## Molecular indicators of microbial community change linked to terrestrial inputs during the Ordovician-Silurian transition (Kentucky, USA)

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The Late Ordovician mass extinction (LOME), one of the largest biocrises of the Phanerozoic, was associated with climatic cooling possibly triggered in part by the spread of early nonvascular land plants. To date, the effects of this biocrisis and the spread of non-vascular land plants on marine microbial communities have received scant attention. We have generated biomarker records for Upper Ordovician to Lower Silurian strata of central Kentucky and southern Indiana (U.S.A.) to investigate contemporaneous microbial community changes and possible controls thereon. Hopane-to-sterane ratios (H/S) document mainly marine algal inputs before and after the Hirnantian Ice Age but enhanced bacterial inputs during the glacial interval (Fig. 1). The first high-H/S interval, dating to the late Katian to early Hirnantian, preceded or coincided with the first stage of mass extinction (LOME-1), which was linked to the onset of Hirnantian glaciation. The second high-H/S interval, dating to the late Rhuddanian and Aeronian, was associated with postglacial warming and thus had a different cause. An increase in long-chain n-alkanes (Fig. 1) may signal increased inputs of land plant biomass, suggesting that an expansion of terrestrial floras in the aftermath of the Hirnantian Glaciation fueled increased marine productivity and anoxia. This second interval is also associated with elevated moretane-to-hopane ratios (M/H), consistent with increased inputs of soil organic matter to the marine system. An increased abundance of C19-C20 long-chain tricyclic terpenes (as proxied by T/H) in the Lower Silurian indicates increased inputs from marine algae, possibly in response to increased nutrient fluxes from terrestrial sources linked to enhanced weathering by non-vascular land plants. These findings are consistent with the hypothesis that the evolution of non-vascular land plants played a major role in marine microbial community changes during the Hirnantian Ice Age and OST, although further testing is needed.

