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**SedaDNA shows that transhumance of domestic herbivores
has enhanced plant diversity over the Holocene in the
Eastern European Alps**

Journal:	<i>The Holocene</i>
Manuscript ID	HOL-24-0103.R1
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Date Submitted by the Author:	14-Oct-2024
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Keywords:	European Alps, <i>sed</i> aDNA, Anthropogenic impacts, Climate change, Austria, Holocene, Metabarcoding, Alpine pasture management, Central Eastern Alps
Abstract:	The Eastern European Alps boasts highly biodiverse ecosystems and a rich archaeological history. However, there is limited research on the enduring impacts of historical climate change and human activities on plant biodiversity in this region. Using sedimentary ancient DNA, we reconstructed plant and animal dynamics from 8.5 thousand years before present (ka BP) around Großer Winterleitensee (Zirbitzkogel, Austria). Variable intensities of human activities since the Middle Bronze Age (~3.5 ka BP) facilitated the persistence of biodiverse Alpine meadow

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	<p>communities and lowered timberlines below their natural limit. Since the end of the Bronze Age (~2.8 ka BP), human activities, particularly pasturing, and increasing temperatures, emerged as significant drivers of plant community dynamics. The introduction of sheep (<i>Ovis aries</i>) did not reduce wild mammal presence, including red deer (<i>Cervus elaphus</i>), hare (<i>Lepus</i>), European mole (<i>Talpa europaea</i>), bank vole (<i>Myodes glareolus</i>), and short-tailed field vole (<i>Microtus agrestis</i>). During the High & Late Mediaeval Period, (~1150 - 450 BP), cattle (<i>Bos taurus</i>) and horses (<i>Equus caballus</i>) became the dominant domesticates, while all wild mammals except the short-tailed field vole and Eurasian water shrew (<i>Neomys fodiens</i>) declined or even disappeared. These changes are also accompanied by a significant transformation of plant community structure. The ability to determine both plant responses and animal drivers from the same palaeolimnological sequence vastly improves our ability to partition causes of vegetation change over the Holocene. Here, we reveal that plant biodiversity is maintained or increased by moderate cattle grazing. Therefore, non-intensive domesticated stock grazing is essential for maintaining diverse Alpine meadows.</p>

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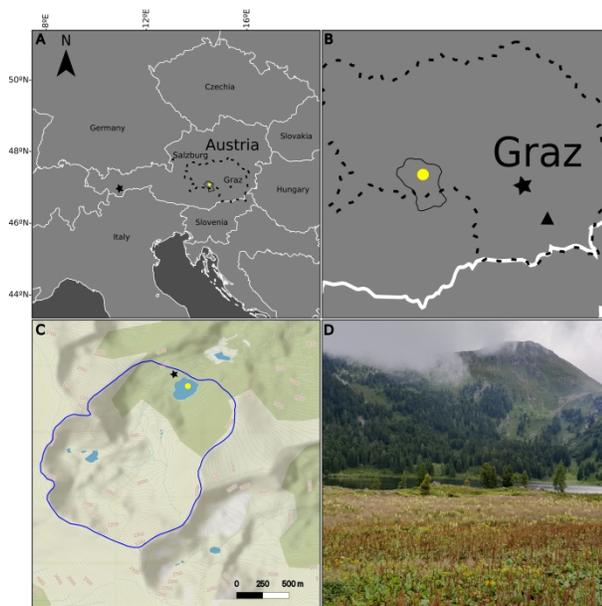


Figure 1

Figure 1. Maps and coring site: **A.** A map of Europe centred around Austria, indicating Styria (dashed line), the Seetaler Alps (solid line), Großes Winterleitensee (yellow circle), and Schwarzsee ob Sölden (black star). Map drawn with vemaps.com basemap. **B.** A zoomed in image of Styria, (dashed border) and the Seetaler Alps (solid border). The triangle indicates Wildon Schlossberg and the yellow circle, Großes Winterleitensee. Map drawn using vemaps.com basemap. **C.** A map of Großes Winterleitensee with the catchment area (blue border), sediment core coring site (yellow circle) and moor core coring site (black star) indicated. Map drawn in QGIS using MapTiler Topo basemap. **D.** Photo taken from downslope of the northwestern side of the lake (I. G. Alsos).

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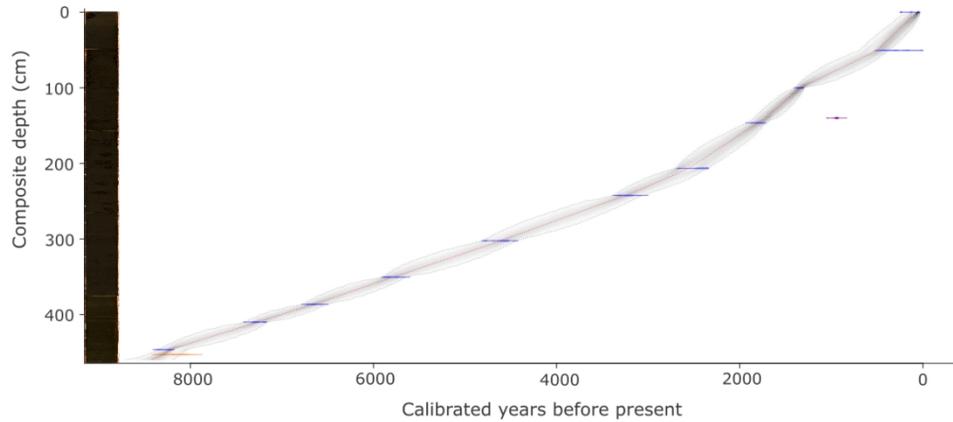


Figure 2. Age depth model, core image and lithology: The Age depth model with the calibrated radiocarbon dates (one standard error) in blue. The age-depth relationship is illustrated by a curve: the most probable calendar ages (darker grey), the 95% confidence interval (grey stippled line), and the optimal model derived from a weighted average of the mean (red line). Two dates were discarded, one with an error margin >100 years (orange) and the other lies outside of the model (purple). The core comprises dark-brown silty-gyttja and some lighter coloured bands throughout.

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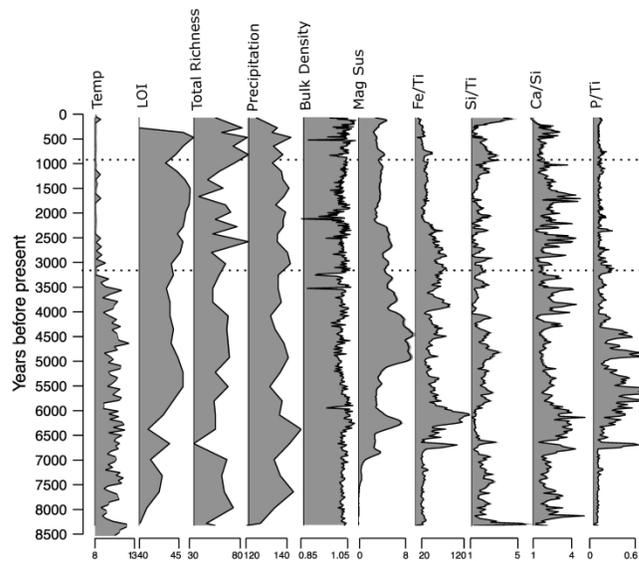
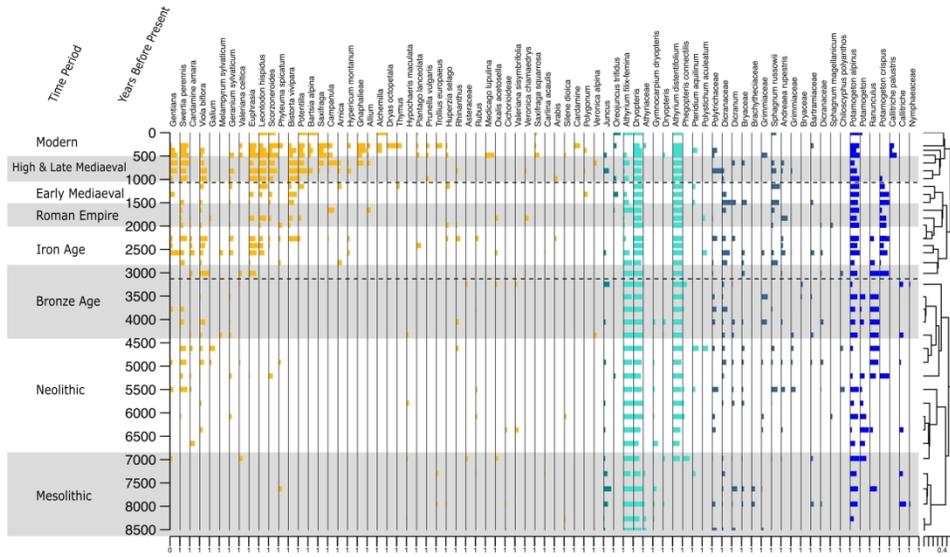


Figure 3 The XRF data with temperature and precipitation data: XRF data of the core taken from Großer Winterleitensee, Austria, alongside mean July temperature (Temp, °C), % loss on ignition (LOI), total plant richness (Hill where $q = 0$), mean precipitation (kg m^{-2}) of water in all phases, bulk density, and magnetic susceptibility (mag sus). Full XRF data shown in Supplementary Figure 1.

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252x146mm (300 x 300 DPI)

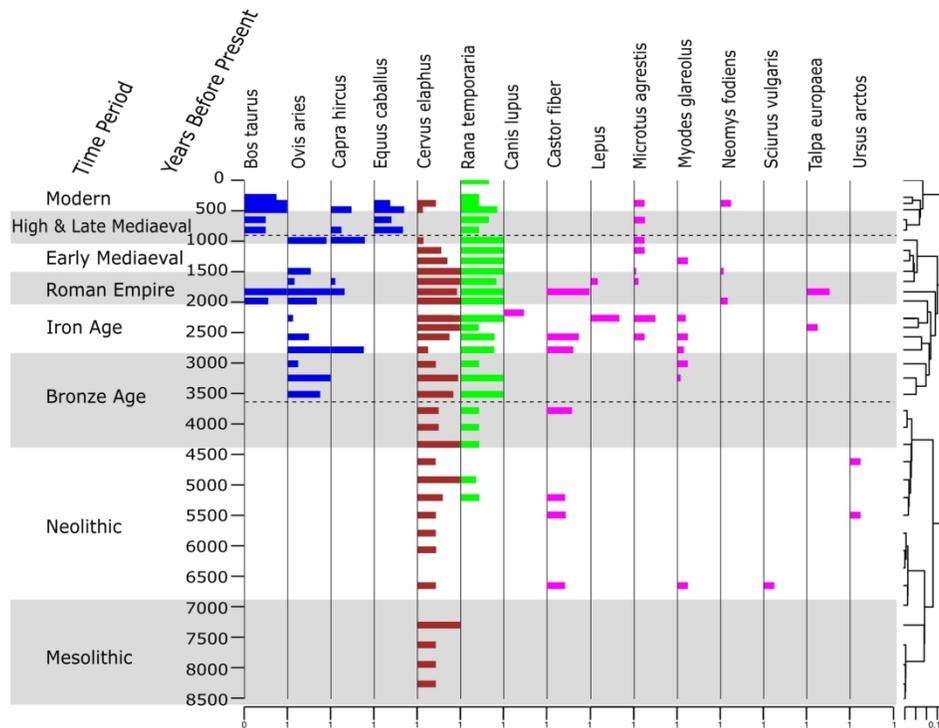


Figure 5. Vertebrate *sedaDNA* diagram The proportion of weighted PCR replicates of the vertebrate *sedaDNA* data where 0 represents *sedaDNA* present in no replicates and 1 represents all 8 replicates. Data is with CONISS statistical zonation using the vertebrate *sedaDNA* data. Archeological time periods are alternately shaded grey and white.

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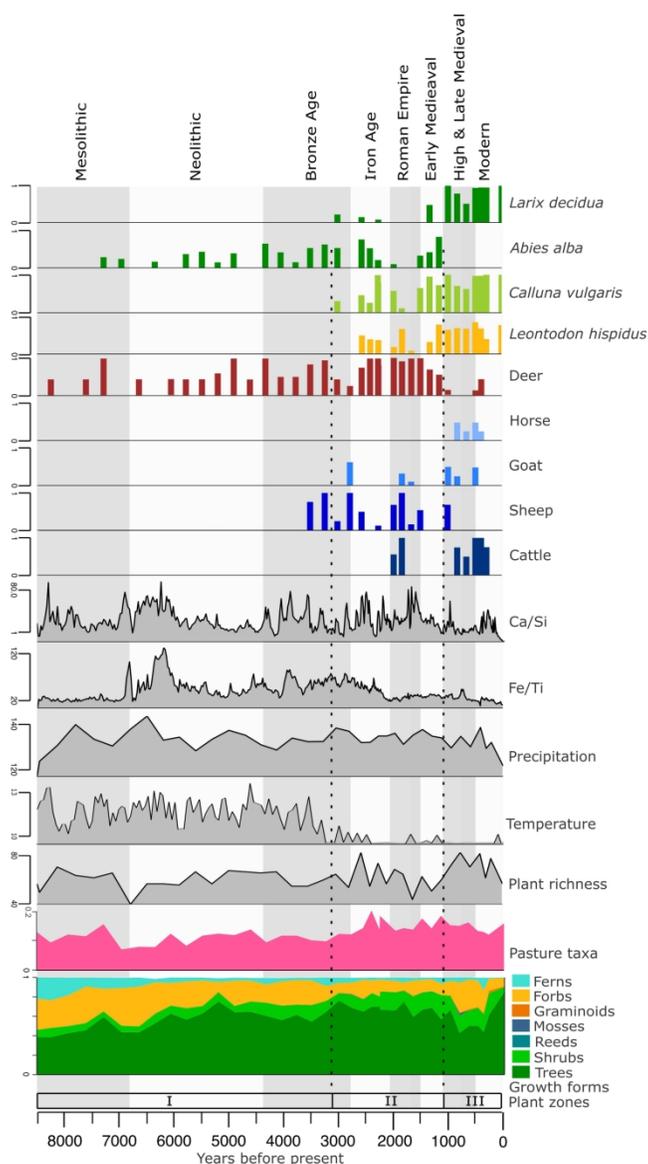


Figure 6 Overall figure: Cultural periods are indicated by the vertical grey and white boxes. Dotted lines are the zones (Plant DNA zones I - III) based on constrained cluster analysis of plant *sed*aDNA data. Plant taxa that are indicative of the changing environment are plotted with red deer (*Cervus elaphus*) and four domesticated taxa from the vertebrate *sed*aDNA data. Also plotted are Ca/Si and Fe/Ti, (indicators of erosion and weathering), precipitation (kg m⁻²), mean July temperature (°C), plant richness (Hill where q = 0), relative proportion of meadow related taxa, and the relative proportions of plants *sed*aDNA taxa reads separated by growth form.
insert Figure 6.

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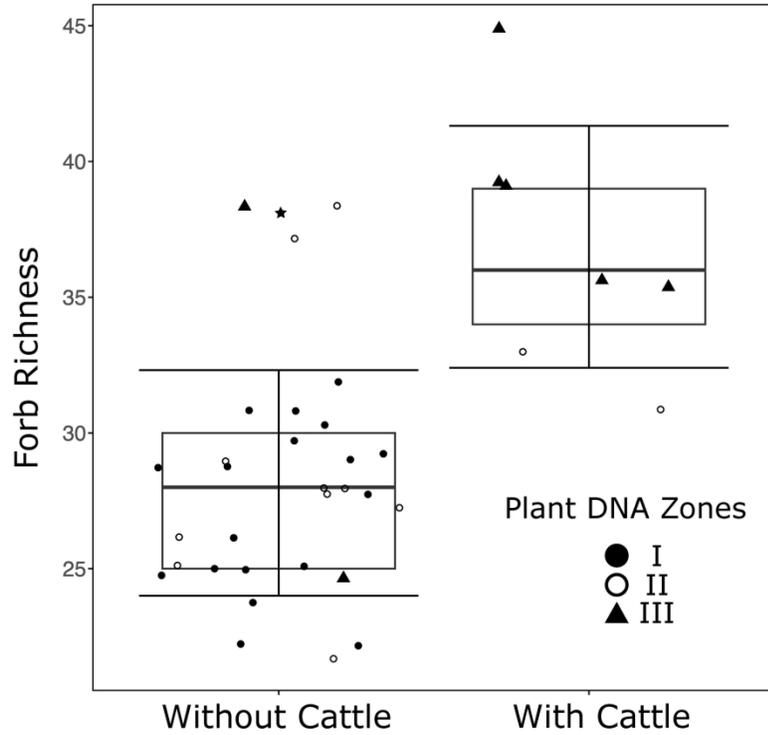


Figure 7 Boxplot: A visual representation showing the statistically significant difference in forb richness (Hill were $q = 0$) with and without the presence of cattle (*Bos taurus*). The Error bars indicate one standard deviation and the points represent the constrained cluster analysis Plant DNA Zones I - III. The outliers are indicated by the star.

219x189mm (300 x 300 DPI)

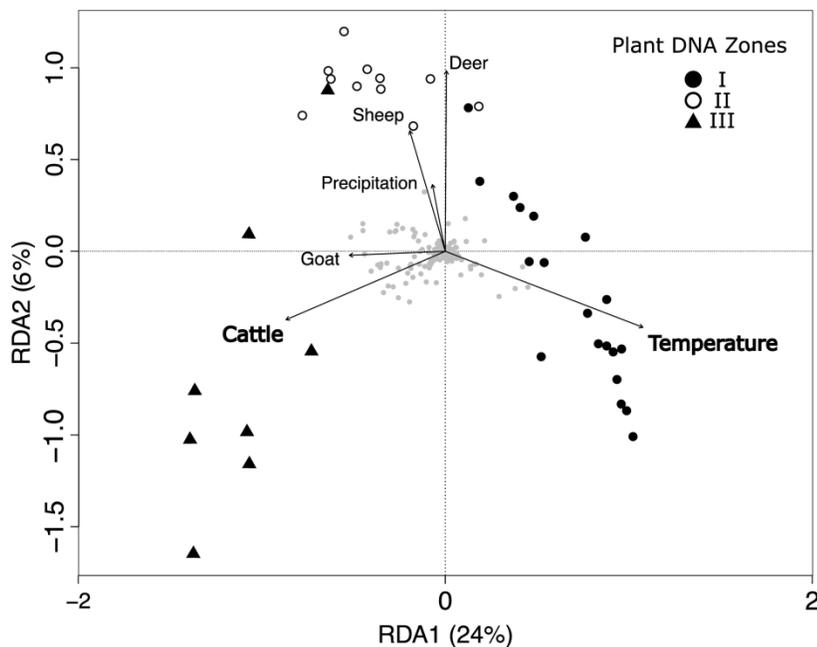
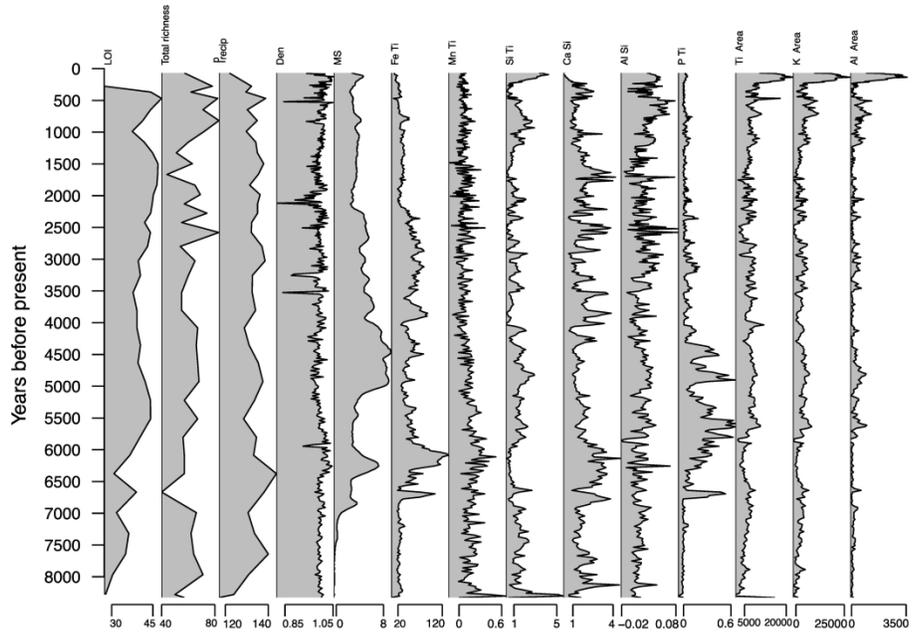


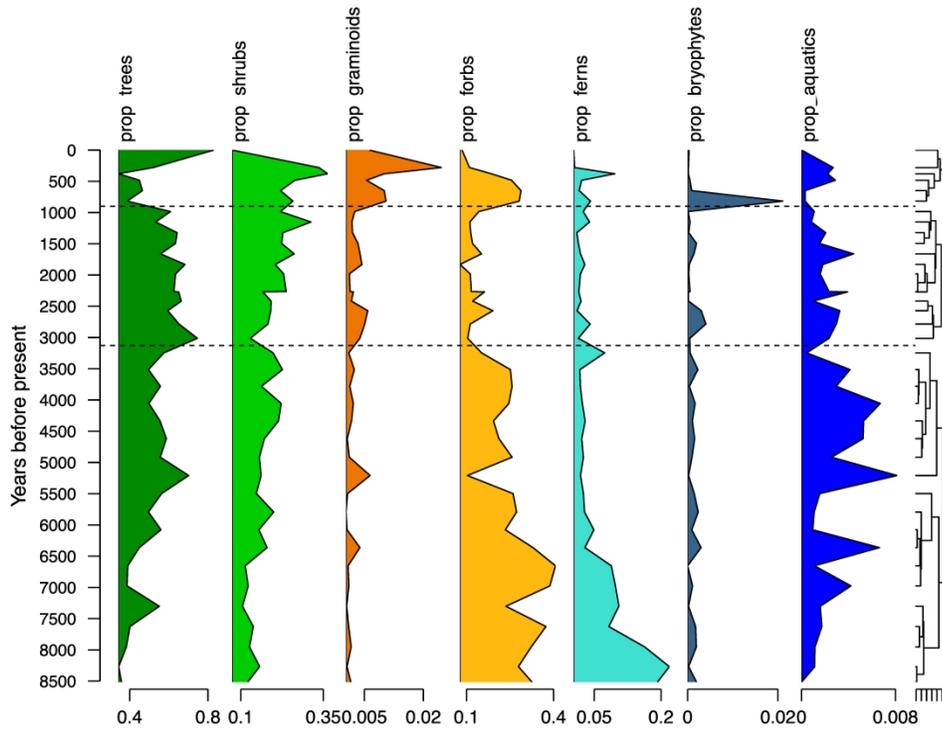
Figure 8. Redundancy Analysis (RDA): Redundancy analysis of the plant *sed*aDNA taxa (quantified as 0-8 weighted PCR repeats) composition across the explanatory variables representing environmental (precipitation (kg m^{-2}), temperature ($^{\circ}\text{C}$)) and animal factors. The sample points' represents the constrained cluster analysis Plant DNA Zones I-III, the grey dots, the plant taxa. The significant variables that explained the plant diversity pattern are shown in bold.

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Supplementary Figure 1. Full XRF data plotted against years before present. Data is plotted with CONISS statistical zonation using the plant *sed*aDNA data

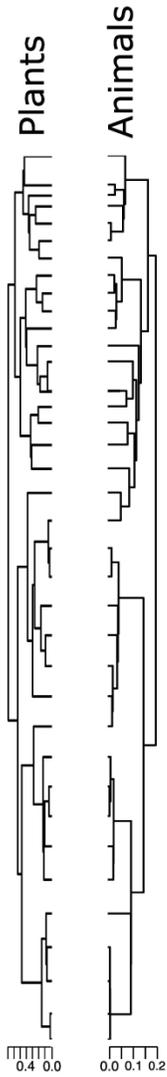
214x154mm (600 x 600 DPI)



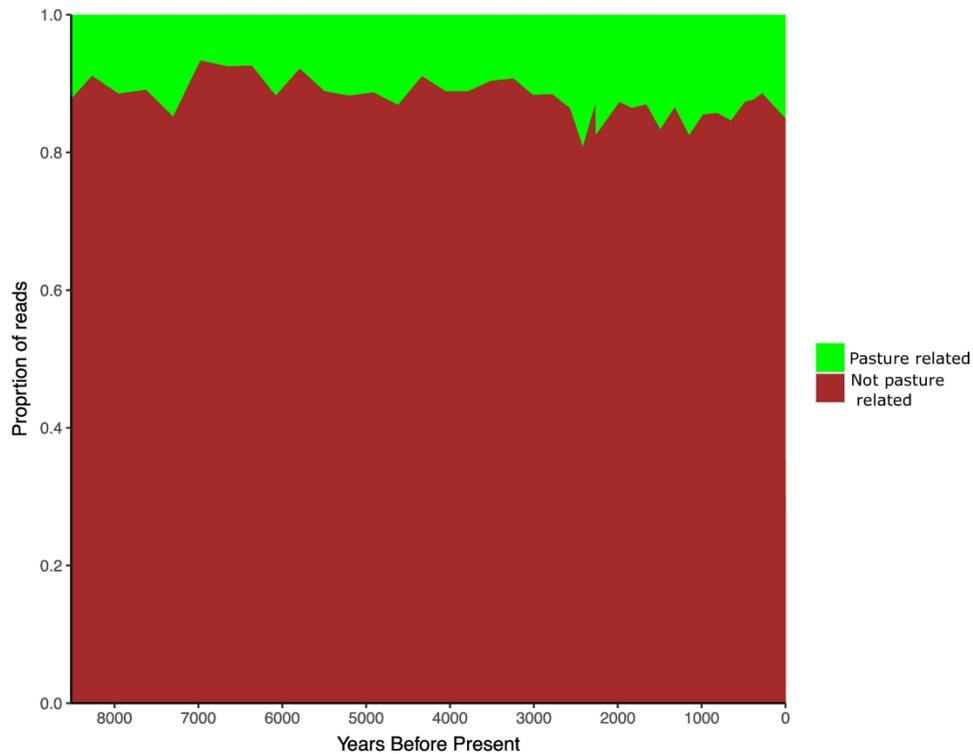
Supplementary Figure 2. Plant growth forms plotted as a proportion of total reads. Data is plotted with CONISS statistical zonation using the plant *sedaDNA* data

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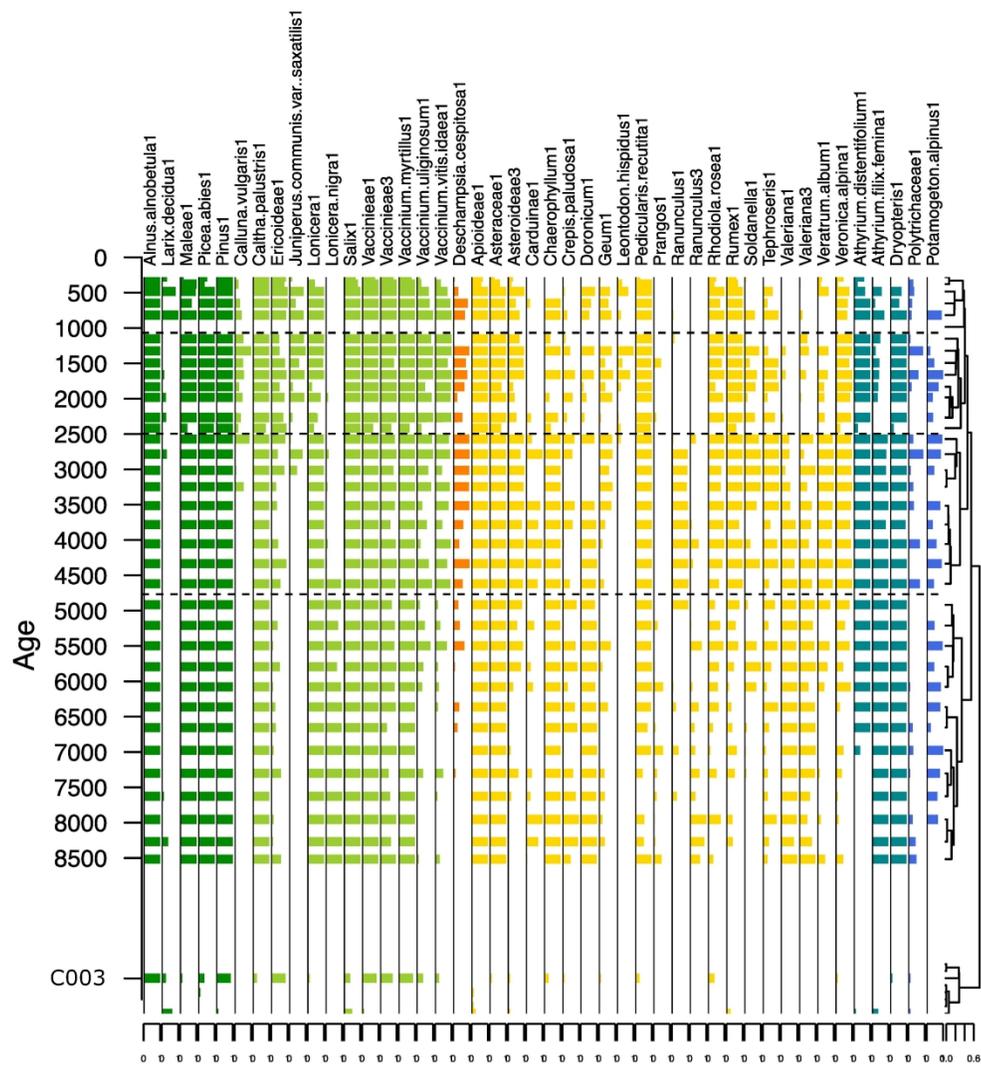


Supplementary Figure 3. Comparison of CONISS statistical zones for the plant and vertebrate *seda*DNA.
103x250mm (600 x 600 DPI)



Supplementary Figure 4. The proportion of reads of 19 alpine pasture related taxa and the remaining taxa, not related to alpine pastures. Alpine pasture related taxa consist of shrubs, graminoids, forbs, and ferns that are commonly found within Alpine pastures. They can be indicators of disturbances from both human and non-human related events. A list of all alpine related taxa can be found in Supplementary table 4"

197x159mm (600 x 600 DPI)



Supplementary Figure 5. Rioja plot of the top 40 taxa from the TEG003 P6 loop data with the switched C003 control and sample no. EG23_087.

146x162mm (600 x 600 DPI)

Supplementary

Supplementary information

Glacial History

Großer Winterleitensee (1845 m a.s.l) is situated within Winterleitenkar, a cirque in the Seetaler Alps, Styria. The lake is near the modern municipality of Neumarkt in der Steiermark. The area is situated on what was the easternmost margin of the Mur Glacial ice sheet during the Würm high glacial period (Gasser et al., 2009). The glacier occupied the basin in and around Neumarkt in der Steiermark and Perchauer pass, up to ~1400 m a.s.l. Winterleitenkar, however, is situated above 1400 m a.s.l, and so was created, and occupied, by hanging glaciers during the last glacial maximum (Lieb, 1989).

Other studies of the lake

Two previous vegetation studies around Großer Winterleitensee have been carried out. A pollen analysis was carried out in 1975 from a core taken near the lake (Zukrigl, 1975) and a contemporary vegetation analysis of Winterleitenkar was done in 2018 (Zernig and Berg, 2018). It is not possible to fully align the core taken for the pollen analysis with ours due as it only has two published radiocarbon dates (3320 +/- 160 BC and 500 +/- 130 BC).

Supplementary Tables

Supplementary table 1. Radiocarbon dates of Großer Winterleitensee. These macrofossil remains were dated in the Poznan (Poz) laboratory. The sample indicated with a star (Figure 2, orange) was removed due to standard deviation of >100 years. The date marked with † fell outside of the age depth model (Figure 2, purple).

Lab. code	Depth [cm]	Material	14C age [BP]
Poz-123846	446 - 447	Plant remains	7490 ± 50 BP
*Poz-131032	453 - 454	* Plant remains & Daphnia eggs	*7350 ± 110 BP
Poz-131034	410 - 411	Plant remains	6350 ± 40 BP
Poz-123847	386 - 387	Plant remains	5840 ± 40 BP
Poz-123848	350 - 351	Plant remains	5035 ± 35 BP
Poz-123849	302 - 303	Plant remains	4085 ± 35 BP
Poz-123850	242 - 243	Plant remains	3030 ± 50 BP
Poz-123851	206 - 207	Plant remains	2380 ± 30 BP
Poz-123852	146 - 147	Plant remains	1900 ± 35 BP
†Poz-131031	140 - 141	† Plant remains	1040 ± 30 BP
Poz-131035	100 - 101	Plant remains	1475 ± 30 BP
Poz-123853	50 - 51	Plant remains	250 ± 90 BP

Supplementary table 2. Summary of plant and vertebrate *sed*aDNA results

Primer region	Plant <i>sed</i> aDNA	Vertebrate <i>sed</i> aDNA
Raw paired-end plant DNA sequences	2 572 655	405 060
After filtering and identification	1 626 989	65 152
Total samples	38	38
Total plant sequences	137	15
Removed sequences	12	95

Supplementary table 3. Taxa with 100% match to a DNA reference library, but removed from the final dataset due to the reasons given. The number of reads of these taxa are <1% of the total number of reads with 100% match within their respective datasets.

Removed taxa	Reason for removal	<i>Sed</i> aDNA data set
Capsicum	Common lab contaminant	Plant
Rutaceae	Common lab contaminant	Plant
Solanum lycopersicum	Common lab contaminant	Plant
Vicia faba	Common lab contaminant	Plant
Tritaceae	Common lab contaminant	Plant
Litorea uniflora	Only in post PCR controls, no samples	Plant
Hippurus Vulgaris	Only in post PCR controls, no samples	Plant
Quercus	Sporadic and unreliable detections	Plant
Asterales	Too high taxonomic level	Plant
Hypnales	Too high taxonomic level	Plant
Indigoferoid clade	Too high taxonomic level	Plant

PACMAD Clade	Too high taxonomic level	Plant
Sus	Only in negative controls	Vertebrate
Sus scrofa	Only in negative controls	Vertebrate
Bilateria	Misidentification of human DNA in reference database	Vertebrate
Catarrhini	Misidentification of human DNA in reference database	Vertebrate
Homininae	Human DNA	Vertebrate
Hominoidea	Human DNA	Vertebrate
Homo	Human DNA	Vertebrate
Homo sapiens	Human DNA	Vertebrate

Supplementary table 4. Plant taxa identified in Großer Winterleitensee in all 38 samples or more than 32 samples (84%).

Trees 100% samples	Shrubs 100% sample	Shrubs > 84% samples	Forbs 100% sample	Forbs > 84% samples	Ferns 100% sample	Ferns > 84% samples	Aquatics > 84% samples
<i>Alnus alnobetula</i>	<i>Salix</i>	<i>Rhododendron</i>	<i>Caltha palustris</i>	<i>Rumex</i>	<i>Dryopteris</i>	<i>Athyrium filix-femina</i>	<i>Potamogeton alpinus</i>
<i>Pinus</i>	<i>Vaccinium myrtillus</i>	<i>Vaccinium vitis-idaea</i>	Apiaceae	<i>Doronicum clusii</i>			
<i>Maleae</i>	<i>Lonicera caerulea</i>	<i>Sambucus racemosa subsp pubens</i>	Asteraceae	Asteroideae			
<i>Picea abies</i>	Vaccinieae	<i>Vaccinium uliginosum</i>	<i>Pedicularis recutita</i>	<i>Tephrosieris integrifolia</i>			
			<i>Chaerophyllu m villarsii</i>	<i>Geum</i>			
				<i>Veratrum album</i>			

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				<i>Rhodiola rosea</i>			
				<i>Veronica alpina</i>			

For Peer Review

Supplementary table 5. Plant taxa typically found in pasture in the Alps today.

Taxa that are commonly found in Alpine Pastures
<i>Plantago lanceolata</i>
<i>Rhinanthus sp.</i>
<i>Deschampsia cespitosa</i>
<i>Juniperus communis s.l</i>
<i>Valeriana officinalis agg.</i>
<i>Veratrum album</i>
<i>Leontodon hispidus</i>
<i>Aegopodium podagraria</i>
<i>Rubus idaeus</i>
<i>Pteridium aquilinum</i>
<i>Anthriscus sylvestris</i>
<i>Chamaenerion angustifolium</i>
<i>Alchemilla vulgaris agg.</i>
<i>Arnica montana</i>
<i>Anthoxanthum alpinum</i>
<i>Medicago lupina</i>
<i>Veronica chamaedrys</i>
<i>Carlina acaulis</i>
<i>Sambucus nigra</i>

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Supplementary Figures

[insert Supp figure 1.]

[insert Supp figure 2.]

[insert Supp figure 3.]

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[insert Supp figure 5]

For Peer Review

References

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17 6 Heintzman, Inger Greve Alsos*

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40 1085.

41 Abstract

42 The Eastern European Alps boasts highly biodiverse ecosystems and a rich archaeological history.
43 However, there is limited research on the enduring impacts of historical climate change and human
44 activities on plant biodiversity in this region. Using sedimentary ancient DNA, we reconstructed
45 plant and animal dynamics from 8.5 thousand years before present (ka BP) around Großer
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17 55 vole and Eurasian water shrew (*Neomys fodiens*) declined or even disappeared. These changes are
18
19 56 also accompanied by a significant transformation of plant community structure. The ability to
20
21 57 determine both plant responses and animal drivers from the same palaeolimnological sequence
22
23 58 vastly improves our ability to partition causes of vegetation change over the Holocene. Here, we
24
25 59 reveal that plant biodiversity is maintained or increased by moderate cattle grazing. Therefore,
26
27 60 non-intensive domesticated stock grazing is essential for maintaining diverse Alpine meadows.

28
29 61
30 62 *Key words:*

31
32 63 European Alps, anthropogenic impacts, climate change, environmental management,
33
34 64 metabarcoding, *sedDNA*

65 66 Introduction

67 The impacts of climate change on alpine plant communities are raising concern due to their
68 potential repercussions on biodiversity, ecosystem functions and services (Liu et al., 2021;
69 Steinbauer et al., 2018; Zu et al., 2021). The rate of climate warming in the European Alps is
70 reaching up to three times the average observed in the northern hemisphere (Hock et al., 2019),
71 which is predicted to result in biodiversity decline in the coming decades (Schwager and Berg,
72 2019). Pressures from human land use could potentially exacerbate these effects causing further

1
2
3 73 losses (Wang et al., 2018). The Central Eastern Alps, recognized as a biodiversity hotspot
4
5 74 harbouring numerous endemic species (Tribisch and Schönswetter, 2003), is now facing significant
6
7 75 ecological threats due to both anthropogenic climate change and land use (Schwager and Berg,
8
9 76 2019). Long-term studies are needed to understand the drivers of such changes, but most
10
11 77 palaeoecological studies so far do not allow for simultaneous statistical analyses of climate and
12
13 78 land use effects.

14
15 79 Recent advances in *sedDNA* (sedimentary ancient DNA) **methods** enable comprehensive
16
17 80 reconstructions of **the surrounding vegetation and husbandry dynamics using** plant and animal
18
19 81 DNA from lake sediment deposits, providing an opportunity for statistical testing to elucidate
20
21 82 drivers of vegetation changes (Garcés-Pastor et al., 2022; Giguët-Covex et al., 2023; van Vugt et
22
23 83 al., 2022). This enhanced understanding can provide pivotal insights into the preservation and
24
25 84 management of these invaluable habitats for future generations, particularly regarding the impact
26
27 85 of grazing in the management of Alpine ecosystems in the face of ongoing climate change.

28
29 86 From the Last Glacial Maximum (Local glacial history in Supplementary information) to the
30
31 87 Holocene **climatic** optimum (~9.5 - 5.5 ka BP (thousand years before present)), the Alps underwent
32
33 88 a progressive increase in temperature (Fohlmeister et al., 2013). The short-lived 8.2 ka BP climatic
34
35 89 event was characterized by generally cooler conditions (Tinner and Lotter, 2001), along with
36
37 90 increased humidity and precipitation (Drescher-Schneider, 2007). Vegetation reconstructions
38
39 91 indicate that the 8.2 ka BP event caused a restructuring of terrestrial plant communities (Tinner
40
41 92 and Lotter, 2001). Following this event, the climate remained relatively stable until the end of the
42
43 93 Holocene climatic optimum at ~5.5 ka BP.

44
45 94 Climate is not the sole driver of plant community dynamics. Throughout the Holocene, Alpine
46
47 95 plant communities have faced significant impacts from human land use practices. These include
48
49 96 early Holocene vegetation clearance through deliberate burning (~9 ka uncalibrated BP) (Bos and
50
51 97 Urz, 2003; Lechterbeck and Rösch, 2021), the artificial lowering of timberlines resulting from
52
53 98 Bronze Age (~4.5 - 3 ka B) mining (~3.5 ka BP) (Knierzinger et al., 2020) and transhumance (Pini
54
55 99 et al., 2017; Schmidl et al., 2005), to modern day recreational hiking (Aziz et al., 2023).

56 100

1
2
3 101 [insert Figure 1.]
4
5 102

6
7 103 Although the Austrian Neolithic period began ~6.9 ka BP (Löcker et al., 2009), the earliest known
8
9 104 human settlement phase in Styria (Figure 1B) dates to ~6.3 ka BP (Wildon Schlossberg) (Brandl
10
11 105 et al., 2015). By this time, the adjacent province to the west (Salzburg) already had evidence of
12
13 106 Neolithic activity at over 2000 m a.s.l (Gilck and Poschlod, 2019). Austria in general remained
14
15 107 sparsely populated until the Late Neolithic (~4.6 ka BP). After which Styria experienced a
16
17 108 significant population increase, becoming progressively more inhabited (Brandl et al., 2015).
18
19 109 Extensive copper ore mining emerged across Styria during the Neolithic to Bronze Age
20
21 110 transition ~4.5 ka BP (Knierzinger et al., 2021). This widespread mining activity led to significant
22
23 111 local deforestation (Drescher-Schneider, 2007) and an increased local demand for animal products.
24
25 112 In the Late Bronze/Early Iron Age, sheep (*Ovis aries*) alpine transhumance, the seasonal mobility
26
27 113 of pastoral activities across altitudes, became a common practice (Saliari et al., 2020). Following
28
29 114 this, during the Iron Age (2.8 - 2 ka BP), there was a shift in farming practices from sheep to cattle
30
31 115 (*Bos taurus*) alpine transhumance. However, a few strongholds of sheep alpine transhumance
32
33 116 remained in East Austria (Schmölcke et al., 2018). The cooler temperatures toward the end of this
34
35 117 period likely decreased the viability of cattle farming, leading to a resurgence of sheep as the
36
37 118 primary domesticate in Austria (Schmölcke et al., 2018). Throughout the period of the Western
38
39 119 Roman Empire (2 - 1.5 ka BP), the prosperity in Austria was mainly derived from mining (stone,
40
41 120 salt, metal ores) and agriculture (Schmidl et al., 2005). Facilitated by a warmer, more stable climate
42
43 121 (Marx et al., 2018), farmers of this period took to a reinvestment in cattle alpine transhumance. To
44
45 122 support both mining processes and cattle pasturing, further tree clearing was undertaken (Drescher-
46
47 123 Schneider, 2007). Following the collapse of the Western Roman Empire ~1.5 ka BP, the Early
48
49 124 Mediaeval Period (~1.5 - 1 ka BP) was a time of war and mass movement across Europe, but also
50
51 125 of an unpredictable climate (Marx et al., 2018). At the onset of the Early Mediaeval Period, the
52
53 126 cooler, wetter climate resulted in a return to sheep alpine transhumance in some areas across
54
55 127 Austria (Marx et al., 2018). A new intensification of cattle alpine transhumance took place at the
56
57 128 start of the High Mediaeval Period (~1 - 0.7 ka BP), once again causing significant habitat

1
2
3 129 disturbances and plant community turnover (Drescher-Schneider, 1998) that has continued to the
4
5 130 present day. This historical reconstruction is based on pollen and archaeological records. It creates
6
7 131 a general narrative, but cannot provide species-specific and local biodiversity data for statistically
8
9 132 testing the drivers of change: climate and grazing.

10
11 133
12
13 134 In this paper, we analyse plant and mammal *sed*aDNA from an Alpine lake (Großer
14
15 135 Winterleitensee, Easternmost Central Alps) to identify species-level ecological histories and test
16
17 136 the main drivers of plant diversity trends. We further aim to identify from when the landscape
18
19 137 around Großer Winterleitensee has been used for Alpine transhumance, which animal species were
20
21 138 the dominant grazers, and when, in order to resolve the debate concerning human impacts on
22
23 139 Alpine biodiversity in the Eastern European Alps. This has further implications for the
24
25 140 management of high-altitude Alpine landscapes in general. If biodiversity has increased through
26
27 141 the grazing of domesticates then it follows that maintaining grazing is essential to sustain high
28
29 142 biodiversity in the face of climate change.

30 31 143 Materials and Methods

32
33
34 144 Großer Winterleitensee is a subalpine lake in Winterleitenkar, Seetaler Alpen, Austrian Alps
35
36 145 (47.089653 N, 14.566058 E, 1845 m a.s.l., Figure 1), with an area of 4.5 ha, a maximum water
37
38 146 depth of 9.6 m, and a pH of 6.98 (July, 2018). The lake catchment is 2.7 km² and comprises a
39
40 147 diverse landscape including mire, Alpine meadows and dwarf shrubs. On the steep south-eastern
41
42 148 facing slope, there is a closed Swiss pine (*Pinus cembra*) forest with scattered spruce (*Picea abies*)
43
44 149 and larch (*Larix decidua*) (Figure 1D). The lake is situated in the Styrian crystalline region, which
45
46 150 is dominated by metamorphic rock (garnet, mica, schist) with rarer occurrences of plagioclase,
47
48 151 gneiss, and pegmatite, and scattered marble and amphibolites on the north-west ridge above the
49
50 152 lake (Zernig and Berg, 2018). Trees in this area can grow at a maximum elevation of 1950 m a.s.l.,
51
52 153 allowing for an elevational difference between lake and upper tree limit of c. 105 m. A moor core
53
54 154 was taken within Winterleitenkar (47.0916667 N, 14.5638888 E, 1850 m a.s.l., Figure 1C) for
55
56 155 pollen analysis (Zukrigl, 1975). However, with only two absolute dates provided (500 ± 130 and
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59
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1
2
3 156 3320 ± 160 BCE or ~2.5 and ~5.3 ka BP) we are unable to fully align this core with our lake
4
5 157 sediment core.

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7 158
8
9 159 A 4.6 m sediment core was taken from the deepest point of the lake from a floating platform using
10
11 160 a Nesje coring system fitted with a 5 m long, 110 mm diameter pipe. For transportation, the core
12
13 161 was cut into one metre sections with the newly exposed ends immediately sealed. A surface
14
15 162 sediment core was also taken with a UWITEC gravity corer using a 1 m long, 100 mm diameter
16
17 163 pipe. All core sections were transported at 4 °C to the Arctic University of Norway in Tromsø
18
19 164 (UiT). Prior to opening, the core sections were scanned for magnetic susceptibility using a
20
21 165 GEOTEK Multi Sensor Core Logger (MSCL-S) with a point sensor at the Department of
22
23 166 Geosciences, UiT. The sections were then cut longitudinally and opened and sampled in a
24
25 167 dedicated ancient DNA laboratory, UiT. We took 37 subsamples at 12 cm intervals for *sedDNA*
26
27 168 analysis from one core half, the other half was archived. During subsampling, samples were also
28
29 169 taken for Loss on Ignition (LOI) and plant macrofossil remains were opportunistically collected
30
31 170 for radiocarbon dating. A subsample from the sediment/water interface was collected from the
32
33 171 surface core in a dedicated environmental DNA laboratory, UiT.

34 172

38 173 **Radiocarbon dating, age-depth model construction, and geochemistry**

40 174 Sixteen terrestrial plant macrofossils were radiocarbon dated at the Poznan Radiocarbon
41
42 175 Laboratory (Goslar et al., 2004) using accelerator mass spectrometry (AMS). The calibration of
43
44 176 AMS dates used the terrestrial IntCal20 curve (Reimer et al., 2020). The age-depth model was
45
46 177 constructed using the Bayesian framework calibration software ‘rbacon’ (v2.5.0) (Blaauw and
47
48 178 Andrés Christen, 2011), executed in R version 4.3.1 (2023-06-16) (R Core Team, 2023).

49 179

51
52 180 The organic content of the sediment samples was measured using the LOI method by Lamb (2004).
53
54 181 The archival core halves were scanned using an AVAATECH XRF core scanner with
55
56 182 measurements taken at 10 mm resolution using a 1.5 mA current and 10 kV voltage for 10 seconds.

1
2
3 183 High-resolution imaging was carried out using a Jai L-107CC 3 CCD RGB Line Scan Camera
4
5 184 mounted to the XRF scanner. The raw peak area data was normalized using either Ti and Si in
6
7 185 order to mitigate the influence of water and matrix effects (Croudace et al., 2006). Both elements
8
9 186 are reliable indicators of input of allochthonous material from the catchment. Iron/titanium (Fe/Ti)
10
11 187 is used to indicate changing redox conditions, phosphorus/titanium (P/Ti) is used as a weathering
12
13 188 indicator and calcium/silicon (Ca/Si) is used as an erosion indicator (Davies et al., 2015). Magnetic
14
15 189 susceptibility, measured using a GEOTEK Multi Sensor Core Logger, can be used as an indicator
16
17 190 for precipitation (Balsam et al., 2011).
18
19 191

192 ***sed*aDNA data generation and sequence assignment**

193 All *sed*aDNA data generation steps mainly followed Rijal *et al.* (2021). Briefly, all 38 samples,
194 four sampling controls, and four extraction negative controls were extracted using a modified
195 DNeasy PowerSoil kit (Qiagen, Germany). Amplification of the samples used two uniquely dual-
196 tagged generic primer sets. For plant *sed*aDNA, the *trnL* P6 loop region of the chloroplast genome
197 was targeted using *gh* primers (Taberlet et al., 2006). For animal *sed*aDNA, we targeted the
198 mitochondrial 16S locus using MamP007 primers (Giguët-Covex et al., 2014) including an
199 updated human blocking primer strategy (Garcés-Pastor et al., 2022). Eight uniquely dual tagged
200 (8 or 9-bp) amplicon replicates were created for both plant and animal *sed*aDNA. PCR reactions
201 and cycling conditions for plants followed Voldstad *et al.* (2020), while animals followed Garcés-
202 Pastor *et al.* (2022). We pooled and cleaned PCR products creating two pools, one for each primer
203 set. A sequencing library was created for each pool and sequenced at Genomics Support Centre
204 Tromsø, UiT on an Illumina NextSeq platform (2x150 bp, mid-output mode, dual indexing).
205 Following data analysis (outlined below), plant negative control EG23_C003 was indiscernible
206 from the plant *sed*aDNA samples, while plant *sed*aDNA sample EG23_087 contained no taxa
207 (Supplementary Figure 4). We suspected a switch between the sample and control. We therefore
208 re-extracted and re-amplified the batch of 20 samples (EG23_B series) in which the switch could
209 have occurred. The resulting library was sequenced using an Illumina MiSeq platform (2x150 bp,

1
2
3 210 mid-output mode, dual indexing) at the Faculty of Biosciences, Fisheries and Economics, UiT. For
4
5 211 downstream data analyses, we combined the re-extracted samples with the remaining unaffected
6
7 212 samples.
8

9 213
10
11 214 Following Rijal *et al.*, (2001), plant *sed*aDNA data was processed using a bioinformatic pipeline
12
13 215 based on the OBITools software package (Boyer *et al.*, 2016). The reference databases PhyloAlps
14
15 216 (Garcés-Pastor *et al.*, 2022), Arctborbryo (Soininen *et al.*, 2015; Sønstebø *et al.*, 2010; Willerslev
16
17 217 *et al.*, 2014), PhyloNorway (Alsos *et al.*, 2020, 2022) and EMBL release 143 (Kanz *et al.*, 2005)
18
19 218 were used. The identified sequences were filtered using custom R scripts (available at
20
21 219 <https://github.com/Y-Lammers/MergeAndFilter>). Sequences were retained if they matched at
22
23 220 100% to at least one reference database, were present in at least three PCR replicates and had a
24
25 221 read count of >10. Sequences that were detected in more replicates of the negative control samples
26
27 222 than the sediment samples and/or are known common laboratory contaminants (Supplementary
28
29 223 Table 3) were removed. Co-occurring sequences were assigned to the same taxon (Alsos *et al.*,
30
31 224 2022). For the animal *sed*aDNA data, we used the aforementioned pipeline with adjustments
32
33 225 outlined in Garcés-Pastor *et al.* (2022). The single reference database, EMBL release 143 was
34
35 226 used. As the concentration of animal *sed*aDNA is typically lower than terrestrial plant *sed*aDNA
36
37 227 (Murchie *et al.*, 2023), we used more relaxed filtering criteria to maximize detections. Sequences
38
39 228 were retained if they were present in at least one replicate, with a read count >1, and a match of
40
41 229 $\geq 95\%$ to the reference database. Co-occurring sequences assigned to the same taxon were merged.
42
43 230 We discarded sequences matching human (*Homo sapiens*), whereas sequences matching
44
45 231 invertebrates were not used in downstream analyses. Sequences identified as *Sus scrofa* were
46
47 232 discarded as we are unable to distinguish domesticated pig from wild boar at this locus. One of the
48
49 233 three unique pig sequences was also present in the extraction control at the same frequency as the
50
51 234 sediment samples, leading us to believe this may be contamination from the extraction reagents.
52
53 235 Sequences that were only present with a read count of one were also removed.
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236 Climate reconstruction and statistical analysis

237 We reconstructed the Holocene climate around Großer Winterleitensee using local temperature
238 and precipitation datasets. The temperature reconstruction is based on chironomid assemblage data
239 taken from the Austrian lake Schwarzsee ob Sölden (SoS) (Ilyashuk et al., 2011; Wick and Tinner,
240 1997), a lake at 2796 m a.s.l, 951 m higher elevation than Großer Winterleitensee. We adjusted
241 the temperature reconstruction using a mean environmental lapse rate of $-6.5\text{ }^{\circ}\text{C km}^{-1}$ (Lute and
242 Abatzoglou, 2021). Therefore, by adding $6\text{ }^{\circ}\text{C}$ to each SoS temperature point an approximate local
243 temperature reconstruction appropriate for Großer Winterleitensee was created. We reconstructed
244 precipitation at 100-year resolution using the CHELSA-TraCE21k v1.0 model (Karger et al.,
245 2023). Precipitation (kg m^{-2}) refers to the mean mass (kg) of water in all phases (rain, snow, etc.)
246 per square metre per 100 years.

247
248 We plotted the proportions of weighted PCR replicates (wtRep) (Rijal et al., 2021) for plant and
249 animal *sed*aDNA data using the Rioja package (Juggins, 2015) as implemented in R. This
250 conservative measure of abundance avoids patterns of change being masked by read-dominant
251 taxa and thereby highlights the diversity detected (Alsos *et al.*, 2022). We conducted a constrained
252 cluster analysis (CONISS) to identify statistically significant changes in the plant and animal
253 community compositions using the Vegan package (Oksanen et al., 2013) in R.

254
255 Box plots were used to determine significant differences in total richness and individual plant
256 growth form richness (Hill number for $q = 0$) with and without the presence of grazing animals.
257 The data for cattle (*Bos taurus*), sheep (*Ovis aries*), horses (*Equus caballus*), goats (*Capra hircus*),
258 and red deer (*Cervus elaphus*) were transformed into binary presence/absence data. Boxplots were
259 plotted using the `geom_boxplot()` and the error bars were created and plotted using `stat_summary()`
260 and `stat_boxplot()` from R package `ggplot2` (Ginestet, 2011). The error bars indicate one standard
261 deviation from each group mean. Plant richness is taken as the total count of taxa identified to

262 family level and lower within each sample. Whereas the plant growth form richness is this data
263 separated into each growth form, e.g tree, shrub etc.

264
265 To explore the effects of temperature, precipitation and animals (wtRep cow, sheep, horse, goat,
266 red deer) on vegetation changes (plant wtRep data), a redundancy analysis (RDA) was performed
267 using Vegan, and plotted using ggplot2. The drivers were checked for co-correlations that could
268 impact the results using cor(). Horse was highly correlated with cattle, thus it was removed. Scaling
269 of the RDA axes was set to two so the angle between the arrows reflects their relative relationship;
270 an angle $<90^\circ$ representing a positive relationship, 90° a neutral relationship, and $>90^\circ$ a negative
271 relationship. A transformation, such as the Hellinger transformation was not required as the data
272 grouping had already reduced the ecological gradient. Model and constraint significance testing
273 was achieved using anova.cca() in Vegan.

274

275 Results

276

277 [insert Figure 2.]

278 Age-depth model and lithology

279 The sixteen AMS radiocarbon dates range between 250 ± 90 and 7490 ± 50 years BP (Supplementary
280 Table 1). Two dates were rejected; one had an error margin of 110 years, and the other fell outside
281 of the model. The age-depth model (Figure 2) displays a near linear sediment accumulation rate
282 (SAR), well captured by the Bayesian model but also well described by two linear rates with a
283 break-point at ~ 2.8 ka BP. At approximately this date the SAR increases $\times 4.5$ from 0.2 mm yr^{-1} to
284 0.9 mm yr^{-1} .

285

1
2
3 286 The core consists of dark-brown silty-gyttja with organic macro-remains and lighter coloured
4
5 287 bands throughout (Figure 2). LOI (Figure 3) indicates a core rich in organic matter. In the oldest
6
7 288 sample (8.5 ka BP), only 20% of the core comprises organic material. Over the following three
8
9 289 thousand years, this percentage increases, culminating in a peak at 5.5 - 5.2 ka BP (44%) before
10
11 290 plateauing and stabilising around a mean of $43\pm 5\%$. The youngest sample however is composed
12
13 291 of only 27% organic content.

14
15 292

16
17 293 [insert Figure 3.]

18
19 294

20 295 XRF data (Figure 3) reveals an increase in Fe/Ti and Ca/Si input in the early Neolithic period ~6.8
21
22 296 - 6 ka BP, indicative of a period of increased weathering and erosion respectively. The ratio of
23
24 297 P/Ti 6.5 - 4.5 ka BP also signals an alteration in precipitation patterns during this period. However,
25
26 298 while a downturn in input takes place, Fe/Ti and Ca/Si remain noisy throughout, suggesting that
27
28 299 while the transport of material into the lake is still occurring, it is at a reduced rate than before,
29
30 300 possibly due to decreased precipitation. The intervals at 2.4 - 2.2 (Iron Age) and 1.3 - 1 ka BP
31
32 301 (Early Mediaeval Period) are intervals characterized by lower erosion as inferred from Ca/Si.
33
34 302 Magnetic susceptibility of this core remains low until ~6.8 ka BP, subsequently peaking at ~4.5 ka
35
36 303 BP and then gradually decreasing towards the upper section of the core, suggesting a decrease in
37
38 304 precipitation regimes and/or a decrease in input of magnetic materials such as Fe.

39
40 305

41 42 43 306 **Precipitation reconstruction**

44
45 307 Modelled precipitation reconstruction data ranges from 117 (8.5 ka BP) to 144 kg m⁻² (6.4 ka BP)
46
47 308 (Figure 3) with the record starting with the lowest precipitation value (until 6.8 ka BP; mean = 129
48
49 309 kg m⁻²). This is followed by a peak with the aforementioned highest value and then decreases
50
51 310 through the Neolithic period (6.9 - 4.4 ka BP; mean = 136 kg m⁻²). The mean precipitation remains
52
53 311 relatively stable (mean = 134 kg m⁻²) until the Modern period, where precipitation decreases once
54
55 312 more (600 years BP - present day; mean = 131 kg m⁻²).

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5
67 314 ***SedaDNA***
89 315
1011 316 [insert Figure 4.]
12
1314 317 **Plant data**
15

16 318 A total of 1,642,012 reads with 100% match to at least one of the reference libraries were obtained
17 319 after bioinformatic filtering (Supplementary Table 2). Following the collapse of homopolymers
18 320 and post-identification filtering, we retained 1,626,989 reads, (99%) across 137 unique sequences:
19 321 11 identified to family-level, 30 to genus-level and 84 species-level (61%) and 12 to other
20 322 taxonomic levels (sub-family, tribe, and sub-tribe). These taxa can be broken down into the
21 323 following growth forms: 8 trees, 16 shrubs, 14 graminoids, 72 forbs, 8 ferns, 13 bryophytes and 6
22 324 aquatic plants (Figure 4). The number of taxa per sample ranged between 40 - 81 with a mean and
23 325 median of 58.5 and 57 taxa respectively. Removed taxa and taxa that are consistently present
24 326 throughout the core can be found in Supplementary Tables 3 and 4, respectively.

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34
35 327 **Animal data**
36

37 328 The animal data comprises 84,062 reads identified with 95% or higher to 246 identified sequences
38 329 (Supplementary Table 2). Fifteen unique sequences representing 15 taxa were retained after post-
39 330 identification filtering and haplotype collapsing, comprising 65,152 reads: one taxon at genus-
40 331 level and 14 at species-level. Whilst these are mammal specific primers, amphibian by-catch does
41 332 occur. The 15 taxa can be broken down into the following groups: 4 domesticate mammals, 10
42 333 wild mammals, and 1 amphibian. Red deer (*Cervus elaphus*) and, from 5.2 ka BP, common frogs
43 334 (*Rana temporaria*) were detected consistently throughout the core, being absent in only a few
44 335 samples across the record (Figure 5).

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52 336
5354 337 [insert Figure 5.]
55
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60

338 CONISS zone analysis

339 Constrained cluster analysis (CONISS) using a broken stick model of both the plant and mammal
340 data identified three statistically significant zones each according to main changes (Supplementary
341 Figure 3). The breakpoints of the CONISS zones for these two data sets are similar. We chose to
342 use the plant CONISS zones as these zones are based on more taxa than those of the mammal data,
343 giving us more confidence in these zones. We call these zones Plant DNA Zones (PDZ) I - III
344 (Figure 6). For comparison, the CONISS zones for the animals are plotted in Figure 5 (See direct
345 comparison of zones in Supplementary Figure 3).

346
347 [insert Figure 6.]

348

349 PDZ I (459 - 235 cm, 8500 - 3010 yrs BP Mesolithic, Neolithic, Bronze Age)

350 PDZ I is characterized by unstable environmental conditions (Figure 6). At the core's base around
351 8.5 ka BP, the models indicate a relatively high temperature (12.02 °C), the lowest precipitation
352 value for the record (117.08 kg m⁻²) and a median starting point for plant richness at 57 taxa.
353 Pasture related plant taxa (Figure 6; Supplementary Table 5) are present across the entire core,
354 however PDZ I displays the lowest proportion (mean = 10±2 %).

355

356 Over the Mesolithic period, Fe/Ti remains stable and low suggesting low weathering. Ca/Si
357 indicates variable inputs of material from erosion processes, while becoming more stable towards
358 the end of the Mesolithic period. At the start of this core, the LOI values are at their lowest, possibly
359 due to few aquatic species and/or less erosion at this time. Progressing through the Mesolithic
360 period (until ~6.8 ka BP), the temperature is fluctuating, and the precipitation is highest in the
361 middle of the period. Total plant richness (Hill q = 0, PDZ I mean = 54.5±6.0) fluctuates in tandem
362 with variations in precipitation. Ferns and forbs have high abundance (average 22% and 32%,
363 respectively), whereas trees only constitute an average of 39% of the reads across these samples.

1
2
3 364 As the climate warms and dries ~7.5 ka BP, the proportion of ferns decreases, while that of trees
4
5 365 increases. Following a peak of pasture related taxa at 7.3 ka BP, these decrease over the subsequent
6
7 366 samples.
8

9 367
10
11 368 The Neolithic Period (6.8 - 4.6 ka BP) begins with the highest precipitation levels of the core and
12
13 369 corresponds with a peak in mineral in-wash (Fe/Ti, Ca/Si & P/Ti; Figure 3 and 6) into the lake and
14
15 370 low abundance of trees. The proceeding drier, more stable climate through the Holocene climatic
16
17 371 optimum is reflected in an increase in trees, the first appearance of beaver (*Castor fiber*) and bank
18
19 372 vole (*Myodes glareolus*), as well as the only record of red squirrel (*Sciurus vulgaris*) at 6.8 ka BP
20
21 373 (Figure 5). We note that red deer decreases during the early Neolithic but increases again during
22
23 374 the Late Neolithic, when also brown bear (*Ursus arctos*) appears.
24

25 375
26
27 376 The cooling throughout the Bronze Age coincided with once again an opening of the forest
28
29 377 environment with a decrease in trees and an increase in forb and shrub growth forms. In the final
30
31 378 500 years of PDZ I, while detecting the domesticated sheep (*Ovis aries*), there is an increase of
32
33 379 trees and ferns once more with a reduction in shrubs and pasture related taxa suggesting, once
34
35 380 again, a closing forest environment. With the exception of one detection at ~6.8 k yrs BP, the bank
36
37 381 vole is first detected in consecutive samples at ~3.25 k yrs BP, coinciding with the aforementioned
38
39 382 increase in forest environment.
40

41 383 **PDZ II (235 - 105 cm, 3010 - 1020 yrs BP, Iron Age, Western Roman Empire, Early Mediaeval**
42
43 **Period)**
44

45
46 385 PDZ II can be characterized as a period where human land use is having a profound effect on plant
47
48 386 dynamics. Trees maintain dominance throughout PDZ II with the proportion of reads fluctuating
49
50 387 around a mean of 68%. The early phase of PDZ II, is represented by the Iron age (2.8 - 2.2 ka BP)
51
52 388 and plant richness (mean = 59.2±9.2 %) and temperature are both decreasing. An initial increase
53
54 389 in shrub diversity includes *Juniperus communis*, *Vaccinium uliginosum*, and *Calluna vulgaris*
55
56 390 indicating habitat disturbance and open land creation, possibly from the pasturing of domesticates.
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4 391 The proportion of pasture related taxa across this zone (Figure 6; mean = 14 ± 0.02 %) is highest at
5 392 2.5 ka BP at 19 %. Pasture related taxa including *Calluna vulgaris*, and *Leontodon hispidus* are
6
7 393 first detected between ~3 and 2.5 ka BP. Taxa that are present only sporadically prior to PDZ II,
8
9 394 are detected more frequently and in more subsequent samples, e.g *Deschampsia cespitosa*,
10
11 395 *Juniperus communis s.l.* The bank vole is detected from the start of PDZ II until the end of the Iron
12
13 396 Age at 2.3 ka BP. The detection of goats (*Capra hircus*) at the Bronze Age/Iron Age boundary
14
15 397 indicates the presence of more domesticate varieties potentially having a more profound effect on
16
17 398 the vegetation than sheep alone. After the introduction of goats, the short-tailed field vole is
18
19 399 detected in two samples (2.5 and 2.2 ka BP), before being detected once again from 1.7 ka BP until
20
21 400 the end of this zone. The presence of Eurasian water shrew (*Neomys fodiens*), European mole
22
23 401 (*Talpa europaea*), hare (*Lepus sp.*) and one instance of wolf (*Canis lupus*) can also be detected in
24
25 402 this zone. *Abies alba*, is a disturbance sensitive species that is not detected when cattle are detected
26
27 403 at this lake. The aquatic plant *Potamogeton crispus* is present almost exclusively in this zone. This
28
29 404 species can persist in nitrogen-rich waters, allowing it to thrive in heavily farmed areas where more
30
31 405 sensitive species cannot. The onset of the Iron Age (2.8 - 2 ka BP) sees an increase and then a
32
33 406 gradual overall decline in plant richness, although there is no sharp change in plant community
34
35 407 structure (Figure 4 and 6).

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37
38 409 The climate during the Roman Empire has less precipitation relative to other time periods.
39
40 410 However, towards the start of the fall of the Western Roman Empire, a warmer temperature is
41
42 411 recorded. Plant richness is overall high through this period, coinciding with the detection of sheep,
43
44 412 cattle (*Bos taurus*) and goats. At 1.8 ka BP, a peak in Ca/Si indicates increased erosion around the
45
46 413 lake. The increased erosion, coupled with the detection of multiple domesticates, points to
47
48 414 heightened human activity in the vicinity.

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50 415
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52 416 The Early Mediaeval Period (1.5 - 1.1 ka BP) has relatively higher precipitation and lower
53
54 417 temperatures. It is characterized by a lower plant richness, however *Abies alba* is detected
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56 418 throughout. Of the domesticates, only sheep are present at the start of this time period. After this,

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3 419 sheep also are no longer detected in the record. Red deer however, maintain their presence around
4
5 420 the lake.
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9 421 **PDZ III (105 - 0 cm, 1020 - 0 yrs BP, High & Late Mediaeval Period, Modern Age)**

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11 422 PDZ III is defined by significant human disturbance and demarcates the discontinuation of *Abies*
12
13 423 *alba*. Of the wild mammals, only red deer, short-tailed field vole, and the Eurasian water shrew are
14
15 424 detected. Red deer however, are only detected in two samples in PDZ III. This could be due to an
16
17 425 increased effect of human activity around the lake, suggesting that throughout previous
18
19 426 domesticated grazing periods, the natural community structure has not been so greatly impacted.
20
21 427 Pasture related taxa remain at around 14±2% throughout this zone, indicating that the grazing of
22
23 428 the domesticated animals is maintaining the openness of the alpine pasture and halting the
24
25 429 expansion of the forest. LOI values are low at this time, possibly due to lower in-lake organic
26
27 430 production as the nitrogen indicator *Potamogeton crispus* is no longer detected. Plant richness
28
29 431 remains high throughout PDZ III.
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31 432
32 433 At the start of the High & Late Mediaeval Period richness is increasing alongside forbs and
33
34 434 graminoids which increase from 15% to 30% and > 0.1% to 1%, respectively. Sheep and goat are
35
36 435 detected during the start of the High & Late Mediaeval Period, with input of Ca/Si indicating
37
38 436 increased erosion. while cattle and horse (*Equus caballus*) are detected later during the Modern
39
40 437 Age. The proportion of tree reads decline, meaning that the relative biomass of trees around the
41
42 438 lake is decreased, suggesting some tree clearing. This is in contrast to the previous periods of
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44 439 pasturing.
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441 Drivers of changes

442 Box plots

443 The box plot (Figure 7) shows that forb richness is significantly higher when there are cattle present
444 compared to when there are not. Samples are plotted with colour representing the different
445 CONISS Zones. There are three outliers in the without cattle group, these three are all samples
446 with sheep present.

447

448 [insert Figure 7.]

449 RDA

450 The RDA (Figure 8) environmental variables (cattle, goat, sheep, red deer, temperature, and
451 precipitation) account for 35% of the variation in plant composition across samples. Only the
452 variables cattle ($F = 2.80$, $p = 0.01$) and temperature ($F = 9.51$, $p = 0.001$) are shown to be
453 significant; the other variables were not and cumulatively accounted for only 3% of the variation
454 in the plant composition. All explanatory variables are included in this RDA plot to emphasize the
455 patterns of the data, however significant variables are in bold. The cluster clearly separates samples
456 belonging to the three different time periods, PDZ I - III. Both RDA axis 1 (24%) and RDA axis
457 2 (6%) are most affected by temperature and cattle. The non-significant grazers (sheep, horses,
458 and red deer) also fall on RDA axis 2, except goats, which falls on RDA axis 1. RDA axis 1
459 separates samples by plant CONISS zones (PDZ I-III), and therefore temporally. RDA 2 separates
460 the samples by animal type showing that sheep cause a similar non-significant effect on the
461 vegetation to that of red deer, and an opposing effect to that of cattle. Thus, cattle cause a different
462 effect on the vegetation from that of large native mammals.

463

464 [insert Figure 8.]

465 Discussion

466 Dynamics before the detection of domesticated animals.

467 Climate drove vegetation composition before the introduction of domesticated animals. Climate
468 change is complex as there are different aspects to which plants can respond. Locally, at Großer
469 Winterleitensee, and regionally across the wider Austrian Alps (Moser et al., 2005), precipitation
470 does not have a significant impact on vascular plant richness. Precipitation however, does have a
471 significant effect on plant richness at Sulsseewli (Garcés-Pastor et al., 2022). The Northern
472 experience relatively high humidity that decreases as we move more towards the interior of the
473 Alps, resulting in a more continental climate (Fink, 1993; Moser et al., 2005). While there is
474 increased humidity in the Northern Alps, there is also greater variability in precipitation through
475 the year causing pronounced drier months (Scherrer et al., 2022). Plant richness in environments
476 with prolonged drier periods, like at Sulsseewli, is more likely to be affected by precipitation
477 regime changes (Korell et al., 2021) than plant richness in environments with more stable regimes.
478 Precipitation in the Seetaler Alpen is more evenly spread throughout the year (Hiebl and Frei,
479 2018) and therefore no relationship between precipitation and plant richness is found. We did not
480 observe any strong increase in plant richness over time, in contrast to results from pollen records
481 from the wider Alps (Giesecke et al., 2019) Taxa expansion occurred at different rates in the
482 Central Eastern Alps relative to the rest of the Alps due to many factors including a more
483 continental climate (Ilyashuk et al., 2011; Wick and Tinner, 1997), human impact (Latałowa and
484 van der Knaap, 2006; Rey et al., 2013; Schwörer et al., 2015), and interspecific competition
485 (Ravazzi, 2002). Pollen analyses revealed the expansion of *Picea abies* in the Eastern European
486 Alps between 10 - 9 ka BP (Drescher-Schneider, 2007) compared to that of the expansion in the
487 Western Alps at 6 - 5 ka BP (Latałowa and van der Knaap, 2006; Thöle et al., 2016). This is
488 corroborated with *P. abies* detected from the start of the Großer Winterleitensee record at ~8.5 ka
489 BP, contrasting with its late detection around ~6 - 5.5 ka BP (Garcés-Pastor et al., 2022; Thöle et
490 al., 2016; Tinner and Theurillat, 2003) in the Swiss Alps. The mass expansion of *P. abies* into the

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3 491 Swiss alps was facilitated by anthropogenic activities such as fire, grazing and logging (Schwörer
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5 492 et al., 2015). *Abies alba*, a taxon that is limited by late frosts and low spring precipitation, is not
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7 493 detected at Großer Winterleitensee until ~7.4 ka BP, some 600 years delayed from presence at
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9 494 Lago Sangiatto in the Italian Alps (van Vugt et al., 2022). This suggests that the change in
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11 495 precipitation regimes and a more oceanic climate (Heiri et al., 2003) allowed for *A. alba* to
12
13 496 establish successfully in the catchment of Großer Winterleitensee. Multiproxy palaeoecological
14
15 497 studies in the Central and Western Alps suggest that summer high-altitude pasturing was already
16
17 498 taking place by the Late Neolithic (Dietre et al., 2014, 2020; Garcés-Pastor et al., 2022; Schwörer
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19 499 et al., 2015). However, no evidence of this is found at Großer Winterleitensee. From the Middle
20
21 500 Neolithic the tree reads decline, we can assume that relative biomass of the trees, and thus forest
22
23 501 cover, around the lake is decreasing. The decline is corroborated by the local pollen core with tree
24
25 502 pollen decreasing at one of the 2 given dates, ~5.3 ka BP (Zukrigl, 1975). This can be attributed
26
27 503 to a known wetting (Zukrigl, 1975) and cold phase ~5.5 - 5 ka BP in the Alpine region (Ilyashuk
28
29 504 et al., 2011; Thöle et al., 2016; Wick and Tinner, 1997). Plant richness was at a low during this
30
31 505 period in agreement with general Alps pollen analyses showing a lower richness in Early compared
32
33 506 to Middle and Late Holocene (Giesecke *et al.*, 2019). While some pasture related taxa are present
34
35 507 around the lake, they are at their lowest level during this period. Indicating that before domesticates
36
37 508 were introduced to pasture, a less diverse alpine meadow was already present. The consistent
38
39 509 detection of wild grazers such as red deer, together with a rich forb community suggests that the
40
41 510 wild grazer population densities were high enough to maintain the openness of such a meadow.
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44 511 **After the introduction of domesticated animals**

46 512 The introduction of sheep around the lake during the late Bronze Age aligns with the notion that
47
48 513 vertical alpine transhumance systems began during this period in the Eastern Alps (Gilck and
49
50 514 Poschlod, 2019; Schmidt et al., 2002). By the Bronze Age, sheep products were integral for daily
51
52 515 life (Grömer and Saliari, 2018). Wool was a valuable resource during the Middle Bronze Age,
53
54 516 used for textiles and tradable goods (Schmölcke et al., 2018) and sheep meat and milk products
55
56 517 were well established dietary staples for the communities of what is now Austria (Schmölcke et
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3 518 al., 2018). A shift in land use around Großer Winterleitensee is reflected in the change of sediment
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5 519 accumulation rate (SAR) from ~2.8 ka BP, the Bronze Age/Iron Age boundary. It coincides with
6
7 520 an increased representation of domesticates in the *sedDNA* record and significant vegetation
8
9 521 change. Human land use, pasturing (Giguet-Covex et al., 2014; Rapuc et al., 2024), and increased
10
11 522 precipitation (Arnaud et al., 2016) can increase be drivers of changing SAR. The opening of the
12
13 523 landscape and greater pasturing could in increase erosion, thereby increasing the SAR and
14
15 524 allowing more *sedDNA* to be transported into the sediment from the wider catchment area. The
16
17 525 delay in SAR increase from the first introduction of sheep during the Bronze Age, and no great
18
19 526 change in precipitation indicate that domesticate pasturing and human disturbance is intensifying.
20
21 527 Later, during the Roman Period, the presence of cattle, sheep, and goats are detected. The wealthy
22
23 528 Romans in Central Europe were known for their advanced culinary culture and their riches
24
25 529 afforded them the luxury of a varied and complex diet (Bakels and Jacomet, 2003) consisting of
26
27 530 goat and sheep meat and milk products from all three animals. Wool manufacturing also played a
28
29 531 crucial role in the Roman economy (Schmölcke et al., 2018), with what is now Austria becoming
30
31 532 a centre for textile manufacturing (Gostenčnik, 2013). The leather of sheep, cattle and goats were
32
33 533 used for garments throughout the Roman Empire, especially those worn by Roman military
34
35 534 personnel (Grömer et al., 2017). All of these factors could have led to the intensification of alpine
36
37 535 transhumance of these animals around Großer Winterleitensee. Towards the end of the Roman
38
39 536 Period and into the Early Mediaeval period, tree clearing may be related to the mining of Noric
40
41 537 iron and a large human population (Drescher-Schneider, 2007). During the High & Late Mediaeval
42
43 538 Period, the abandonment of sheep farming after 1 ka BP coincided with the intensification of cattle
44
45 539 farming and dairying, and the introduction of horses around the lake. Horses during this period
46
47 540 were used for, among other things, rural heavy transportation (Henning, 2014) and could have
48
49 541 been used to cart heavy items to and from the area around Großer Winterleitense, such as logs
50
51 542 from tree clearance processes.

52 543

53
54 544 While there is an overall increase in plant taxa from pre to post introduction of domesticated
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56 545 mammal grazing, much of the local flora already had arrived prior to human alteration of the

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3 546 landscape. Conversely, in the Western Alps richness is increased greatly due to the presence of
4
5 547 domestic animals (Thöle et al., 2016), especially cattle (Garcés-Pastor et al., 2022). At Großer
6
7 548 Winterleitensee, there is a reorganisation of the existing plant communities around the lake. The
8
9 549 introduction of domesticated animals to an area can heavily modify vegetation and soil through
10
11 550 several factors caused by animals at varying intensities; husbandry, grazing, excretion
12
13 551 (fertilisation) and trampling. Cattle and sheep have largely differing grazing methods, while sheep
14
15 552 prefer to graze on forbs and close to the ground surface, cattle prefer to eat more moderately high
16
17 553 level forage (Cutter et al., 2022). Another way in which cattle can facilitate forb growth is
18
19 554 impeding the growth of trees and shrubs, thus diminishing the forest expansion (Wieczorkowski
20
21 555 and Lehmann, 2022). We observed the highest mean total richness in the periods of cattle presence.
22
23 556 The trampling of cattle has a strong influence on ground cover by forming bare patches
24
25 557 (Hiltbrunner et al., 2012) suitable for the germination of seeds and the establishment of less
26
27 558 dominant taxa such as pasture related taxa *Leontodon hispidus* and *Calluna vulgaris* (Mitchell et
28
29 559 al., 2008). Seeds could arrive via wind transportation, but also deposited through cattle faecal
30
31 560 matter (Traba et al., 2003) A potential way cattle presence caused a significant change to forb
32
33 561 richness may be the larger body size and differing grazing patterns compared to both sheep and
34
35 562 goats and the usually larger population density than the horses. Conversely, at Sulsseewli both
36
37 563 sheep and cattle that showed a significant relationship with plant richness (Garcés-Pastor et al.,
38
39 564 2022), possibly due to a higher sheep density than at Großer Winterleitensee. While both sheep
40
41 565 and cattle have a trampling effect (Chai et al., 2019), the cattle would have a greater impact as they
42
43 566 are larger and heavier than sheep (Yang et al., 2019). Despite the differences, both these lakes
44
45 567 display that light to moderate grazing of either animal increases plant biodiversity.

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48 569 *Abies alba* was not detected around Großer Winterleitensee at multiple periods, suggesting
49
50 570 significant human disturbance likely by tree removal, browsing from domesticates, and forest
51
52 571 regeneration prevention. *Abies alba* germinates within thick humus layers, so regenerates best in
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54 572 forest environments. It is also a browsing intolerant taxon, where dense populations of even wild
55
56 573 ungulates can significantly hinder its growth and subsequent regeneration (Frei et al., 2024;

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2
3 574 Kupferschmid et al., 2015; Unkule et al., 2022). While *A. alba* populations demonstrate resilience
4
5 575 mostly to the presence of sheep, there is a disappearance of *A. alba* once at 2.8 ka BP and then
6
7 576 every time cattle are present. The *A. alba* population declines in the Bernese Alps, Switzerland
8
9 577 (Rey et al., 2013; Schwörer et al., 2015) at 5.5 ka BP, attributed to anthropogenic disturbances
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11 578 such as fire, grazing and logging, and the expansion of *Picea abies*, a taxon that is ever present
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13 579 around Großer Winterleitensee. In the Lepontine Alps, Italy (van Vugt et al., 2022) the *A. alba*
14
15 580 population declines and 5.1 ka BP, also attributed to intense human land use. The final collapse of
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17 581 *A. alba* at Großer Winterleitensee is ~1ka BP coinciding with heavy disturbance and tree removal
18
19 582 around the lake for grazing of domesticates. *Larix decidua* is seen to establish a persistent
20
21 583 population around Großer Winterleitensee instead, at ~1 ka BP. Normally, *L. decidua* stands would
22
23 584 occur where soil is exposed, as the seeds of *L. decidua* are dispersed by wind and thus are very
24
25 585 efficient at colonising bare ground and disturbed habitats (index of colonising success of 7/10)
26
27 586 (Prach et al., 2017). While *L. decidua* is an efficient colonizer and more robust against disturbances
28
29 587 than *A. alba*, it was also spread by humans to form larch forest-meadows for grazing and timber
30
31 588 production (van Vugt et al., 2022). Species-rich *L. decidua* stands were already detected by the
32
33 589 Bronze Age in the neighbouring Bernese Alps, Switzerland (Rey et al., 2013) and Lepontine Alps,
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35 590 Italy (van Vugt et al., 2022). While a smaller presence of *L. decidua* is detected around the lake at
36
37 591 these times, a continued strong detection of *L. decidua* occurs much later around Großer
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39 592 Winterleitensee, in the High & Late Medieval Period, suggesting an extremely long delay in the
40
41 593 creation of these stands.

594 **Wild animals around the lake**

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46 595 Contrary to subalpine lake Sulsseewli record (Garcés-Pastor et al., 2022) the introduction of
47
48 596 domesticated animals did not coincide with the disappearance of red deer (*Cervus elaphus*). This
49
50 597 may be since the domestic grazing pressure around Großer Winterleitensee was relatively low
51
52 598 during this period, unlike Sulsseewli. Thus, enough tree coverage was maintained, or habitat
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54 599 disturbance was not intense enough, and the red deer population was able to maintain a presence
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56 600 at the lake. From the High & Late Mediaeval Period, ~1 ka BP, the red deer are no longer detected.

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3 601 Red deer live between woodland and open grassland areas, suggesting the intensification of
4
5 602 farming and escalation of tree removal forced the red deer to retreat from this lake, and it did not
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7 603 fully re-establish or the population was kept low due to hunting. Other wild animals are also
8
9 604 affected by the plant growth forms around the lake. The bank vole's preferred habitat is forests
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11 605 with high canopy and shrub cover (Hille and Mortelliti, 2011) while the field vole's preferred
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13 606 habitat is forests with dense herbaceous cover and wet meadows (Mathias et al., 2017). We see
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15 607 that the bank vole disappears from the record during the Roman Period, however the field vole
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17 608 remains through the intensification of human land use.
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19

20 609 **Implications for conservation**

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23 610 The preservation of Alpine meadows has become increasingly important in recent years with
24
25 611 respect to climate change and Alpine pasture abandonment (Piccinelli et al., 2020; Thöle et al.,
26
27 612 2016). The conservation of Alpine pastures not only directly impacts plant biodiversity, but also
28
29 613 other organisms dependent upon the open grassland (Cutter et al., 2022). In the past, prolonged
30
31 614 heavy grazing has led to significant harm, causing impoverished soils and decreased biodiversity
32
33 615 (Cislaghi et al., 2019). However, the undergrazing, or complete abandonment of these pastures
34
35 616 leads to an expansion of trees and progressive ecological succession to closed forest (Cislaghi et
36
37 617 al., 2019). Compounding this, increasing temperatures are further promoting the growth of trees
38
39 618 (Snell et al., 2022) and therefore leads to a decrease in plant biodiversity. Our data shows that the
40
41 619 light to moderate grazing of cattle increases not only forb richness, but also total plant richness.
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43 620 This is in agreement with the intermediate disturbance hypothesis which suggests that moderate
44
45 621 levels of habitat disturbance allows for highest plant species diversity (Hobbs and Huenneke,
46
47 622 1992). Furthermore, it shows that grazing by sheep has a similar effect on the plant diversity to
48
49 623 that of red deer. Moderate levels of cattle or sheep alpine transhumance should be continued to
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51 624 encourage the maintenance of these pastures and upkeep of plant biodiversity. Especially in a
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53 625 manner that could help mitigate the promotion of climate change on tree growth.
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626 Conclusion

627 This sedaDNA-based research from Großer Witterleitensee emphasizes the importance of
628 interdisciplinary approaches to unravel complex ecosystem dynamics over long timescales. By
629 using a multi-proxy approach, we are able to tease-apart and evaluate the impacts of climate
630 change, native mammals and alpine transhumance on the vegetation at high taxonomic resolution.
631 Our study represents the first in the Eastern European Alps identifying how and when alpine
632 transhumance occurred using *sedaDNA* and DNA-barocoding technology. Our findings
633 demonstrate that moderate-intensity cattle grazing significantly enriches the plant community. The
634 insights gained from this research contributes to a deeper understanding of the historical and
635 ongoing drivers of Alpine plant communities, thereby providing a foundation for informed
636 conservation efforts and sustainable, evidence-lead, management practices.

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20
21 664 IGA designed the research and raised the funding and provided resources. IGA, AGB, AT, SGP,
22
23 665 KW and PDH did the fieldwork. SZ did the DNA lab work with input from SGP. TG performed
24
25 666 radiocarbon dating. SZ performed XRF interpretation with input from AGB. AGB and SZ
26
27 667 performed age-depth modelling with input from PDH. SZ verified and curated the plant sequences
28
29 668 with input from SGP and AT, whereas PDH did the same for animals. YL and SZ performed the
30
31 669 bioinformatics. SZ performed the statistical analysis with input from SGP and IGA. SZ wrote the
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36

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