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Research paper

Quantitative climate reconstruction from late-glacial and early Holocene plant macrofossils in western Norway using the probability density function approach

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ABSTRACT

Climate changes during the deglaciation are often derived from proxies such as chironomids and pollen but reconstructions are particularly difficult during cold periods. Plant macrofossils in lake sediments can be numerous during cold, treeless periods. They can often be identified to species level and therefore have the potential to be used for quantitative climate reconstructions in treeless situations such as the late-glacial in western Norway.

To explore the potential of using plant macrofossils to quantify late-glacial climate change we prepared a modern data-set by digitizing 600 arctic circumpolar species distributions. We combined them with gridded climate data to determine their species-climate envelopes for mean January and July temperatures. As a test, we selected species that grow in arctic Fennoscandia today and applied a probabilistic indicator species approach (probability density functions — pdf) to their modern occurrence data and found that contemporary temperatures can be reconstructed within the uncertainty ranges.

We applied the approach to a late-glacial and early Holocene plant macrofossil sequence from Kråkenes, western Norway (5°E 62°1′N) and compared it to existing reconstructions made from pollen and chironomid fossil data. The reconstructed deglacial climate based on the plant macrofossil assemblage was comparable to the other proxy reconstructions except that the mean July temperature was higher during the coldest phase. Plant macrofossils provide additional information to the other proxy reconstructions and a probabilistic approach gives robust uncertainty estimates. This is a good starting point for obtaining more knowledge on late-glacial climate change using plant macrofossils.

1. Introduction

The climate warming in much of the arctic during the last few decades is dramatic (Smol et al., 2005) and unique over the last 200,000 years (Axford et al., 2009). A comparison of natural rapid climate changes over the last deglacial period allows the effects of anthropogenic influence on the climate system to be better understood, and, through modelling, to improve understanding of forcing and feedbacks. In the Arctic and Northern Europe there were large and rapid climate fluctuations during and after the deglaciation (e.g. Lowe et al., 1995) and this is therefore a particularly useful period to use for comparison with current climate change. However, past climate changes have to be reconstructed from proxy data. With more than one proxy reconstruction we can be more certain about the rates and magnitudes of the changes. However, these depend on the reliability of the proxy reconstructions.

Proxies reflecting past climate change can be found in lake sediments and climate reconstructions through the past are often based on biological proxies such as pollen (Bartlein et al., 1986; Guiot, 1987; Huntley, 1993; Seppä and Birks, 2001; Seppä et al., 2004) or chironomids (Lotter et al., 1997; Walker et al., 1997; Olander et al., 1999; Brooks and Birks, 2001; Toivonen et al., 2001). In general they all reflect the pronounced climate fluctuations during the deglaciation that are also shown in the Greenland ice-core records (Rasmussen et al., 2006; see for example Brooks and Birks, 2001).

However, it is still difficult to reconstruct climate at northern latitudes during cold periods such as the Younger Dryas based on biological proxies. This is mainly because organisms are at the limits of their tolerance so diversity is lower than in warmer areas (Gaston, 2000; Velle et al., 2011). This limits any reconstruction of past climate. In addition, fossil remains in sediments can be sparse. In the case of pollen, cold-climate reconstructions are affected by the relatively large amount of far-distance transported pollen, mostly tree pollen from warmer areas, in both the fossil assemblages and in the modern samples comprising calibration datasets (Seppä et al., 2004; Birks and Birks, 2006). The influence of far-transported tree pollen biases

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temperature optima for both the arctic and alpine species and for the tree taxa (Bjune et al., 2010). Low taxonomic resolution is also a problem for pollen reconstructions, as grains are infrequently identifiable to species (Birks, 2003; Seppä et al., 2004; Ortu et al., 2006). This is critical for modern analogue methods that try to reconstruct temperatures from pollen assemblages in periods when trees were absent (Guiot et al., 1993; Bigler et al., 2002; Jackson and Williams, 2004). Pollen assemblages in the late glacial and early Holocene may have no modern analogues due to species' different responses to climate change, including ecological factors such as competition and reproductive capacity that affect migration and establishment.

To reduce these problems, plant macrofossils have been applied to qualitatively infer or validate interpretations of past environmental conditions from other proxies, particularly pollen (Birks, 1993; Birks, 2003; Bjune et al., 2004; Eide et al., 2006; Birks and Birks, 2008). For example Huntley (1993) used the abundance of pollen taxa in two dimensional climate space (pollen–climate response surfaces) to infer the climate from a fossil assemblage. Macrofossils were then used to constrain which of the fossil climate analogues represented by the pollen spectrum in a certain sample is most likely (Huntley, 1994). Plant macrofossils provide unique palaeoecological information, because they can often be identified to species level, originate locally, and are often numerous and species rich during cold treeless periods (see Birks, 2001 for a review). Thus they complement the information obtained from pollen (Birks and Birks, 2000).

Macrofossils have also been used as the main proxy to qualitatively infer past climate change. Birks (1993) and Birks and van Dinter (2010) used an approach based on modern vegetation analogues to reconstruct temperature ranges within the late-glacial and early Holocene periods. Thompson et al. (1999, 2008) applied a quantitative modern analogue technique to plant macrofossil assemblages using the geographical overlap of species at the present to find the closest analogue climate to the past. However, macrofossils have rarely been used in quantitative climate reconstructions because they are recorded as concentrations which are difficult to handle statistically.

A different approach is to use the presence of “climate-indicator” taxa to reconstruct late-glacial climate (Iversen, 1954). This approach can incorporate information from plant macrofossils. Recently the probability density function (pdf) method, a quantitative indicator method, has been developed (Kühl et al., 2002). The pdf method is a probabilistic approach that is based on the present geographic distributions of species (Kühl et al., 2002). It is not dependant on modern analogue species assemblages because it uses the climate envelopes of individual species; the species do not need to overlap geographically today. The pdf method performs well when compared to reconstructions of the same data using a modern analogue method (Kühl and Litt, 2003) and has been applied to pollen records of different warm periods in central Europe (Kühl et al., 2007; Litt et al., 2009; Kühl and Gobet, 2010; Kühl et al., 2010), the Early Weichselian (Kühl et al., 2007), and Holocene changes in the Near East (Neumann et al., 2007). As the pdf method uses presence/absence data and not relative abundance as its basis it can potentially be used with proxy data such as plant macrofossils (Kühl et al., 2002) where presence/absence is important. If it is applied to pollen the pdf method could potentially miss information because relative abundance of pollen is important in reflecting vegetation and hence climate.

Here we aim to explore the potential of the pdf method using plant macrofossils to quantitatively reconstruct late-glacial and Holocene climate at high latitudes. We construct a database of arctic species distributions, run a modern test, and use the pdf method to reconstruct climate based on plant macrofossil data from Kråkenes, western Norway. The Kråkenes multi-proxy project (Birks and Wright, 2000) offers the opportunity to compare the quantitative probabilistic mean July temperature reconstructions made using the plant macrofossil record with temperature reconstructions based on other proxies (pollen, chironomids) derived from the same core using transfer functions (Birks et al., 2000; Brooks and Birks, 2000; Bjune et al., 2010).

2. Methods

Species were selected for digitization based on their presence in Arctic Fennoscandia and/or Svalbard based on the Pan Arctic Flora list (Elven, 2007 onwards). Over 600 species distribution-areas are in the database. This comprehensive database of Arctic species distributions includes species found as fossils in Fennoscandia.

2.1. Digitizing species distribution data

To gather information on Arctic species-climate envelopes modern species distribution data were obtained from atlases of circumpolar plants (Hultén and Fries, 1986).

To prepare the original maps for statistical analysis, they were given a spatial reference (i.e. latitude and longitude). Each map was scanned and georeferenced using geographical information systems (GIS) using ESRI ArcGIS^{tm} in a Lambert polar equidistant projection. During georeferencing, ten tie-points were used between the scanned map and the surface of known coordinates. A third order polynomial function was used to adjust the image (scanned map) to obtain the best fit. This procedure gives each pixel in the scanned map a coordinate.

The presences of the species were then gathered from the georeferenced image. This was done by keeping to Hultén's original design by digitizing the distributions of individual species as point, continuous polygonal, and discontinuous (line) presences (feature classes) (Fig. 1). The distribution data were stored in a geodatabase in vector format (*.gdb).

Only the points and continuous distribution areas were used as the basis for the species-climate envelope calculations because the discontinuous distribution area represents uncertain or approximate species distribution areas (Fig. 1). Such a distribution area may give ambiguous information on species presence and potentially contribute more noise to the more precise presence categories. Some species are only available as discontinuous presence and were therefore excluded from further analysis.

In order to combine the distribution data with the climate data, and for further numerical analysis, the species-occurrence data were referenced on a grid of latitude and longitude. The presences were reprojected and rasterised to the same grid as the climate data (Section 2.2) with a resolution of 0.5°×0.5° latitude longitude. This was considered an appropriate resolution given the scale of the original maps (1: 88 000 000). The data were exported as a presence/absence text file with latitude and longitude as a grid reference for each occurrence.

2.2. Climate data

New et al. (1999) constructed a global climatology that is based on climate station data. By using a thin-plate spline to interpolate between known points as a function of latitude, longitude, and elevation, they constructed a continuous climate surface of the world. Climate parameters that are generally thought to be relevant for plant growth on a macro-scale and that are frequently used in climate reconstructions based on plants were extracted from the gridded climate dataset. The climate parameters we used were mean July temperature (TJul) and mean January temperature (TJan).

2.3. The pdf method

To quantify the species–climate relationship the pdf-method (Kühl et al., 2002; Neumann et al., 2007) was followed. The pdf-method uses the combined species and climate data on a grid as the basis from which to extract vectors of climate variables (TJul, TJan)