

A31 Ringwood, Hampshire diatom analysis and environmental reconstruction

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Introduction

A diatom assessment was carried out for 6 samples taken from a sediment sequence (WS603) at the A31 Ringwood site (AOC Archaeology 2023, Appendix 3). The 6 samples for diatom assessment were selected from a 4m sequence of gravel, sand, alluvium and foreshore river margin deposits from the River Avon, Hampshire. Of the 6 samples assessed, 4 samples were found to be suitable for diatom analysis. These samples have been analysed and 2 new samples have been prepared and analysed for diatoms. Diatom analysis of this sequence is reported here.

Methods

Diatom preparation followed standard techniques (Battarbee *et al.* 2001). Two coverslips of different concentrations were made from each sample and fixed in Naphrax for diatom microscopy.

Diatom counting was carried out a magnification of x1000 under phase contrast illumination using a Leica microscope. Diatom floras and taxonomic publications were consulted to assist with diatom identification; these include Werff & Huls (1957-1974), Hartley *et al.* (1996) and Krammer & Lange-Bertalot (1986-1991).

Diatom-based total phosphorus (TP) reconstruction was carried out using the European Diatom Database (EDDI) (Battarbee *et al.* 2000) Combined TP dataset. The C2 program (Juggins 2003) was used for the manipulation of data formats, taxonomic harmonisation, weighted average environmental reconstruction and for plotting diagrams.

Results

The results of percentage diatom analysis for the 6 samples from WS603 are presented in Figure 1. A summary diagram of diatom lifeform and habitat groups is presented in Figure 2. The results of TP (total aquatic phosphorus) reconstruction are shown in Figure 3 and in Tables 1 & 2.

The diatom assemblages throughout the A31 Ringwood sequence are dominated by freshwater, non-planktonic diatoms that include aerophilous, benthic, epiphytic, and other non-planktonic species. Only traces of open-water planktonic species (*Aulacoseira* sp., *Cyclotella kuetzingiana* agg. *Cyclotella*

meneghiniana) are present in the bottom and top samples (Figure 1). The dominance of non-plankton indicates a shallow-water environment.

Rheophilous diatom taxa are associated with flowing water. These river and stream diatoms include *Melosira varians*, *Meridion circulare* and *Rhoicosphaenia curvata* that are present in all samples, with peaks of rheophilous diatoms of 10% and 7% at 2.41 m bgl and 1.66 m bgl respectively. Rheophilous diatoms are less abundant in the top 2 samples.

Several *Fragilaria* species are common through the WS603 sequence and can form a significant proportion of the diatom assemblages, particularly in the upper part of the core. These diatoms include *Fragilaria pinnata*, *Fragilaria construens*, *Fragilaria construens* var. *venter*, *Fragilaria brevistriata*, *Fragilaria vaucheriae*, *Fragilaria capucina* var. *mesolepta*, *Fragilaria leptostauron*, *Fragilaria leptostauron* var. *martyii* and *Fragilaria lapponica*. These *Fragilaria* spp. have wide environmental ranges for example enabling resistance to periods of drying out because of fluctuations in water levels or allowing the species to grow in water with a wide range of nutrient concentrations. These opportunistic diatoms can also colonise disturbed environments for example.

Denys (1988) has observed that some *Fragilaria* spp fit into the classical model of organisms favoured by r-selection (relatively small valve size, production of large numbers of cells and wide range of ecological tolerance). As a result of their high turnover rates, these opportunistic diatoms may quickly form blooms and temporarily become dominant. This can be seen where there are sudden changes in environment, such as rapid changes in water levels and parallel changes in the habitats available for colonisation and growth. Such *Fragilaria* taxa have a wide range of tolerance and the ability to grow rapidly in newly formed habitats.

Aerophilous diatoms are at a maximum of 14% in the bottom sample (2.41 m bgl). The quality of diatom preservation is also poorest in this sample, probably reflecting exposure of the sediments to the air for longer periods resulting in significant diatom breakage and silica dissolution. Aerophilous taxa such as *Ellerbeckia arenaria*, *Hantzschia amphioxys*, *Navicula mutica*, *Pinnularia major* and *Pinnularia microstauron* can live with periods of desiccation.

A diverse flora of benthic diatoms including *Diploneis ovalis*, *Sellaphora pupula*, *Navicula elginensis* and *Navicula tripunctata* represent shallow water, mud-surface habitats. The benthic species comprise from 4% to 8% of the diatoms in the samples. Other attached, non-planktonic diatoms also represent the dominance of shallow water habitats, increasing from 47% at the base of the sequence to between 77% to 82% of the assemblages in 4 of the top samples, but with a decline to 56% at 1.66 m bgl where there are maxima of epiphytic and rheophilous diatoms.

The cumulative abundance of epiphytic species such as *Cocconeis placentula*, *Cocconeis pediculus* and *Epithemia turgida* reach a maximum at

1.66 m bgl reflecting increased growth of aquatic macrophytes. The peak of *Cocconeis placentula* reflects a maximum of TP in the aquatic environment (see TP reconstruction below). In the EDDI diatom TP training set *Cocconeis placentula* has a high TP optimum ($132 \mu\text{g l}^{-1}$) an important factor driving the maximum reconstructed TP value (see TP reconstruction below).

There is no evidence, from diatom valve morphology (teratological forms) or species composition, of heavy metal contamination in the aquatic environment here.

Diatom-based TP reconstruction

Inferring the values of past aquatic phosphorus or other chemical or environmental variables, from fossil diatom remains preserved in sediments involves two stages (e.g., Cameron *et al.* 1999). First the relationship between diatom abundances and the contemporary environmental variable of interest is modelled using a modern training or calibration set comprised of surface sediment diatom samples and associated water chemistry. These relationships are used to derive a transfer function. The second stage is to use the transfer function to infer past values from the fossil diatom assemblages.

Diatom-based TP reconstruction was carried out for the A31 Ringwood sediment sequence using the combined European TP dataset. This training set is derived from a training set of 347 lakes across Europe (Battarbee *et al.* 2000). The diatom taxonomy of the A31 fossil samples was first harmonised with the EDDI combined TP training set. TP reconstruction was then carried out by Weighted Averaging (WA) using both inverse and classical regression methods. Generally, these regressions have provided similar results for the sediment sequence with low standard errors of prediction, high r^2 , and low root mean square errors (RMSE). The results of the quantitative reconstructions for TP are shown in Table 1 and Table 2 and results are shown graphically in Figure 3.

The taxa in the fossil samples from the A31 sediment sequence are well represented in the combined European TP dataset. Most of the species from the 6 samples analysed for diatoms are present in the training set. A high proportion of the total fossil flora in the samples is also present in the training set (91% to 96%) (Table 1). However, in the less well-preserved bottom sample the representation of the fossil flora in the modern training set is reduced to 81% of the fossil assemblage represented in the training set. Overall, the combined European TP dataset therefore provides good analogues to produce TP reconstructions for these samples.

Table 1. Total number of diatom species in Ringwood A31 fossil samples compared with the number of these species present in the combined European TP training set; and percentage sum of diatoms in the fossil samples represented by species in the training set

Diatom Sample Top Depth (m) bgl	Diatom Sample Bottom Depth (m) bgl	Total number of diatom species in fossil sample	Number of fossil diatom species present in the TP training set	% Sum of diatoms in fossil sample present in the TP training set
1.23	1.25	41	32	95
1.40	1.42	38	31	96
1.50	1.52	50	43	94
1.65	1.67	45	36	91
1.86	1.88	45	37	95
2.40	2.42	34	26	81

Table 2. TP reconstruction for the Ringwood A31 sequence using the Combined European TP dataset. (The R^2 values for the reconstructions vary from 0.76 for the two models with tolerance downweighting and 0.71 for the models without down weighting).

Diatom Sample Top Depth (m) bgl	Diatom Sample Bottom Depth (m) bgl	TP ($\mu\text{g l}^{-1}$) with Inverse Regression model	TP ($\mu\text{g l}^{-1}$) with Classical Regression	TP ($\mu\text{g l}^{-1}$) with Inverse Regression model and Tolerance Downweighting	TP ($\mu\text{g l}^{-1}$) with Classical Regression model and Tolerance Downweighting
1.23	1.25	43.98	44.49	46.42	47.63
1.40	1.42	56.07	62.63	64.09	72.74
1.50	1.52	66.29	79.27	58.65	64.75
1.65	1.67	119.07	180.81	127.78	179.99
1.86	1.88	73.65	91.95	72.07	84.86
2.40	2.42	74.71	93.81	75.56	90.30

There are a range of predicted TP values for each sample between models for diatom-based reconstructions of TP (Table 2). It is not clear here which is the most appropriate to use for the A31 Ringwood diatom assemblages. This variation is seen between Inverse and Classical regression models, with higher predicted values using Classical Regression. There are also differences between these models and their respective variants using tolerance down weighting, where species with a wide range of nutrient tolerance (and therefore less predictive value) are given less weight in the model. However, the reconstructed TP levels are consistently relatively high ($>44 \mu\text{g l}^{-1}$) and similar **trends** are apparent in all the reconstruction models (Figure 3). The reconstructed TP levels are highest in the lower sediments (2.41 m bgl, 1.87 m bgl), reaching a maximum at 1.66 m bgl (in the range 120 to 180 $\mu\text{g l}^{-1}$).

depending on the model chosen). The high levels of TP may be indicative of nutrient enrichment from a variety of possible sources, but the reconstructed TP appears to reflect consistently high background levels. The TP levels remain relatively high but decline in the top 3 samples from around $80 \mu\text{g l}^{-1}$ to about $45 \mu\text{g l}^{-1}$.

The diatom-inferred total phosphorus (TP) values can be compared with nutrient levels defined as follows (Smol 2008):

oligotrophic (TP < $10 \mu\text{g l}^{-1}$), low levels of nutrients and biological productivity;

mesotrophic (TP $10 \mu\text{g l}^{-1}$ – $20 \mu\text{g l}^{-1}$), intermediate levels of nutrient concentration and biological productivity;

eutrophic (TP > $30 \mu\text{g l}^{-1}$), nutrient rich, highly productive.

Comparison with present day and historical nutrient levels reconstructed using diatom-based transfer functions (e.g. Bennion *et al.* 1996; Cameron in Keevil 2004) shows that the values for reconstructed TP in the A31 sequence are consistently high, whichever model for reconstruction is used. The water would be classified as eutrophic (TP > $30 \mu\text{g l}^{-1}$). These high nutrient levels could derive from a range of sources including organic waste from human settlement, animal grazing in the catchment or for example because of the presence of significant bird populations. The highest nutrient levels, recorded by the TP value at 1.66 m bgl, appear to be driven largely by the maximum of the epiphytic species *Cocconeis placentula* that has a high TP growth optimum of $132 \mu\text{g l}^{-1}$ and comprises 26% of the assemblage at 1.66 m bgl. The radiocarbon results place 1.66 m bgl within the Early Medieval period (AOC 2023).

Conclusions

1. Six samples from the A31 sequence have been analysed for diatoms including 2 new samples not examined during the assessment stage.
2. The diatom assemblages are dominated throughout by freshwater, non-planktonic, shallow-water species from epiphytic, benthic, and other attached habitats. Epiphytic diatoms reflect the importance of the aquatic macrophyte habitat particularly at 1.66 m bgl.
3. Diatoms, notably a group of *Fragilaria* spp. with wide environmental tolerances and the ability to grow rapidly in disturbed habitats are common, particularly in the top part of the sequence. This suggests the presence of unstable, shallow water habitats subject to changes such as fluctuating water levels or variable nutrient levels.
4. Rheophilous diatom species, that are associated with moving water, form a relatively small but consistent component of the assemblages. These flowing water diatoms are less common in the top 2 samples of the sequence perhaps indicating a decrease in flow.

5. Diatom-based TP reconstruction shows consistently high values of TP through the A31 Ringwood sequence. The high TP values may result from input from several possible nutrient sources. There is a maximum of reconstructed TP at 1.66 m bgl.
6. The diatoms do not show evidence of heavy metal contamination at the site.

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