



## Using preserved extractable lipids in a multi-proxy reconstruction of past vegetation patterns

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Analysis of fossil pollen and of stable carbon isotopes of organic matter preserved in soils and sediments are the most commonly used proxies to reconstruct past vegetation patterns. Unfortunately, fossil pollen analysis normally does not distinguish beyond family or generic level, while its spatial resolution is limited by windblown dispersal of pollen. At the same time stable carbon isotopes can only be used in cases of a transition in time between C3 and C4 vegetation. As a result a multi-proxy approach combining only fossil pollen and stable isotope analysis often does not suffice for a detailed reconstruction of past vegetation patterns. Therefore, we developed a new biomarker application to be used in conjunction with the previously mentioned proxies. The biomarker application is based on the analysis of plant-specific groups of n-alcohols and n-alkanes with chain lengths of 20 – 36 carbon atoms preserved in sediments or soils. The biomarker patterns are subsequently unraveled into the plant species of origin by the newly developed VERHIB model[1]. Here we describe the VERHIB model and present the results of its application to reconstruct the natural position of the upper forest line in the Ecuadorian Andes from biomarkers preserved in a peat deposit and three soil monoliths along an altitudinal transect. We compare the results with those from fossil pollen and stable carbon isotope analysis from the same archives and show how the combined application yields a reconstruction of past vegetation composition with previously unattainable detail.

[1] Jansen et al. (2010) *Palaeogeog. Palaeocl.* 385, 119-130.