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IMPROVED SOURCE APPORTIONMENT OF SOIL AND SEDIMENT ORGANIC MATTER USING INVERSE MODELING OF BIOMARKER COMPOSITION (VERHIB 2.0)

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Identifying the sources of organic matter in terrestrial and aquatic systems can lead to a greater understanding of the organic matter cycle as well as local palaeovegetation and palaeoclimate conditions. A variety of proxies have been used to study organic matter composition, including stable isotopes ($\delta^{13}\text{C}$, $\delta^2\text{H}$, $\delta^{18}\text{O}$), radioactive isotopes (radiocarbon, ^{14}C), and molecular proxies (e.g. lignin monomers, suberin/cutin monomers, phospholipid fatty acids, or free extractable lipids like alkanes, alcohols, and fatty acids). Commonly, most studies only investigate and interpret a limited number of molecular markers, so quantitative information is often not consistent among different molecular marker classes and joint evaluation of data is weak. Additionally, most molecular markers are ubiquitous, which is why species cannot be identified by individual markers, but by unique patterns of those markers.

To overcome these limitations, the VERHIB (Vegetation Reconstruction by the Help of Inversed modelling and Biomarkers) model was established, which gave the unique opportunity to implement quantitative data of numerous molecular marker classes to reconstruct and quantify the contribution of different source vegetation to soil organic matter. The VERHIB model uses linear regression to describe how vegetation development in an archive at a specific location results in the accumulation of certain biomarkers. By inverting the forward model, palaeovegetation can be reconstructed from the observed biomarker signal. The VERHIB model was first tested with artificial data and then applied to observed data beginning with the *n*-alkane and *n*-alcohol signals found in a peat sequence in Ecuador (Jansen et al., 2010). The biomarker analysis was compared with a previously performed reconstruction created using pollen analysis. It was found that the biomarker analysis was better for local vegetation reconstruction and could supplement the regional reconstruction obtained through pollen analysis. Difficulties associated with biomarker analysis included problems with identifying separate species that have similar biomarker signals as well as a limited ability to identify taxa not in the biomarker database. Later, the VERHIB model was applied to biomarker signals found in soil from Ecuador (Jansen et al., 2013) and a polycyclic driftsand sequence in the Netherlands (van Mourik, Jansen, 2013).

As the VERHIB model has not been updated significantly since its advent, there is much room for improvement to incorporate the latest insights in molecular proxy dynamics in soils and sediments, and to broaden its applicability. The model will be tested with existing and new datasets including a complex soil sequence from the Netherlands, a peat sequence from Central Germany, and lake sediments from Switzerland. The improved VERHIB 2.0 model has the potential to become a widely applied tool in soil science, limnology, sedimentology, geochemistry, palaeoecology and other disciplines and will provide new insights into comprehensive molecular marker analyses.

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