *Juncaceae*. These are plant families that are rather difficult to determine, especially in the non-flowering state, and therefore require some prior knowledge and experience. Also, the number of different observers, critically considered by Verheyen et al. (2017), is certainly a relevant reason for differences in determination between the two years in this comparative study.

Due to the rapidly changing weather conditions during this year's analyses and the partly very steep topography at the selected plots, the occurrence of false determinations due to the site conditions mentioned by Morrison (2016) is not unlikely.

The observation errors that have occurred underline the importance of using comparable survey methods and a unified research team for long-term studies. They also show how important good plant knowledge is for such studies. With regard to future Summer Schools therefore the authors recommend a distribution of a list of vascular plant species and their characteristics in advance to make the determination more reliable.

In order to determine possible environmental influences on the change in vegetation structure, data from temperature loggers were also included in the statistical analysis. However, due to the short period of time available, it is difficult to accurately interpret the temperature data and the length of the snow cover and its possible influence on the vegetation. Nevertheless, Böhm et al. (2001) emphasize that the inclusion of temperature loggers in long-term studies is of great relevance, since air temperatures in mountain regions are expected to increase twice as much as the global mean air temperature.

A closer look at the duration of snow cover, including ridges and slope inclination in Val Mulix would be relevant in the future, as some studies show that warmer winters lead to a shift of biodiversity to higher mountain ranges and an increase in shrub layer, which could lead to a loss of habitat specialists (Cannone et al., 2007; Choler, 2018; Theurillat & Guisan, 2001). Choler (2018) also assumes that the winter snow cover is a key parameter for the performance of frost-sensitive plants. However, Theurillat and Guisan (2001) are critical of a holistic height shift of vegetation, since the species will not find equivalent areas with similar physiographic conditions at higher altitudes due to steep slopes and stony soil conditions.

In future vegetation analyses in Val Mulix, it might also be interesting to integrate the management systems of the selected areas into the analysis in order to find out how changes in agricultural structures affect the grasslands there or how floristic shifts occur (Peter, 2007).

In conclusion, the versatile data obtained in this study provide an important knowledge base for understanding the influence of environmental parameters on plant communities in the Alpine regions and their biodiversity. It is therefore important to incorporate this data into future political decisions such as the Energy Strategy 2050, which focuses on mountain regions as a location for future hydroelectric power plants and other renewable energies (Bundesamt für Umwelt, 2009).

## Conclusion

As expected, we could not detect any change in the diversity and composition of the vascular plants in Val Mulix within one year. For this reason, we were not able to validate the drivers responsible for the long-term changes in the vascular plants in investigated Alpine region. Nevertheless, the analysis of our report can serve as a template for future summer schools, as changes in the occurrence and distribution of the Alpine vascular plant community are predicted.

As we noted in the discussion, many observers and different levels of experience often lead to observation errors. Possible misdeclared species turnover should therefore be taken into account in future reports. The collected data should always be carefully reviewed and adjusted if necessary. To avoid observation errors already in the field, it is important that survey teams have a balanced level of experience and work accurately, which in turn requires sufficiently planned time.

We expect that already in two years, when the next summer school in Preda is planned, the collected temperature data will provide more information on the relationship between temperature, snow cover and species occurrence. In addition, the new monitoring data can re-evaluate whether some species changes are emerging.

In general, we are confident that the long-term biodiversity study in Val Mulix, one of the few high-altitude transects in Europe, can provide important insights into the loss of biodiversity and changes in the Alpine plant community.

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## Patterns of alpine plant diversity in Preda (GR)

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### Abstract

Various environmental factors as well as human management practices influence the plant composition of alpine vegetation. This study contributes to the general knowledge of plant diversity patterns in the swiss alps. We analyzed the alpine and sub-alpine flora in two neighboring valleys located near the Albula pass, characterized by locally varying bedrock, diverse vegetation types and elevation gradients. We recorded vascular plant species composition in 19 100 m<sup>2</sup> plots, each with two series of nested subplots ranging from 0.0001 to 10 m<sup>2</sup>, as well as a set of environmental parameters. We analyzed species richness at different special scales. For the 10 m<sup>2</sup> and 100 m<sup>2</sup> plots, we calculated the species richness, evenness and Shannon index which we modelled as a function of the environmental parameters by linear and generalized linear models. We found a significant positive effect of the heat index on evenness, Shannon index and species richness. The vegetation type forest had a negative influence on plant diversity. Controversially, the soil-pH has a negative effect on Shannon index and evenness, while it has a positive effect on species richness. Also, the tree cover showed different effects on our response variables: a negative effect on species richness and a positive effect on evenness. Interestingly elevation has a slight negative effect on the Shannon index and evenness. Finally, we suggest including precipitation and microrelief as predictors as well as further taxonomic groups for subsequent studies.

### Introduction

The composition of alpine semi-natural grasslands in Europe results from the influence of various environmental factors and human management (Bätzig, 2005; Pittarello et al., 2020). Within the mountain habitats, meadows and pastures have the highest plant diversity. They have an important production function as well as a high natural value (Väre et al., 2003). Alpine grasslands also provide ecosystem services (Haines-Young & Potschin-Young, 2018). Identifying the drivers of plant diversity is the aim of many vegetation ecology studies (Baumann et al., 2016; Palpurina et al., 2017; Polyakova et al., 2016; Turtureanu et al., 2014). The effect of environmental factors, for example elevation, pH-value or nutrient input on plant diversity is often hump shaped (Baumann et al., 2016; Pittarello et al., 2018).

A possible driver for plant diversity is the soil-pH, influenced by the underlying or surrounding bedrock. The soil pH-plant diversity relationship is explained by physiological stress, which occurs at the extreme ends of the pH gradient. These findings relate to the intermediate stress hypothesis (Grime, 1979) and the physiological tolerance hypothesis (Currie et al., 2004). Acidic soils with a pH < 4, are thought to constrain the plant diversity because of high phytotoxicity (Abedi et al., 2013; Tyler, 1996). Nutrient limitation is also thought to play a role in limiting species richness on acidic soils (Rorison, 1980). In turn, on soils with pH >7, phosphorus and iron have decreased solubility gradients which could play a role in limiting the fine-scale species richness (Tyler, 1996; Zohlen & Tyler, 2000). But even considering these findings, the effect of the soil pH on the plant diversity is not univocal. For instance, the soil pH has been

found to have a positive, a negative, a hump-shaped or no effect on plant species diversity of dry grasslands (Polyakova et al., 2016).

Elevational gradients are also considered as of high relevance for understanding plant diversity patterns and community assembly rules (Baumann et al., 2016). An increase in elevation goes hand in hand with major changes in temperature and amount of precipitation, among others (Rahbek, 2005). The resulting steep environmental gradients exemplify how biodiversity responds to major environmental changes (Baumann et al., 2016). Some studies show a unimodal relationship between species richness and elevation, but the support for these findings are not unanimous, indicating that other environmental factors must be considered as well (Baumann et al., 2016).

Other environmental variables that are frequently analyzed to explain plant diversity include soil fertility, grazing intensity and land use, microrelief, topographic wetness, soil humidity, and climate. Yet, the effect and importance of many of these factors have also been found to vary significantly between studies and cannot be generalized (Polyakova et al., 2016). Scale dependence, meaning that the effect of environmental factors on plant diversity is different depending on the spatial grain size, which is considered, might be a possible explanation for diverging results (Baumann et al., 2016; Turtureanu et al., 2014).

The aim of our study is to contribute to the general knowledge of plant diversity patterns in the Swiss alps. The study area, located on the Albula pass in the canton of Grisons, is particularly suited for this project because of the locally varying bedrock, the diverse vegetation types and the elevation gradients present in the region. We sampled vascular plant composition in nested plots of different sizes along edaphic, bioclimatic and topographic gradients to answer the following questions: (i) Which environmental parameters affect plant diversity in Val Mulix and Val Zavretta (canton GR)? (ii) How does plant diversity differ across different spatial scales?

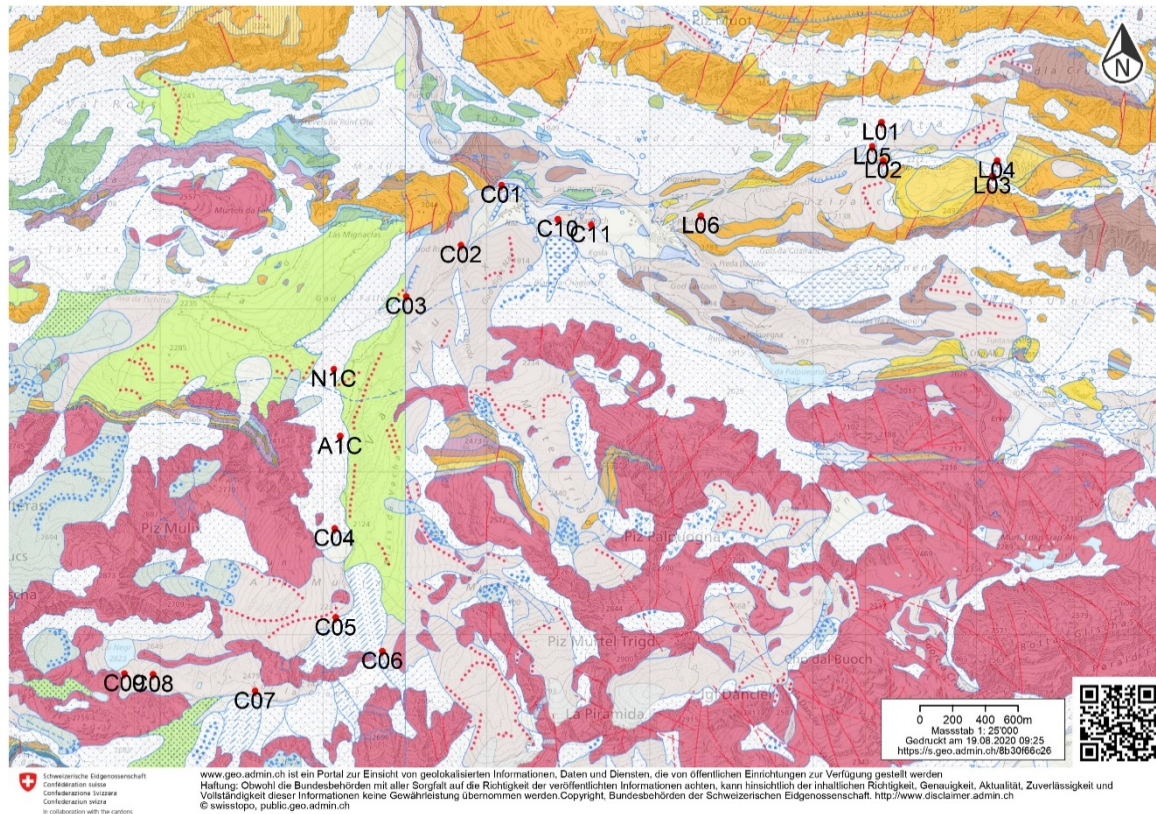
## Methods

### Study site

The investigated plots are located in the area of the Val Mulix (1746-2623 m a.s.l.) and Val Zavretta (1789-2888 m a.s.l.) in the canton of Grisons in the Swiss alps. Interestingly, these two neighbouring valleys lie under the influence of two different geological formations. The Val Mulix lies on debris of mostly Granodiorite (silicate stone), whilst the Val Zavretta is formed by moraines of Dolomit (limestone) (Swisstopo, 2020). The pH of the soil is dependent of numerous factors but, in general, it is rather alkaline when the bedrock is formed of limestone and rather acidic when the bedrock consists of silicate (Agroscope, 2014). Considering the geological map of the region (Figure 1), the soil-pH of the Val Mulix was expected to be predominantly acidic whilst the soil-pH of the Val Zavretta was expected to be rather alkaline. The annual average temperature is 1.9 °C and the average precipitation is 700 mm (data 1981- 2010, climate station Samedan). The landscape of the region is characterized by alluvial plains, subalpine forests, dwarf-shrub heath, subalpine and alpine grasslands, thus offering a wide array of different vegetation types and site characteristics which can be studied and compared.

We based our study on 19 permanent (square-shaped) 100 m<sup>2</sup> plots which correspond to the European Dry Grassland Group (EDGG) multi-scale “biodiversity plots” (Dengler et al., 2016). In general, they were chosen as to capture the biggest variability of local vegetation types. 13 Plots were installed during the

summer school 2019. 11 of those plots are situated along an elevation transect in the Val Mulix. They are placed every approximately 100 m of elevation between 1750 and 2650 m a.s.l. in near-natural vegetation (plots C01-C09 and N1C). An additional plot is situated at approximately 2650 m a.s.l. as to include secondary grassland vegetation (plot A1C) as well as near-natural forest vegetation (plot N1C) of the same altitude. Finally, two plots are situated where the two valleys meet, in the alluvial plain of the Albula river: one in open vegetation (plot C10) and the other in forested vegetation (plot C11) (Figure 1). In 2020 six additional plots were set up in the Val Zavretta. Their location was chosen subjectively, with the aim to represent the variability of the vegetation on limestone (plots L01-L06).



**Fig. 1.** Geological map showing the spatial distribution of the studied plots. The red surfaces indicate granodiorit (silicate) bedrock. The orange surfaces indicate dolomit (limestone) bedrock (Swisstopo, 2020).

## Field sampling

The sampling was carried out in August 2020 by master students and lecturers of the University of Applied Sciences in Wädenswil (ZHAW). The nested-plot approach (“biodiversity plots”) according to Dengler et al. (2016) was used. The species were recorded in subplots of 0.0001, 0.001, 0.01, 0.1, 1, and 10 m<sup>2</sup>, located in two opposite corners (NW and SE) of a 100 m<sup>2</sup> (10 m × 10 m) plot. The species cover in percentage was estimated in the 10 m<sup>2</sup> subplots. The 100 m<sup>2</sup> plots were examined for additional species which were systematically attributed a cover of 0.01 % if not of particular importance. Cryptogams and fungi were not recorded because of lacking capacity. Additional structural and environmental variables were recorded in the 10 m<sup>2</sup> subplots according to Dengler et al. (2016). Table 1 provides a list of the recorded structural and environmental parameters.



**Table 1.** Summary of recorded environmental and structural variables

Environmental parameter	Recording method	min	max	mean
Elevation	Measured in m a.s.l.	1705	2594	2115.90
Aspect	Measured in °	0	355	175.30
Inclination	Measured in °	2	52	27.10
Maximum microrelief	Measuring the highest relief structure (cm)	5	60	23.00
Soil depth	Depth measured with an iron pole at five spots (cm)	2.6	45.8	14.10
Height of herb layer	Measured with a disc along a pole at five spots (cm)	0	95	9.02
Tree cover	Estimated (%)	0	80	9.20
Shrub cover	Estimated (%)	0	75	9.05
Herb cover	Estimated (%)	5	96	62.26
pH	Measured from with the multimeter (pH)	3.94	7.91	6.20
ec	Measured with the multimeter (mS/cm)	31	480	168.90
Veg. Type	Classifications in field	Floodplain, forest, subalpine heathland, grassland		
Land Use	Classifications in field	Grazed, abandonment, managed		
Relief position	Classifications in field	Upper slope, middle slope, lower slope, plain		
Litter	Estimated (%)	0.1	95	26.00
Dead wood	Estimated (%)	0	20	2.32
Fine soil cover	Estimated (%)	3	100	71.50
Gravel cover	Estimated (%)	0	60	6.36
Stone cover	Estimated (%)	0	80	18.11
Total stone cover	Sum of gravel and stone cover (%)	0	97	24.46

The soil pH and electrical conductivity were derived from a mixed soil sample, taken from the top 10 cm in several random locations within the 10 m<sup>2</sup> subplots. The soil samples were air-dried for further analysis. 10 g of the sieved soil sample was mixed with 25 g of distilled water (aqua dest.) in a 50 ml plastic test tube. Before measurement, the mixture was left to stand for at least one hour. During this time the samples were shaken once. Afterwards the pH and electrical conductivity were measured with the multi meter (HI991300, HANNA instruments) (Dengler et al., 2016).

### Data analysis

All statistical evaluations were performed with the software R Studio Version 1.2.1335 (R Core Team, 2019). From the results of the vegetation surveys the species richness (S), Shannon index (H) and evenness (E) were calculated with the R-Package vegan (Oksanen et al., 2019). The species richness was calculated for all plot sizes. Since the Shannon index and evenness take the cover of the species into account (Begon et al., 1996), these indices were calculated for the 10m<sup>2</sup> subplots and the 100m<sup>2</sup> plot respectively. These three indices are the dependent variables in our models. As independent variable we used the heat index (calculated from aspect and inclination according to Olsson et al., 2009) soil depth, tree cover, pH-value, electrical conductivity, elevation and total stone cover.

To assess the influence of environmental variables on the Shannon index and evenness, a multi linear model with the function `lm` (Chambers, 1992) within the R-Package `stats` (R Core Team, 2019) was calculated. For species richness, a general linear model (`glm`) with poisson distribution of errors from the `stats` package was used (R Core Team, 2019).

To assess the correlation among the predictor variables, the function `correlation_test` from the package `lme4` (Bates et al., 2015) was used. Due to data distribution the Kendall method was used. In case of a strong correlation (Kendall-R >0.7) between two variables, we kept the one we considered ecologically more meaningful. Correlations were found between total stone cover and fine soil as well as total stone cover and stones. Therefore, only total stone cover was used for the variable selection.

For each variable a model with the linear term and a model with the linear and quadratic term was calculated. The AICc values of the models were compared with the function `AICcTab` from the R-Package `MuMIn` (Barton, 2019). For automatic variable selection with the `dredge` function from the package `MuMIn` (Barton, 2019), the terms with lower AICc were selected if  $\Delta AICc > 2$  to build the full-model. Considering the Principle of Parsimony, only the linear term was chosen in the case of  $\Delta AICc < 2$  (Busemeyer et al., 2015). The model averaging, including the direction of the relationship between the predictor and the responds variable, was done with the function `model.avg` from the package `MuMIn`. The weights of the different variables were calculated with the importance function (Barton, 2019). For the final model, only those variables were considered whose contribution to the model is > 0.5. With the function `summary` from the package `base` (R Core Team, 2019) an overview of the contribution of the variables was generated and the adjusted R<sup>2</sup> (only for the `lm`) was calculated. The results were visualized with the functions `plot_model` and `tab_model` from the package `sjPlot` (Lüdecke et al., 2019) and `plot_grid` from the package `cowplot` (Wilke, 2019).

In order to test the distributions of the residuals of the models, residual plots were conducted. The visual inspection showed mostly homogeneity of variance and normal distributed residuals. Further, spatial auto correlation for all subplots within the biodiversity plots was tested by Moran's I test based on a list of neighboring plots, using the `ape` package (Paradis & Schliep, 2019). Finally, the GLM was tested for over dispersion by the function `testDispersion` from the package `DHARMA` (Hartig, 2020).

## Results

### Species richness at different spatial scales

Counting all the plots together, we identified a total of around 349 species. This number fails to be very precise due to the missing precision in the determination of a few specimens. Nevertheless, we consider this number as being representative of the species richness over the surface of all the plots. Considering the 100 m<sup>2</sup> plots, the most common vascular plants that were found were *Homogyne alpina* (in 14 plots), *Juniperus communis* subsp. *alpina* (in 12 plots), *Festuca rubra*, *Leontodon helveticus*, *Rhanunculus montanus*, *Solidago virgaurea* and *Vaccinium vitis-idaea* (in 10 plots).

Mean total species richness varied between 2.3 species at the smallest spatial scale (0.0001 m<sup>2</sup>) and 48.5 species at 100 m<sup>2</sup> scale. Considering the 100 m<sup>2</sup> plots, the total species richness was lowest in plot N1Cx, located in forest vegetation at 1974 m a.s.l. It was highest in plot C10x located in open vegetation of the alluvial plain (Table 2).



**Table 2.** Overview of the species richness encountered in the all nested-plot series and normal plots of the study

Area in m <sup>2</sup>	Species richness			Evenness			Shannon-Index		
	min	max	mean	min	max	mean	min	max	mean
0.0001	0	6	2.3						
0.001	0	8	3.3						
0.01	0	11	6.2						
0.1	2	21	11.3						
1	3	36	18.8						
10	9	56	30.1	0.17	0.81	0.56	0.38	2.76	1.87
100	14	88	48.5	0.25	0.70	0.56	0.83	3.10	2.13

### Species diversity– environment relationships

Table 2 and Figure 2 show the influence of the environmental parameters on the final model for the Shannon index, evenness and species richness.

#### *Shannon index*

The heat index and the vegetation types “grassland” and “subalpine heathland” have a positive influence on the Shannon index, with only the heat index being significant. Except tree cover, all variables (elevation, ec, tree cover, pH) have a significant negative influence on the Shannon index. 58.1% of the model for the Shannon index can be explained by the variables (adjusts R<sup>2</sup>).

#### *Evenness*

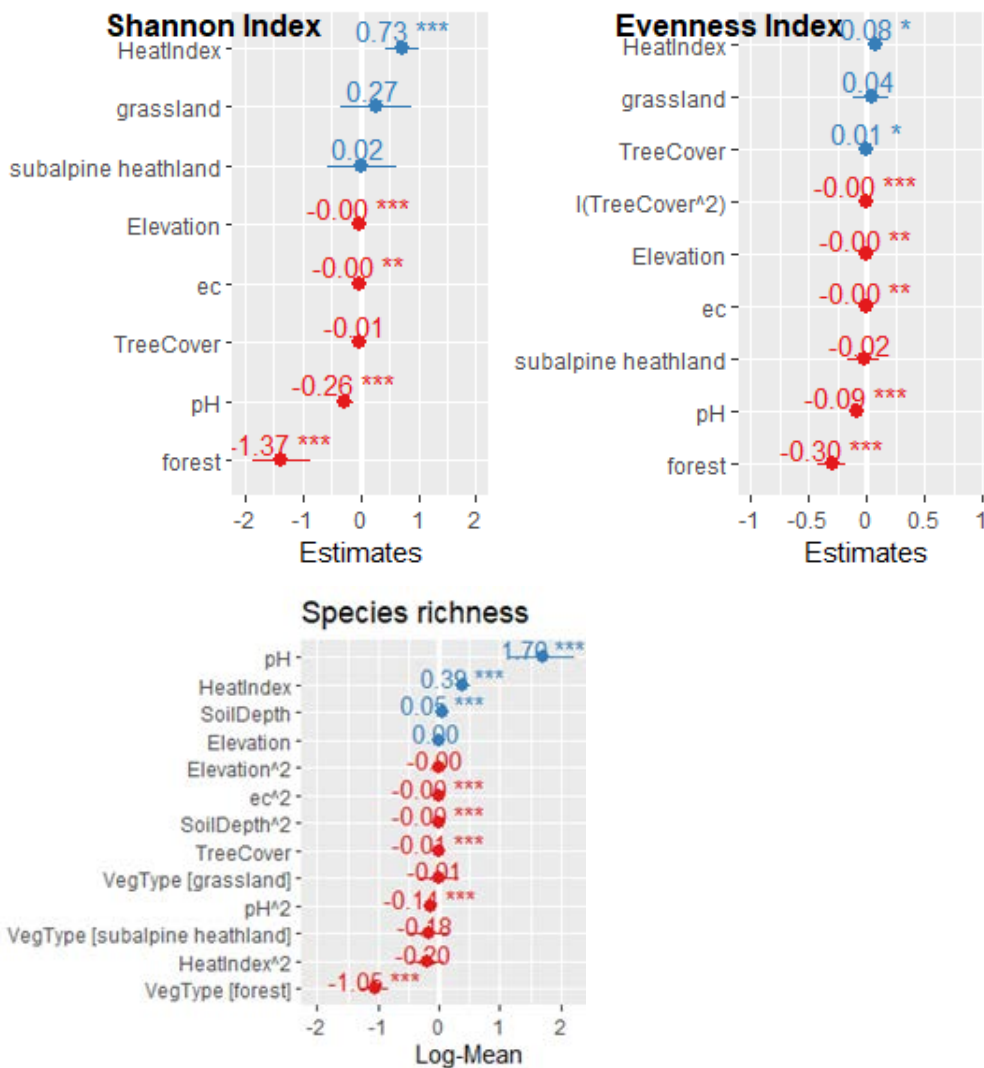
The environmental parameters heat index, the vegetation type “grassland” and tree cover have a positive effect on evenness, whereas the latter variable has no significant influence. The parameters elevation, ec, the vegetation type forest and the pH value and the square term of tree cover have a significant negative effect on evenness. The vegetation type subalpine heathland also has a negative effect but is not significant. The evenness model is explained to 54.4% by the variables.

#### *Species richness*

The heat index and the pH value have a significant positive influence on species richness. For the pH value, the negative square term must also be considered. The vegetation type forest and the tree cover had a negative influence on the number of species. For electrical conductivity, the negative square term has a significant effect on species richness.

**Table 2.** Influences of individual variables on Shannon index, evenness and species richness. Ec = electrical conductivity; Est = Estimate; std. err = standard error.

Predictors	Shannon Index			Evenness Index			Species richness		
	Est	std. err	p	Est	std. err	p	Est	std. err	p
Intercept	7.926	1.116	<0.001	1.852	0.257	<0.001	-4.033	2.339	0.085
Veg. type: forest	-1.367	0.249	<0.001	-0.297	0.060	<0.001	-1.053	0.121	<0.001
Veg. type: grassland	0.269	0.311	0.391	0.041	0.074	0.576	-0.010	0.171	0.953
Veg. type: subalpine heathland	0.024	0.294	0.934	-0.023	0.070	0.739	-0.182	0.181	0.314
ec	-0.002	0	0.003	0.000	0.000	0.007			
ec <sup>2</sup>							0.000	0.000	<0.001
Elevation	-0.002	0	0.001	0.000	0.000	0.008	0.003	0.002	0.191
Elevation <sup>2</sup>							0.000	0.000	0.068
Heat Index	0.729	0.139	<0.001	0.077	0.032	0.021	0.392	0.063	<0.001
Heat Index <sup>2</sup>							-0.200	0.139	0.151
pH	-0.264	0.069	<0.001	-0.086	0.016	<0.001	1.697	0.271	<0.001
pH <sup>2</sup>							-0.144	0.022	<0.001
Tree cover	-0.008	0.004	0.052	0.007	0.003	0.015	-0.005	0.002	<0.001
Tree cover <sup>2</sup>				0.000	0.000	<0.001			



**Fig. 2.** Graphical representation of influence of the variables on Shannon index, evenness and species richness.

## Discussion

### Species richness at different spatial scales

Our findings show that species richness at different grain sizes vary greatly from one plot to another. Comparing the 10 m<sup>2</sup> subplots with the large 100 m<sup>2</sup> plots, a difference of the Shannon index and of the evenness can also be observed (Table 2). A further step would be to model species richness at the seven different grain sizes (0.0001–100 m<sup>2</sup>) as a function of the environmental predictors, as it was done by Baumann et al. (2016) and Turtureanu et al. (2014) amongst others. This would enable us to find out if different environmental factors are of particular influence on species richness at different scales. As several authors have found (e.g. Baumann et al., 2016; Polyakova et al., 2016; Turtureanu et al., 2014), we expect the environment – species richness relationship to be scale dependent. For instance, the conceptual model of (Shmida & Wilson, 1985) states that diversity at finest scales is driven predominantly by niche relations, while the heterogeneity of the environment is more relevant at intermediate scales. Furthermore, climatic variables have been found to gain importance with increasing grain size (Field et al., 2009; Siefert et al., 2012).

Another analysis which could be undertaken to assess the species – area relationship is the calculation of the z-values. The Power law can usually give a good approximation of Species – Area relationship (SARs) at any spatial scale (Dengler, 2009). The exponent z of the power law has been successfully used as an informative tool to compare beta-diversity between habitats, taxa and scales (Drakare et al., 2006).

### Species diversity – environment relationships

Overall, in accordance with our expectations, Shannon index, evenness and species richness showed contrasting patterns in relation to the predictors. Comparing the varying influence of different environmental parameters on different indices of biodiversity enables us to acquire a more holistic view of the patterns driving vegetation diversity.

The predictor which has a significant negative influence on all three indices is the vegetation type “forest” (Table 2). As a matter of fact, the two most species-poor plots (C1 and C2) are situated in forested vegetation. This result emphasizes the risks of land abandonment and the importance of maintaining a variety of land-use types to preserve species diversity (Maurer et al., 2006).

Further, a significant positive effect of heat index on all indices can be observed. In other studies, solar radiation has repeatedly been found to have a positive effect on grassland diversity in regions where extreme summer drought is not an issue (Klimek et al., 2007; Turtureanu et al., 2014). Also, as inclination is included in the heat index calculation, our results are in accordance with the findings of previous research showing that plant-diversity is positively affected by slope (Pittarello et al., 2020).

We found that elevation has a slight negative effect on the Shannon index and evenness. This finding is surprising, as we would have expected an increase in species richness with elevation (with a slight decrease in the highest elevation), based on a study of the BAFU (2009). Our results might partially be explained by the fact that we sampled the alluvial plain, representing the highest plant diversity over all the plots, which is located at the lowest elevation.

Controversially, the Soil-pH has a slightly negative influence on Shannon index and evenness, while it has a positive effect on species richness. These results are to be interpreted with caution. In literature, examples of strong and weak, positive and negative effects of soil-pH on plant diversity can be found

(Polyakova et al., 2016; Turtureanu et al., 2014). As supported by (Pärtel, 2002), the regional context influences the species richness – soil pH relationship. For instance, Palpurina et al. (2017) have found that precipitation, uniquely or together with soil-pH explain more variation in species richness than pH alone. Also, the tree cover showed different effects on our response variables: a negative effect on species richness and a positive effect on evenness. There are other studies that show differing reactions of evenness and species richness (Yeboah et al., 2016; Reitalu et al., 2009). We suppose that low pH value and increasing tree cover are causing stress to certain species but have a positive effect on evenness of species distribution.

For future studies, we recommend to consider precipitation, as many authors point to its strong effect on plant diversity (e.g. Palpurina et al., 2017; Pittarello et al., 2020). Further, the microrelief should be included in the Modell, because it provides an array of ecological niches, benefiting plant diversity (Pittarello et al., 2020).

Finally, research shows that the study of one single taxonomic group is not a good indicator of biodiversity abundance. (Berglund & Jonsson, 2001). Kuzemko et al., (2016) have found that the different studied taxonomic groups reacted differently to the drivers of biodiversity. Including other taxa in the study would be greatly beneficial to its quality.

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## Appendix I: List of all observed species

*Compiled by Jürgen Dengler and Jamyra Gehler*

In the following, we provide a list of all species that have been recorded in the permanent plots, in the other student research projects plus some observations from along the trails. The species are grouped into vascular plants (nomenclature according to Juillerat et al. 2017), orthoptera, lepidoptera, birds, reptiles, amphibians, mammals and fungi (nomenclature according to Index Fungorum Partnership 2020). They are arranged into five geographical units “Around Sonnenhof”, “Val Mulix” below and above tree line and “Val Zvretta” below and above treeline. Additionally there are fungi observations from the trail to Lai Palpuegna. Very few species could not be assigned post hoc to one of the sites.

The list summarizes the findings of the Summer Schools in 2019 and 2020. Records from the projects in 2020 are in blue, those from findings along the trails in 2020 in green. If a species was recorded for the first time in 2020, also the species name is in colour. In total we have recorded so far 458 vascular plant, 203 fungal, 8 orthopteran, 18 lepidopteran, 1 amphibian, 1 reptile, 38 bird and 16 mammal taxa.

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Species	Without site information	Around Sonnenhof (alluvial plain, mires, grasslands, woodlands)	Val Mulix below treeline	Val Mulix above treeline	Trail to Lai Palpuegna	Val Zvretta below treeline	Val Zvretta above treeline
<b>Vascular plants</b>							
<i>Achillea atrata</i>							x
<i>Achillea erba-rotta</i> subsp. <i>moschata</i>							
<i>Achillea millefolium</i> aggr.		x	x	x			
<i>Achillea nana</i>			x	x			
<i>Aconitum lycoctonum</i> subsp. <i>neapolitanum</i>			x	x			
<i>Aconitum lycoctonum</i> subsp. <i>vulparia</i>				x			
<i>Aconitum napellus</i>		x	x	x			
- <i>Aconitum napellus</i> subsp. <i>vulgare</i>			x				
<i>Aconitum variegatum</i> subsp. <i>paniculatum</i>				x			
<i>Adenostyles alliariae</i>			x	x			

Species	Without site information	Around Sonnenhof (alluvial plain, mires, grasslands, woodlands)	Val Mulix below treeline	Val Mulix above treeline	Trail to Lai Palpuogna	Val Zvretta below treeline	Val Zvretta above treeline
<i>Adenostyles leucophylla</i>				x			
<i>Aegopodium podagraria</i>		x					
<i>Agrostis alpina</i>							x
<i>Agrostis capillaris</i>		x	x	x			
<i>Agrostis gigantea</i>		x					
<i>Agrostis rupestris</i>				x			x
<i>Agrostis schleicheri</i>				x			x
<i>Agrostis schraderiana</i>			x	x			
<i>Agrostis stolonifera</i>		x	x				
<i>Ajuga genevensis</i>			x				
<i>Ajuga pyramidalis</i>		x	x	x			
<i>Alchemilla alpina</i> aggr. s.l.		x	x	x			
<i>Alchemilla</i> sp.				x			
<i>Alchemilla vulgaris</i> aggr. s.l.		x	x	x			
- <i>Alchemilla splendens</i> aggr.				x			
<i>Alnus viridis</i>			x				
<i>Androsace chamaejasme</i>				x			x
<i>Androsace obtusifolia</i>				x			
<i>Anemone narcissiflora</i>							x
<i>Antennaria dioica</i>							x
<i>Anthoxanthum odoratum</i> aggr.			x	x			
- <i>Anthoxanthum alpinum</i>				cf./x			
- <i>Anthoxanthum odoratum</i>		x	x	x			
<i>Anthriscus nitida</i>			x				
<i>Anthyllis vulneraria</i>		x	x				x
- <i>Anthyllis vulneraria</i> subsp. <i>alpestris</i>		cf./x	x	x			x
<i>Aquilegia alpina</i>							x
<i>Aquilegia atrata</i>	x						
<i>Aquilegia vulgaris</i>						x	
<i>Arabis bellidifolia</i> subsp. <i>stellulata</i>							x
<i>Arabis caerulea</i>		x	x				
<i>Arabis subcoriacea</i>		x					
<i>Arctostaphylos alpina</i>	x						x
<i>Arctostaphylos uva-ursi</i>		x	x				x
<i>Arnica montana</i>		x	x	x			
<i>Arrhenatherum elatius</i>			x				
<i>Artemisia genipi</i>							x
<i>Asplenium viride</i>			cf.				x



Species	Without site information	Arround Sonnenhof (alluvial plain, mires, grasslands, woodlands)	Val Mulix below treeline	Val Mulix above treeline	Trail to Lai Palpuogna	Val Zvretta below treeline	Val Zvretta above treeline
<i>Aster bellidiastrum</i>		x	x	x	x		x
<i>Astragalus alpinus</i>		x	x				
<i>Astragalus penduliflorus</i>			x				
<i>Astrantia major</i>		x					
<i>Athyrium distentifolium</i>				x			
<i>Avenella flexuosa</i>		x	x	x			
<i>Bartsia alpina</i>		x	x	x			x
<i>Biscutella laevigata</i>			x	x			
<i>Botrychium lunaria</i>			x	x			
<i>Briza media</i>		x	x	x			
<i>Calamagrostis epigejos</i>			x				
<i>Calamagrostis varia</i>		x	x			x	x
<i>Calamagrostis villosa</i>		x	x	x			
<i>Caltha palustris</i>		x					
<i>Calluna vulgaris</i>		x	x				
<i>Caltha palustris</i>		x	x				
<i>Campanula barbata</i>		x	x	x		x	
<i>Campanula caenisia</i>							x
<i>Campanula cochleariifolia</i>		x					
<i>Campanula rotundifolia</i>			x	x			
<i>Campanula scheuchzeri</i>		x	x	x			x
<i>Cardamine amara</i>		x					
<i>Carduus defloratus</i>		x	x	x		x	x
<i>Carex alba</i>						x	
<i>Carex atrata subsp. atrata</i>			x				x
<i>Carex atrata subsp. aterrima</i>				x			
<i>Carex curvula</i>				x			
<i>Carex davalliana</i>		x	x				
<i>Carex digitata</i>			x	x			
<i>Carex elata</i>		x					
<i>Carex ferruginea</i>							x
<i>Carex firma</i>							x
<i>Carex flacca</i>		x	x			x	x
<i>Carex flava</i>		x	x				
<i>Carex frigida</i>				cf.			
<i>Carex lepidocarpa</i>		x	x				
<i>Carex leporina</i>			x				
<i>Carex montana</i>		x				x	

Species	Without site information	Around Sonnenhof (alluvial plain, mires, grasslands, woodlands)	Val Mulix below treeline	Val Mulix above treeline	Trail to Lai Palpuogna	Val Zvretta below treeline	Val Zvretta above treeline
<i>Carex nigra</i>		x		x			
<i>Carex ornithopoda</i>		x	x			x	x
<i>Carex pallescens</i>			x	x			
<i>Carex panicea</i>		x					
<i>Carex paniculata</i>		x					
<i>Carex pilulifera</i>				cf.			
<i>Carex sempervirens</i>		x	x	x		x	x
<i>Carlina acaulis</i>		x	x				x
<i>Centaurea nervosa</i>		x	x				
<i>Centaurea scabiosa</i>		x	x				
<i>Cerastium alpinum</i>							x
<i>Cerastium arvense</i>				x			
- <i>Cerastium arvense</i> subsp. <i>strictum</i>			x				
<i>Cerastium fontanum</i>		x		x			
- <i>Cerastium fontanum</i> subsp. <i>fontanum</i>				x			
- <i>Cerastium fontanum</i> subsp. <i>vulgare</i>			x				
<i>Cerastium latifolium</i>							Cf.
<i>Cerastium uniflorum</i>			x				
<i>Chaerophyllum hirsutum</i>		x	x			x	
<i>Chaerophyllum villarsii</i>		x	x	cf.			
<i>Chenopodium bonus-henricus</i>		x	x				
<i>Cirsium helenioides</i>		x	x				
<i>Cirsium oleraceum</i>		x	x				
<i>Cirsium spinosissimum</i>				x			
<i>Coeloglossum viride</i>			x	x			x
<i>Corallorhiza trifida</i>		x					
<i>Cotoneaster integerrimus</i>			x				
<i>Crepis alpestris</i>		x		x			x
<i>Crepis aurea</i>	x			x			x
<i>Crepis bocconeii</i>			x				
<i>Crepis conycifolia</i>			x				
<i>Crepis foetida</i>				x			
<i>Crepis kernerii</i>							x
<i>Crepis paludosa</i>		x	x				
<i>Cystopteris alpina</i>		x					
<i>Cystopteris fragilis</i> aggr.			x	x			
<i>Dactylis glomerata</i>		x	x	x			
<i>Dactylorhiza incarnata</i>		x	x				

Species	Without site information	Around Sonnenhof (alluvial plain, mires, grasslands, woodlands)	Val Mulix below treeline	Val Mulix above treeline	Trail to Lai Palpuogna	Val Zvretta below treeline	Val Zvretta above treeline
<i>Dactylorhiza maculata</i>		x	x				
- <i>Dactylorhiza maculata</i> subsp. <i>fuchsii</i>			x				
<i>Dactylorhiza majalis</i>		x	x	x			
<i>Dactylorhiza</i> sp.		x					
<i>Daphne mezereum</i>			x				
<i>Daphne striata</i>				x		x	x
<i>Deschampsia cespitosa</i>		x	x	x			
<i>Dianthus superbus</i>	x	x	x				
<i>Diphysastrum alpinum</i>				x			
<i>Doronicum clusii</i>				x			
<i>Draba aizoides</i>							x
<i>Draba fladnizensis</i>			x				
<i>Draba hoppeana</i>							x
<i>Dryas octopetala</i>		x	x				x
<i>Dryopteris carthusiana</i>			x				
<i>Dryopteris dilatata</i> aggr.			x				
<i>Elyna myosuroides</i>		x					
<i>Empetrum nigrum</i>		x	x	x			
- <i>Empetrum nigrum</i> subsp. <i>hermaphroditum</i>				x			
<i>Epilobium alsinifolium</i>		x					
<i>Epilobium angustifolium</i>		x	x				
<i>Epilobium fleischeri</i>		x	x	x			
<i>Epipactis atrorubens</i>						x	
<i>Equisetum palustre</i>		x					
<i>Equisetum variegatum</i>		x	x				
<i>Erica carnea</i>		x	x			x	x
<i>Erigeron alpinus</i> aggr.							x
<i>Eriophorum angustifolium</i>		x					
<i>Eriophorum scheuchzeri</i>				x			
<i>Euphorbia cyparissias</i>		x	x			x	
<i>Euphrasia minima</i> aggr.			x	x			x
<i>Euphrasia picta</i>		x					
<i>Euphrasia rostkoviana</i>		x	x	cf.			
- <i>Euphrasia rostkoviana</i> subsp. <i>rostkoviana</i>				x			
<i>Euphrasia salisburgensis</i>							x
<i>Festuca pulchella</i>		x	x				x
<i>Festuca quadriflora</i>							x
<i>Festuca rubra</i> aggr.		x	x	x		x	

Species	Without site information	Around Sonnenhof (alluvial plain, mires, grasslands, woodlands)	Val Mulix below treeline	Val Mulix above treeline	Trail to Lai Palpuogna	Val Zvretta below treeline	Val Zvretta above treeline
- Festuca rubra		x	x	x			
- Festuca nigrescens		x		x			
Festuca violacea aggr.				x			
Fragaria vesca		x	x			x	
Galeopsis tetrahit			x				
Galium album		x					
Galium anisophyllum			x				x
Galium boreale		x	x				
Galium pumilum aggr.		x	x	x			
- Galium pumilum		x					
- Galium anisophyllum		x	x	x			
Gentiana acaulis			x	x			
Gentiana asclepiadea		x	x	x			
Gentiana bavarica subsp. bavarica				x			
Gentiana brachyphylla				x			
Gentiana campestris		x	x	x			x
Gentiana clusii		x					x
Gentiana germanica				x			
Gentiana lutea			x	x			
Gentiana nivalis			x	x			
Gentiana punctata			x	x			
Gentiana ramosa				x			
Gentiana utriculosa		x					
Gentiana verna				x			
Geranium sylvaticum		x	x	x			
Geum montanum			x	x			
Geum rivale				x			
Globularia cordifolia							x
Globularia nudicaulis							x
Gnaphalium supinum				x			
Gymnadenia conopsea		x	x				x
Gymnadenia odoratissima			x				x
Gypsophila repens		x	x				x
Hedysarum hedysaroides				x			x
Helianthemum alpestre			x				x
Helianthemum nummularium		x	x	x			x
- Helianthemum nummularium subsp. grandiflorum							x
- Helianthemum nummularium subsp. obscurum		x	x				

Species	Without site information	Around Sonnenhof (alluvial plain, mires, grasslands, woodlands)	Val Mulix below treeline	Val Mulix above treeline	Trail to Lai Palpuogna	Val Zvretta below treeline	Val Zvretta above treeline
<i>Helictotrichon pubescens</i>		x					
- <i>Helictotrichon pubescens</i> subsp. <i>laevigatum</i>		x					
<i>Helictotrichon versicolor</i>		x	x	x			
<i>Hepatica nobilis</i>						x	
<i>Heracleum sphondylium</i>		x	x				
<i>Hieracium alpinum</i>				x			
<i>Hieracium hoppeanum</i>		Cf.					
<i>Hieracium lachenalii</i>			x				
<i>Hieracium lactucella</i>				x			
<i>Hieracium murorum</i> aggr.		x	x	x		x	x
<i>Hieracium piliferum</i>				x		x	
<i>Hieracium pilosella</i>			x				
<i>Hieracium</i> sp.				x			
<i>Hieracium villosum</i> aggr.				x			x
- <i>Hieracium pilosum</i>			x				x
<i>Hippocrepis comosa</i>		x				x	x
<i>Homogyne alpina</i>		x	x	x		x	x
<i>Huperzia selago</i>		x		x			
<i>Hypochaeris uniflora</i>				x			
<i>Juncus articulatus</i> aggr.		x	x				
- <i>Juncus alpinoarticulatus</i>		x					
<i>Juncus jacquinii</i>		x		x			
<i>Juncus trifidus</i>				x			
<i>Juncus triglumis</i>			x				
<i>Juniperus communis</i>			x				
- <i>Juniperus communis</i> subsp. <i>alpina</i>		x	x	x			x
<i>Knautia arvensis</i>		x					
<i>Knautia dipsacifolia</i>		x	x			x	
<i>Koeleria pyramidata</i>	x	x					
<i>Larix decidua</i>		x	x				
<i>Laserpitium latifolium</i>		x	x			x	x
<i>Lathyrus pratensis</i>		x					
<i>Leontodon helveticus</i>		x	x	x			x
<i>Leontodon hispidus</i>		x	x	x			x
- <i>Leontodon hispidus</i> subsp. <i>danubialis</i>			x			x	
- <i>Leontodon hispidus</i> subsp. <i>hispidus</i>		x	x				x
- <i>Leontodon hispidus</i> subsp. <i>pseudocrispus</i>			x				
<i>Leontodon incanus</i>				x			x

Species	Without site information	Around Sonnenhof (alluvial plain, mires, grasslands, woodlands)	Val Mulix below treeline	Val Mulix above treeline	Trail to Lai Palpuogna	Val Zvretta below treeline	Val Zvretta above treeline
<i>Leontodon montanus</i>				Cf.			
<i>Leontodon</i> sp.				x			
<i>Leontopodium alpinum</i>							x
<i>Leucanthemopsis alpina</i>				x			
- <i>Leucanthemopsis alpina</i> subsp. <i>alpina</i>				x			
- <i>Leucanthemopsis alpina</i> subsp. <i>minima</i>							x
<i>Leucanthemum vulgare</i> aggr.			x	x			
- <i>Leucanthemum adustum</i>		x	x	x		x	x
<i>Ligusticum mutellina</i>			x	x			x
<i>Ligusticum mutellinoides</i>			x	x			
<i>Lilium martagon</i>			x				
<i>Linaria alpina</i>		x		x			x
<i>Linnea borealis</i>			x				
<i>Linum catharticum</i>		x	x	x			x
<i>Listera ovata</i>		x	x			x	
<i>Loiseleuria procumbens</i>				x			
<i>Lonicera caerulea</i>			x				
<i>Lonicera nigra</i>						x	
<i>Lonicera xylosteum</i>			x				
<i>Lotus corniculatus</i> aggr.		x	x			x	x
- <i>Lotus alpinus</i>		x	x	x			x
- <i>Lotus corniculatus</i>		x	x	x			
<i>Luzula alpina</i>		x	x	x			
<i>Luzula alpinopilosa</i>				x			
<i>Luzula lutea</i>			x				
<i>Luzula luzulina</i>			x				
<i>Luzula luzuloides</i> subsp. <i>rubella</i>		x	x				
<i>Luzula multiflora</i>			x	x			
<i>Luzula pilosa</i>							x
<i>Luzula sieberi</i>		x	x				x
<i>Luzula</i> sp.			x				
<i>Luzula spicata</i>				x			
- <i>Luzula spicata</i> subsp. <i>mutabilis</i>			x				
<i>Luzula sudetica</i>		x		Cf.			
<i>Luzula sylvatica</i>			x				
<i>Lycopodium</i> sp.				x			
<i>Maianthemum bifolium</i>			x				
<i>Medicago lupulina</i>		x					



Species	Without site information	Arround Sonnenhof (alluvial plain, mires, grasslands, woodlands)	Val Mulix below treeline	Val Mulix above treeline	Trail to Lai Palpuogna	Val Zvretta below treeline	Val Zvretta above treeline
<i>Medicago sativa</i>		x					
<i>Melampyrum pratense</i>		x	x	x			
<i>Melampyrum sylvaticum</i>		x	x	x		x	
<i>Melica nutans</i>		x				x	
<i>Moeheringia ciliata</i>							x
<i>Moeheringia trinervia</i>			x				
<i>Molinia caerulea</i> aggr.		x					
- <i>Molinia caerulea</i>		x	x				
<i>Moneses uniflora</i>		x	x				
<i>Myosotis alpestris</i>			x	x			x
<i>Myosotis alpina</i>				x			
<i>Myosoton aquaticum</i>		x					
<i>Nardus stricta</i>		x	x	x			
<i>Orthilia secunda</i>			x	x			
<i>Oxalis acetosella</i>			x				
<i>Oxyria digyna</i>				x			x
<i>Oxytropis campestris</i>		x	x				
<i>Parnassia palustris</i>		x	x				x
<i>Pedicularis rostratospicata</i> subsp. <i>helvetica</i>					x		
<i>Pedicularis verticillata</i>							x
<i>Petasites paradoxus</i>		x	x				
<i>Peucedanum ostruthium</i>			x	x			
<i>Phleum alpinum</i> aggr.				x			
- <i>Phleum rhaeticum</i>		x	x	x		x	
<i>Phleum hirsutum</i>							x
<i>Phyteuma betonicifolium</i>		x	x	x			x
<i>Phyteuma hemisphaericum</i>				x			
<i>Phyteuma orbiculare</i>		x	x				x
<i>Phyteuma scheuchzeri</i>			x				
<i>Picea abies</i>		x	x			x	x
<i>Pimpinella major</i>		x	x				
<i>Pinguicula alpina</i>		x	x				x
<i>Pinguicula vulgaris</i>		x					
<i>Pinus cembra</i>		x	x			x	x
<i>Pinus mugo</i> subsp. <i>mugo</i>			x				
<i>Pinus mugo</i> subsp. <i>uncinata</i>		x	x			x	
<i>Plantago atrata</i>			x	x			
<i>Plantago lanceolata</i>		x					

Species	Without site information	Around Sonnenhof (alluvial plain, mires, grasslands, woodlands)	Val Mulix below treeline	Val Mulix above treeline	Trail to Lai Palpuogna	Val Zvretta below treeline	Val Zvretta above treeline
<i>Plantago major</i> subsp. <i>major</i>		x					
<i>Plantago media</i>			x				
<i>Plantago serpentina</i> aggr.				x			
- <i>Plantago alpina</i>		x	x	x			
<i>Poa alpina</i>			x	x			x
<i>Poa minor</i>							x
<i>Poa pratensis</i>		x	x				
<i>Poa trivialis</i>		x					
<i>Polygala alpestris</i>		x	x				x
<i>Polygala amara</i> aggr.				x			
- <i>Polygala amarella</i>		x					
<i>Polygala chamaebuxus</i>							x
<i>Polygala</i> sp.							x
<i>Polygala vulgaris</i>			x				
<i>Polygonatum verticillatum</i>						x	
<i>Polygonum viviparum</i>		x	x	x			x
<i>Potentilla aurea</i>			x	x			
<i>Potentilla crantzii</i>		x	x	x			x
<i>Potentilla erecta</i>		x	x				
<i>Prenanthes purpurea</i>			x				
<i>Primula farinosa</i>		x	x				x
<i>Primula hirsuta</i>				x			
<i>Primula integrifolia</i>				x			x
<i>Primula latifolia</i>				x			
<i>Primula</i> sp.				x			
<i>Pritzelago alpina</i> subsp. <i>alpina</i>							x
<i>Prunella grandiflora</i>		x					
<i>Prunella vulgaris</i>			x				
<i>Pseudorchis albida</i>				x			
<i>Pulmonaria australis</i>			x				
<i>Pulsatilla alpina</i> subsp. <i>alpestris</i>							x
<i>Pulsatilla alpina</i> subsp. <i>apiifolia</i>				x			
<i>Pyrola minor</i>		x		x			x
<i>Pyrola rotundifolia</i>		x	x	x			x
<i>Ranunculus acris</i>			x				
<i>Ranunculus alpestris</i>							x
<i>Ranunculus bryenius</i>							x
<i>Ranunculus montanus</i> aggr.		x	x	x			

Species	Without site information	Arround Sonnenhof (alluvial plain, mires, grasslands, woodlands)	Val Mulix below treeline	Val Mulix above treeline	Trail to Lai Palpuogna	Val Zvretta below treeline	Val Zvretta above treeline
- <i>Ranunculus montanus</i>		x	x	x			x
- <i>Ranunculus villarsii</i>				x			
<i>Ranunculus thora</i>							x
<i>Rhinanthus alectorolophus</i>		x					
<i>Rhinanthus glacialis</i>			x				
<i>Rhinanthus minor</i>		x	x	x			
<i>Rhododendron ferrugineum</i>			x	x			
<i>Rhododendron hirsutum</i>							x
<i>Rosa pendulina</i>		x	x				
<i>Rubus caesius</i>			x				
<i>Rubus idaeus</i>			x				
<i>Rubus saxatilis</i>		x	x			x	
<i>Rumex acetosella</i>			x				
<i>Rumex obtusifolius</i>		x	x				
<i>Rumex scutatus</i>			x	x			
<i>Salix appendiculata</i>		x	x	x			
<i>Salix breviserrata</i>				x			
<i>Salix caesia</i>		x	x				
<i>Salix foetida</i>		x	x				
<i>Salix herbacea</i>				x			
<i>Salix myrsinifolia</i>		x	x	x			x
<i>Salix purpurea</i>		x	x				
<i>Salix repens</i>		x					
<i>Salix reticulata</i>							x
<i>Salix retusa</i>				x			x
<i>Salix waldsteiniana</i>				x			
<i>Sanguisorba officinalis</i>		x	x				
<i>Saussurea alpina</i>			x	x			
<i>Saxifraga aizoides</i>		x	x	x			x
<i>Saxifraga bryoides</i>				x			
<i>Saxifraga caesia</i>							x
<i>Saxifraga paniculata</i>				x			x
<i>Saxifraga rotundifolia</i>			x				
<i>Saxifraga stellaris</i>		x					
<i>Scabiosa columbaria</i> aggr.			x				
- <i>Scabiosa lucida</i>		x					x
<i>Sedum</i> sp.				x			x
<i>Sedum villosum</i>				cf.			cf.

Species	Without site information	Around Sonnenhof (alluvial plain, mires, grasslands, woodlands)	Val Mulix below treeline	Val Mulix above treeline	Trail to Lai Palpuogna	Val Zvretta below treeline	Val Zvretta above treeline
<i>Selaginella selaginoides</i>		x	x	x			x
<i>Sempervivum montanum</i>			x	x			
<i>Senecio abrotanifolius</i>							x
<i>Senecio doronicum</i>			x	x			x
<i>Senecio hercynicus</i>			x				
<i>Senecio incanus</i>				x			
- <i>Senecio incanus</i> subsp. <i>carniolicus</i>				x			
<i>Senecio ovatus</i> aggr.			x				
<i>Senecio rupestris</i>		x					
<i>Sesleria caerulea</i>		x	x	x		x	x
<i>Sibbaldia procumbens</i>			x				
<i>Silene acaulis</i>							x
<i>Silene dioica</i>		x					
<i>Silene nutans</i>	x						
- <i>Silene nutans</i> subsp. <i>nutans</i>							x
<i>Silene pratensis</i>		x	x				
<i>Silene rupestris</i>				x			
<i>Silene vulgaris</i> subsp. <i>vulgaris</i>		x	x	x			x
<i>Soldanella alpina</i>		x					x
<i>Soldanella pusilla</i>			x	x			x
<i>Soldanella</i> sp.				x			
<i>Solidago virgaurea</i>		x	x	x		x	x
<i>Sorbus aucuparia</i>			x				
<i>Stellaria nemorum</i>			x				
<i>Taraxacum officinale</i> aggr.		x	x	x			
<i>Taraxacum</i> sp.							x
<i>Thalictrum aquilegifolium</i>			x	x			
<i>Thalictrum minus</i>						x	
<i>Thesium alpinum</i>		x	x	x			x
<i>Thesium pyrenaicum</i>		x	x	x			
<i>Thymus alpestris</i>		x	x	x			
<i>Thymus praecox</i> subsp. <i>polytrichus</i>		x	x				x
<i>Thymus praecox</i> subsp. <i>praecox</i>		x	x	x		x	x
<i>Thymus pulegioides</i>		x					
- <i>Thymus pulegioides</i> subsp. <i>pulegioides</i>			x				
<i>Tofieldia calyculata</i>		x	x				x
<i>Trichophorum cespitosum</i>		x	x	x			
<i>Trifolium alpinum</i>			x	x			

Species	Without site information	Arround Sonnenhof (alluvial plain, mires, grasslands, woodlands)	Val Mulix below treeline	Val Mulix above treeline	Trail to Lai Palpuogna	Val Zvretta below treeline	Val Zvretta above treeline
<i>Trifolium aureum</i>			cf.				
<i>Trifolium badium</i>			x	x			
<i>Trifolium medium</i>		x					
<i>Trifolium montanum</i>		x					
<i>Trifolium pratense</i>			x				
- <i>Trifolium pratense</i> subsp. <i>nivale</i>			x	x			
- <i>Trifolium pratense</i> subsp. <i>pratense</i>			x	x			x
<i>Trifolium repens</i>		x		x			
<i>Trifolium thalii</i>			x	x			
<i>Trollius europaeus</i>		x		x			x
<i>Tussilago farfara</i>		x	x	x			
<i>Urtica dioica</i>		x	x				
<i>Vaccinium myrtillus</i>		x	x	x			
<i>Vaccinium uliginosum</i> aggr.		x	x	x			
- <i>Vaccinium gaultherioides</i>			x	x			x
<i>Vaccinium vitis-idaea</i>		x	x	x		x	x
<i>Valeriana diversifolia</i>			x				
<i>Valeriana montana</i>		x	x	x		x	
<i>Valeriana officinalis</i>			x				
<i>Veratrum album</i>			x	x			
<i>Veratrum album</i> subsp. <i>lobelianum</i>			x				
<i>Veronica alpina</i>				x			
<i>Veronica bellidioides</i>				x			
<i>Veronica fruticans</i>				x			
<i>Veronica officinalis</i>			x				
<i>Vicia cracca</i>		x	x				
- <i>Vicia cracca</i> subsp. <i>incana</i>		x					
<i>Viola biflora</i>		x	x	x			
<i>Viola palustris</i>		x					
<i>Viola sylvestris</i> aggr.			x	x			
<b>Fungi</b>							
<i>Agaricus comtulus</i>				x			
<i>Agaricus langei</i>					x		
<i>Agaricus porphyrocephalus</i>				x			
<i>Albatrellus ovinus</i>					x		
<i>Amanita muscaria</i>		x	x				
<i>Amanita submembranacea</i>			x		x		

Species	Without site information	Around Sonnenhof (alluvial plain, mires, grasslands, woodlands)	Val Mulix below treeline	Val Mulix above treeline	Trail to Lai Palpuogna	Val Zvretta below treeline	Val Zvretta above treeline
<i>Amanita vaginata</i>				x			
<i>Ampulloclitocybe clavipes</i>					x		
<i>Amylostereum areolatum</i>			x				
<i>Armillaria ostoyae/borealis</i>			x				
<i>Arrhenia griseopallida</i>	x						
<i>Arrhenia oniscus</i>			x				
<i>Arrhenia velutipes</i>				x			
<i>Ascobolus</i> sp.				x			
<i>Atheniella flavoalba</i>			x	x			
<i>Atractosporocybe inornata</i>					x		
<i>Bankera violascens</i>				x			
<i>Bisporella citrina</i>			x				
<i>Boletus edulis</i>			x				
<i>Bovista plumbea</i>				x			
<i>Bovistella utriformis</i>			x				
<i>Bryoglossum gracile</i>				x			
<i>Calocera viscosa</i>					x		
<i>Calocybe carnea</i>				x			
<i>Cantharellus cibarius</i>		x	x				
<i>Cerocorticium</i> sp.			x				
<i>Chalciporus piperatus</i>		x	x				
<i>Cheilymenia stercorea</i>			x	x			
<i>Chroogomphus helveticus</i>		x	x				
<i>Clavaria fragilis</i>				x			
<i>Clitopilus scyphoides</i>			x				
<i>Clitopilus</i> sp.				x			
<i>Collybia cookei</i>					x		
<i>Conocybe fuscimarginata</i>			x				
<i>Conocybe ochrostriata</i>				x			
<i>Coprinopsis nivea</i>			x	x			
<i>Coprinopsis patouillardii</i>				x			
<i>Coprinopsis</i> sp.				x			
<i>Coprinopsis tigrinella</i>				x			
<i>Coprobia granulata</i>			x	x			
<i>Cortinarius distans</i>			x				
<i>Cortinarius crassifolius</i>			x				
<i>Cortinarius</i> sect. <i>Phlegmacium</i>					x		
<i>Cudonia confusa</i>			x				

Species	Without site information	Arround Sonnenhof (alluvial plain, mires, grasslands, woodlands)	Val Mulix below treeline	Val Mulix above treeline	Trail to Lai Palpuogna	Val Zvretta below treeline	Val Zvretta above treeline
<i>Cuphophyllus virgineus</i>			x				
<i>Dacrymyces stillatus</i>					x		
<i>Deconica montana</i>			x	x			
<i>Entoloma longistriatum</i>				x			
<i>Entoloma mougeotii</i>			x				
<i>Entoloma serrulatum</i>			x				
<i>Entoloma sodale</i>				x			
<i>Exidia nigricans</i>			x				
<i>Exobasidium juelianum</i>				x			
<i>Exobasidium myrtilli</i>			x				
<i>Exobasidium rhododendri</i>	x						
<i>Exobasidium vaccinii</i>			x	x			
<i>Fayodia gracilipes</i>			x	x	x		
<i>Fomes fomentarius</i>					x		
<i>Fomitopsis pinicola</i>					x		
<i>Galerina marginata</i>					x		
<i>Gliophorus irrigatus</i>		x					
<i>Gliophorus psittacinus</i>			x				
<i>Gloeocystidiellum leucoxanthum</i>					x		
<i>Gloeophyllum abietinum</i>			x				
<i>Gomphidius glutinosus</i>		x			x		
<i>Gymnopilus junonius</i>					x		
<i>Gymnopus androsaceus</i>				x			
<i>Gymnopus dryophilus</i>			x	x	x		
<i>Gymnosporangium cornutum</i>			x				
<i>Hebeloma mesophaeum</i>					x		
<i>Hemimycena</i> sp.				x			
<i>Hydnellum caeruleum</i>			x				
<i>Hydnellum conrescens</i>			x				
<i>Hydnum repandum</i>		x					
<i>Hygrocybe chlorophana</i>		x					
<i>Hygrocybe conica</i>			x	x			
<i>Hygrocybe flavescens</i>			x				
<i>Hygrocybe miniata</i>				x			
<i>Hygrocybe nigrescens</i>				x			
<i>Hygrocybe punicea</i>		x					
<i>Hygrophorus atramentosus</i>					x		
<i>Hygrophorus chrysodon</i>		x					



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Hymenoscyphus sp.				x			
Infundibulicybe gibba					x		
Inocybe geophylla			x				
Inocybe mixtilis			x				
Inocybe sp.				x			
Laccaria montana				x			
Lachenllula suecica			x				
Lactarius badiosanguineus			x				
Lactarius deterrimus		x					
Lactarius pseudouvidus				x			
Lactarius rufus			x		x		
Lactarius scrobiculatus					x		
Lactarius semisanguifluus		x			x		
Lactarius trivialis					x		
Lactarius turpis					x		
Lactarius zonarioides					x		
Laetiporus sulphureus			x				
Lasiobotrys loniceriae				x			
Leccinum scabrum					x		
Lepista nuda					x		
Leucocybe connata					x		
Lichenomphalia umbellifera		x					
Lophodermium pinastri			x				
Lycoperdon molle					x		
Lycoperdon lividum			x				
Lycoperdon perlatum			x				
Lycoperdon pratense			x				
Mallocybe fulvipes		x					
Mallocybe leucoblema			x				
Marasmiellus ramealis					x		
Marasmius androsaceus			x	x			
Melampsora epitea				x			
Melanoleuca melaleuca			x				
Melanoleuca subalpina		x		x			
Mensularia radiata			x				
Mollisia sp.			x				
Mucronella calva			x				
Mycena abramsii			x				

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<i>Mycena aetites</i>				x			
<i>Mycena alcalina</i>			x				
<i>Mycena amicta</i>			x				
<i>Mycena aurantiomarginata</i>			x				
<i>Mycena capillaripes</i>				x			
<i>Mycena epipterygia</i>			x				
<i>Mycena filopes</i>			x				
<i>Mycena galericulata</i>			x				
<i>Mycena galopus</i>			x				
<i>Mycena laevigata</i>			x				
<i>Mycena leaiana</i>			x				
<i>Mycena maculata</i>			x				
<i>Mycena metata</i>			x				
<i>Mycena olivaceomarginata</i>				x			
<i>Mycena pura</i>					x		
<i>Mycena sp.</i>				x			
<i>Mycena strobilicola</i>			x				
<i>Mycena xantholeuca</i>			x				
<i>Mycocentrodochium curvisporum</i>				x			
<i>Neolentinus lepideus</i>			x				
<i>Panaeolina foenicisecii</i>			x				
<i>Panaeolus papilionaceus</i>			x				
<i>Panaeolus semiovatus</i>			x				
<i>Parasola misera</i>				x			
<i>Peniophora aurantiaca</i>			x	x			
<i>Phaeoclavulina flaccida</i>		x			x		
<i>Phaeolus schweinitzii</i>			x		x		
<i>Phloeomana alba</i>			x				
<i>Phloeomana clavata</i>				x			
<i>Pholiota scamba</i>			x				
<i>Pilobolus sp.</i>				x			
<i>Protostropharia semiglobata</i>			x	x			
<i>Pseudosperma rimosum</i>					x		
<i>Puccinia bistortae</i>				x			
<i>Puccinia festucae</i>			x	x			
<i>Pyxidiophora sp.</i>				x			
<i>Ramaria largentii</i>			x				
<i>Rhizopogon odoratus</i>			x				

Species	Without site information	Around Sonnenhof (alluvial plain, mires, grasslands, woodlands)	Val Mulix below treeline	Val Mulix above treeline	Trail to Lai Palpuogna	Val Zvretta below treeline	Val Zvretta above treeline
<i>Rickenella mellea</i>		x					
<i>Rickenella</i> sp.			x				
<i>Roridomyces roridus</i>			x				
<i>Russula acrifolia</i>			x				
<i>Russula adusta</i>			x				
<i>Russula alutacea</i>			x				
<i>Russula consobrina</i>					x		
<i>Russula decolorans</i>					x		
<i>Russula densifolia</i>					x		
<i>Russula laccata</i>				x			
<i>Russula montana</i>				x			
<i>Russula nana</i>				x			
<i>Russula nauseosa</i>			x				
<i>Russula rhodopus</i>					x		
<i>Russula</i> sp.			x				
<i>Russula subrubens</i>				x			
<i>Russula viscida</i>			x				
<i>Rutstroemia bolaris</i>			x				
<i>Scutellinia scutellata</i>				x			
<i>Spathularia flavida</i>			x		x		
<i>Steccherinum ochraceum</i>			x				
<i>Stereum sanguinolentum</i>				x	x		
<i>Suillus cavipes</i>			x				
<i>Suillus granulatus</i>			x				
<i>Suillus grevillei</i>			x				
<i>Suillus placidus</i>			x				
<i>Suillus plorans</i>			x				
<i>Suillus variegatus</i>			x		x		
<i>Suillus viscidus</i>		x	x				
<i>Trichaptum abietinum</i>			x				
<i>Tricholoma atosquamosum</i>					x		
<i>Tricholoma inamoenum</i>			x				
<i>Tricholoma psammopus</i>					x		
<i>Tricholoma scalpturatum</i>			x				
<i>Tricholoma sulphureum</i>			x				
<i>Tricholoma terreum</i>			x				
<i>Tricholomopsis decora</i>			x				
<i>Tricholomopsis rutilans</i>					x		

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<i>Tubaria conspersa</i>			x				
<i>Tubulicrinis glebulosus</i>			x				
<i>Uromyces cacaliae</i>				x			
<i>Uromyces solidaginis</i>				x			
<i>Uromyces trifolii-repentis</i>			x	x			
<i>Uromyces veratri</i>				x			
<i>Xerocomellus chrysenteron</i>					x		
<b>Orthoptera</b>							
<i>Chorthippus apricarius</i>			x				
<i>Chorthippus parallelus</i>			x	x			
<i>Gomphocerus sibiricus</i>				x			
<i>Metrioptera brachyptera</i>			x				
<i>Miramella alpina</i>			x	x			
<i>Omocestus viridulus</i>			x	x			
<i>Stethophyma grossum</i>			x				
<i>Tetrix bipunctata</i>			x				
<b>Lepidoptera</b>							
<i>Aglais urticae</i>		x					
<i>Agnis aglaja</i>			x				
<i>Boloria pales</i>			x	x			
<i>Boloria titania</i>		x	x	x			
<i>Coenonympha gardetta</i>				x			
<i>Erebia mnestra</i>			x	x			
<i>Erebia montana</i>			x				
<i>Erebia tyndarus</i>				x			
<i>Fabriciana niobe</i>		x	x				
<i>Hesperia comma</i>			x				
<i>Parnassius apollo</i>			x				
<i>Parnassius phoebus</i>				x			
<i>Pieris napi</i>		x					
<i>Plebejus idas</i>			x				x
<i>Polyommatus coridon</i>							x
<i>Pyrgus alevus</i>			x				
<i>Speyeria aglaja</i>		x					
<i>Thymelicus lineola</i>			x				

Species	Without site information	Arround Sonnenhof (alluvial plain, mires, grasslands, woodlands)	Val Mulix below treeline	Val Mulix above treeline	Trail to Lai Palpuogna	Val Zvretta below treeline	Val Zvretta above treeline
<b>Amphibians</b>							
<i>Rana temporaria</i>				x			
<b>Reptiles</b>							
<i>Vipera berus</i>			x				
<b>Birds</b>							
<i>Acanthis flammea</i>			x				
<i>Anthus spinoletta</i>							x
<i>Aquila chrysaetos</i>				x			
<i>Ardea cinerea</i>		x					
<i>Buteo buteo</i>		x					
<i>Cinclus cinclus</i>		x		x			
<i>Corvus corone corone</i>		x					
<i>Dendrocopos major</i>		x	x				
<i>Dryocopus martius</i>		x	x				
<i>Falco tinnunculus</i>				x			x
<i>Ficedula hypoleuca</i>		x					
<i>Fringilla coelebs</i>		x					
<i>Garrulus glandarius</i>		x					
<i>Lophophanes cristatus</i>		x	x			x	
<i>Loxia curvirostra</i>		x					
<i>Motacilla cinerea</i>		x	x				
<i>Nucifraga caryocatactes</i>		x	x			x	
<i>Oenanthe oenanthe</i>							x
<i>Parus major</i>		x	x				
<i>Periparus ater</i>		x	x				
<i>Phoenicurus ochruros</i>		x	x	x		x	x
<i>Phoenicurus phoenicurus</i>		x					
<i>Phylloscopus collybita</i>		x					
<i>Picus viridis</i>		x					
<i>Poecile montanus</i>		x	x			x	
<i>Prunella collaris</i>							x
<i>Ptyonoprogne rupestris</i>				x			x
<i>Pyrrhocorax graculus</i>				x			x
<i>Pyrrhula pyrrhula</i>		x	x				
<i>Regulus regulus</i>		x	x				
<i>Saxicola rubetra</i>			x				

Species	Without site information	Around Sonnenhof (alluvial plain, mires, grasslands, woodlands)	Val Mulix below treeline	Val Mulix above treeline	Trail to Lai Palpuogna	Val Zvretta below treeline	Val Zvretta above treeline
<i>Sitta europaea</i>		x					
<i>Spinus spinus</i>		x					
<i>Sylvia curruca</i>		x					
<i>Troglodytes troglodytes</i>		x	x				
<i>Turdus merula</i>		x					
<i>Turdus pilaris</i>		x					
<i>Turdus viscivorus</i>		x	x				
<b>Mammals</b>							
<i>Apodemus sp.</i>		x	x	x			
<i>Capra ibex</i>					x		
<i>Capreolus capreolus</i>			x	x			
<i>Cervus elaphus</i>			x	x			
<i>Chionomys nivalis</i>					x		
<i>Marmota marmota</i>			x	x			x
<i>Microtus arvalis</i>					x		
<i>Microtus sp.</i>		x					
<i>Mustela erminea</i>					x		
<i>Myodes glareolus</i>		x	x	x			
<i>Pitymus sp.</i>		x					
<i>Rupicapra rupicapra</i>					x		x
<i>Sorex alpinus</i>		x					
<i>Sorex araneus aggr.</i>				x			
<i>Sorex minutus</i>		x	x				
<i>Sorex sp.</i>		x	x				

## Appendix II: Photo plates

Compiled by Tom Bischof, photos by Tom Bischof, Jürgen Dengler and Hanna Schreiber

### The Group House “Sonnenhof”



Our accommodation in the middle of nature with impressive views of the Albula Region.



At times, the trees around the house were full of migrating songbirds such as Pied flycatcher *Ficedula hypoleuca*, Common Redstart *Phoenicurus phoenicurus* and Eurasian siskin *Spinus spinus*.



## The Abula alluvial plain



In the habitat mosaic close to the Sonnenhof, the vegetation was sampled (middle) and photo traps were hidden (bottom left). Observed species included White-throated Dipper *Cinclus cinclus* (top left), Dark green fritillary *Argynnis aglaia* (middle left), *Gentiana asclepiadea* (middle right), Crested Tit (bottom middle) and *Pyrgus alveus* (bottom right).



## Biodiversity monitoring fieldwork at Val Mulix



Along the whole Val Mulix transect, permanent sampling plots were assessed using a multi-scale approach. Some animals were also observed. Common Adder *Vipera berus* (right) was discovered below the tree line. Green Mountain Grasshopper *Miramella alpina* (left) was the most abundant insect in the meadows.





The higher part of the Val Mulix is home to a diverse plant community. Flowering species included *Solidago virgaurea*, *Phleum rhaeticum*, *Aconitum napellus*, *Aconitum lycoctonum*, *Dianthus superbus* and *Lilium martagon* (LTR). At the top of the slopes a large deer herd (*Cervus elaphus*) was seen grazing between the rocks (bottom right).





Fieldwork was conducted at high altitudes. Scheuchzer's cottongrass *Eriophorum scheuchzeri* (left) grows at the border of Lai Negr at 2600 m a.s.l. Evening time was spent identifying plants and listening to the group's presentations (bottom half).



## Small mammal monitoring



The small mammal group conducted a monitoring using “Mammalia” photo traps. Additionally, dead animals found on the paths (e.g. *Sorex* sp.) were collected and identified. Identification was also practiced on Anette’s collection (bottom).



## Grouse field trip



Introduction by Roland Graf to the habitat assessment for Western Capercaillie *Tetrao urogallus* and Hazel grouse *Tetrastes bonasia*, two bird species suspected to live in the area. But no traces were found. Among other fungi, Chanterelle *Cantharellus cibarius* (middle) and Sulphur porling *Laetiporus sulphureus* (middle left) were abundant.



## Val Zavretta



The vegetation in Val Zavretta surprised with a high number of species. Diversity here is favoured by alkaline conditions: *Gymnadenia conopsea* (left), *Saxifraga paniculata* (middle right) and Edelweiss *Leontopodium alpinum* (bottom right).





Even well above the tree line the species richness was impressive: *Agrostis alpina*, *Saxifraga paniculata*, Alpine accentor *Prunella collaris*, Alpine marmot *Marmota marmota*, *Linaria alpina*, Chalkhill blue *Polyommatus coridon*, Northern Wheatear *Oenanthe oenanthe*, *Campanula cenisia*, *Silene acaulis*.



## Last evening in Preda



A delicious barbecue dinner was followed by an outdoor presentation about bats by Annette. Everyone enjoyed eating outside for once before cleaning the house the next morning.