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Shedding light on sporopollenin chemistry, with reference to UV reconstructions

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Abstract

Sporopollenin, which forms the outer wall of pollen and spores, contains a chemical signature of ultraviolet-B flux via concentrations of UV-B absorbing compounds (UACs), providing a proxy for reconstructing UV irradiance through time. Although Fourier transform infrared (FTIR) spectroscopy provides an efficient means of measuring UAC concentrations, nitrogen-containing compounds have the potential to bias the aromatic and hydroxyl bands used to quantify and standardise UAC abundances. Here, we explore the presence and possible influence of nitrogen in UV reconstruction via an FTIR study of Lycopodium spores from a natural shading gradient. We show that the UV-sensitive aromatic peak at 1510 cm⁻¹ is clearly distinguishable from the amide II peak at 1550 cm⁻¹, and the decrease in aromatic content with increased shading can be reconstructed using standardisation approaches that do not rely on the 3300 cm⁻¹ hydroxyl band. Isolation of the sporopollenin results in the loss of nitrogen-related peaks from the FTIR spectra, while the aromatic gradient remains. This confirms the lack of nitrogen in sporopollenin and its limited potential for impacting on palaeo-UV reconstructions. FTIR is therefore an appropriate tool for quantifying UACs in spores and pollen, and information on UV flux should be obtainable from fossil or processed samples.

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1. Introduction

Pollen and spores (collectively sporomorphs), the reproductive vectors of land plants, contain a chemical signature of prevailing ultraviolet-B flux that can be used as a proxy for reconstructing UV-B through time (Rozema et al., 2009; Fraser et al., 2014a). Plant tissues contain UV-B absorbing compounds (UACs), a natural sun block that protects the cellular machinery from the harmful effects of UV-B (Rozema et al., 2009; Lomax et al., 2008; Fraser et al., 2014a). Plant tissues contain UV-B absorbing compounds (UACs), a natural sun block that protects the cellular machinery from the harmful effects of UV-B (Rozema et al., 2009; Lomax et al., 2008; Fraser et al., 2014a). Plant tissues contain UV-B absorbing compounds (UACs), a natural sun block that protects the cellular machinery from the harmful effects of UV-B (Rozema et al., 2009; Lomax et al., 2008; Fraser et al., 2014a). Plant tissues contain UV-B absorbing compounds (UACs), a natural sun block that protects the cellular machinery from the harmful effects of UV-B (Rozema et al., 2009; Lomax et al., 2008; Fraser et al., 2014a). Plant tissues contain UV-B absorbing compounds (UACs), a natural sun block that protects the cellular machinery from the harmful effects of UV-B (Rozema et al., 2009; Lomax et al., 2008; Fraser et al., 2014a). Plant tissues contain UV-B absorbing compounds (UACs), a natural sun block that protects the cellular machinery from the harmful effects of UV-B (Rozema et al., 2009; Lomax et al., 2008; Fraser et al., 2014a). Plant tissues contain UV-B absorbing compounds (UACs), a natural sun block that protects the cellular machinery from the harmful effects of UV-B (Rozema et al., 2009; Lomax et al., 2008; Fraser et al., 2014a). Plant tissues contain UV-B absorbing compounds (UACs), a natural sun block that protects the cellular machinery from the harmful effects of UV-B (Rozema et al., 2009; Lomax et al., 2008; Fraser et al., 2014a). Plant tissues contain UV-B absorbing compounds (UACs), a natural sun block that protects the cellular machinery from the harmful effects of UV-B (Rozema et al., 2009; Lomax et al., 2008; Fraser et al., 2014a). Plant tissues contain UV-B absorbing compounds (UACs), a natural sun block that protects the cellular machinery from the harmful effects of UV-B (Rozema et al., 2009; Lomax et al., 2008; Fraser et al., 2014a). Plant tissues contain UV-B absorbing compounds (UACs), a natural sun block that protects the cellular machinery from the harmful effects of UV-B (Rozema et al., 2009; Lomax et al., 2008; Fraser et al., 2014a). Plant tissues contain UV-B absorbing compounds (UACs), a natural sun block that protects the cellular machinery from the harmful effects of UV-B (Rozema et al., 2009; Lomax et al., 2008; Fraser et al., 2014a). Plant tissues contain UV-B absorbing compounds (UACs), a natural sun block that protects the cellular machinery from the harmful effects of UV-B (Rozema et al., 2009; Lomax et al., 2008; Fraser et al., 2014a). Plant tissues contain UV-B absorbing compounds (UACs), a natural sun block that protects the cellular machinery from the harmful effects of UV-B (Rozema et al., 2009; Lomax et al., 2008; Fraser et al., 2014a). Plant tissues contain UV-B absorbing compounds (UACs), a natural sun block that protects the cellular machinery from the harmful effects of UV-B (Rozema et al., 2009; Lomax et al., 2008; Fraser et al., 2014a). Plant tissues contain UV-B absorbing compounds (UACs), a natural sun block that protects the cellular machinery from the harmful effects of UV-B (Rozema et al., 2009; Lomax et al., 2008; Fraser et al., 2014a).

Sporopollenin, which forms the outer wall of pollen and spores, contains a chemical signature of ultraviolet-B flux via concentrations of UV-B absorbing compounds (UACs), providing a proxy for reconstructing UV irradiance through time. Although Fourier transform infrared (FTIR) spectroscopy provides an efficient means of measuring UAC concentrations, nitrogen-containing compounds have the potential to bias the aromatic and hydroxyl bands used to quantify and standardise UAC abundances. Here, we explore the presence and possible influence of nitrogen in UV reconstruction via an FTIR study of Lycopodium spores from a natural shading gradient. We show that the UV-sensitive aromatic peak at 1510 cm⁻¹ is clearly distinguishable from the amide II peak at 1550 cm⁻¹, and the decrease in aromatic content with increased shading can be reconstructed using standardisation approaches that do not rely on the 3300 cm⁻¹ hydroxyl band. Isolation of the sporopollenin results in the loss of nitrogen-related peaks from the FTIR spectra, while the aromatic gradient remains. This confirms the lack of nitrogen in sporopollenin and its limited potential for impacting on palaeo-UV reconstructions. FTIR is therefore an appropriate tool for quantifying UACs in spores and pollen, and information on UV flux should be obtainable from fossil or processed samples.

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−3300 cm$^{-1}$, since this is internally stable in FTIR sporopollenin spectra (Watson et al., 2007; Lomax et al., 2008).

FTIR provides an efficient, economic, and non-destructive means of accumulating large data sets to assess sporomorph chemistry, enabling proxy development. However, there are possible confounding factors in measuring UAC concentrations from FTIR spectra. In particular, the presence of nitrogen-containing compounds may bias measurement of the 1510 cm$^{-1}$ aromatic peak (Rozema et al., 2009). Nitrogen is known to occur in proteins in sporomorphs, and occurs in vibrational spectra through amide groups that represent the protein backbone, and other bonds that relate to specific amino acid side-chains (Barth and Zscherp, 2002; Schulte et al., 2008).

Of particular relevance is the position of the amide II band in sporomorph vibrational spectra. This band results primarily from the out-of-phase combination of NH bending and CN stretching (Barth and Zscherp, 2002; Miller, 2003), and typically occurs at $\sim 1550$ cm$^{-1}$ but can also be present at sufficiently low wavenumbers (Miller, 2003) to be conflated with, or impact upon, the 1510 cm$^{-1}$ aromatic peak. The amino acid tyrosine, which has previously been identified in pollen grains (Schulte et al., 2008), also occurs as an aromatic peak at $\sim 1517$ cm$^{-1}$ (Barth and Zscherp, 2002), within the frequency range of the UAC peak. The height of the 3300 cm$^{-1}$ hydroxyl band that is used to normalise the 1510 cm$^{-1}$ aromatic peak may also be influenced by amide groups, either from the amide A and B bands, which represent NH stretching and occur at $\sim 3300$ and 3170 cm$^{-1}$ (Barth and Zscherp, 2002; Miller, 2003; Rozema et al., 2009), respectively, or through overtones of the amide II band (Miller, 2003). It has been suggested (Rozema et al., 2009) that the aromatic/hydroxyl ratio may relate partly to sporopollenin macromolecular structure, rather than UAC concentrations.

Critical to understanding the influence of nitrogen on UAC quantification is the location of nitrogen-containing compounds within sporomorphs. Proteins are known to occur in the cytoplasm and in compounds external to the sporomorph wall (Traverse, 2007; Pummer et al., 2012; Pummer et al., 2013), but GC–MS analysis of sporopollenin itself has not yielded nitrogen-containing compounds (Watson et al., 2007; Mackenzie et al., 2015). If this is the case the influence of nitrogen on FTIR spectra should be limited when applied to fossil or processed sporomorphs where only the sporopollenin component remains. However, the impact of nitrogen has not been explicitly studied across a UV-B gradient, and this and other potential confounding effects need to be understood for the successful analysis of both modern (experimental and herbarium) and fossil samples.

Here, we address these issues by re-analysing the FTIR dataset of Fraser et al. (2011), which documents statistically significant changes in the UAC concentrations of Lycopodium annotinum Linnaeus spores across a natural shading gradient. Specifically, we:

1. Attempt to identify both amide and UAC peaks in the FTIR spectra.
2. Study changes in the 1510 cm$^{-1}$ aromatic peak height across the shading gradient, from spectra that have been standardised to zero mean and unit variance (i.e. z-scores; Jardine et al., 2015). This standardisation approach removes the effect of sample thickness on the peak heights, and so does not rely on normalising against the 3300 cm$^{-1}$ hydroxyl band. This allows us to determine whether the previously reconstructed UAC gradient (Fraser et al., 2011) is still present without the influence of the hydroxyl band.
3. Compare the spectra of untreated and acetylated spores. Acetylation is an oxidation technique that efficiently removes all of the non-sporopollenin components of sporomorphs, including the cytoplasm, inner wall, and outer proteins and lipids (Traverse, 2007; Jardine et al., 2015). This allows us to determine whether the amide peaks remain following acetylation and therefore the likely influence of nitrogen-containing compounds on UAC measurement in fossil or processed sporomorphs.

2. Materials and methods

The published FTIR dataset of Fraser et al. (2011) comprises samples of Lycopodium annotinum spores from Abisko, Sweden (68° 21′ N, 18° 49′ E). The samples were collected in September 2006 from six plants: three in the full shade of the tree canopy (samples E10-6A, E10-6B and E10-6C), two in partial shade at the forest margin (samples E10-5A and E10-5B), and one under open sky (sample E10-7B). The Fraser et al. (2011) dataset comprises five replicate FTIR spectra from each sample, except for sample E10-6A where four replicates were analysed. We have used the same samples to carry out FTIR analysis of acetylated spores.

The spore exine was isolated by acetylating the samples for 10 min at 90°C in a water bath, using a standard preparation of nine parts acetic anhydride ([CH₃CO]O) to one part sulfuric acid (H₂SO₄) (Faegri and Iversen, 1989). After 10 min the centrifuge tubes were topped up with glacial acetic acid (CH₃COOH) to stop the reaction, centrifuged and the supernatant decanted. The centrifuge tubes were then topped up with water, centrifuged and decanted a further three times.

FTIR analysis of the acetylated spores was carried out using the same equipment and protocol as in the original study (Fraser et al., 2011). Specifically, we used a Thermo Scientific (Waltham, MA, USA) Nicolet Nexus FTIR bench unit with a Continuum IR microscope fitted with a MCT-A liquid nitrogen-cooled detector in transmission mode using a Reflechromat 15 × objective lens. To remove atmospheric H₂O and CO₂ interference within spectra the entire system (bench unit, microscope and sample stage) was purged with air that has been dried and scrubbed of CO₂ using a Peak Scientific (Billerica, MA, USA) ML85 purge unit. We collected five replicate scans for each sample, using an aperture size of 100 × 100 μm at 512 scans per replicate and a resolution of 1.928 cm$^{-1}$ wavenumbers. A background scan was taken before each analytical run and automatically subtracted from the sample spectrum.

All data manipulation and analysis was carried out in R version 3.2.1 (R Development Core Team, 2015). Baseline drift was corrected for by subtracting a linear baseline from each sample. Baseline removal was carried out using the R package ‘baselinel1.2–0’ (Liland and Mevik, 2015) with the ‘modpolyfit’ method, which fits the baselines by least squares polynomial curve fitting, in this case with a first-order polynomial baseline (Lieber and Mahadevan-Jansen, 2003). Following baseline correction, each spectrum was standardised to zero mean and unit variance (z-scores) using the equation $(x − \bar{x}) / \sigma$, where $x$ is the absorbance value, $\bar{x}$ is the spectrum arithmetic mean, and $\sigma$ is the spectrum standard deviation.

For each standardised FTIR spectrum the heights of the 1510 cm$^{-1}$ aromatic peak and the 3300 cm$^{-1}$ hydroxyl peak were measured. Peak heights were measured by taking the maximum value within a given range, which was 1505 to 1525 cm$^{-1}$ for the aromatic peak, and 3190 to 3550 cm$^{-1}$ for the hydroxyl peak. For comparison with the standardised peak heights both peaks were also measured in the baseline corrected, unstandardised spectra, and the aromatic/OH ratio calculated. The statistical significance of differences in peak heights among the three shading levels was assessed with non-parametric Kruskal-Wallace tests (Hammer and Harper, 2006). Other bands were assigned to functional groups and sporomorph components (i.e., sporopollenin, proteins, lipids) using the literature (Coates, 2000; Mayo, 2003; Watson et al., 2007; Schulte et al., 2008; Schulte et al., 2010; Zimmermann, 2010; Fraser et al., 2011; Larkin, 2011; Fraser et al., 2012; Pummer et al., 2013; Fraser et al., 2014b; Zimmermann and Kohler, 2014; Baàcoglu et al., 2015; Zimmermann et al., 2015a; Zimmermann et al., 2015b); those discussed in this paper are summarised in Table 1. All raw spectral data and R code used for data analysis are included in the Supplementary Information.
Table 1
Band assignments for absorbance bands discussed in the text. Interpretation follows the literature (Coates, 2000; Mayo, 2003; Watson et al., 2007; Schulte et al., 2008; Schulte et al., 2010; Zimmermann, 2010; Fraser et al., 2011; Lackin, 2011; Fraser et al., 2012; Pummer et al., 2013; Fraser et al., 2014b; Zimmermann and Kohler, 2014; Başçıoğlu et al., 2015; Zimmermann et al., 2015a; Zimmermann et al., 2015b).

<table>
<thead>
<tr>
<th>Wavenumber (cm(^{-1}))</th>
<th>Band assignment</th>
<th>Interpretation</th>
</tr>
</thead>
<tbody>
<tr>
<td>3300</td>
<td>(\nu)OH</td>
<td>Hydroxyl</td>
</tr>
<tr>
<td>2925</td>
<td>(\nu)sCH(_n)</td>
<td>Aliphatic, lipids and sporopollenin</td>
</tr>
<tr>
<td>2850</td>
<td>(\nu)sCH(_n)</td>
<td>Aliphatic, lipids and sporopollenin</td>
</tr>
<tr>
<td>1740</td>
<td>(\delta)C = O</td>
<td>Lids</td>
</tr>
<tr>
<td>1710</td>
<td>(\delta)C = O</td>
<td>Carboxyl, sporopollenin</td>
</tr>
<tr>
<td>1650</td>
<td>(\nu)C = C</td>
<td>Aromatic, proteins</td>
</tr>
<tr>
<td>1600</td>
<td>(\nu)C = C</td>
<td>Aromatic, sporopollenin</td>
</tr>
<tr>
<td>1550</td>
<td>(\delta)NH, (\nu)C-N</td>
<td>Amide II, proteins</td>
</tr>
<tr>
<td>1510</td>
<td>(\nu)C = C</td>
<td>Aromatic, sporopollenin</td>
</tr>
<tr>
<td>1460</td>
<td>(\delta)CH(_2)</td>
<td>Aliphatic, lipids</td>
</tr>
<tr>
<td>1440</td>
<td>(\delta)CH(_2)</td>
<td>Aliphatic, proteins and sporopollenin</td>
</tr>
<tr>
<td>1265</td>
<td>(\delta)NH, (\nu)C-N</td>
<td>Amide III, proteins</td>
</tr>
<tr>
<td>1160</td>
<td>(\nu)C-H</td>
<td>Aromatic, sporopollenin</td>
</tr>
<tr>
<td>1030</td>
<td>(\nu)C-H</td>
<td>Aromatic, sporopollenin</td>
</tr>
<tr>
<td>853</td>
<td>(\delta)C-H</td>
<td>Aromatic, proteins and sporopollenin</td>
</tr>
<tr>
<td>817</td>
<td>(\delta)C-H</td>
<td>Aromatic, sporopollenin</td>
</tr>
</tbody>
</table>

3. Results

Analysis of FTIR spectra from untreated Lycopodium spores shows that both amide and aromatic peaks are present and identifiable (Fig. 1A and B). The amide I peak, which relates to \(C=O\) stretching and occurs at \(-1650\) cm\(^{-1}\) (Barth and Zscherp, 2002; Miller, 2003; Schulte et al., 2008) is more prominent than the amide II peak at \(1550\) cm\(^{-1}\). The amide III peak, which is the in-phase combination of NH bending and CN stretching (Barth and Zscherp, 2002; Miller, 2003), has previously been identified in Raman spectra at \(-1270\) cm\(^{-1}\) (Schulte et al., 2008) but is not strongly expressed in FTIR (Miller, 2003) and is not identifiable in the Lycopodium spectra. The aromatic peak at \(1510\) cm\(^{-1}\) is clearly detectable, and importantly this peak and the amide II peak are distinguishable from each other.

A number of other peaks identified in previous studies (Watson et al., 2007; Schulte et al., 2008; Schulte et al., 2010; Zimmermann, 2010; Fraser et al., 2011; Fraser et al., 2012; Pummer et al., 2013; Fraser et al., 2014b; Zimmermann and Kohler, 2014; Başçıoğlu et al., 2015; Zimmermann et al., 2015a; Zimmermann et al., 2015b) can be identified in the Lycopodium spectra (Fig. 1A and B, Table 1). Peaks relating to \(C=C\) or \(C=H\) bonds in aromatic ring structures (Coates, 2000) are present at \(1510\) cm\(^{-1}\), \(1550\) cm\(^{-1}\), and \(1460\) cm\(^{-1}\), in addition to the aromatic peak at \(1650\) cm\(^{-1}\). A carbonyl (\(C = O\)) band at \(1740\) cm\(^{-1}\) and an aliphatic (\(CH\(_2\)) band at \(1460\) cm\(^{-1}\) represent lipids (Başçıoğlu et al., 2015). Prominent \(\nu\)sCH\(_n\) and \(\nu\)sCH\(_n\) aliphatic peaks also occur at \(2925\) and \(2850\) cm\(^{-1}\), respectively. Carbohydrates occur as small peaks in the \(1200\) to \(900\) cm\(^{-1}\) range (Başçıoğlu et al., 2015).

The distributions of peak height measurements within samples are shown as box plots (Fig. 2) while the shading treatment medians are displayed in bar charts (Fig. 3). Peak heights from the standardised spectra show that the \(1510\) cm\(^{-1}\) aromatic peak (Figs. 2A and 3A) responds as expected across the shading gradient, with a statistically significant (\(H = 6.62, df = 2, p = 0.037\)) decrease in height with increased shading, consistent with earlier findings (Fraser et al., 2011). The hydroxyl peak shows no clear relationship with shading level (Figs. 2C and 3C; \(H = 1.49, df = 2, p = 0.48\)). Standardising the aromatic peak by the hydroxyl peak (Figs. 2E and 3E) shows the same overall relationship as the z-score standardised peak height (Figs. 2A and 3A), with a significant decrease in peak height ratio across the shading gradient (\(H = 10.23, df = 2, p = 0.006\)).
Acetolysis leads to a simplification of the FTIR spectra, with a number of peaks reducing in size or disappearing altogether (Fig. 1C and D). While the 1510 cm\(^{-1}\) aromatic peak remains distinct the amide I and II peaks are reduced in height, to the extent that they almost completely disappear from the spectrum. Acetolysis also reduces or removes other peaks relating to lipids, carbohydrates, and aromatic compounds (Fig. 1C and D). The vsCH\(_2\) and vsCH\(_3\) aliphatic peaks at 2925 and 2850 cm\(^{-1}\) are reduced in height, the 1460 cm\(^{-1}\) peak almost disappears, but a broad absorbance band remains at 1440 cm\(^{-1}\). The 1740 cm\(^{-1}\) carbonyl peak disappears, and the small carbohydrate peaks in the 1200 to 900 cm\(^{-1}\) region are also removed. The aromatic peak at 850 cm\(^{-1}\) disappears, and an aromatic peak at 1600 cm\(^{-1}\) (Fraser et al., 2014b; Jardine et al., 2015) emerges. A carboxyl peak at 1710 cm\(^{-1}\) also emerges following acetolysis, as does a prominent peak at 1030 cm\(^{-1}\) which is only weakly apparent in the fresh material, and probably represents ferulic acid (Bağcioğlu et al., 2015). The peaks at 1370 and 1160 cm\(^{-1}\) remain in a simplified form. The shape of the hydroxyl absorbance band at ~3300 cm\(^{-1}\) also changes, with the main peak shifting to higher wavenumbers.

Box plots and bar charts of peak heights for the acetolysed spores show that the aromatic gradient is still present after acetolysis (Figs. 2B and 3B), with a significant difference in median peak height among the shading levels (\(H = 9.46, df = 2, p = 0.009\)). The hydroxyl peak (Figs. 2D and 3D) shows slightly more variability compared to the fresh material (Figs. 2C and 3C), but the range of values is still similar across the shading gradient and the difference in peak height is not statistically significant (\(H = 2.52, df = 2, p = 0.28\)). Standardising the aromatic peak by the hydroxyl peak (Figs. 2F and 3F) leads to a similar reconstruction to the z-score standardised aromatic peak (Figs. 2B and 3B), and the difference among shading levels is again significant (\(H = 6.44, df = 2, p = 0.04\)). Importantly, the overall magnitude of the aromatic peak height decrease from the open to partially and fully shaded samples is similar in the fresh and acetolysed material (~0.25 standard deviations in the z-score standardised spectra, and ~0.1 in terms of the aromatic/hydroxyl ratio [Fig. 3]).
5. Conclusion

We have shown that the presence of nitrogen in the proteins of sporomorphs does not hinder the measurement of UAC concentrations using FTIR. The amide groups are clearly distinct from the UV-B responsive 1510 cm$^{-1}$ aromatic peak, do not alter the height of the hydroxyl band that has been used to normalise the aromatic peak, and are entirely or mostly limited to compounds occurring external to the sporopollenin, and so are of little relevance to studies of fossil sporomorphs. We have also demonstrated that the same phenolic gradient that is present in fresh (i.e., unprocessed) spores and pollen when evaluating sporopollenin chemistry, and the impact of other substances on it, is essential for these activities, and FTIR provides a rapid method for assessing this.

Our results highlight the importance of using the spectra of acetolysed (or otherwise processed) spores and pollen when evaluating sporopollenin chemistry, rather than the spectra of fresh grains. This is important first because strong peaks in the acetolysed spectra, such as the peak at 1030 cm$^{-1}$ (Fig. 1), can be obscured in the fresh spectra. Second, and as already noted, some aromatic and aliphatic peaks relate in part to the labile components outside of the sporopollenin (Pummer et al., 2012; Pummer et al., 2013; Jardine et al., 2015), and are reduced in height when the sporopollenin is isolated. In the current study this is observed in the aromatic peak at 850 cm$^{-1}$ and the aliphatic peaks at 2925 and 2850 cm$^{-1}$, which are reduced with acetolysis. In these cases it is likely that the peaks relate to compounds that occur both within the sporopollenin and external to it, and it is only with the spectra of isolated exines that accurate estimates of sporopollenin chemistry can be derived.

Acknowledgements

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Appendix A. Supplementary data

Supplementary data to this article can be found online at http://dx.doi.org/10.1016/j.revpalbo.2016.11.014.

References


