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Ancient sedimentary DNA reveals long-term impact of climate change on northern flora

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Arctic and alpine species are disproportionately affected by climate change, and knowledge about their ability to survive or disperse is essential for their long-term conservation. Ancient sedimentary DNA (sedaDNA) has improved as a proxy for reconstructing past floras, and may now be applied in high throughput analyses. Our lab has analysed, or is in the process of analysing, sedaDNA from ~40 long (up to 26 000 years old) and 11 short (0-1000 years old) lake sediment cores from the Europe (Alps, Norway, Svalbard, Iceland, Polar Urals). Both general and site-specific patterns have emerged from these data. For example, the taxa recorded in sedaDNA often indicate a warmer climate than that which has been inferred based on pollen records; this is in concordance with macrofossil evidence. Also, the limits of past northern tree lines may have been underestimated based on pollen studies. Some heathland species, such as *Vaccinium* spp. and *Empetrum*, often show a time lag in arrival compared with other species with similar climatic requirements. Thus, despite the fact that they have berries and therefore are well adapted to long-distance dispersal by birds, our data show they are constrained from rapid responses to climate changes. Other patterns are site-specific. For example, we see a stepwise doubling of floristic richness from the Last Glacial Maximum to the Holocene in the Polar Urals, which is barely detectable in the pollen analyses. Further, the majority of taxa with a mainly arctic-alpine distributions survived the early-Holocene climate warming, when shrub and trees entered the region, probably due to a very heterogeneous landscape that allows co-existence of species with different requirements. In contrast, arctic-alpine taxa disappear from the catchment a subset of the lakes studied in North Norway after shrub and forest expansion. Linking this type of information to characteristics of these biogeographic regions may provide useful when planning for future nature reserves. In the near future, the combination of many sites, complete DNA reference libraries, and emerging molecular methods will allow for the tracking of individual species through time and space.

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