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PALEOENVIRONMENTAL RECONSTRUCTION OF THE HOLOCENE BEERBERG PEATLAND SEQUENCE (THURINGIA, GERMANY) - THE ADDED VALUE OF INVERSED MODELING OF BIOMARKER COMPOSITION

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Introduction

Paleoenvironmental reconstruction has been frequently applied to various terrestrial archives, including peat sequences to better understand local and regional climate and environmental changes. Numerous tools have been applied with biomarkers as one of the most powerful tools in this respect. However, commonly single biomarkers of a set of individual compounds were applied, which often results in some contradictory results in between different substance classes. On the Beerbergmoor sequence from Thuringia, Germany, that covers the last ca. 6000 years before present, we applied various biomarkers such as alkanes, fatty acids and alcohols to trace changes in the vegetation composition. In addition, we applied for the first time an inversed model to assess quantitative shifts in vegetation composition among all investigated biomarker classes. The overall aim was to determine, whether inversed modeling can provide more comprehensive and quantitative changes of plant communities in such paleoenvironmental records.

Results

Carbon and nitrogen concentrations as well as C/N ratio already showed that peat samples represent a mixture of organic matter incorporated by roots of higher plants, *Sphagnum* moss and aboveground biomass of higher plants currently growing at that site. At a depth below 250 cm higher nitrogen and carbon concentration and lower C/N ratios suggest contribution of biomass from various origins, while between 250 cm and 100 cm depth the high C/N ratio argue for predominantly *Sphagnum*-derived biomass. At the top of the sequence (<20 cm depth) very high nitrogen concentrations point to strong atmospheric nitrogen deposition during recent years.

The biomarker composition of recent plants did not enable a clear distinction between *Sphagnum* species and higher plant biomass, which was observed in former studies. However, in the depth interval between 100 and 250 cm the aquatic to terrestrial ratio $[(C_{23}+C_{25})/(C_{23}+C_{25}+C_{29}+C_{31}) n\text{-alkanes}]$ also pointed to stronger contribution of *Sphagnum* plant biomass. Similar observations could be made using the fatty acid composition, while alcohols did not reveal special trends.

In addition to various molecular proxies also polycyclic aromatic hydrocarbons (PAH) were investigated. In depth intervals below 250 cm more PAH (predominantly 3-ring structures and to a lower magnitude also 4-ring-molecules) were observed than in the depth between 100 cm and 250 cm, arguing for more burning residues at a larger depth of this sequence. Above 100 cm two maxima of PAH abundance were observed: at 50-70 cm depth 4-ring

moieties predominate, whereas above 20 cm 4-7 ring structures appear in high concentrations. The PAH composition argues for more natural burning at large profile depth, most likely during the phase of neolithic settlements in that area. The larger ring structures incorporated in the upper meter of the sequence argue for more intense burning probably during the middle ages and recent times since the industrial revolution.

Reconstructed temperatures based on glycerol dialkyl glycerol tetraethers (GDGTs) revealed a subsequent temperature increase from 6°C to 10°C until 130 cm depth. Above values dropped to 6°C within 20 cm. Between 100 cm and 50 cm temperatures were slightly lower, whereas the minimum of <6°C at 50 cm most likely indicated the little ice age in the late Medieval, followed by temperatures maximising above 10°C in the uppermost 20 cm. As such, the temperature curve is in good agreement with other climate reconstructions over the past ca. 6000 years that are covered by the Beerberg peatland sequence.

Apart from the molecular composition that still remains fragmented and does not allow for quantitative vegetation shifts, inversed modeling was applied to reconstruct the lipid composition in the peat sequence by the lipid composition of recent plants and roots obtained from that site. To achieve this, all quantified biomarker results from alkane, fatty acid and alcohol fractions were evaluated together. The inversed modeling revealed that roots contribute ca. 5-30% to the overall organic matter in the different depths of the sequence with a tendency of higher contributions below 250 cm depth. At the same depth *Calluna vulgaris* and *Sphagnum capellifolium* showed the closest match to the peat material and thus contributed up to 55% and 10%, respectively, to the peat signal. Between 100 and 250 cm depth roots play a minor role (5-20%) and grass-type biomass like *Eriophorium vaginatum* seemed to be the most likely contributor to the majority of the peat biomass, apart from *Sphagnum* species. Within the uppermost 100 cm roots played the largest role among the whole profile and contributed mostly more than 20% to peat biomass. Although this inversed modeling exercise still requires more fine-tuning, the first attempts already showed the strengths of this attempt to better quantify the contribution of different biomass sources to the bulk organic matter than by just looking at different molecular proxies like average chain length, carbon preference index and others, individually. As such, inversed modeling is a powerful tool to improve our paleoenvironmental understanding, not only in peat sequences, but also in other soil and sedimentary settings.