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Shell palaeoproteomics: First application of peptide mass fingerprinting for the rapid identification of mollusc shells in archaeology

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ABSTRACT

Molluscs were one of the most widely-used natural resources in the past, and their shells are abundant among archaeological findings. However, our knowledge of the variety of shells that were circulating in prehistoric times (and thus their socio-economic and cultural value) is scarce due to the difficulty of achieving taxonomic determination of fragmented and/or worked remains. This study aims to obtain molecular barcodes based on peptide mass fingerprints (PMFs) of intracrystalline proteins, in order to obtain shell identification. Palaeoproteomic applications on shells are challenging, due to low concentration of molluscan proteins and an incomplete understanding of their sequences. We explore different approaches for protein extraction from small-size samples (< 20 mg), followed by MALDI-TOF-MS analysis. The SP3 (single-pot, solid-phase) sample preparation method was found to be the most successful in retrieving the intracrystalline protein fraction from seven molluscan shell taxa, which belong to different phylogenetic groups, possess distinct microstructures and are relevant for archaeology. Furthermore, all the shells analysed, including a 7000-year-old specimen of the freshwater bivalve *Pseudunio*, yielded good-quality distinctive spectra, demonstrating that PMFs can be used for shell taxon determination. Our work suggests good potential for large-scale screening of archaeological molluscan remains.

Significance: We characterise for the first time the peptide mass fingerprints of the intracrystalline shell protein fraction isolated from different molluscan taxa. We demonstrate that these proteins yield distinctive PMFs, even for shells that are phylogenetically related and/or that display similar microstructures.

Furthermore, we extend the range of sample preparation approaches for "shellomics" by testing the SP3 method, which proved to be well-suited to shell protein extraction from small-size and protein-poor samples.

This work thus lays the foundations for future large-scale applications for the identification of mollusc shells and other invertebrate remains from the archaeological and palaeontological records.

1. Introduction

Molluscs have been an important natural resource throughout human history; they were exploited as a foodstuff and their shells were perforated and, presumably, worn as ornaments by both early modern humans [e.g. 1–3] and Neanderthals [e.g. 4]. The tradition of "shell jewelry" continued throughout the Middle and Upper Palaeolithic and further expanded during the Neolithic, when shells were extensively used as a raw material, fashioned into pendants, bracelets and beads of a variety of shapes and types [5]. While research into Palaeolithic ornaments has been especially fruitful, the same cannot be said for later prehistory and historical times [6], despite the growing number of studies at the regional and supra-regional scale, particularly for the European Neolithic (e.g. [7,8]). One line of enquiry concerns the discovery of the diversity of shells used as raw materials by prehistoric societies, and, above all, the reasons behind their choice: was the selection of certain species based on their prestige, material qualities or socio-cultural significance [6,9,10]? Answering these questions could help us to better understand shifting cultural and biological boundaries in the past, to track people's interactions, migrations and mobility, as well as to reconstruct their strategies for adapting to new environments [8,11–13].

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Archaeological shell artefacts, particularly ornaments or tools, are often found heavily fragmented, worked and/or degraded and thus taxonomic identification becomes problematic, if not impossible [14]. This is because most (if not all) morphological features, such as outer surface ornamentations, are usually absent. The microstructural/mineralogical characteristics of the material can only give broad information on the shell type used [15,16], because the most commonly encountered microstructure types, such as nacreous, prismatic and crossed-lamellar, are found across many different mollusc families, chiefly among bivalves and gastropods [17]. The development of different biomolecular tools has advanced research into the origin of small, old and fragmented biological remains from archaeological and paleontological contexts. In particular, in the past decade, ancient protein research (palaeoproteomics) has been extremely successful with respect to collagen-based and keratin-based substrates [18–24], while newer applications include the characterisation of more complex mineralised proteomes, such as those of dental calculus, dental enamel and avian eggshell [16,25–29]. Peptide mass fingerprinting (PMF) by MALDI-TOF has been particularly useful, allowing rapid large-scale screening of artefacts for species identification [30]. However, mollusc shells, and more generally all invertebrate organisms, are still underrepresented in palaeoproteomic studies.

Mollusc shells are organo-mineral nanocomposites of calcium carbonate (calcite and/or aragonite) and a small organic fraction (~0.01–2%) comprising a mixture of proteins, saccharides, lipids and pigments [31]. There are two key features that make shells a very interesting system for ancient protein studies. Firstly, shell protein sequences can vary considerably across taxa [32–34], which is useful when attempting to determine specific molecular "barcodes". Secondly, shells retain a small fraction of their proteins within the mineral crystals. These are known as "intracrystalline proteins" and may represent a so-called 'closed system', remaining inaccessible to environmental contamination and protected from rapid degradation processes (e.g., microbial) and thus persisting over archaeological/geological timescales [35–40].

However, shells are also a challenging substrate for biomolecular studies, partially explaining why "palaeoshellomics" is only just beginning to catch up. The main challenges are due to the low abundance of the intracrystalline proteins and our limited knowledge of shell protein sequences. Firstly, the intracrystalline shell protein fraction, which is typically isolated by a strong bleaching step, represents around 0.001–0.01% of the total shell mass [37]. Nacreous shells such as the freshwater mother-of-pearl mussels (e.g. *Unio* and *Margaritifera*), pearl oysters (*Pinctada*), abalone shells (*Haliotis*) and many others, have a relatively organic-rich framework. These structures are dominated by *inter*crystalline organics, which can constitute up to 1–2% by weight of the total shell [37,41]. In contrast, for crossed-lamellar shells, e.g. *Spondylus, Glycymeris, Cardiidae, Strombus* and some foliated shells, e.g. *Pecten, Crassostrea*, the shell matrix content may be as low as ~0.004% by weight [42–45]. Therefore, considering that sample size is usually a limiting factor for the application of palaeoproteomics to unique archaeological artefacts, sample preparation protocols commonly employed on small samples (typically, < 20 mg) of other biomineralised tissues, e.g. eggshell [26,46,47], may not be adequate for most mollusc shell substrates, and will need to be revised.

Secondly, there is a great diversity of mollusc shell proteins, most of which are currently not fully characterised and thus remain largely unknown [48]. The peculiarity of shell proteins is attested by the fact that they neither carry a simple phylogenetic signal, nor are associated to specific microstructural features [33,49,50]. One of their most prominent characteristics is the presence of repetitive low complexity domains (RLCDs) [34,50], which are made of blocks of several to tens of poly-Ala, poly-Gly and poly-Ser amino acids. Such domains are difficult to cleave with routinely used proteases (e.g. trypsin), thus are often "missed" in proteomic analyses. The presence of different post-translational modifications (such as glycosylation, phosphorylation) may also hinder the detection/characterisation by mass spectrometric analyses [48,51].

This work therefore aimed to develop a simple proteomic approach based on MALDI-TOF mass spectrometry, in order to obtain molecular barcodes for the taxonomic identification of archaeological shell artefacts. The main objectives were:

1) Method development: to test different preparation protocols, which could be used for small-size shell samples (< 20 mg).
2) Application: to explore the viability of generating peptide mass fingerprints (PMFs) for the intracrystalline proteins of different mollusc shell taxa.

To achieve the first objective, three specimens of *Unio pictorum* (Bivalvia, Unionida, Unionidae - freshwater), *Ostrea edulis* (Bivalvia, Ostreida, Ostreidae - marine) and *Spondylus gaederopus* (Bivalvia, Pectinida, Spondylidae - marine) were used in order to develop a suitable method for shell protein extraction and characterisation. These three species are important for archaeological research in the Mediterranean basin and in central-northern Europe. In addition, they represent three different microstructures: aragonitic nacre, calcitic foliated and aragonitic crossed-lamellar. They were also selected on the basis of their bulk amino acid composition: in the dataset reported by ref. [14] (their Figure 3) *Unio* sp. could easily be distinguished from other taxa, while both *Spondylus* and *Ostrea* yielded a more uncertain classification. Our hypothesis was that, by retrieving the peptide mass fingerprints (PMFs) of the intracrystalline shell proteins, more secure taxonomic identification could be achieved, especially as new data on *Spondylus* showed that this mollusc shell has a very distinct protein makeup [45]. This encompasses the second objective of this work, i.e. to apply the optimised preparation method to a further set of shells: *Pecten maximus* (Bivalvia, Pectinida, Pectinidae - marine), *Patella vulgata* (Gastropoda, Patellidae - marine), *Phorcus turbinatus* (Gastropoda, Trochida, Trochidae - marine) and a 7000-year-old archaeological specimen, *Pseudunio auricularius* (Bivalvia, Unionida, Margaritiferidae - freshwater) [52,53]. These taxa were selected as they had been previously tested for their ability to preserve a fraction of intracrystalline proteins, which is stable over archaeological and geological timescales [16,39,40,44,54].

2. Materials and methods

2.1. Samples

2.1.1. Method development

Three bivalve species were studied in order to optimise a suitable method for shell protein analysis, testing different bleaching and protein extraction techniques in small-size samples (< 20 mg):

1) *Spondylus gaederopus* is a Mediterranean bivalve, which belongs to a small family, Spondylidae (order Pectinida), and has a complex microstructure, composed of aragonitic crossed-lamellar and prismatic layers and an upper calcitic foliated layer. The shell was purchased from Conchology, Inc. [55]; it had been collected alive by diving to a depth of 15 m in the area of Saronikos, Greece, in 2010 (as indicated by the vendors);
2) *Unio pictorum* is a freshwater bivalve and belongs to the family Unionidae. Its shell is completely aragonitic, comprising nacreous and prismatic layers. The shell used in this study was collected in a stream close to Izeure (Burgundy, France) by one of the authors (F.M.);
3) *Ostrea edulis* is a marine bivalve, commonly known as the European flat oyster, and belong to the family Ostreidae. The shell is foliated calcitic with the presence of discontinuous chalky lenses. The specimen was collected in northern Jutland (Denmark), and obtained from the personal collection of collaborator Søren H. Andersen [16].

2.1.2. Method application

Three modern shells (specimens from the reference collection of one of the authors, B.D.) and one archaeological shell were studied to evaluate the optimal method for intracrystalline protein extraction and analysis by peptide mass fingerprinting (PMF).

- *Patella vulgata* is a marine gastropod with calcite and aragonite layered in several different microstructures (prismatic, foliated, crossed-lamellar). The intracrystalline shell proteins display a closed-system behaviour [39];
- *Phorcus turbinatus* is a marine gastropod, mainly nacreous (aragonitic) with a thin upper calcitic layer (prismatic and foliated). The intracrystalline protein fraction was observed to behave as a closed system [40,54];
- *Pecten maximus* is a marine bivalve, commonly known as the great scallop. The shell is composed mainly of foliated calcite. *Pecten* shells also retain a small intracrystalline protein fraction that was found to behave as a closed system [44];
- *Pseudunio auricularius* is a freshwater bivalve with a fully aragonitic shell, comprising nacreous and prismatic layers. This specimen comes from the Neolithic site of Isorella, Italy, dated to 5226–5023 cal BCE [16,52,53].

2.2. Analytical procedure: method development

All of the shell samples were already available as fine-grained powders (particle size: 200–500 μm) as they had been used for previous studies [14,16,39,44,45]. The powders represent the bulk fraction of the shell, i.e. where all (or most) microstructural layers are represented.

2.2.1. Bleaching

Bleaching is a vigorous cleaning approach which involves the use of sodium hypochlorite (NaOCl) in order to remove surface contamination and/or weakly bound intercrystalline organics from targeted samples. It is used routinely to treat biomineralised tissues and organisms, such as eggshell, mollusc shell or coral, before ancient protein analysis. Developed originally for amino acid racemization geochronology [36,37] it is also used in shell proteomics in order to reduce the pool of analysed proteins and isolate those that are truly associated to the mineral phase [56].

Unio, Spondylus and *Ostrea* shell powders were carefully weighted and placed in clean eppendorf vials. Twelve 20 mg samples were prepared for each shell (Fig. 1) so that three different bleaching exposures could be tested on four 20 mg aliquots:

1) Mild bleaching: 1 mL of NaOCl (diluted to an approximate concentration of 1.0–1.5%) was added and powders were left to soak for 4 h; this type of bleaching was selected as it was used in a previous palaeoshellomics study [16];
2) Intermediate bleaching: 1 mL of NaOCl (diluted to an approximate concentration of 1.0–1.5%) was added and powders were left to soak for 24 h; this type of bleaching was selected as an intermediate step between the "mild" and "strong";
3) Strong bleaching: 1 mL of NaOCl (concentrated, 10–15%) was added and the powders soaked for 48 h - this step is typically used to isolate the intracrystalline fraction of proteins in mollusc shells [37]. In this paper, for convenience, we refer to this 48-h-bleached fraction as "intracrystalline". However, we note that a series of experiments should be performed for each of the shells separately in order to verify the optimal bleaching times and to test the closed-system behaviour (see e.g. [57]).

After bleaching, all of the samples were thoroughly rinsed with ultrapure water (5 times) and air-dried.

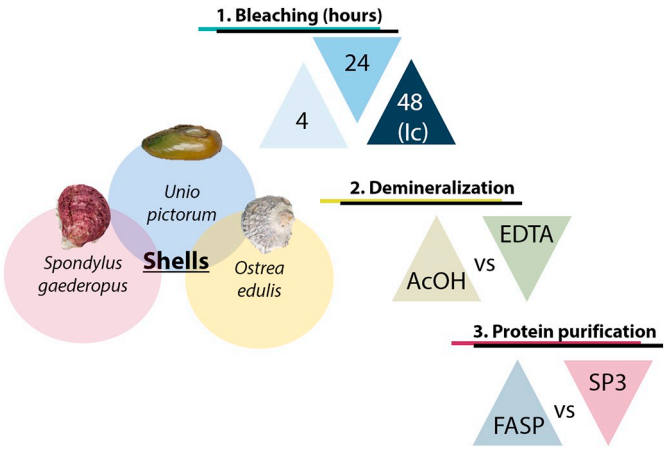

Fig. 1. Scheme showing the different approaches tested for shell protein extraction. "Mild" and "Intermediate" bleaching steps (4 and 24 h) were performed using diluted ~1.0–1.5% NaOCl; "strong" 48-h bleaching was performed using concentrated ~10–15% NaOCl, which isolates the "operational" intracrystalline fraction (Ic). Demineralisation was achieved using 10% acetic acid (AcOH) or EDTA (0.5 M). Two different protein purification methods were evaluated and compared: filter aided sample preparation (FASP) vs single-pot, solid-phase sample preparation (SP3).

Table 1
List of shell protein extraction treatments tested in this study. FASP - filter aided sample preparation; SP3 - Solid-phase sample preparation; for demineralisation, 10% cold acetic acid (AcOH) and 0.5 M EDTA solutions were tested. "Mild" and "intermediate" bleaching steps (4 and 24 h) were carried out using diluted NaOCl (1.0–1.5%), while the "strong" bleaching step (for a duration of 48 h) was carried out to isolate intracrystalline fraction (Ic) using concentrated NaOCl (10–15%).

No.	Method annotation	Bleaching (h)	Demineralisation	Protein purification
1	4hrs_AcOH_FASP	4	AcOH (10%)	FASP
2	24hrs_AcOH_FASP	24		
3	Ic_AcOH_FASP	48 (Ic)		
4	4hrs_EDTA_FASP	4	EDTA (0.5 M)	
5	24hrs_EDTA_FASP	24		
6	Ic_EDTA_FASP	48 (Ic)		
7	4hrs_AcOH_SP3	4	AcOH (10%)	SP3
8	24hrs_AcOH_ SP3	24		
9	Ic_AcOH_ SP3	48 (Ic)		
10	4hrs_EDTA_ SP3	4	EDTA (0.5 M)	
11	24hrs_EDTA_ SP3	24		
12	Ic_EDTA_ SP3	48 (Ic)		

2.2.2. Demineralisation

The bleached powders of each shell were divided into two subsets in order to test two demineralisation approaches (Table 1):

1) Acetic acid: the first set was demineralised with cold acetic acid (10% v/v) adding 100 μL every hour, thoroughly mixing, to a final volume of 300 μL (in the case of *Spondylus*, which was not fully demineralised, an additional 30 μL aliquot was added to obtain complete demineralisation);
2) EDTA: the second set was demineralised with a 0.5 M EDTA solution (Sigma-Aldrich, E7889, pH 8, ~0.5 M) by adding 500 μL to each of the powdered samples and thoroughly mixing with a vortex for ~4 h.

All of the extracts were kept at 4 °C until the protein purification step was carried out.

2.2.3. Protein purification and processing

All of the demineralised shell samples were again divided into two subsets and two separate desalting/protein purification approaches were applied: filter aided sample preparation (FASP) and single-pot, solid-phase sample preparation (SP3) (Table 1).

2.2.3.1. FASP extraction. The extracts were concentrated using PALL Nanosep centrifugal devices (3 kDa, 0.5 mL). For the acetic acid extracts, which resulted in a mixture of acid soluble and acid insoluble matrices (ASM and AIM), these were mixed and loaded to the same centrifugal device to minimise loss due to separate washes. The EDTA extracts were solubilised and homogeneous. The solutions were loaded onto spin filter columns and the samples were concentrated and desalted washing five times with HPLC-grade water (0.5 mL, centrifuging at 11000 rpm, room temperature), before exchanging to buffer (50 mM ammonium bicarbonate, pH 7.5–8). The extracts were reduced using 1 M DL-dithiothreitol (Sigma, Canada) for 1 h at 65 °C, alkylated with 0.5 M iodoacetamide (Sigma, USA) for 45 min at room temperature in the dark and digested with trypsin (0.5 μg, Promega, V5111, proteomics grade) overnight. Digestion was stopped with 10% TFA (to a final TFA concentration of 0.1%), samples were purified using C18 solid-phase extraction tips (Pierce zip-tip; Thermo-Fisher) and evaporated to dryness.

2.2.3.2. SP3 extraction. The samples were processed as described in a previous study [58]. For the EDTA extracts, reduction and alkylation were performed before processing with the SP3 beads, and for the acetic acid extracts it was performed after SP3 extraction and buffer exchange. 8 μL of Sera-Mag SpeedBeads (1:1 mixture of hydrophobic and hydrophilic) were added to each of the extracts. To induce binding, 100% EtOH (HPLC-grade) was added to a final EtOH concentration of 50% and incubated at 24 °C for 5 min at ~1000 rpm. The tubes were then placed on a magnetic rack for separation, the supernatant removed and discarded. The proteins bound to the beads were cleaned with 80% EtOH (3×), exchanged to buffer (50 mM ammonium bicarbonate, pH 7.5–8) and the mixture sonicated for 30 s. After this step, for the EDTA extracts, enzymatic digestion was carried out directly, while for the acidic extracts, reduction and alkylation were performed first. Trypsin was added (0.5 μg, Promega, proteomics grade) for overnight digestion at 37 °C and light shaking was applied (~1000 rpm). Afterwards, the extracts were centrifuged for 1 min, placed on a magnetic rack, the supernatants containing the digested peptides were transferred to separate tubes, acidified with 10% TFA (to a final TFA concentration of 0.1%) and the samples purified using C18 solid-phase extraction tips. Eluted peptides were evaporated to dryness.

Table 1 shows the full list of the twelve different treatments tested for each of the three shells (a total of 36 samples were analysed). Additionally, four blank samples were included in the study (AcOH vs EDTA; FASP vs SP3).

2.3. MALDI-MS analysis

The samples were resuspended in 10 μL TFA solution (0.1%) and 0.7 μL aliquots were mixed with 0.7 μL of α-cyano-4-hydroxycinnamic acid matrix solution (1%, prepared in 50% acetonitrile / 0.1% trifluoroacetic acid (v/v/v)) directly on a MBT Biotarget 96 MALDI plate. All the samples were analysed on a bench-top Microflex LRF MALDI-TOF mass spectrometer (Bruker Daltonics, Germany). Samples were analysed in reflector mode, using the following parameter settings: ion source 1 18.96 kV; ion source 2 16.02 kV; lens voltage 9.05 kV, reflector 20.01 kV, laser power 22–28%. Shell proteomes of *Ostrea edulis* and *Pseudunio auricularius* were analysed with higher laser power (28%) than the rest of the shells (22%). The spectrum collected for each sample resulted from the sum of 1000 laser shots. Mass range was 800–4000 *m/z* and peptide masses below 650 Da were suppressed. The peptide calibration standard (#8206195, Bruker Daltonics, Germany), a mixture of seven peptides (Angiotensin II *m/z* = 1046.541, Angiotensin I *m/z* = 1296.685, Substance_P *m/z* = 1347.735, Bombesin *m/z* = 1619.822, ACTH (1–17 clip) *m/z* = 2093.086, ACTH (18–39 clip) *m/z* = 2465.198 and Somatostatin *m/z* = 3147.471) was used for external mass calibration to maximise mass accuracy. The spectra were exported as text files and further processed using mMass, an open access mass spectrometry interpretation tool [59]. Two spectra were obtained and averaged for each sample. All of the resulting spectra were processed by performing baseline correction (precision: 100%, relative offset: 10–30%) and by smoothing (Savitzky-Golay method, with a window size of 0.3 *m/z*, 1.5 cycles). Peak picking was performed selecting an S/N threshold ≥6, picking height of 100% and deisotoping using standard mMass parameters. Internal mass calibration was carried out using trypsin, keratin and matrix *m/z* values (reported in Supplementary material 1). All the spectra are reported in Supplementary material 1.

2.4. PMF library preparation

For marker peaks identification, samples were extracted in duplicate using the Ic_EDTA_SP3 method. Any *m/z* values corresponding to common laboratory contaminants (i.e. keratin, trypsin, α-cyano MALDI matrix) were excluded from data interpretation (mass tolerance for peak matching: 0.1 Da). Furthermore, in order to ensure that all possible contaminants were taken into account, *m/z* values identified in blank samples (four samples prepared with the AcOH/EDTA and FASP/SP3 methods) were added to the common contaminants peak list, which was then used to exclude these values from samples PMFs. Finally, each shell spectrum was checked manually for additional recurring peaks, i.e. if the same peak was observed in most shell spectra, it was not taken into account; these might be genuine shell peptides and not contamination, but their occurrence across taxa would prevent their use as "markers". We note that shell protein sequences can be very different in phylogenetically distant taxa, therefore there is a high probability that recurring *m/z* values do not represent the same peptide but different, isobaric, sequences. The full list of identified contaminant peaks is presented in Supplementary material 2.

2.5. Method application

For the four shells included in this part of the study (*Phorcus, Patella, Pecten* and archaeological *Pseudunio*), the intracrystalline shell proteins were extracted using the optimal method, noted as Ic_EDTA_SP3 (Table 1, method no. 12). In brief, intracrystalline proteins were isolated after 48 h of bleaching with concentrated NaOCl (10–15%). Powders were demineralised using EDTA and proteins were extracted and purified using the SP3 method. Enzymatic digestion, peptide desalting and MS analyses were carried out as detailed in Sections 2.2.3 and 2.3.

3. Results and discussion

The first part of the results and discussion section aims to assess the most suitable approach for extracting shell proteins for peptide mass fingerprint (PMF) characterisation. In the second part we show the applicability of the optimised method to a wider variety of molluscan taxa, including an archaeological specimen. Finally, the PMFs for the different shell taxa are presented.

3.1. Method development

For shell proteomics by MALDI-TOF, different bleaching, demineralisation and protein purification steps were evaluated on three molluscan taxa (Fig. 1, Table 1). We note that the conditions needed to isolate the intracrystalline protein fraction in shells may differ for each species and should be tested individually. However, as the future scope

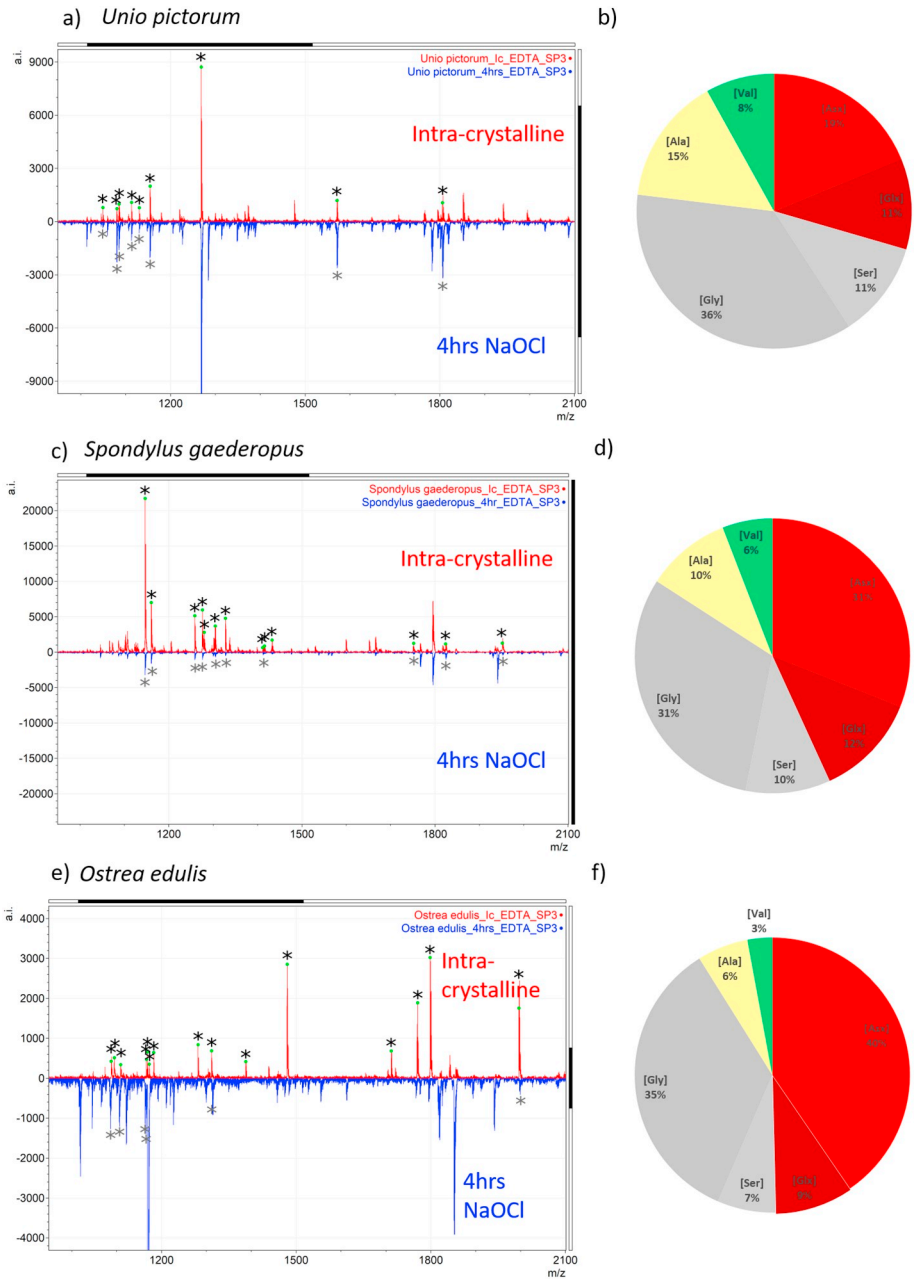

Fig. 2. *Unio pictorum, Spondylus gaederopus* and *Ostrea edulis* (inter + intra)crystalline vs intracrystalline (Ic) peptide mass fingerprints (PMFs) (a, c, e) and bulk amino acid (AA) compositions corresponding to the Ic fraction (b, d, f) obtained from previously published work [14]. Intracrystalline proteins (Ic) isolated by "strong bleaching" are shown in red and (inter + intra)crystalline proteins, obtained via "mild" bleaching, are shown in blue. Asterisks indicate the marker peptides for these shells. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

of this project is to create a large library of "intracrystalline PMFs", in this work, we give an "operational" definition of the "intracrystalline" proteins as the fraction which can be isolated via a 48-h bleaching step using concentrated NaOCl (~12%). Previous studies have shown that this treatment to be effective for all shell taxa tested thus far, regardless of their age (modern vs fossil) or provenance [14,36–40,45,57].

3.1.1. Intracrystalline shell proteins and effect of bleaching

Mollusc shell proteins were successfully isolated, extracted and characterised by MALDI-TOF-MS from all three samples - *Unio, Spondylus* and *Ostrea* (Fig. 2). Comparing the PMFs of the intracrystalline shell protein fraction (Fig. 2a, c, e; spectra in red) and the fraction obtained via "mild" bleaching (spectra in blue), we note that the two spectra are very similar only for *Unio* (Fig. 2a), while for *Spondylus* and *Ostrea* (Fig. 2c, e), the spectra of the fraction obtained after "mild" bleaching were of lower quality. This was particularly evident for *Spondylus* (Fig. 2c), for which the PMF of the Ic fraction was significantly better than that obtained from both the 4-h (Fig. 2c, in blue) and the 24-h bleached samples (Supplementary material 1). Therefore, the "strong bleaching" step is preferable for the isolation and characterisation of shell proteins by MALDI-TOF-MS. Importantly, *Unio, Spondylus* and *Ostrea* yielded individual intracrystalline PMFs (Fig. 2a, c, e), and we find that most of the potential marker peaks for these shells appear in the 1000–2000 *m/z* range. The corresponding bulk amino acid compositions are presented as pie charts next to the spectra (Fig. 2b, d, f) and clearly show that the differences in PMFs are far more evident than the differences in relative amino acid composition.

The results showed that intracrystalline PMFs can be obtained from

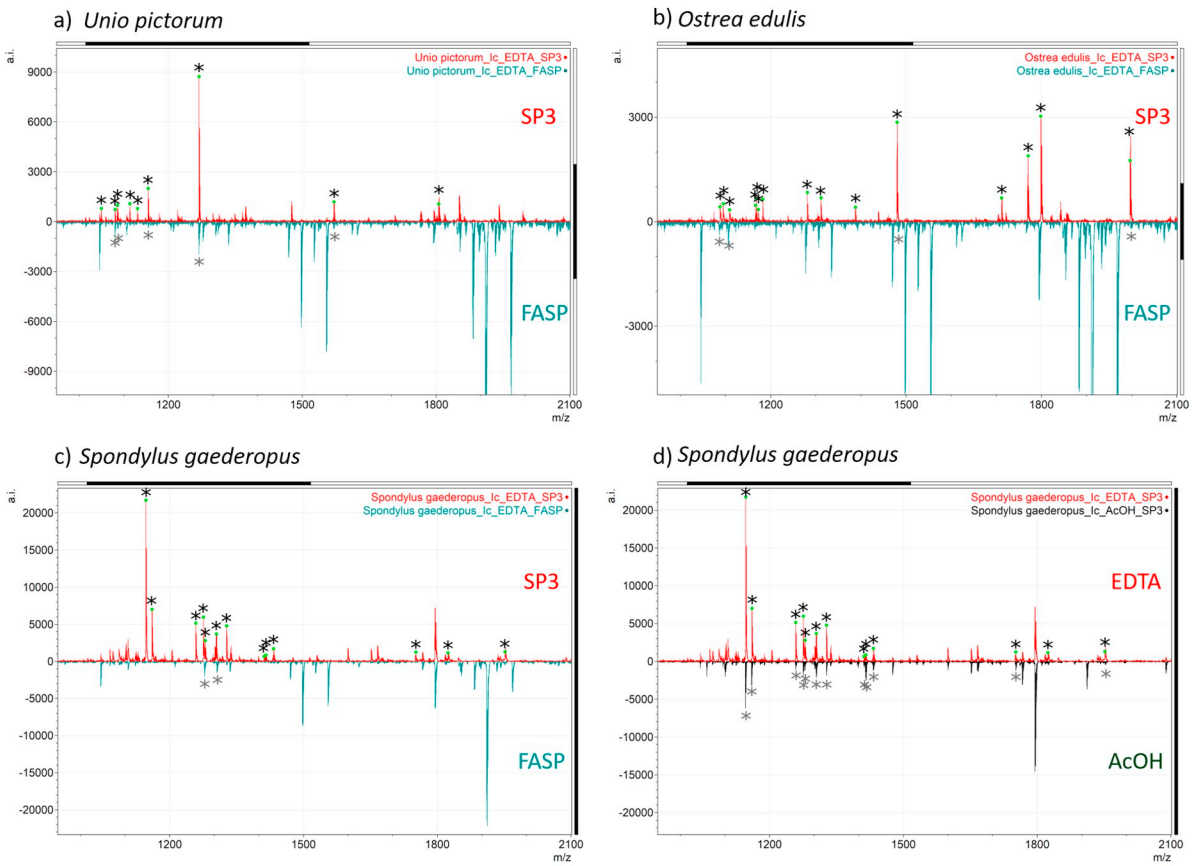

Fig. 3. Peptide mass fingerprints (PMFs) of the intracrystalline shell protein fraction extracted from *Spondylus gaederopus, Unio pictorum* and *Ostrea edulis.* Spectra a-c show PMFs of a) *Unio*, b) *Spondylus* and c) *Ostrea,* obtained by single-pot, solid-phase sample preparation (SP3, in red) or filter aided sample preparation (FASP, in green). *Spondylus* spectra in d) compare the demineralisation with EDTA (red) and AcOH (dark green). Asterisks indicate the marker peptides identified for these shells. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

20 mg shell samples, regardless of their different microstructures (nacreous, crossed-lamellar, foliated) and their variable organic content: even the most organic-poor microstructure (i.e. crossed-lamellar in *Spondylus*) retained a sufficient fraction of Ic proteins.

Furthermore, we did not observe any simple correlation between bleaching time/NaOCl concentration and the number of potential marker peptides - i.e. shorter bleaching times do not imply better MALDI-TOF spectra and, vice versa, harsh bleaching treatments do not necessarily mean that protein concentrations will be too low for proteomics. This is interesting as many "shellomics" studies encourage bleaching as a cleaning pretreatment [56], but generally avoid higher concentrations of NaOCl and longer exposure times, presuming that shell proteins would be fully hydrolyzed. In the case of *Unio*, no compelling difference was observed between the spectra of the (inter + intra)crystalline fraction ("mild" bleaching) and the intracrystalline (Ic) fraction ("strong" bleaching). Remarkably, for *Spondylus*, the intensity and number of potential marker peaks is considerably higher in the intracrystalline fraction compared to the spectra obtained after just 4 h of bleaching, for which the PMFs were barely detectable. This effect has also been observed in other shells [60], including a study of the *Spondylus* proteome by tandem mass spectrometry [45], and may be due to the difficulty of breaking down complex networks of proteins with other shell matrix macromolecules, such as chitin. It is likely that the presence of glycosylated proteins, lipoproteins, phospholipids, or proteins with repetitive low complexity domains (RLCD), could influence signal detection (or suppress it completely) [51,61]. This would explain why a strong oxidative treatment, which removes a large quantity of these macromolecules, may be advantageous in shell protein analyses. In addition, the intracrystalline proteins have more acidic domains, which bind to the mineral [25], and thus are preferentially ionised, therefore their detection is favoured when analysed by MALDI-TOF mass spectrometry.

3.1.2. Extraction and purification

The SP3 method for shell protein isolation and purification was found to be more effective than FASP. The intracrystalline PMFs obtained by SP3 were of better quality and displayed a higher number of marker peaks for *Unio, Ostrea* and *Spondylus* (Fig. 3a-c, spectra in red). On the contrary, in the FASP PMFs, the relative proportion between marker peaks and the trypsin/keratin peaks (common laboratory contaminants) was severely skewed towards the latter (Fig. 3a-c, green spectra). This is probably due to the fact that the (minimal) loss of proteins which occurs during ultrafiltration is especially noticeable for protein-poor samples, with enzymes and common contaminants thus being over-represented in the resulting spectrum. The SP3 extraction is therefore better suited to shell samples [62].

In general, the issue of protein concentration will principally affect MALDI-TOF analyses of proteins from crossed-lamellar and foliated microstructures; for example, a 20-mg *Spondylus* sample may contain as low as ~200 ng of intracrystalline proteins. For nacroprismatic shells, which are generally more organic-rich, we can speculate that 10-15 mg samples should be sufficient for obtaining good-quality PMFs. Obviously, diagenesis will inevitably impact on the limit of detection.

There was no significant difference between the spectra of samples demineralised with EDTA or acetic acid (Fig. 3d), but we note that it was much easier to handle the EDTA extracts because 1) demineralisation with EDTA is less vigorous and 2) EDTA yields fully demineralised extracts, while the acidic decalcification results in two

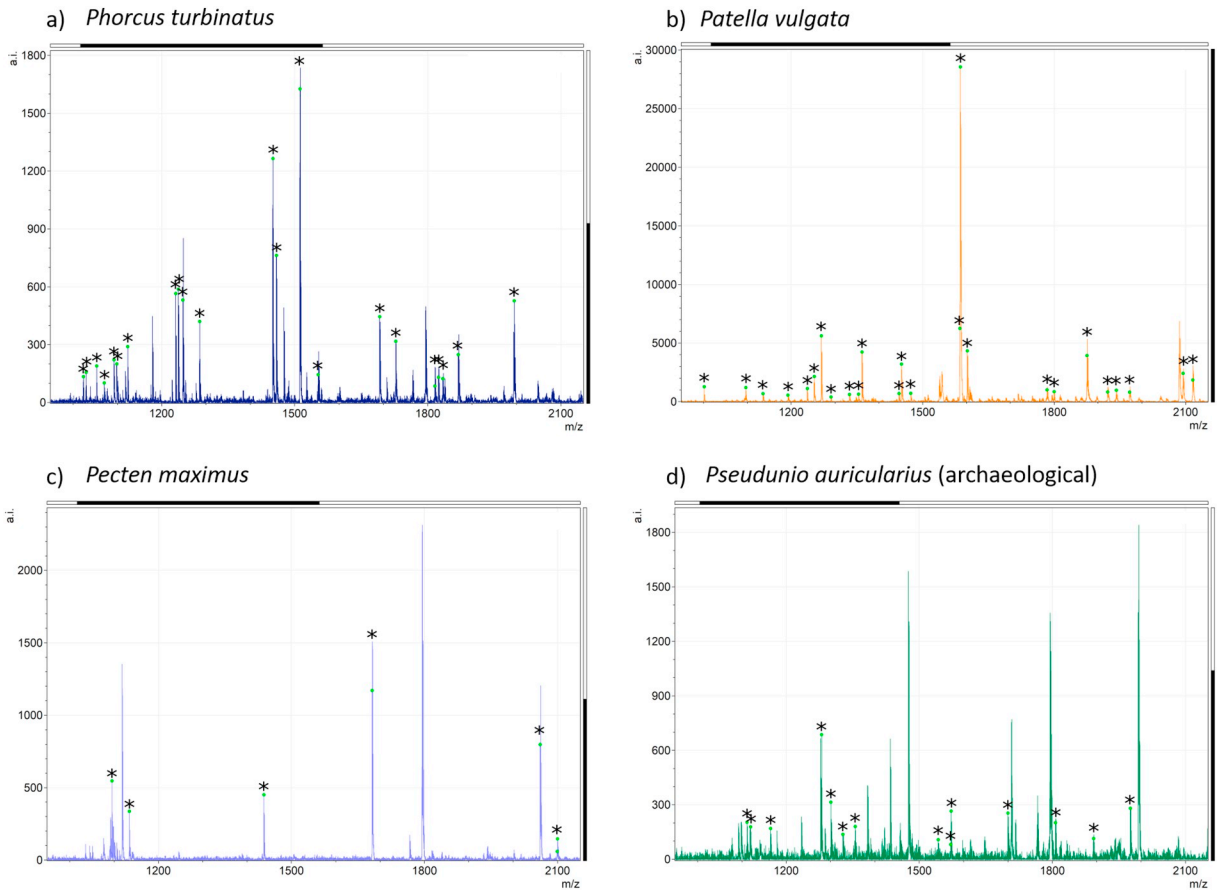

Fig. 4. Intracrystalline PMFs of the four different shell species that were used to validate the protein extraction method (Ic_EDTA_SP3): a) *Phorcus turbinatus* (modern), b) *Patella vulgata* (modern), c) *Pecten maximus* (modern), *Pseudunio auricularius* (Neolithic, 5226–5023 cal BCE). Asterisks indicate the marker peptides identified for these shells.

fractions - the acid soluble (ASM) and acid insoluble (AIM) matrices.

The SP3 method, which had been developed for low-concentration samples [58], showed very good results for shell proteins, and it appeared to be time and cost-effective (for such small-size samples, and assuming similar cost for consumables, the SP3 method is ~25 times cheaper than FASP). To our knowledge this is the first application of SP3 extraction for "shellomics", and it is not yet routinely employed in palaeoproteomics [63]. The efficiency of SP3 was especially visible for "protein-poor" shells such as *Spondylus*. SP3 enabled us to obtain good-quality spectra of the Ic fraction, whereas the same samples extracted by FASP did not show any peptide markers at all. Therefore, SP3 outperforms FASP, a method used in previous studies on molluscan shells and archaeological substrates.

Considering the results of all the tests conducted here, we conclude that the optimal method for shell protein analyses is Ic_EDTA_SP3 (Table 1, method no.12), which consists of three steps:

1) isolation of the intracrystalline protein fraction by bleaching the shell powder for 48 h using concentrated NaOCl (10–15%),
2) demineralisation of the shell powder using EDTA (0.5 M).
3) protein purification by single-pot, solid-phase sample preparation (SP3).

3.2. The application of "palaeoshellomics": Shell PMFs

The extraction approach Ic_EDTA_SP3 was tested on a set of different shells, in order to validate the method. The set included a marine bivalve shell (the scallop *Pecten maximus*), two gastropods (*Patella vulgata* and *Phorcus turbinatus*) and an archaeological freshwater mussel, *Pseudunio auricularius*. Protein extraction was successful for all shells, including the archaeological *Pseudunio*. Fig. 4 shows the PMFs obtained; as noted for *Spondylus, Ostrea* and *Unio* (Fig. 2), most of the marker peptides were observed in the 1000–2000 *m/z* range (Fig. 4a-d, markers represented by asterisks).

Table 2 summarises the peaks that were found to be taxon-specific in this pilot study, i.e. did not pertain to any of the identified laboratory contaminants (see Section 2.4 for more details) and did not occur in any of the other species tested (except for *Unio* and *Pseudunio*, which are phylogenetically close and have similar proteomes, see discussion below). Excluding *m/z* values which may represent genuine shell peptides but which recur in different taxa is a cautious approach, but in the absence of sequence information we are unable to evaluate if these *m/z* values represent identical peptides or different peptides with the same mass, and therefore assess their phylogenetic significance. We hope to revise this information in the future. Nonetheless, the unique peptides were sufficient to discriminate between taxa. The two gastropod shells, *Patella* and *Phorcus,* yielded very distinctive PMFs, with 24 and 18 markers identified respectively. Among the marine bivalves, 6 markers were identified for *Pecten,* 13 markers for *Spondylus* and 15 markers for *Ostrea.* The freshwater mother-of-pearl mussel *Unio* yielded 10 individual markers and 14 peptide markers were identified from the archaeological *Pseudunio* (Table 2). Overall, there is noticeable variation in the number of markers identified per taxon; this may imply that *Pecten* (6 markers) may be more difficult to identify than *Patella* (24 markers) in the archaeological record, as diagenesis is expected to cause the disappearance of some of these markers over time. We are currently conducting artificial diagenesis experiments on *Spondylus* intracrystalline proteins and preliminary data show the persistence of eight (out of

Table 2
Peptide markers (*m/z* values) for *Unio pictorum, Spondylus gaederopus, Ostrea edulis, Phorcus turbinatus, Patella vulgata, Pecten maximus* and *Pseudunio auricularius* (intracrystalline protein fraction). Values in bold indicate shared markers.

	Shells						
Age	Modern						Archaeological
Dominant microstructure	Foliated		Crossed-lamellar		Nacreous		
Mineralogy	Calcitic		Mostly aragonitic (thin upper layer - calcitic)	Calcitic and Aragonitic	Mostly aragonitic (thin calcitic prisms)	Aragonitic	
Taxonomy	Bivalvia, Ostreida, Ostreidae	Bivalvia, Pectinida, Pectinidae	Bivalvia, Pectinida, Spondylidae	Gastropoda, Patellidae	Gastropoda, Trochida, Trochidae	Bivalvia, Unionida, Unionidae	Bivalvia, Unionida, Margaritiferidae
Species	*Ostrea edulis*	*Pecten maximus*	*Spondylus gaederopus*	*Patella vulgata*	*Phorcus turbinatus*	*Unio pictorum*	*Pseudunio auricularius*
Marker *m/z*values	1087.9	1095.5	1146.6	1001.5	1023.5	1049.5	1111.6
	1095.0	1134.6	1160.6	1096.6	1029.6	1080.6	1119.6
	1109.2	1437.7	1258.7	1135.6	1053.5	1085.6	1164.7
	1166.5	1681.8	1275.7	1192.6	1070.5	1113.4	1279.7
	1168.5	2060.9	1279.6	1252.7	1123.6	1130.5	1300.7
	1172.7	2100.0	1304.6	1268.8	1231.7	1154.5	1327.7
	1182.7		1327.7	1290.8	1247.8	1268.5	1355.7
	1281.4		1411.7	1332.8	1285.6	**1570.8**	1542.7
	1311.5		1415.7	1353.8	1450.8	1764.8	**1570.8**
	1387.9		1432.7	1361.8	1458.9	1805.8	1571.8
	1480.1		1751.8	1445.8	1511.9		1699.8
	1711.8		1823.9	1451.7	1552.8		1806.8
	1770.6		1951.9	1472.8	1691.7		1892.9
	1798.5			1584.9	1727.8		1975.9
	1996.3			1585.9	1815.9		
				1601.8	1824.0		
				1783.9	1833.9		
				1799.9	1868.9		
				1874.9			
				1921.9			
				1941.9			
				1972.0			
				2094.0			
				2116.0			

thirteen) peptide markers after 96 h continuous heating at 80 °C and of three after 4800 h (Sakalauskaite et al., unpublished data).

Some interesting observations can be made with regard to the similarities (or lack thereof) of species that are phylogenetically related. For example, the remarkable difference between *Spondylus* and *Pecten* PMFs supports a recent study showing that spondylids may have followed a distinct evolutionary pathway from the other pectinoid molluscs [45]. Furthermore, we identified one marker peak (*m/z* 1570.8), that likely corresponds to a peptide shared by the two Unionida shells (freshwater bivalves) *Unio pictorum* (family Unionidae) and *Pseudunio auricularius* (family Margaritiferidae). We suggest that the peptide at *m/z* 1570.8 (Table 2) belongs to protein Hic74 [64], which was found to be the dominant protein in unionoid shells [16]. The peak can be assigned to peptide sequence EAD(-18.01)DLALLSLLFGGR and it was previously identified by LC-MS/MS analyses.

In summary, distinct PMFs can be obtained for intracrystalline shell proteins for different taxa (Fig. 4). Our suggested extraction approach was effective on 20 mg bleached shell samples of both bivalves (freshwater and marine) and gastropods, regardless of their microstructure. The method was also successful in extracting and characterising proteins from an archaeological sample of *Pseudunio auricularius*.

We highlight that:

1) shells with the same microstructure, e.g. nacre (*Unio/Pseudunio*), foliated (*Pecten/Ostrea),* crossed lamellar (*Patella/Spondylus*), yielded distinct PMFs;
2) species that belong to the same order (e.g. Pectinida: *Pecten/Spondylus*; Unionida: *Unio/Pseudunio*) display different PMFs (with the exception of one marker peak that is likely shared by *Pseudunio* and *Unio*).

4. Conclusions

In this work we find that:

- The most suitable method for mollusc shell protein extraction from small-size samples includes a strong bleaching step (12% NaOCl for 48 h), followed by EDTA demineralisation and SP3 extraction. This is the first application of the SP3 method for "shellomic" studies.
- Using this method, the intracrystalline shell proteins can be successfully extracted and analysed by MALDI-TOF-MS and they yield unique PMFs, which enable us to discriminate between different shell taxa;
- The optimised method was employed to study several modern shells and one archaeological specimen, showing the effectiveness of this approach, regardless of species, microstructure or age of the samples.

Overall, this preliminary work strongly indicates that different molecular barcodes based on PMFs of intracrystalline shell proteins can be obtained from small-size samples and used for taxonomic identification of shells. Importantly, the method was found to be effective on a sub-fossil shell, suggesting excellent potential for archaeological applications. We also highlight current challenges facing "palaeoshellomics". First of all, many shell species, including those that were widely exploited in the past, lack reference sequences at genomic or transcriptomic level. In the future we will build a larger reference dataset of molluscan shell PMFs and test the intra-specific variability by analysing a higher number of specimens per taxon. We also hope to link PMFs to sequence data and thus be able to test patterns of phylogenetic relatedness more rigorously. The second challenge concerns our poor understanding of peptide bond stability over archaeological timescales;

however, artificial diagenesis experiments show that intracrystalline shell proteins yield identifiable PMFs even after prolonged heating. Moreover, previous studies on Neolithic shell ornaments had already demonstrated excellent protein sequence recovery [16].

Fast and reliable molecular identification of shells from archaeological sites could represent an important contribution to archaeological, palaeoenvironmental and geoarchaeological research. Given the challenges above, we are focusing our investigation on taxa that are especially relevant for the study of the past, such as molluscs exploited as a food resource (e.g. oysters, mussels) or as raw materials for making tools and ornaments (e.g. pearl mussels, *Spondylus, Glycymeris*). As an example, in this study we report that *Spondylus* displays a set of unique markers. This is archaeologically significant, because *Spondylus* was one of the most important and prestigious shells in prehistory, with numerous archaeological finds from both Neolithic Europe and pre-Columbian South America [65–68]. However, the majority of presumed *Spondylus* ornaments are poorly preserved and morphologically undiagnostic, therefore our work will allow archaeologists to gain a deeper insight into the circulating "shell economy" of prehistoric times.

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Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.jprot.2020.103920.

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