Data on vegetation composition, soil edaphic variables and fungal communities in 1-13 year old clearcuts in central Sweden

SND-ID: 2025-23. **Version**: 1. **DOI**: https://doi.org/10.5878/vfre-f585

Download data

CarryOverNeffects_EnzymeAssayData.txt *(13.03 KB)*

CarryOverNeffects_OTUtable.txt *(5.24 MB)*

CarryOverNeffects_PlotData.txt *(22.65 KB)*

CarryOverNeffects_Rscript.r *(53.76 KB)*

CarryOverNeffects_SoilRespirationData.txt *(129.06 KB)*

CarryOverNeffects_TreeGrowthRateData.txt *(12.92 KB)*

CarryOverNeffects_TreeHeightData.txt *(140.93 KB)*

CarryOverNeffects_VegetationPlotData.txt *(23.43 KB)*

CarryOverNeffects_VegetationSubPlotData.txt *(132.81 KB)*

Associated documentation

Data_readme.txt *(18.18 KB)*

SessionInfo_Rscript.txt *(1.53 KB)*

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2025-23-1.zip *(~5.78 MB)*

Citation

Boeraeve, M., Granath, G., Lindahl, B. D., Clemmensen, K. E., & Strengbom, J. (2025) Data on vegetation composition, soil edaphic variables and fungal communities in 1-13 year old clearcuts in central Sweden (Version 1) [Data set]. Swedish University of Agricultural Sciences. Available at: https://doi.org/10.5878/vfre-f585

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Principal's reference number

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Description

Data collected from clearcuts, 1 to 13 years after clearcutting, in central Sweden (Uppland and Västmanland). It contains data on the vegetation composition, height and growth rate of trees, soil organic layer carbon and nitrogen stocks, enzyme activities in the soil organic layer (for only a part of the samples) and the soil fungal communities.

Data contains personal data

No

Language

English

Time period(s) investigated

2022-05 – 2023-10

Data format / data structure

Text

Species and taxons

Pinus sylvestris
Picea abies
Betula
Ericales
Fungi

Data collection 1

- Mode of collection: Measurements and tests
- Description of the mode of collection:
  1. Study area and design
  The research was conducted in central Sweden (59-60° N) in two study areas in the transition between the hemiboreal and boreal zone. In total, 36 clearcuts were selected: 18 clearcuts of previously fertilized forests paired with 18 clearcuts of unfertilized forests with similar characteristics (site index, time since clearcutting, soil type). All forests were property of Sveaskog AB, who provided the data necessary to select them.
  In the fertilized sites, 150 kg N ha-1 had been applied once (n = 14) or twice (n = 4) between 1973 and 2006 in the form of the commonly used Skog-CAN, which is ammonium nitrate with added dolomite (CaMg(CO3)2), to reduce the risk of acidification, and 0.2% boron (B). A space-for-time substitution approach was used to determine the change over time in soil conditions, plant and fungal communities after clearcutting. The forests were clearcut between 2009 and 2018 and sampled between May and September 2022, i.e. 4-13 years after clearcutting. All clearcuts had underwent mechanical soil preparation and had been planted with tree seedlings (Pinus sylvestris and Picea abies). On each clearcut, three circular plots with a radius of 10 m were delineated away from any retention trees. In these plots soil samples were taken, soil respiration was measured, ground vegetation and tree layer were surveyed and young trees were sampled to estimate tree growth rate. Soil samples and soil respiration measurements were taken in the parts of the plot that were undisturbed during soil preparation, i.e. where the soil organic layer was intact.

  After analysing the results from this first field campaign, an additional sampling campaign in August

2023 was set up to collect soil samples and measure soil respiration in more recent clearcuts, i.e. within a year before sampling (clearcut in 2022 or the beginning of 2023, before the start of the growing season). In this campaign, 6 clearcuts of previously fertilized forests were selected and paired with 6 clearcuts of unfertilized stands with similar characteristics.
In the fertilized sites, 150 kg N ha-1 had been applied once between 2004 and 2012. After clearcutting, the soil was mechanically prepared in two of the six pairs and no tree planting had taken place yet in any of the clearcuts. The soil sampling and soil respiration measurements were conducted in the same way as during the first sampling campaign.

2. Tree and ground vegetation survey
Composition of ground vegetation was determined using a 1x1 m frame divided into 25 quadrats. The number of quadrats in which a taxon was present was recorded for each vascular plant species and for mosses, lichens and vascular plants as a group. For tree species, a distinction was made between individuals belonging to the tree layer (> 1.2 m) or the ground vegetation (< 1.2 m). This was repeated six times across each 10-m-radius plot. In each plot, a circular subplot with radius 3 m was delineated, in which the species and height of all trees (> 1.2 m) were recorded, from which tree density and tree layer composition were later calculated. In the clearcuts from 2009-2015, three individuals (> 1.2 m) of both Picea abies and Pinus sylvestris were sampled for estimation of tree growth rate.
If less than three individuals of a species were present in a plot, the species was not sampled. Sampling was done by cutting the tree at the base and collecting a disc of the stem. These cross-sections were taken back to the laboratory where they were sanded and scanned. Tree ring widths were measured using the measuRing R package (Lara et al., 2015), and growth rates (yearly diameter increase, in mm) were extracted from linear regressions of cumulative tree ring width against year, plotted for each individual tree separately.

3. Soil respiration
Soil CO2 flux was measured on rain-free days in two rounds: one in spring (16 May – 9 June 2022) and one in summer (22 August – 12 September 2022).
During the second sampling campaign in 2023, only one round of soil CO2 flux measurements was conducted (11-17 August 2023). In each plot, respiration was measured at five locations: one in the middle and four closer to the edge, using a closed chamber constructed from a dark, non-transparent PVC-collar (diameter = 23.5 cm, height = 15 cm) equipped with a portable infrared CO2 gas analyzer (Vaisala GMP343) and a humidity and temperature meter (Vaisala HM70). All living ground vegetation was removed before gently pushing the chamber 0-1 cm into the soil, minimizing soil disturbance while making sure that no gaps were present between the collar and the soil surface. CO2 concentration was then recorded for 3 min at 15s intervals. A quadratic function was fitted between CO2 concentration and time, and CO2 flux was calculated from the linear term on a per area basis (mg C m-2 h-1), accounting for chamber temperature and volume according to standard equations (Kutzbach et al., 2007).
After each CO2 measurement, the soil water content and temperature, as well as the depth of the organic layer were determined. Soil water content was measured four times with a soil moisture sensor (Meter GS3 with a Pro-Check reader) and the mean value was used in further analyses. Soil temperature was measured at 3 cm depth.

4. Soil sampling
25 soil cores (diameter 3 cm) were taken in a grid pattern across each plot, the mineral layer was removed and the organic layer, including litter, was pooled into one soil sample.
Parts of the plot were the soil organic layer was removed during soil preparation were avoided. Soil samples were stored on ice until frozen at -20° C.

5. Soil CN and pH analyses

After weighing and homogenisation in a freeze-mill, a subsample was freeze-dried, weighed (before and after to determine % dry weight), and assessed for carbon and nitrogen content using a combustion elemental analyser (TruMac CN; LECO, St. Joseph, MI, USA). A 5 g subsample of freshly frozen, homogenised soil was shaken in 25 mL of deionised water for 10 min at 650 rpm and left to equilibrate for 15 min before measuring pH with a PHM93 pH meter (Radiometer, Copenhagen). The carbon and nitrogen stocks of the organic layer were calculated by multiplying the dry weight of the soil sample by the carbon and nitrogen content, respectively, and scaling it up to tonnes ha-1 based on the total area of the soil cores.

6. Soil enzyme assays (only for the soil samples from 1yo clearcuts)

From the frozen homogenised soil samples of the 2023 sampling campaign, potential enzymatic activities of five hydrolytic enzymes (cellobiohydrolase, β-glucosidase, β-xylosidase, β-N-acetyl-glucosaminidase and acid phosphatase) and of manganese peroxidase were determined (Kyaschenko et al., 2017; Saiya-Cork et al., 2002).

Soil suspensions were made by shaking a volume of frozen soil equivalent to 2 g dry soil in 200 mL sodium acetate buffer (50 mM, pH 5) for the hydrolytic enzyme assay, and the equivalent to 5 g dry soil in 50 mL sodium acetate buffer for the manganese peroxidase assay. For the hydrolytic enzymes, the soil suspensions were further

diluted 10 times and 50 µL fluorogenic umbelliferyl substrate was added to 200 µL soil suspensions (0.001 g dry weight soil ml-1). After incubating in the dark for 2h, 10 µL 0.5 M NaOH was added to stop the reaction, and fluorescence was measured, controlling for background fluorescence (assays without the incubation step).

The soil suspensions were also incubated with a standard methylumbelliferone solution as a quenching control. Soil suspensions with too high quenching were further diluted and the assay was repeated. Net fluorescence was converted to enzyme activity expressed per min and g organic matter. For the manganese peroxidase assay,

50 µL of clear supernatant of soil suspensions (0.1 g dry weight soil ml-1) were added to a buffer solution with 3-dimethylaminobenzoic acid and 3-methyl-2-benzothiazolinone hydrazone hydrochloride and either MnSO4 or EDTA (which chelates Mn). Four combinations were done: one with Mn and H2O2 (peroxidase activity including Mn-dependent), one with EDTA and H2O2 (Mn-independent peroxidase activity), one with EDTA (negative control) and one with Mn, H2O2 and a commercial horseradish peroxidase (Sigma-Aldrich, Burlington, MA, USA) (positive control). Immediately after mixing the reagents, plates were put in the plate reader and absorbance was measured every 3 min for 30 min.

Mn-dependent activity was calculated as total peroxidase activity minus Mn-independent peroxidase activity and expressed as absorbance per minute and g organic matter.

7. soil metabarcoding

A 0.25 g subsample of freeze-dried and ball milled soil was used for DNA extractions with the Nucleospin Soil kit (Macherey-Nagel) following the manufacturer's instructions. About 1000 bp long markers, including the ITS2 region together with parts of the large subunit, were amplified from diluted DNA extracts (1 ng/µl), using the

forward primer gITS7 and the reverse primer TW13 with unique identification tags attached to both primers (Ihrmark et al., 2012; Tedersoo et al., 2018).

Amplification was done in 50 µl reactions consisting of 0.5 µM forward primer, 0.3 µM µl reverse primer, 0.25 µl DreamTaq polymerase, 5 µl dNTPs, 5 µl DreamTaq buffer, 1.5 µl MgCl2, 3.25 µl H2O and 25 ng template DNA under the following conditions: 5 min at 94° C, 21-25 cycles of 30 s at 94° C, 30 s 56° C and 1 min at 72° C

and finally 8 min at 72° C. PCR products were equimolarly pooled and cleaned with the E.Z.N.A.

Cycle Pure Kit (Omega Bio-Tek). After a quality control by Bioanalyzer (Agilent tech), the amplicon pool was sequenced on the PacBio Sequel II platform (Pacific Biosciences) at SciLifeLab NGI (Uppsala, Sweden).
Sequence data was submitted to the NCBI Sequence Read Archive under BioProject PRJNA1191207.

8. qPCR quantification
Copy numbers of the ITS2 region were quantified from diluted DNA extracts (0.5 ng per reaction) on a CFX Connect Real-Time System (Bio-Rad) using the forward primer gITS7 (Ihrmark et al., 2012) and reverse primers ITS4 and ITS4arch (Sterkenburg et al., 2018; White et al., 1990) in duplicates. The ITS2 copy numbers were converted to ITS2 copy number mg-1 organic matter and corrected to fungal ITS2 copy number mg-1 organic matter by multiplying total copies with the ratio of fungal sequences in that sample, based on the metabarcoding data (to correct for non-target amplification e.g. of plant DNA).

- Time period(s) for data collection: 2022-05 – 2023-11
- Data collector: Swedish University of Agricultural Sciences
- Instrument: Vaisala GMP343 - a portable infrared CO2 gas analyzer
- Instrument: TruMac CN; LECO - a combustion elemental analyser for carbon and nitrogen
- Instrument: PacBio Sequel II - sequencing
- Instrument: CFX Connect Real-Time System (Bio-Rad) - qPCR
- Source of the data: Biological samples
- Spatial resolution: 100 metres

Geographic spread

Geographic location: Sweden

Geographic description: Uppland and Västmanland, Sweden (59-60° N)

Responsible department/unit

Department of Ecology

Funding

- Funding agency: Vinnova
- Funding agency's reference number: 2019-03167_Vinnova
- Project name on the application: Forest management for improved natural carbon sequestration
- Funding information:
  Purpose and goal:
  If climate effects are to be kept within manageable limits, we must quickly reduce greenhouse gas emissions and find innovative solutions to reduce the CO2 concentration in the atmosphere. One solution is to increase the forest´s carbon storage through forest management. The project´s objective is to clarify the climate benefits with large-scale forest fertilization, and describe how other ecosystem services and biodiversity might be affected, and to what extent refined stand selection can improve the climate benefit of fertilization and limit its negative environmental impact.

  Expected results and effects:
  We will clarify what the maximum climate benefit large-scale forest fertilization, as currently practiced, the potential of more intensive fertilization treatments, with and without thinning, and what negative side effects the different alternatives can cause. The results will clarify expected climate benefit over different periods and will provide a basis for future policy on if, and how, forestry should be used to counteract climate change. The results are therefore relevant to several

of the national and international environmental and sustainability goals.

Approach and implementation:
We study how forestry can reduce CO2 concentration in the atmosphere by analyzing how operative and more intensive forest fertilization affects forest production, timber assortment and soil carbon stock. To evaluate climate impacts, we conduct LCA analyzes of forest raw materials and soil C storage. We will also examine fertilization effects on other ecosystem services and biodiversity. By analyzing in which stands that fertilization is most effective, and relate the effect to the national availability of such land, we can estimate the net effect of forest fertilization.

Research area

Ecology (Standard för svensk indelning av forskningsämnen 2011)

Environment (INSPIRE topic categories)

Keywords

Soil, Species distribution, Carbon cycle, Forest vegetation, Mycorrhizal fungi, Soil respiration, Clearcuttings, Forest fertilisation

Publications

Boeraeve, Margaux; Granath, Gustav; Lindahl, Björn; Clemmensen, Karina; Strengbom, Joachim (accepted) Fertilizer-induced soil carbon rapidly disappears after clearcutting in boreal production forests. Journal of Applied Ecology.

Polygon (Lon/Lat)

17.550659, 59.910976
17.990112, 59.772992
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Polygon (Lon/Lat)

15.811043, 59.630052
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15.811043, 59.630052

Accessibility level

Access to data through SND
Data are freely accessible

Use of data

Things to consider when using data shared through SND

License

Versions

Version 1. 2025-02-28

Contacts for questions about the data

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