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Year-round methane cycling activity in a European alpine peatland with large spatial and temporal variability

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Abstract

Peatlands are well-known emitters of methane (CH_4). European alpine peatlands share certain characteristics with boreal peatlands, despite being located at temperate latitudes, such as a strong seasonality with snowfall in winter and a short summer and growing season. Unlike boreal peatlands, they experience relatively large temperature fluctuations between day and night and are more likely to be sloping. It is unknown how these factors affect CH_4 dynamics. Furthermore, winter CH_4 dynamics have rarely been studied. We quantified the soil-atmosphere CH_4 flux at an alpine peatland in Austria (1670 m a.s.l), with a focus on the spatial and temporal heterogeneity in this ecosystem. In summer, CH_4 emissions were high (0.7 - 206 mg m^2 h^{-1}), whereas in spring, shortly after snowmelt, both CH_4 uptake and emissions were observed at different locations within the alpine peatland (ranging from -4 mg m^2 h^{-1} to 11 mg m^2 h^{-1}). In winter, a local snow-free patch persisted at the peatland due to the year-round influx of 5°C spring water. Both CH_4 uptake and emission were observed in winter, with emissions also observed at snow-covered locations (fluxes ranging from -41 mg m^2 h^{-1} to 6 mg m^2 h^{-1}). The spatial heterogeneity in summer was further investigated by high resolution chamber measurements and soil analyses of temperature, carbon and nitrogen content, and 16S rRNA analyses of the microbial community. These showed a grouping that likely resulted from the input of redox-active components by the spring water that entered the peatland in a non-uniform pattern, which was revealed by soil temperature measurements. Overall, our research shows that alpine peatlands are unique systems with complex spatial and temporal patterns, which have strong implications for soil microbiology and CH_4 cycling.

1. Introduction

Peatlands and wetlands are, in general, major sources of methane (CH_4) to the atmosphere, due to their anoxic nature and high carbon stocks (Turetsky et al., 2014). CH_4 is produced in the anoxic, carbon-rich soil by methanogenic archaea. Part of this CH_4 may be consumed by methanotrophic bacteria or archaea prior to emissions, but (modelling) studies have shown that a large proportion of the produced CH_4 is emitted to the atmosphere (Arah and Stephen, 1998; Couwenberg and Fritz, 2012). Boreal and arctic wetlands have been studied intensively and have also been shown to emit large amounts of CH_4 (Kuhn et al., 2025). Little research has, however, been conducted at alpine peatlands. Although located at a different latitude, boreal wetlands and alpine peatlands share certain characteristics such as a long winter snow cover and a short growing season. It is however largely unknown whether alpine peatlands behave similarly to boreal wetlands in terms of CH_4 dynamics.

High latitude (arctic) and high-altitude (alpine) peatlands have predominantly been studied during the summer season due to the practical limitations of visiting these snow-covered places in the winter season. As a result, global models lack inputs on winter CH_4 fluxes from these systems. A recent modelling study pointed to non-growing season wetland CH_4 emissions as the main source of uncertainty in modelling CH_4 emissions (Kuhn et al., 2025). Winter in the high-alpine region (>1500 m a.s.l.) is characterized by a consistent snow cover and temperatures below freezing from November to April (Geosphere Austria, (Matiu et al., 2021)). With May and September and October as the shoulder season, the summer season only covers approximately 3 months per year and is therefore not an accurate representation of the year-round greenhouse gas fluxes. Additional research is required for a proper estimation of the contribution of alpine peatlands to local and national emission estimates.

Alpine ecosystems are expected to experience further increases in air and soil temperature, as well as changing precipitation regimes, due to climate change (Gobiet et al., 2014). Temperature, soil moisture content, and plant-effects are all known to play a role in wetland CH_4 emission dynamics (Whalen and Reeburgh, 1996), but their effects are intertwined and complex. Warming experiments with saturated soils have shown that an increase in temperature can result in an increase of both the CH_4 production and CH_4 oxidation potential (Li et al., 2020). The net effect on the emissions depends on the balance between these two. In natural, non-manipulated settings, CH_4 emissions and temperature have been shown to have a direct relationship(Wei et al., 2015). In a recent modelling assessment on the future of CH_4 emissions in boreal wetlands, both temperature and the lengthening of the growing season were important factors causing increased emissions with future climate warming (Kuhn et al., 2025). The vegetation can affect CH_4 emissions by plant characteristics such as root and shoot length and gas transport potential, but the vegetation composition within wetlands itself is also driven by the water availability and hydrologic variables (Harbert and Cooper, 2017; Koch et al., 2007). The water table depth in itself can create physical limitations for diffusive gas transport, often leading to anoxic conditions in soils. Several studies have shown a correlation between water table depth and CH_4 fluxes (Chen et al., 2013; Koch et al.,

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Preprint. Discussion started: 5 June 2026

2007; Li et al., 2020; Wei et al., 2015), but the mechanisms behind this correlation are often unknown.

We investigate the CH_4 fluxes of an alpine peatland located in the European Alps (1670 m a.s.l.) over different seasons. We also study the high spatial heterogeneity in CH_4 fluxes within this peatland and use soil and water temperature and chemistry to assess the effect of water transport through the peatland on summer and winter CH_4 dynamics. Alpine peatlands are unique in their sloping nature, which likely results in short water residence times and high spring water inputs compared to other peatland systems. We hypothesize that these features have a major impact on CH_4 dynamics in summer, spring and winter.

2. Material and methods

2.1 Site description

The Auenfeld alpine peatland is located at 47°14'27.21"N 10° 7'54.74"E (42.4210, 10.13200), at 1670 m a.s.l. in Schröcken, Voralberg, Austria. It is ca 0.7 ha in size and located in a wide alpine valley (Fig. 1). The area is part of the Northern Calcareous Alps (GeoSphere Maps). In summer it is used for extensive grazing with cows. In winter it is located within a well-used ski area but is not part of the ski runs or prepared snow paths. Sampling campaigns took place on 9 July 2024, 20 February 2025, 13 May 2025, 31 July – 1 Aug 2025, 14-16 August 2025, and 30 January 2026. Unless otherwise specified, gas sampling was always performed between 11:00 and 16:00.
Maps were created using Google Earth Pro (2025). The peatland experiences a strong seasonality, with a snow cover from on average November until April, with occasional snowfall from September onwards (Fig. A1).

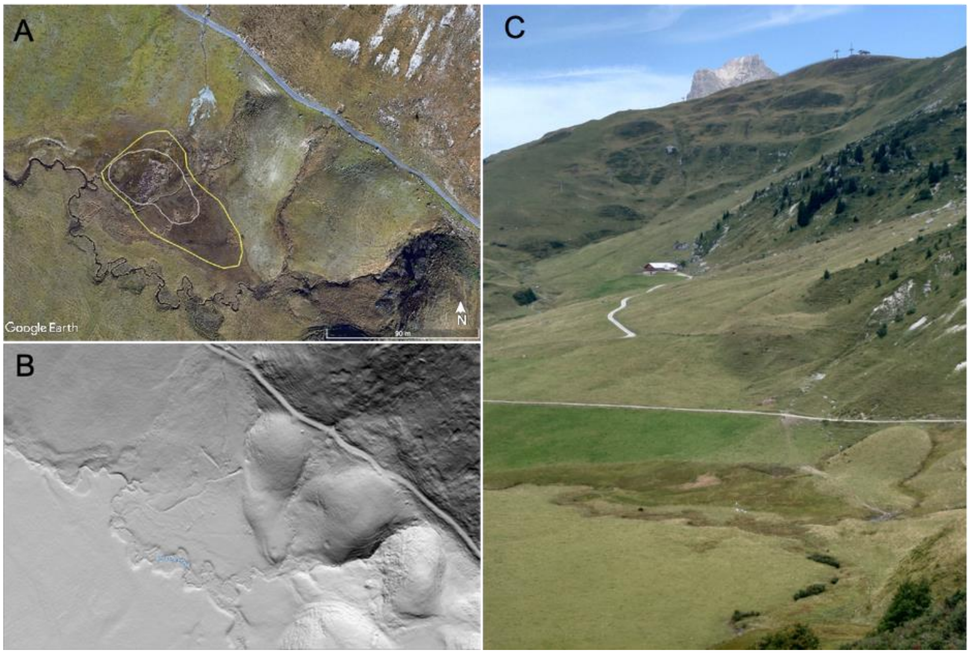

Fig. 1. Geographic setting of the Auenfeld alpine peatland site. A) Satellite imagery (Imagery © 2026 Airbus, Maxar Technologies, © Swisstopo, Map data © 2026 Google) with in yellow and white the outlines of respectively the spring/summer and winter sampling areas. B) Hillshade representation of the digital elevation model from the 3rd laser scanning survey of Vorarlberg 2023, 25 cm grid resolution (source: GeoAtlas Voralberg (GeoAtlas Voralberg, n.d.)). C) Picture from August 2025, showing the alpine peatland on the bottom part of the slope, recognizable by its dark green colour. More details on the sampling locations are shown in Fig. A2.

2.2 CH_4 gas flux measurements

CH_4 fluxes were measured with static chambers, spread over the alpine peatland, within the areas indicated in Fig. 1A and Fig. A2 and as depicted in Fig. A3. The locations were manually selected during each field campaign, chambers were therefore not placed at exactly the same spots during different campaigns, as initial measurements during summer 2024 showed that aiming for the same spots was of limited value (discussed in Results & Discussion). Both the chambers and chamber bases were constructed in-house from transparent polypropylene boxes (Ikea Samla). The volume of the chambers was 5 L, the volume of the bases 2 L. Bases were only used during summer campaigns and were placed in the soil minimum 1 hour before measurements. When no chamber bases were used, the chambers were weighed down with single rectangular 725 ml water bottles to ensure a good contact between the chamber edge and the soil. After chamber installation, 4 (spring and summer) or 6 (winter) discreet gas samples were collected over 25 – 60 min. Each gas sample was collected through a sampling port consisting of a butyl stopper with a long (10 cm) needle which' tip was located in the central part of the chamber. The air inside the chamber was mixed prior to each sample collection. Samples (15 ml) were used to flush and then fill one 3 ml exetainer vial with 3 ml overpressure. The exetainers were then transported to the laboratory and CO_2 and CH_4 were

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analysed using a gas chromatograph (Thermo Fisher SCIENTIFIC TRACE 1310, Thermo Fisher Waltham, Massachusetts, USA) equipped with two pulsed discharge ionization detectors (PDD).

Gas flux rates were calculated by linear regression. For both the linear regression analysis and the creation of the boxplots, Rstudio was used (packages dplyr and ggplot2, plus readr and RColorbrewer for enhanced visualisation (Hadley Wickham, 2016; Yarberry, 2021)). Only linear regression results with an $R^2 > 0.5$ were included in the analyses, others were discarded. The coefficient of the linear regression was corrected for chamber volume and footprint, the temperature at 14:00 local time (according to the values of measurement station 11305 (Warth, 1478 m) on the day of sampling, Geosphere Austria), and one set value for the atmospheric pressure to calculate the flux in mg CH_4 m^{-2} h^{-1}. Atmospheric pressure was estimated at 0.83 atm for 1670 m elevation. Seasonal variation in the atmospheric pressure (~±2%) was considered negligible relative to other sources of uncertainty in the flux measurements.

2.3 Soil and vegetation characteristics

The Auenfeld peatland was sampled and surveyed for soil and vegetation characteristics at 9 locations within (and 1 location ca. 3 m outside) the peatland area in August 2025 (locations shown in Fig. A2). Each location was photographed and marked. Soil temperature was measured in situ in triplicate at 10 cm depth using a digital soil thermometer. Vegetation assessment was done by estimating the canopy cover of the most prominent vascular plant species and classifying them according to the Braun-Blanquet method (Westhoff and Van Der Maarel, 1978).

At each sampling site, a soil core of ca. 20 cm deep was cut from the soil with a knife. From these cores, we sampled the soil at 4 – 6 cm depth, stored it in plastic bags and kept it in the dark at 4°C until processing. In the lab, part of the material was dried for 24 - 36 hours at 60°C, after which it was milled using a ball-mill and used for C:N analysis on a multi N/C 2100 (Analytic Jena, Germany, analytical duplicates). Measurements were done in triplicate and values were averaged.

Before and after drying, the samples were weighed to determine the gravimetric water content (calculated as $\text{Weight}_{\text{water}} / \text{Weight}_{\text{dry soil}} * 100\%$). A second part of the material was kept at 4°C until DNA extraction with the Qiagen Powersoil DNA extraction kit. 16s rRNA sequencing was performed by GENEWIZ Azenta Life Sciences Europe, targeting the V3 and V4 regions with primers CCTACGGRRBGCASCAGKVRVGAAT (F) and GGACTACNVGGGTWTCTAATCC (R), resulting in on average 80.000 reads per sample. The raw data was processed with Genewiz Europe pipelines to produce 16S rRNA OTU tables of the microbial community of each sample. Of one specific location (V7), two individual samples were collected in the field, from the same soil core. These two duplicate samples were processed separately, to assess the variability within the soil core. Both samples were used for DNA extraction and sequencing, and are shown in the manuscript as samples V7-1 and V7-2. As the samples showed high similarity, only one sample of each of the other locations was used for sequencing and analyses.

2.4 Water sampling and analysis

Water samples of the springs above the peatland were collected in July 2025. Locations are marked in Fig. A4. The water temperature was measured at the surface with the same digital soil thermometer that was used to record soil temperatures. Water samples were collected directly from the streams into plastic syringes, filtered (0.45 μm syringe filters), placed in 12 mL exetainer vials, and stored at 4°C until analysis. DOC was quantified using a multi N/C 2100 (Analytik Jena, Germany) and using continuous Flow Injection Analysis (AA3, Seal analytical; UK). Major anions and cations were quantified by ion chromatography, using a ion chromatograph Compact IC Flex (Metrohm, Switzerland) equipped with an automated filtration unit and an autosampler. Certified quality controls at different concentrations were measured every 20th sample and at the start and end of each run.

2.5 Statistical analyses and graphics

All statistical analyses were performed using R. To assess differences in CH4 flux among seasons and months, we first evaluated the assumptions of normality and homogeneity of variance. Normality of residuals within each season was tested using the Shapiro-Wilk test, and homogeneity of variances was assessed using Levene's test.

Due to the violation of the assumption of homogeneity of variance (Levene's test: $F_{2,192} = 5.54$, $p = 0.005$), a non-parametric approach was used. Differences in CH_4 flux between seasons were tested using the Kruskal-Wallis rank sum test. Where significant differences were detected ($p < 0.05$), pairwise comparisons were conducted using Dunn's test with Bonferroni correction for multiple comparisons.

16S rRNA sequencing data was processed in R to determine the diversity and differences between samples at the family level. Deeper taxonomy was available but was not used for statistical analyses, due to the large number of zeroos in the OTU tables at the genus and species level. To analyze the Bray-Curtis distance and diversity parameters, the R packages phyloseq, vegan, and dplyr were used.

Visualisation of spatial properties, as in Fig. 5 and Fig. 6, was done using the packages ggplot2 and scales, with map excerpts from Google Earth (extracted in 2026) as background.

3. Results and discussion

The Auenfeld alpine peatland, located at 1670 m a.s.l. (Fig. 1), was sampled in high spatial and temporal resolution in both a diurnal and seasonal matter. It was a strong source of CH_4 to the atmosphere in summer (CH_4 emission of 34 mg m^2 h^{-1} on average on a warm summer day, 10 mg m^2 h^{-1} on a cold summer day, Fig. 2, Fig. 3), with local rates of over 140 mg m^2 h^{-1} and 45 mg m^2 h^{-1}, respectively. These local hotspots emit an amount of CH_4 per m^2 within one hour that other previously reported alpine peatlands emit over periods of 24 hours to one month. Other research reported summer CH_4 emissions of 2 mg m^2 h^{-1} (Monte Bondone, IT, 1563m)(Pullens et al., 2016); up to 8 mg m^2 h^{-1} (Tibetan plateau, swamps and peatlands below 3000 m, reviewed by Wei et al., 2015(Wei et al., 2015) but also the Swiss Oberaar-fen, at 2320 m and three fens in the Autrian Rotmoos area at 2250 m a.s.l. (Henneberger et al., 2015; Koch et al., 2007)); ±10 mg m^2 h^{-1} at Goeschenen, CH (1915 m) (Liebner et al., 2012) or 3 – 30 mg m^2 h^{-1} in a comparison study of 15

Swiss fens (Franchini et al., 2014). Our reported average rates are thus 1.5 – 25 times higher than in comparable systems, placing it on the high end of the peatland CH_4 emissions spectrum. Hirota et al. (2005) reported emissions that were on the high end for the Tibetan plateau (± 35 mg m^2 h^{-1}). Interestingly, they reported these rates after a livestock grazing experiment, which showed that grazing increased CH_4 emissions significantly, most likely due to the resulting shortening of the vegetation. Our peatland is used for extensive grazing, unlike most of the previously investigated alpine fens and bogs. Whether grazing causes our peatland to have emission rates that are so much higher than reported in other studies needs to be determined.

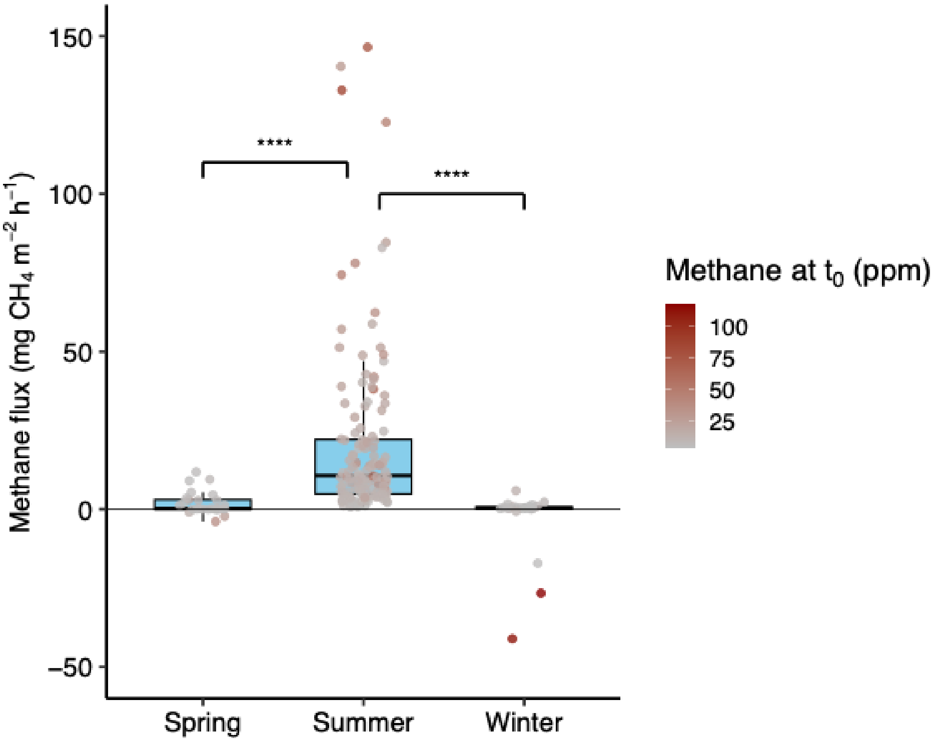

Fig. 2. CH_4 fluxes from the Auenfeld peatland soil during different seasons (spring n = 26, summer n = 144, winter n = 26, only fluxes with an R^2 of >0.5 are included). The colours of the points indicate the CH_4 concentration in the static chambers at the t_0 sampling point. Post-hoc Dunn's tests with Bonferroni correction revealed that summer CH_4 flux differed significantly from both Spring ($p < 0.001$) and Winter ($p < 0.001$), while no significant difference was detected between spring and winter. One outlier in the summer period (flux of 206 mg CH_4 m^{-2} h^{-1}) was omitted to enhance the visibility of the data points in the lower areas of the graph.

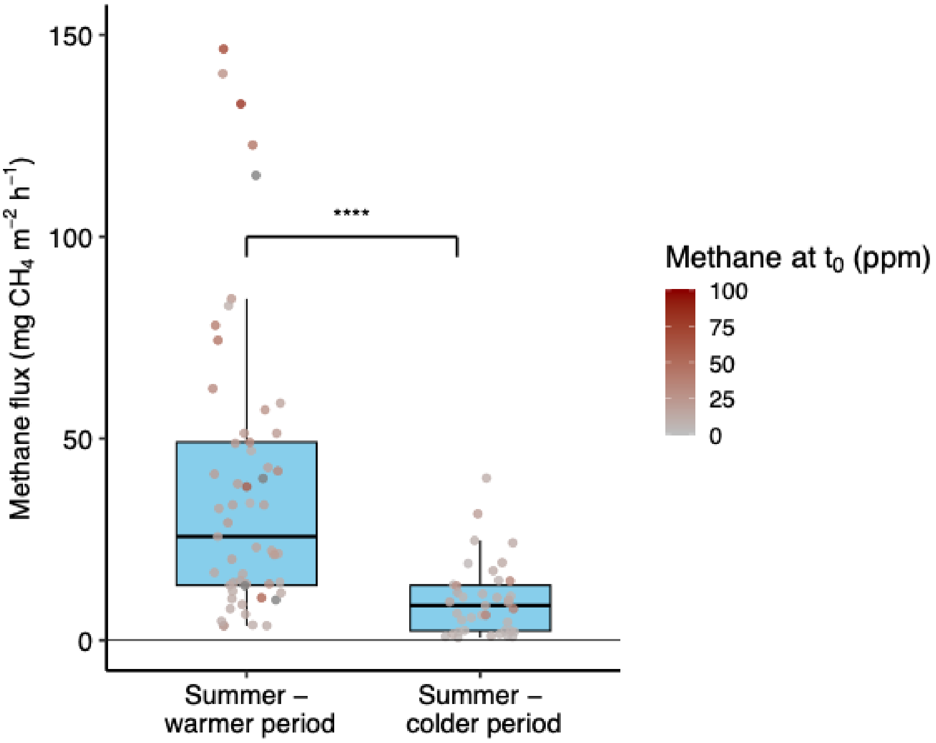

Fig. 3. CH_4 fluxes from the Auenfeld peatland soil during two different summer periods, one in 2024 and one in 2025 (cold n = 39, warm n = 58, only fluxes with an R^2 of >0.5 are included). One outlier in the warm summer period (flux of 206 mg CH_4 m^{-2} h^{-1}) was omitted to enhance the visibility of the data points in the lower areas of the graph. The colours of the points indicate the CH_4 concentration in the static chambers at the t_0 sampling point. Post-hoc Dunn's tests with Bonferroni correction revealed that the CH_4 flux differed significantly between the two measurement periods ($p < 0.05$). The two winter seasons that were sampled, in 2025 and 2026, did not differ significantly.

3.1 Spatial variability in CH_4 emissions and soil characteristics

3.1.1 CH_4 emissions

Although our summer CH_4 emissions were consistently high, we observed a large spatial variation (Fig. 4). Our detailed summer study design investigated both the spatial variability within 1 m^2 and within the whole peatland. Overall, the emission rates during daytime ranged from 11 – 138 mg m^2 h^{-1} on average (Fig. 4). The static chambers were divided into three groups that were 5-10 m apart and each contained four chambers within 1 m^2 (see Fig. A2 and A3 for the setup and location of the chambers). The CH_4 emissions from group 1 differed significantly from those of group 2 during the daytime ($p < 0.01$), but not from that of group 3 (Fig. 4). Interestingly, also the variation within the groups was large, despite the small distance between the chambers within one group (Fig. 4). No significant differences between individual chambers were found, likely due to the number of observations per chamber (n=5), but the differences in means and medians indicated that the small-scale variation seemed as important as the larger scale variation between the sites. During the night, the emission rates were significantly lower than during the day (2.7 – 14.2 mg m^2 h^{-1}; Fig. 4, $p < 0.0001$) but the large spatial variation persisted, with significantly different rates between the groups, and a large variation between chambers within the 1 m^2 groups. The chambers that were on average emitting most CH_4 during the day (Chambers A, C, K, N), were not the same chambers that on average emitted the most CH_4 during the night (Chambers B, D). Significant day-night differences in summertime CH_4 emissions have also been reported for boreal peatlands and Tibetan alpine peatlands (Long et al., 2010; Peng et al., 2019), where it was attributed to the air and/or soil temperature difference between day and night.

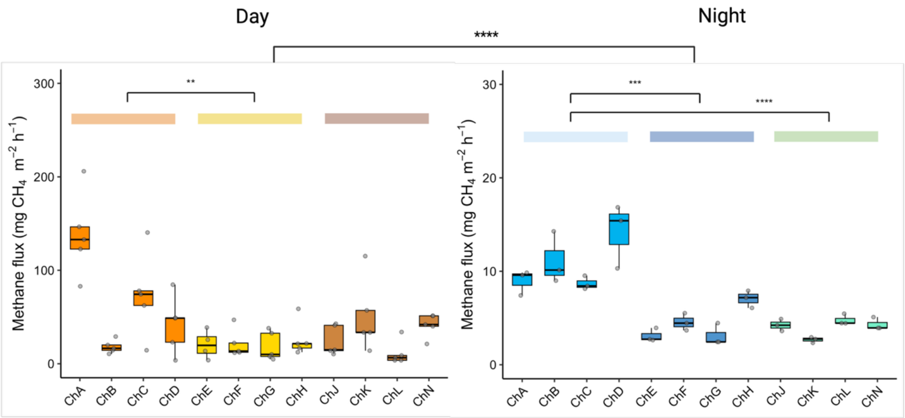

Fig. 4. Spatial diversity of CH_4 fluxes in the Auenfeld peatland in July 2024, during the day (left) and night (right). Note the difference in the y axis. Boxes of the same colour indicate that those chambers were located within 1 m^2. The three m^2-groups were 5 – 10 m apart from one another, as shown in the map of Fig. A2. For a picture of the setup, see Fig. A3. Groups that were significantly different are indicated (** $p<0.01$, *** $p<0.0005$, **** $p<0.0001$).

Small scale spatial differences in CH_4 fluxes within peatland sites were also observed by (Wei et al., 2015) in a swamp meadow, where they were directly correlated with soil moisture content, which ranged from 60 to 80 v%. In our peatland, the moisture content is expected to be high throughout, as the groundwater table was never observed to be deeper than 10 cm, and is therefore unlikely to be the only factor explaining the spatial heterogeneity in CH_4 emissions, as the correlation between soil moisture and CH_4 emissions disappeared above a soil moisture content of 80% in the study of (Wei et al., 2015). Different vegetation is known to have different gas transport characteristics and may therefore influence gas dynamics locally. Lai et al. (2014) reported different CH_4 emissions based on the dominant vegetation at different sites within a Canadian peatland, similarly to (Heiskanen et al., 2021) for a Finish peatland. This effect may be further enhanced by grazing (Hirota et al., 2005). The one study on spatial variability that was performed in the European Alps focusses on the variation between different fens, not on variation within one fen (Franchini et al., 2014), and these results are therefore hard to extrapolate to our study.

3.1.2 Soil characteristics

To understand the factors controlling spatial heterogeneity in our peatland ecosystem, we analysed several soil characteristics. These also showed a high spatial variability. We sampled the soil at 4 – 6 cm depth and found a large variation in gravimetric water content (371 – 1105%) and in soil carbon and nitrogen content (TOC of 9 – 41%, TIC 0.04 - 6.2%, C:N ratio 40 – 98; Fig. 5 & 6, SI Table A2). A vegetation survey also showed large differences within the peatland, despite its small size (SI Table A2, also visible as differences in the dominant colour of the vegetation in Fig. 1C). To study the cause of this large variation on an unconventionally small scale, we measured soil temperature within the peatland and the temperature of its water sources during a warm and sunny summer day (air temperature 22°C). The soil temperature at 10 cm depth ranged from 7.8 to 20.8°C within the peatland (Fig. 6) and showed a clear spatial pattern that aligned with the observed vegetation patterns. The water that flows upstream and downstream of the peatland has a temperature of 4.8 – 6.3°C (data not shown, sampling locations visible in Fig. A4). Directly above this peatland is a steep slope (Fig. 1C) with several water springs at the bottom (conceptual figure in Fig. A4). These springs lay just above the peatland and are present year-round.

The soil temperature data, that differs strongly between different locations of the peatland and is remarkably low for a warm summer period (Fig. 6), suggests that the peatland is fed by the spring water, but not in a homogeneous matter. The low temperatures of the soil, despite the warm and sunny weather in the week before the measurements were taken, indicate that the spring water cools the soil in specific locations. A conceptual figure of the water flow, hypothesized based on the soil temperature, is available in Fig. A4. When measuring the solutes in the spring water sampled above the peatland (for locations, see Fig. A4), we observed nitrate and sulfate, albeit in low concentrations (0.6 – 1.0 mg NO_3 L^{-1}, 3.5 – 5.3 mg SO_4 L^{-1}, n = 3). These, along with potential oxygen delivered with the water influx, likely affect biochemical cycling (including CH_4 cycling) in the peatland soil. DOC concentrations in the spring water were low (4.9 – 5.6 mg C L^{-1}, n=3). The soil temperature variation that we observed suggests that certain locations receive more spring water inputs than others, and that the residence time of the water in the peatland is most likely short. Overall, we hypothesize that the spatially heterogeneous influx of spring water into this peatland is a result of the complex topography of the area surrounding the peatland and the sloping nature of the peatland itself, which are both common for the European Alps, and is the reason for the high spatial variability in CH_4 flux that was observed during the summer season (Fig. 1, 2, 3). More research, including hydrological modelling, would be needed to further test this hypothesis.

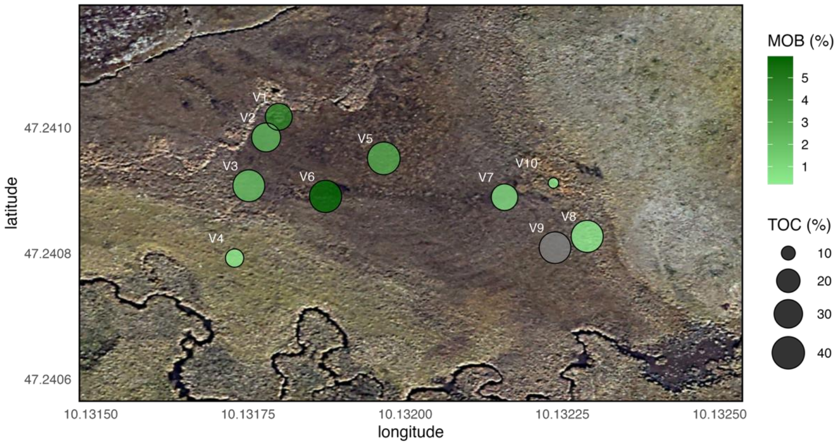

Fig. 5. CH_4 oxidizing bacteria (MOB) relative abundance (colour scale, as % of 16S rRNA reads) and total organic carbon (TOC, symbol size, as % of dry soil mass) content of soil samples of 4-6 cm depth of different locations within the alpine peatland. No microbial community data is available for location V9. For information on the microbial groups that contributed to the total MOB abundance, see SI Table A1. V4 is a reference location outside the peat area. Values are reported in SI Table A2. (Background map - Imagery © 2026 Airbus, Maxar Technologies, © Swisstopo, Map data © 2026 Google)

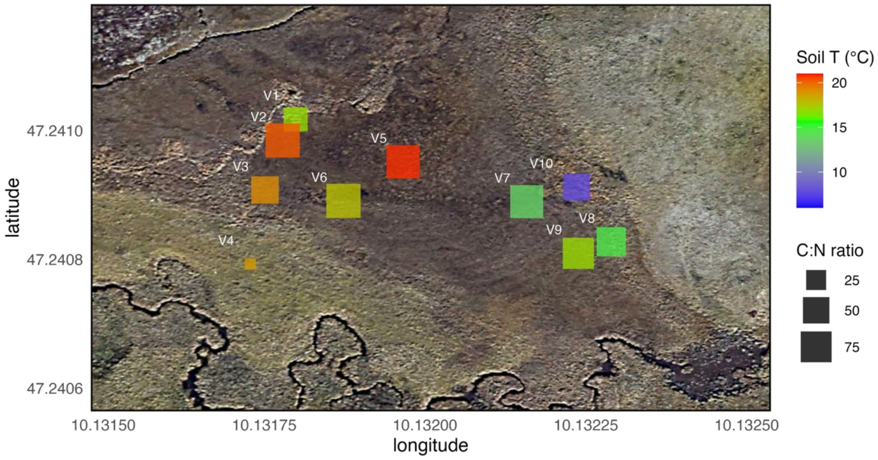

Fig. 6. Soil temperature at 10 cm depth (colour scale) and carbon to nitrogen ratio of soil samples of 4-6 cm depth (symbol size) of different locations within the alpine peatland. V4 is a reference location outside the peat area. Values are reported in SI Table A2. (Background map - Imagery © 2026 Airbus, Maxar Technologies, © Swisstopo, Map data © 2026 Google)

3.1.3 Soil microbial community and CH_4 cycling organisms

In addition to the CH_4 emissions and the soil characteristics, also the soil microbial community composition varied within the peatland. The same samples that were used for the physicochemical soil characterization were used for DNA extraction and microbial community analysis (Fig. A5).

Using Bray-Curtis distance analysis combined with hierarchical clustering, we can observe a grouping of the samples, based on the composition of the entire soil microbial community (Fig. 7). Sample V4, which is located outside of the peatland (Fig. A2), is an outlier on the dendrogram, which confirms the hypothesis that the peatland conditions (permanently water logged, reduced environment) shape a significantly different microbial community than non-peatland conditions, and that these soil characteristics are more important in determining the microbial community than other environmental characteristics that prevail in the entire area, such as climate or land use. Interestingly, also sample V1 is a strong outlier, even though this sample is spatially very close to other sampling locations within the peatland. Likely, the specific conditions created by the plant community in this location (dominated by Carex rostrata, Table A2), in combination with the hydrological conditions (Fig. A4), creates unique conditions for the soil microbial community. When considering the other sampling locations, two clusters can be noticed: V2 – V6, which are all located in the lower and middle part of the peatland, elevation-wise, and V7 – V10, which are all located at the higher part of the peatland. V7.1 and V7.2 are duplicate samples of the same location, which were processed independently. Their tight grouping indicates that variability within one location is small and provides confidence to the grouping of the other samples.
Interestingly, this observed grouping in locations based on their elevation seems to reflect that the spatial location in the peatland in terms of water influx is more important in shaping the microbial community than soil characteristics such as the TOC or C:N ratio (compare Fig. 5, 6 and 7). This supports our hypothesis that the influx of spring water has a large importance in shaping the biological conditions in the soil, leading to differences in microbial community structure, and greenhouse gas emissions.

The elevation-based grouping also appears when analysing the CH_4-related microbial community. The lower- and middle locations show higher abundances of CH_4 oxidizing bacteria and methanogenic archaea (2.0 – 6.0% MOB, 0.12 – 0.36 % methanogens) than the higher locations (0.3 – 0.9% MOB, 0% methanogens). A correlation between methanotroph and methanogen abundance was observed (Fig. A6, $R^2 = 0.85$). In earlier studies on methanotrophic and methanogenic microorganisms in alpine peatlands, opposing trends in methanotroph and methanogen abundance were observed instead (Tian et al., 2024). It must be noted that our results reflect the microbial community at 4-6 cm depth. It is likely that higher relative abundances of methanogens can be found deeper in the soil, where conditions are more reduced, and that higher abundances of methanotrophs can be find in the topsoil, where more oxygen is available. No statistically significant correlation between soil characteristics (TOC, TIC, C:N, temperature) and the CH_4 cycling community was found, possibly due to the low sample size. In previous studies on methanogen and methanotroph abundances in alpine soils, soil temperature explained the variation found between locations along a hydrological or elevation gradient (Hofmann et al., 2016; Tian et al., 2024). No direct comparison between CH_4 fluxes and the microbial community of our study site could be made, because samples were not taken at exactly identical locations and/or sampling times.

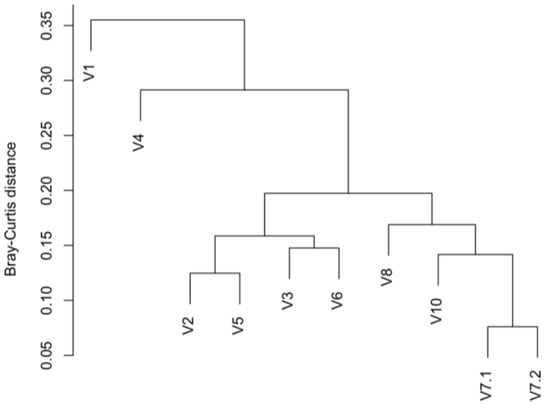

Fig. 7. Hierarchical clustering based on Bray-Curtis distance analyses of the microbial community, classified to family level, in the alpine peatland samples (locations indicated in Fig. 4). Samples V7.1 and V7.2 are duplicate samples from the same location (see Methods). Sample V4 is a reference location outside the peat area.

‰3.2 Weather-dependent and seasonal variability

3.2.1 Weather effects on summer CH_4 emissions

Besides the spatial and diurnal diversity that was observed in our summer campaign, a large variation was also observed between two separate summer sampling campaigns (Fig. 3) that differed in weather conditions during and in the week before the measurements. The warmer summer measurement campaign had an average air temperature of 15.7°C during the 4 days before the measurement, with on average 6.5 h of sunshine per day, whereas the 4 days before the colder summer campaign had an average air temperature of 9.7°C, with only 0.8 h of sunshine per day (GeoSphere Austria). We observed significantly higher CH_4 emissions during the warmer measurement period, compared to the colder period (Fig. 3, $p < 0.05$). Both periods were in the alpine summer months (July – Aug). The week-long warmer period likely resulted in a higher topsoil temperature, compared to a week-long colder period, as other research in wet alpine fen soils showed a strong response of the soil temperature at 5 cm depth with time of day, following air temperature and solar influx (Koch et al., 2007). In that study, the temperature at 15 cm depth showed only a very limited response, and the temperature at 35 cm showed no diurnal trend at all. Microbial processes in soils are known to generally increase at higher temperatures, due to higher enzymatic activities (Barnard et al., 2020). It is, however, unknown which process rates are specifically increasing with higher temperatures in our alpine peatlands. Other weather-related factors that may have affected the CH_4 flux may be a result of precipitation. We observed an increased water flow in waterways above the peatland, which may have resulted in an increased influx of water into the peatland, creating less reducing conditions and therefore reducing the methanogenic potential and/or increasing the methanotrophic potential. Previous studies have shown an effect of the water table depth on the methanogenic and methanotrophic community in Tibetan alpine peatlands (Tian et al., 2024).

3.2.2 Seasonal dynamics

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Post-snowmelt (spring): CH_4 uptake and emission

During the spring period, shortly after snowmelt, the vegetation biomass in the alpine peatland is small (Fig. A1). We measured CH_4 fluxes in several locations within the peatland during this post-snowmelt season and again observed large spatial differences. Both CH_4 emission and CH_4 uptake occurred, measured fluxes ranged from emissions of 12 mg m^2 h^{-1} to uptake rates of -4 mg m^2 h^{-1}, all within the 0.7 ha peatland area (Fig. 2). The CH_4 emissions were significantly different from the summer period ($p< 0.001$). Li et al. (2020) also reported CH_4 uptake from a saturated alpine soil on the Tibetan plateau during the spring season, although the fluxes reported in that study were significantly lower (-0.01 to +0.04 mg CH_4 m2 h) than the fluxes we report. Pullens et al. (2016) reported an increase in CH_4 emissions after snow melt, rather than a decrease. Seasonal dynamics were also studied by (Drollinger et al., 2019) using eddy covariance tower flux data from a peatland in the lower alpine area (630m elevation). They reported positive fluxes year-round, with lowest fluxes in winter and highest in summer, with no noticeable change in spring/snow melt season.

Winter: Snow-free patches as key CH_4 cycling locations

Previous research on CH_4 fluxes from alpine soils, wetlands and peatlands has had a strong focus on the snow-free season. The Auenfeld peatland, although located at 1670 m and surrounded by snow-covered soils (Fig. A1), remains partially snow-free during the winter season. This phenomenon was observed in the field during our sampling campaigns (2024, 2025 and 2026, 2024 data not shown) and is also visible on historical winter aircraft images of this location (GeoAtlas Voralberg). Soil temperature measurements showed that the soil temperature at the snow-free area was consistently elevated compared to the surrounding snow-covered soil (2 - 4.6°C in the snow-free peatland, versus -0.1 – 1.0°C in the snow-covered peatland areas). The soil temperature in the snow-free patches was close to that of the spring water that flows through the peatland and that has a constant year-round temperature of 4 - 7°C. We therefore hypothesize that the spring water is warming up the alpine peatland soils in winter, creating snow-free areas.

We are the first to measure CH_4 dynamics at an alpine peatland with these snow dynamics. Although several locations in winter were sources of CH_4, certain locations within the snow-free patches showed CH_4 uptake, with uptake rates of up to 41 mg m^2 h^{-1} (Fig. 2). Previous research on snow-free peatlands has either only included locations that have an ice layer instead of snow on the soil surface (Chen et al., 2008; Gazovic et al., 2010) or were studies on artificial snow cover manipulation, without any CH_4 flux measurements (Bombonato and Gerdol, 2012; Robroek et al., 2013). The effect of the snow-free nature of this alpine peatland in winter on the long-term soil carbon storage is currently unknown. Sites with early snowmelt have been shown to have higher organic matter decomposition rates than sites with late snow melt (Venn et al., 2021), but the higher soil temperatures in this peatland could also support plant and algae growth which may enhance carbon uptake and storage. Surprisingly, we also observed CH_4 emissions from the parts of the peatland that were covered in deep snow (8.3 - 26 mg m^2 h^{-1}, 73 - 130 cm snow, n = 5). Although the alpine peatland CH_4 emissions were significantly ($p < 0.001$) lower in winter than in summer, they are still relevant given the long winter period at these altitudes of the European Alps.

3.2.3 CH_4 sinks and sources

The observed CH_4 uptake rates in our spring and winter campaigns are potentially underestimating the CH_4 sink potential of these soils, as CH_4 may likely become limiting during 25 – 60 minute chamber deployments. In the chambers that were deployed in spring and winter, a correlation between the starting concentration at t_0 and the CH_4 uptake/emission rate was observed ($R^2 = 0.71$). It is therefore likely that the CH_4 uptake potential of these soils is higher than estimated based on our measurements. The high starting concentrations that were observed in some of our chambers was likely created due to the accidental release of trapped CH_4 bubbles from the soil, upon chamber placement. In summer, no net CH_4 uptake was observed, neither in chambers with high nor low starting concentrations (Fig. 2). Overall, our data shows that the CH_4 emissions and uptake patterns are complex and dependent on both hydrological and biogeochemical factors. More research is needed to detangle the effects of hydrology, vegetation characteristics, and physicochemical soil characteristics. In addition, more research is needed to estimate the contribution of alpine peatlands to overarching alpine greenhouse gas balances. Our study shows high CH_4 emission rates that indicate that alpine peatlands should not be ignored when estimating regional or national greenhouse gas balances.

4. Data availability

All data and R scripts will be made available in the public repository Zenodo upon publication.

5. Author contribution

SvG designed the study, wrote the first draft, and lead the data interpretation. FJ and SK performed field experiments and laboratory analyses. AK contributed to the experimental design and the writing and proofreading of the manuscript.
The authors declare that they have no conflict of interest.

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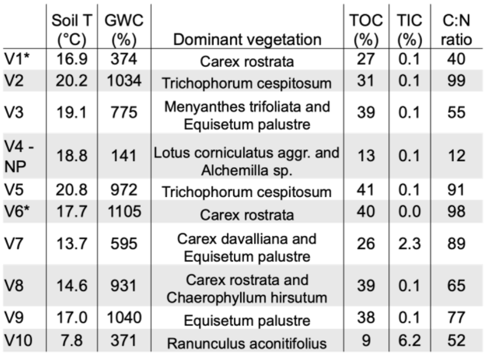
Appendix A

Supplemental figures and tables

Table A1. OTU table showing all OTUs, with taxonomic classification, that were classified as methanotrophic bacteria.

Type I Methane oxidizing bacteria																
	V1	V10	V2	V3	V4	V5	V6	V7-1	V7-2	V8	taxonomy					
	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Methylococcales		
	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.01	0.00	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Methylococcales		
	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Methylococcales		
	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Methylococcales		
	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Methylococcales		
	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Methylococcales		
	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Methylococcales		
	0.04	0.00	0.01	0.00	0.00	0.00	0.01	0.00	0.00	0.00	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Methylococcales		
	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Methylococcales	f__Crenotrichaceae	g__Crenothrix
	1.76	0.01	0.52	0.27	0.00	0.61	2.66	0.10	0.20	0.01	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Methylococcales	f__Crenotrichaceae	g__Crenothrix
	0.67	0.00	0.20	0.31	0.01	0.64	0.80	0.03	0.05	0.00	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Methylococcales	f__Crenotrichaceae	g__Crenothrix
	0.01	0.06	0.09	0.72	0.00	0.33	0.29	0.05	0.09	0.01	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Methylococcales	f__Crenotrichaceae	g__Crenothrix
	0.45	0.01	0.02	0.00	0.00	0.02	0.40	0.02	0.09	0.00	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Methylococcales	f__Crenotrichaceae	g__Crenothrix
	0.20	0.01	0.06	0.12	0.00	0.01	0.43	0.01	0.04	0.02	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Methylococcales	f__Crenotrichaceae	g__Crenothrix
	0.40	0.00	0.02	0.01	0.00	0.10	0.01	0.03	0.03	0.00	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Methylococcales	f__Crenotrichaceae	g__Crenothrix
	0.14	0.00	0.03	0.00	0.00	0.00	0.14	0.00	0.00	0.00	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Methylococcales	f__Crenotrichaceae	g__Crenothrix
	0.00	0.00	0.00	0.00	0.00	0.03	0.09	0.01	0.00	0.00	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Methylococcales	f__Crenotrichaceae	g__Crenothrix
	0.00	0.00	0.01	0.00	0.00	0.04	0.01	0.00	0.03	0.00	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Methylococcales	f__Crenotrichaceae	g__Crenothrix
	0.00	0.00	0.00	0.03	0.00	0.00	0.01	0.01	0.01	0.00	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Methylococcales	f__Crenotrichaceae	g__Crenothrix
	0.01	0.00	0.00	0.00	0.00	0.02	0.02	0.00	0.00	0.00	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Methylococcales	f__Crenotrichaceae	g__Crenothrix
	0.00	0.00	0.01	0.01	0.00	0.00	0.00	0.00	0.00	0.00	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Methylococcales	f__Crenotrichaceae	g__Crenothrix
	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Methylococcales	f__Crenotrichaceae	g__Crenothrix
	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Methylococcales	f__Crenotrichaceae	g__Crenothrix
	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Methylococcales	f__Crenotrichaceae	g__Crenothrix
	0.00	0.00	0.00	0.01	0.00	0.37	0.02	0.00	0.00	0.00	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Methylococcales	f__Crenotrichaceae	g__Crenothrix
	0.01	0.00	0.04	0.02	0.00	0.13	0.01	0.04	0.06	0.03	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Methylococcales	f__Methylococcaceae	
	0.00	0.00	0.14	0.00	0.00	0.00	0.00	0.00	0.00	0.00	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Methylococcales	f__Methylococcaceae	
	0.12	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Methylococcales	f__Methylococcaceae	
	0.00	0.00	0.00	0.00	0.00	0.01	0.01	0.00	0.00	0.00	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Methylococcales	f__Methylococcaceae	
	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Methylococcales	f__Methylococcaceae	
	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Methylococcales	f__Methylococcaceae	
	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Methylococcales	f__Methylococcaceae	
	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Methylococcales	f__Methylococcaceae	
	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Methylococcales	f__Methylococcaceae	
	0.00	0.00	0.04	0.00	0.00	0.01	0.00	0.00	0.00	0.00	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Methylococcales	f__Methylococcaceae	
	0.12	0.00	0.14	0.16	0.00	0.30	0.32	0.09	0.11	0.05	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Methylococcales	f__Methylococcaceae	g__
	0.10	0.00	0.12	0.04	0.00	0.01	0.06	0.00	0.01	0.01	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Methylococcales	f__Methylococcaceae	g__Methylocaldum
	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Methylococcales	f__Methylococcaceae	g__Methylocaldum
	0.01	0.03	0.04	0.01	0.00	0.07	0.42	0.00	0.01	0.01	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Methylococcales	f__Methylococcaceae	g__Methylomonas
Sum	**4.05**	**0.16**	**1.56**	**1.73**	**0.01**	**2.71**	**5.76**	**0.37**	**0.75**	**0.15**						
Type II Methane oxidizing bacteria																
	V1	V10	V2	V3	V4	V5	V6	V7-1	V7-2	V8	taxonomy					
	0.33	0.00	0.39	0.13	0.00	0.02	0.02	0.00	0.00	0.01	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhizobiales	f__Methylocystaceae	
	0.05	0.00	0.04	0.00	0.19	0.05	0.01	0.00	0.00	0.00	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhizobiales	f__Methylocystaceae	g__
	0.13	0.01	0.34	0.03	0.00	0.01	0.01	0.00	0.00	0.01	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhizobiales	f__Methylocystaceae	g__
	0.03	0.01	0.01	0.07	0.00	0.05	0.06	0.04	0.03	0.05	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhizobiales	f__Methylocystaceae	g__Methylosinus
	0.04	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhizobiales	f__Methylocystaceae	g__Methylosinus
	0.03	0.04	0.04	0.06	0.00	0.10	0.09	0.08	0.09	0.06	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhizobiales	f__Methylocystaceae	g__Pleomorphomonas
	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhizobiales	f__Methylocystaceae	g__Pleomorphomonas
	0.04	0.15	0.02	0.01	0.01	0.02	0.01	0.03	0.04	0.03	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhizobiales	f__Methylocystaceae	g__Rhodoblastus
Sum	**0.64**	**0.20**	**0.84**	**0.31**	**0.20**	**0.25**	**0.20**	**0.15**	**0.16**	**0.15**						

Table A2. Soil characteristics across the peatland. The soil temperature reported here was measured at 10 cm depth. GWC: gravimetric water content, TOC: total organic carbon as % of dry soil weight, TIC: Total inorganic carbon as % of dry soil weight. * indicates surface water at this location. V4-NP: Non-peatland location, as reference. The location of the other samples can be found in Fig. A2.



	Soil T (°C)	GWC (%)	Dominant vegetation	TOC (%)	TIC (%)	C:N ratio
V1*	16.9	374	Carex rostrata	27	0.1	40
V2	20.2	1034	Trichophorum cespitosum	31	0.1	99
V3	19.1	775	Menyanthes trifoliata and Equisetum palustre	39	0.1	55
V4 - NP	18.8	141	Lotus corniculatus aggr. and Alchemilla sp.	13	0.1	12
V5	20.8	972	Trichophorum cespitosum	41	0.1	91
V6*	17.7	1105	Carex rostrata	40	0.0	98
V7	13.7	595	Carex davalliana and Equisetum palustre	26	2.3	89
V8	14.6	931	Carex rostrata and Chaerophyllum hirsutum	39	0.1	65
V9	17.0	1040	Equisetum palustre	38	0.1	77
V10	7.8	371	Ranunculus aconitifolius	9	6.2	52

Fig. A1. The Auenfeld alpine peatland sampling site accross different seasons.

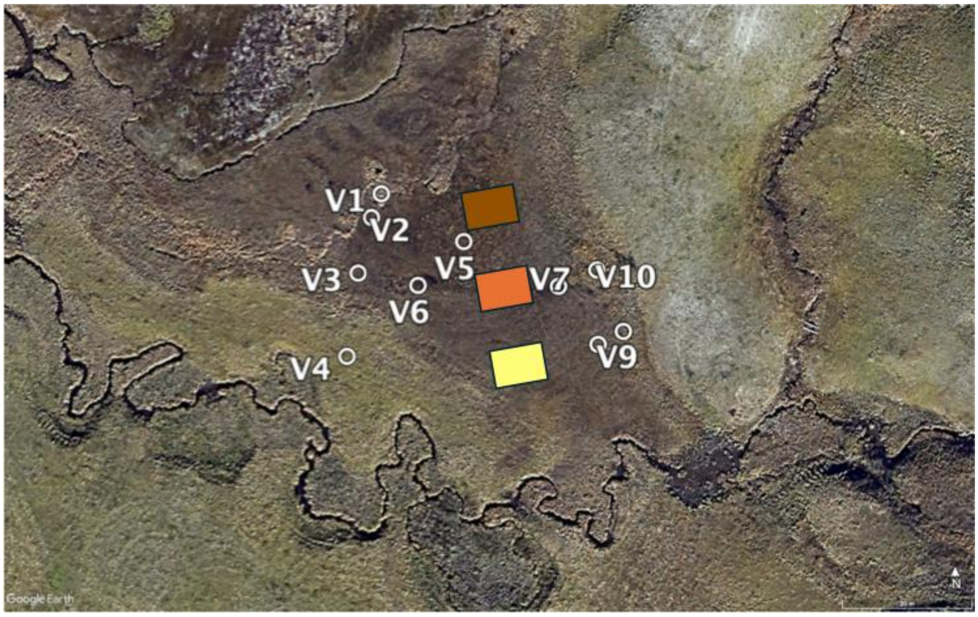


Fig. A2. Sampling locations within the alpine peatland. The coloured boxes represent the sampling areas of July 2024, of which the data is displayed in Fig. 3, and a picture is shown in Fig. A3. In each coloured box, 4 chambers were places within 1 m^2. Locations V1-V10 were used for soil sampling. The chamber measurements during other campaigns (spring, winter, summer 2025) were spread out over the summer sampling or winter sampling area indicated in Fig. 1. (Background map - Imagery © 2026 Airbus, Maxar Technologies, © Swisstopo, Map data © 2026 Google)

Fig. A3. Pictures of the group-wise setup of the chambers within the Auenfeld alpine peatland. Left: overview with the three groups visible. Right: the setup of the 4 chambers within one group.

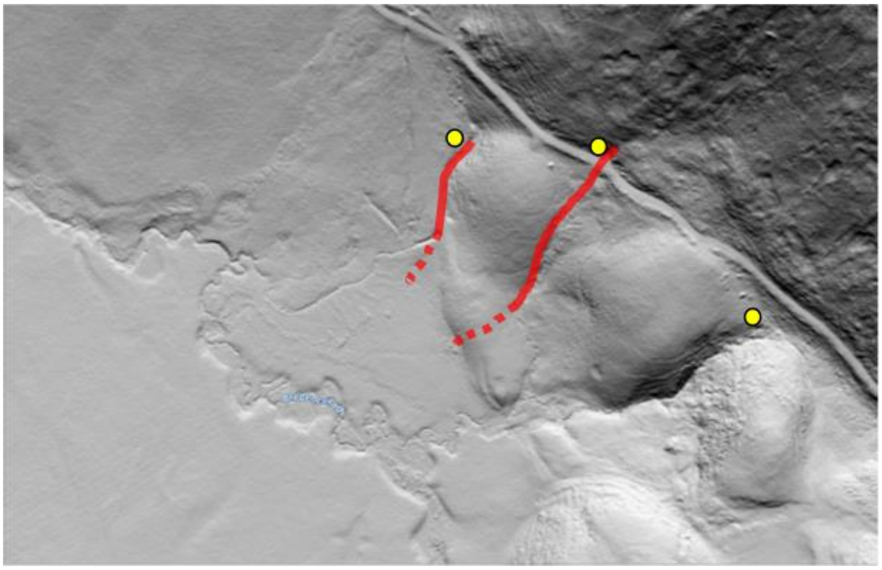


Fig. A4. Hypothesized hydrology of the alpine peatland. Red lines indicate the expected water influx paths. Solid lines indicate observed water flow in the field, dashed lines indicate suspected below ground water flow. Yellow circles indicate water sampling locations for water chemistry.

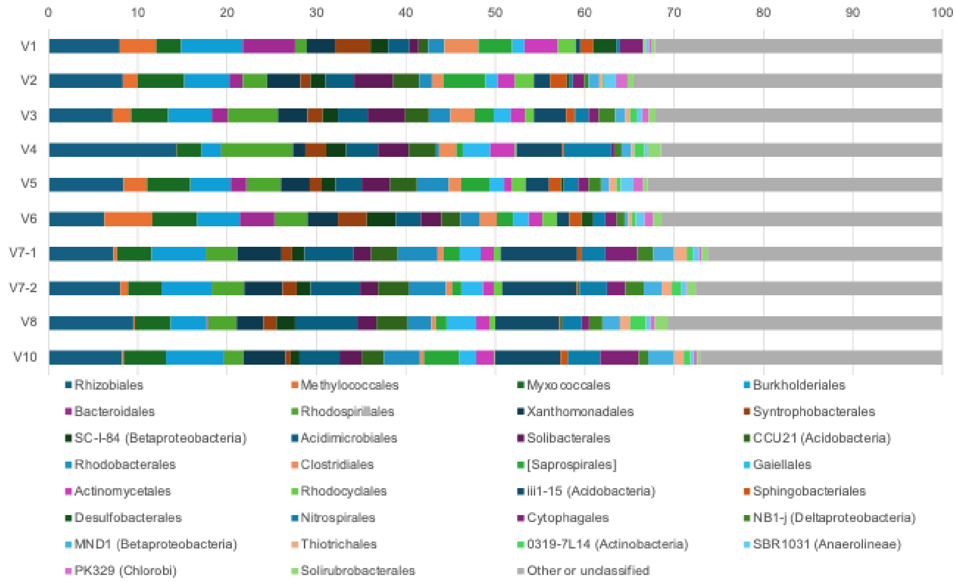


Fig. A5. Microbial community classified at order level (relative abundance, % of 16S rRNA reads) of 4-6 cm depth soil samples of the alpine peatland. All orders that had at least 1% abundance in at least 2 of the 10 samples, are shown. V7-1 and V7-2 represent duplicate samples from one soil core.

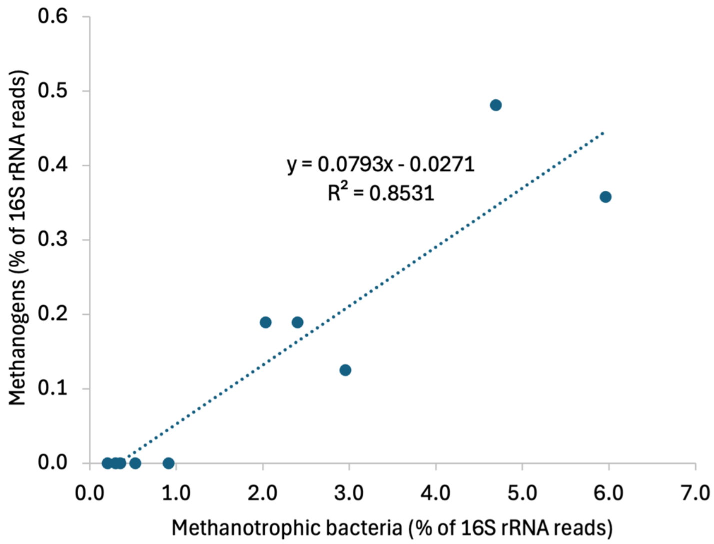


Fig. A6. Correlation between the abundance of methanotrophic bacteria and methanogenic archaea in soil samples of the alpine peatland.