

Supporting Information

A milk and ochre paint mixture used 49,000 years ago at Sibudu, South Africa

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S4 Text. Chemical analyses

Gas chromatography/mass spectrometry (GC/MS) of the MOD flake

Micro-samples (3.3 mg from the MOD flake and less than 1 mg from the other samples, see below) were collected from the specimens and submitted to an analytical procedure (GC/MS) in order to identify lipids, waxes, proteins, resinous materials and saccharides [1-2]. GC/MS had already been successfully employed for the characterization of organic materials from Border Cave [3].

Reagents

All the solvents were Baker HPLC grade and were used without any further purification. Trifluoroacetic acid (99% purity) and anhydrous pyridine were from Fluka (Milan, Italy). Ethanethiol (ETSH; 99.5%), sodium azide (NaN₃; 99.5%), *N,O*-bis(trimethylsilyl)trifluoroacetamide (BSTFA) with and without 1% trimethylchlorosilane, *N-tert*-butyldimethylsilyl-*N*-methyltrifluoroacetamide (MTBSTFA) with 1% trimethylchlorosilane, 1,1,1,3,3,3-hexamethyldisilazane (HMDS, 99.9%) and triethylamine were from Sigma-Aldrich. The following solutions, apart from those for the amino acids, were prepared by weighing pure substances and were used as standards: (i) amino acid solution in 0.1 M HCl (Sigma-Aldrich) and containing 12.5 µmol/mL of proline (Pro) and hydroxyproline (Hyp) and 2.5 µmol/mL of aspartic acid (Asp), glutamic acid (Glu), alanine (Ala), arginine, cysteine, phenylalanine (Phe), glycine (Gly), hydroxylysine, isoleucine (Ile), histidine, leucine (Leu), lysine (Lys), methionine (Met), serine (Ser), tyrosine (Tyr), threonine, and valine (Val); (ii) solution of fatty and dicarboxylic acids in acetone, containing lauric acid (0.24 mg/g), suberic acid (0.27 mg/g of Su), azelaic acid (0.28 mg/g of A), myristic acid (0.25 mg/g of My), sebacic acid (0.3 mg/g of Se), palmitic acid (0.25 mg/g of P), oleic acid (0.51 mg/g of O), stearic acid (0.51 mg/g of S) [all acids (purity >99%) from Sigma-Aldrich]; (iii) norleucine solution in bidistilled water (Sigma-Aldrich; purity 99%, 138.66 µg/g) was used as a derivatization internal standard for amino acids; (iv) tridecanoic acid solution in isooctane (Sigma-Aldrich; purity 99%, 135.48 µg/g) was used as a lipid-resinous fraction derivatization internal standard; (v) hexadecane solution in isooctane (Sigma-Aldrich; purity 99%, 80.34 µg/g) was used as an injection internal standard; (vi) monosaccharides and uronic acids solution in bidistilled water containing D-(+)-galactose (0.1 mg/g), L-(-)-fucose (0.1 mg/g), L-(+)-arabinose (0.1 mg/g), L-(-)-ramnose (0.1 mg/g), L-(-)-mannose (0.1 mg/g), D-(+)-xylose (0.1 mg/g), D-(+)-glucose (0.1 mg/g), D-glucuronic

acid (0.1 mg/g), D-galacturonic acid (0.1 mg/g) monohydrate; and (xi) mannitol in bidistilled water (0.1 mg/g) was used as a derivatisation internal standard for aldoses and uronic acids. All monosaccharides and uronic acids (purity 99%) were purchased from Sigma-Aldrich (Milan, Italy). All standard solutions were stored at 4 °C.

Analytical procedure and instrumentation

The sample treatment, needed prior to GC/MS analysis, consists in a multistep chemical pre-treatment based on the ammonia extraction of proteins and polysaccharide materials, in order to separate them from lipid and resinous materials. The extraction is then followed by the separation and purification of proteinaceous and polysaccharide materials before hydrolysis. Lipids and resins are saponified/salified separately. Three fractions are generated, derivatised with silylating agents and analyzed separately by GC/MS, thus enabling a quantitative analysis to be performed.

The acidic hydrolysis of proteins and gums and the saponification of lipids were performed using a microwave oven model ETHOS One (High Performance Microwave Digestion System) Milestone (Sorisole, Bergamo, Italy). The GC/MS instrumentation consists of a 6890N Network GC System (Agilent Technologies, Palo Alto, CA, USA) equipped with a PTV injector and coupled to a 5973 MS detector with quadrupole analyser. MS was set with an electron impact ionisation (EI, 70 eV) in positive mode, ion source temperature at 230 °C, scan range of 50-700 m/z, and interface temperature of 280 °C. GC separation was performed using a HP-5MS column (J&W Scientific, Agilent Technologies: stationary phase 5% phenil–95% methylpolysiloxane, 30 m length, 0.25 mm i.d., 0.25 m film thickness) connected to a deactivated fused silica precolumn (J&W Scientific, Agilent Technologies: 2 m length, 0.32 mm i.d.). GC conditions for the lipid-resinous fraction involved the use of the PTV injector in splitless mode at 300 °C; the chromatographic oven was programmed at 80 °C for 2 min isothermal, 10 °C/min up to 200 °C, 4 min isothermal, 6 °C/min up to 280 °C, 40 minutes isothermal; constant He flow 1.2 mL/min, injector temperature 280 °C. GC conditions for the protein fraction involved the PTV injector used in splitless mode at 220 °C; the chromatographic oven was programmed with an initial temperature of 100 °C, isothermal for 2 min, then 4°C/min up to 280 °C, and 280 °C isothermal for 15 min. GC conditions for the saccharide fraction involved the PTV injector used in splitless mode at 250 °C; the chromatographic oven was programmed at 50 °C isothermal for 2 min, 5°C/min up to 190 °C, 190 °C isothermal for 20 min 5 °C/min up to 280 °C, and 280 °C isothermal for 15 min. Structural assignments are based on literature data, NIST and Wiley mass spectra libraries and spectra interpretation.

Analysis of sample D6d MOD: results

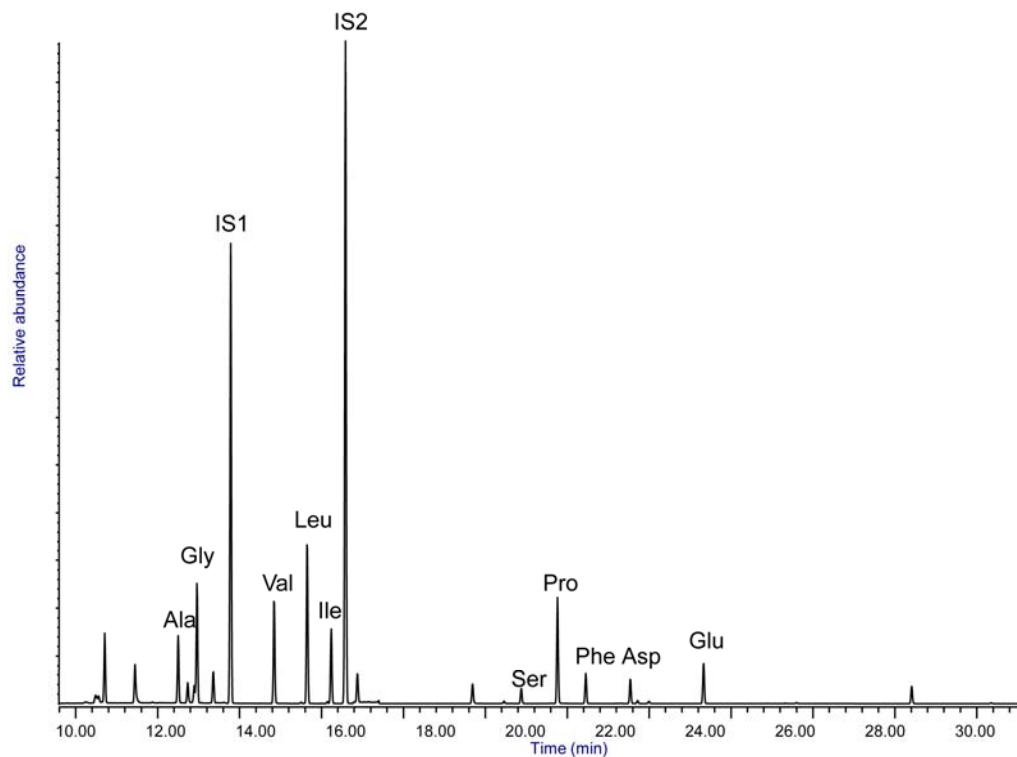


Fig. A. Gas chromatogram of the proteinaceous fraction of sample D6 MOD acquired in SIM mode (Ala = alanine, Gly = glycine, Val= valine, Leu = leucine, Ile = isoleucine, Pro = proline, Phe = phenylalanine, Asp = aspartic acid, Glu = glutamic acid, Hyp = hydroxyproline, IS1 = hexadecane, IS2 = norleucine).

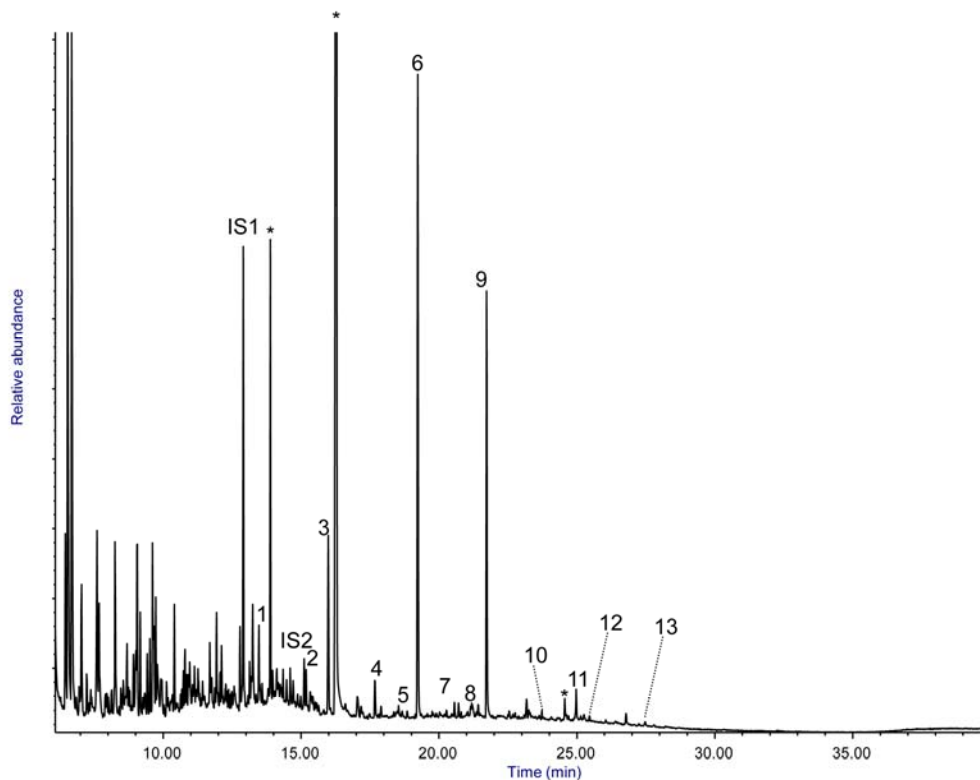


Fig. B. Gas chromatogram of the lipid-resinous fraction of the MOD flake residue (IS1 = hexadecane, IS2 = tridecanoic acid). The peak assignment is given in Table A.

Table A. Peak assignment for Fig. B. Acids and alcohols are identified as their trimethylsilyl (TMS) derivatives.

Peak n°	Retention time (min)	Identified compound
1	13.85	dodecanoic acid (lauric)
2	15.65	α,ω -nonanedioic acid (azelaic)
3	16.54	tetradecanoic acid (myristic)
4	18.24	pentadecanoic acid (also branched)
5	18.83	cis-9-hexadecenoic acid (palmitoleic)
6	19.72	hexadecanoic acid (palmitic)
7	21.02	heptadecanoic acid (also branched)
8	21.42	cis-9-octadecenoic acid (oleic)
9	21.74	octadecanoic acid (stearic)
10	23.73	eicosanoic acid
11	24.97	unknown peak (m/z 217, 315, 371, 463)
12	25.46	docosanoic acid
13	27.48	tetracosanoic acid

GC/MS analysis of samples of Howiesons Poort backed segments and other tools

Six stone artifacts with ochre lines and possible residue in the hafting area have been analyzed using the same procedures applied to the MOD flake. The samples are:

- the backed edge of three Howiesons Poort segments from Sibudu (GR C6c, PGS B5a and GSII B6a, dated between 64.7 ± 2.3 and 61.7 ± 2.0 [4]; Fig. C;
- the backed edge of one segment from Rose Cottage (MAL IH no. 16; described with residues in [5: fig. 2:4);
- the base of a unifacial point in layer Co (C3a CO, final MSA, dated to 38.0 ± 2.6 ka by OSL [6];
- the thick back of a side scraper (from MOD C3a).

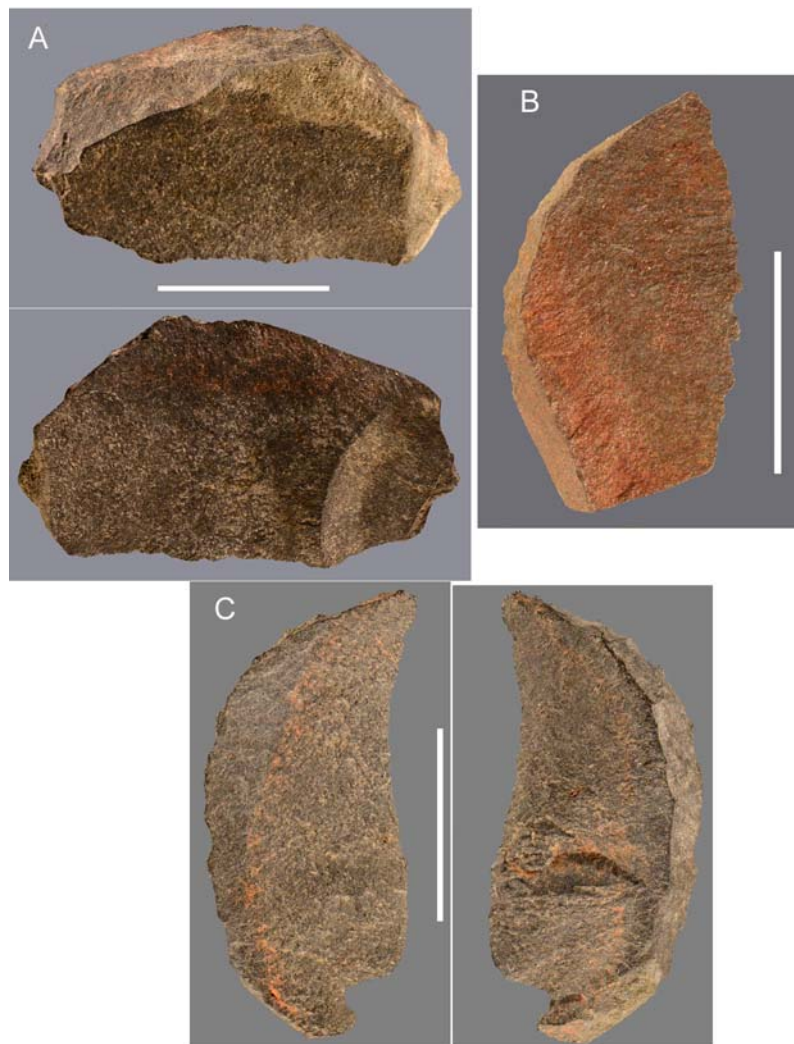


Fig. C. Three backed pieces from the Howiesons Poort layers of Sibudu, all hornfels. (A) PGS B5a no. 69. (B) GR C6c, broken at base. (C) GSII B6a. All three were dipped in solvent prior to analysis but only A and B gave significant results. Scale bar = 1 cm.

All six samples were lightly scraped in the described area. No significant molecular markers of organic material were detected in four samples. Three backed segments, PGS B5a, GR C6c and GSII B6a were then dipped in the extraction solvent for the first step of the combined procedure. Two gave significant results illustrated by Figs. D-E for PGS B5a and GR C6c, respectively. Peak assignment is reported in Table B.

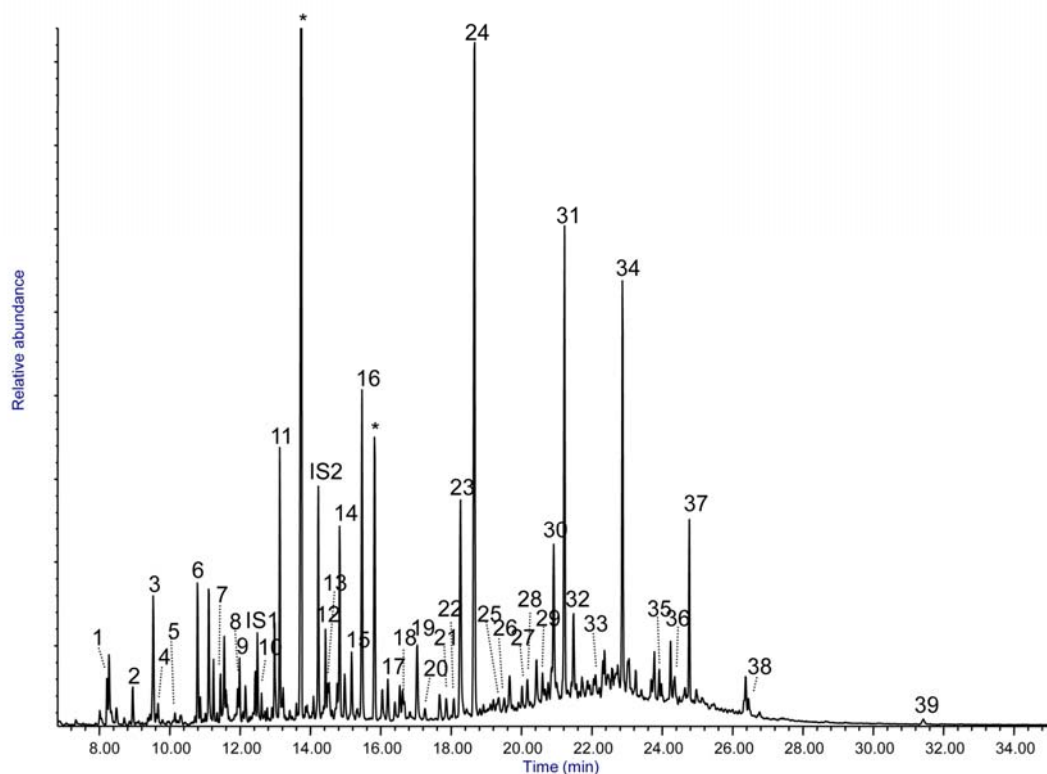


Fig. D. Gas chromatogram of the total lipid-resinous fraction of sample B5a PGS (IS1 = hexadecane, IS2 = tridecanoic acid). Peak assignment is reported in Table B.

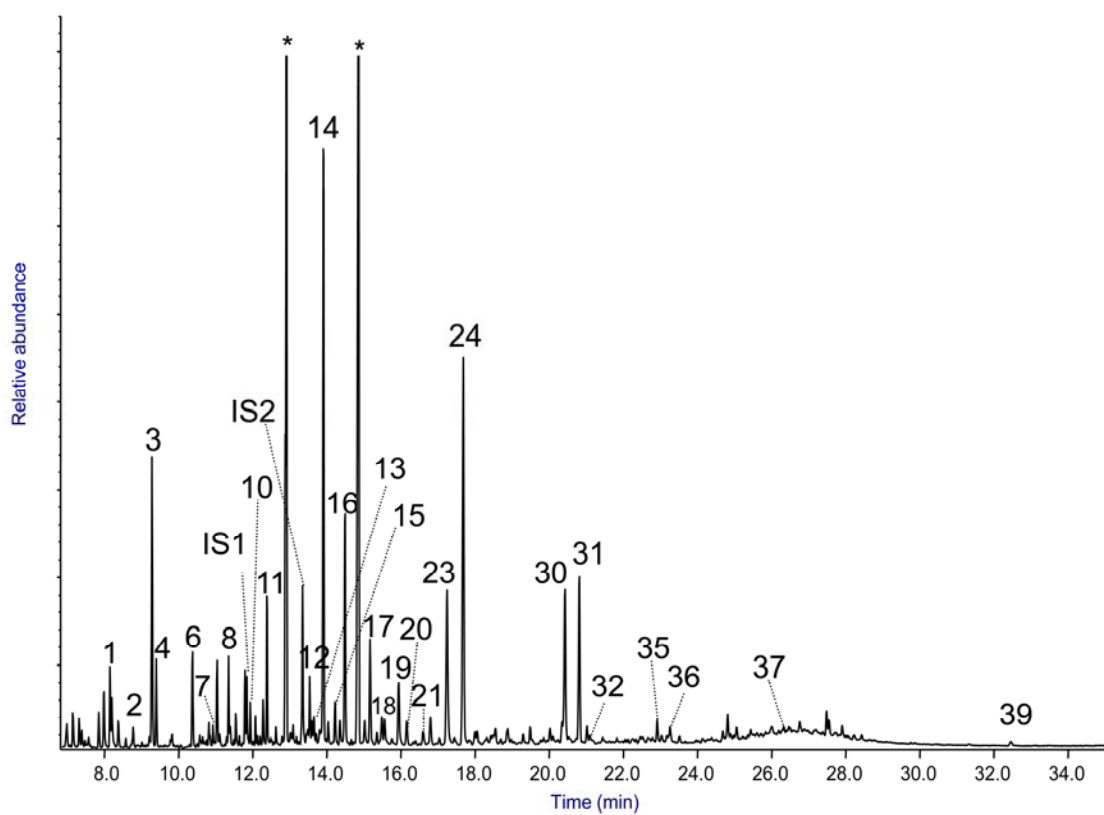


Fig. E. Gas chromatogram of the total lipid-resinous fraction of sample C5c GR (IS1 = hexadecane, IS2 = tridecanoic acid). Peak assignment is reported in Table B.

Table B. Peak assignment for figs. D-E.

Peak #	Tr (min)	Compound	Peak #	Tr (min)	Compound
1	8.29	octanoic acid	20	17.26	hexadecanol
2	8.95	succinic acid	21	17.85	undecandioic acid
3	9.53	nonanoic acid	22	18.08	12-hydroxydodecanoic acid
4	9.68	2-hydroxy heptanoic acid	23	18.27	cis-9-hexadecenoic acid (palmitoleic)
5	10.15	pentanedioic acid (glutaric acid)	24	18.66	hexadecanoic acid (palmitic)
6	10.80	decanoic acid	25	19.35	dodecandioic acid
7	11.44	hexanedioic acid (adipic acid)	26	19.51	13-hydroxytridecanoic acid
8	11.93	2-hydroxy nonanoic acid	27	20.00	heptadecanoic acid (also branched)
9	11.98	undecanoic acid	28	20.17	octadecanol (stearyl alcohol)
IS1	12.49	hexadecane	29	20.61	tridecanedioic acid
10	12.62	heptanedioic acid	30	20.91	cis-9-octadecenoic acid (oleic)
11	13.13	dodecanoic acid (lauric)	31	21.20	octadecanoic acid (stearic)
IS2	14.22	tridecanoic acid	32	21.48	isopimaric acid
12	14.43	p-hydroxy hydrocinnamic acid	33	22.10	16-hydroxyhexadecanoic acid
13	14.48	vanillic acid	34	22.86	dehydroabietic acid
14	14.83	nonandienoic acid (azelaic acid)	35	23.92	didehydroabietic acid
15	15.17	myristoleic acid (9-tetradecenoic acid)	36	24.34	9,10-dihydroxyoctadecanoic acid
16	15.46	tetradecanoic acid (myristic)	37	24.76	7-oxo-dehydroabietic acid
17	16.20	decanedioic acid (sebacic acid)	38	26.45	15-hydroxy-7-oxodehydroabietic acid
18	16.62	pentadecenoic acid	39	31.43	Cholesterol
19	16.51	pentadecanoic acid (also branched)			

The most abundant compounds contained in samples B5a PGS and C6c GR are linear monocarboxylic fatty acids (from C8 to C18), the most abundant being palmitic (hexadecanoic acid, C16:0) and stearic acids (octadecanoic, C18:0). The samples also contain dicarboxylic acids (in particular azelaic acid – nonandioic acid). These oxidation products of unsaturated fatty acids indicate that the lipids originally present in the samples contained a relevant amount of oleic acid (9-octadecanoic), which has undergone a degradative oxidation process, which is also revealed by the presence of 9,10-hydroxy-octadecanoic acids. The presence of odd chain length fatty acids and cholesterol indicates animal origin of fats. Odd-branched (C15 and C17) fatty acids suggest animal fats, or that the lipids have undergone bacterial degradation. On the basis of the observed lipid profile, it is not possible to say whether a vegetal-origin lipid material had been added to the mixture or not. In both samples, a diterpenic fraction was present, whose main

components are abietadienic acids: dehydroabietic (#34), didehydroabietic (#35), 7-oxo-dehydroabietic (#37) and 15-hydroxy-7-oxodehydroabietic (#38). Pimaradienic acids such as peak #32 (isopimaric acid) were also detected (pimaric, sandaracopimaric, palustric, levopimaric acids were detected as minor components). The diterpenic profile of the sample suggests that the hafting material contained a resin extracted from a plant belonging to the conifer family. In particular, *Pinaceae*, *Podocarpaceae* or *Araucariaceae* may produce a resin containing abietadienic and pimaradienic components. Amongst our database of South African plants, the wood of *Afrocarpus* (syn. *Podocarpus*) *falcatus* contains relevant amount of these compounds and is thus a probable candidate as the source of the resin used as hafting material. Analysis of charcoal from the HP layers of Sibudu shows that *Podocarpus* was predominant while *Acacia* is absent (7). The hypothesized use of plant gum as a hafting adhesive at Sibudu requires further testing.

Proteomic analyses

Proteinaceous material was identified on the MOD flake following a minimally invasive proteomic analytical procedure described by [8], aimed at preserving the integrity of the archeological piece. The micro-black sample n°87 of ca. 4 mg was directly submerged in 100 µl ammonium bicarbonate 10 mM pH 8.0, and trypsin digested in heterogeneous phase enzymatic by adding proteomics-grade trypsin 0.1 µg/µl at 37 °C for 16 h. The supernatant was then recovered by centrifugation and the peptide mixture was filtered on 0.22 µm PVDF membrane (Millipore), concentrated and purified using a reverse-phase C18 Zip Tip pipette tip (Millipore). The eluate was analyzed by LC-MSMS on a 6520 Accurate-Mass Q-ToF LC/MS System (Agilent Technologies, Palo Alto, CA, USA) equipped with a 1200 HPLC System and a chip cube (Agilent Technologies). After loading, the peptide mixture was first concentrated and washed on a 40 nl enrichment column (Agilent Technologies chip), with 0.1% formic acid in 2% acetonitrile as eluent. The sample was then fractionated on a C18 reverse-phase capillary column (Agilent Technologies chip) at a flow rate of 400 nL/min, with a linear gradient of eluent B (0.1% formic acid in 95% acetonitrile) in A (0.1% formic acid in 2% acetonitrile) from 7% to 80% in 50 min. Peptide analysis was performed using data-dependent acquisition of one MS scan (mass range from 300 to 2000 m/z) followed by MS/MS scans of the three most abundant ions in each MS scan. MS/MS spectra were measured automatically when the MS signal surpassed the threshold of 50,000 counts. Double and triple charged ions were preferably isolated and fragmented. Each LC-MSMS analysis was preceded and followed by blank runs to avoid carryover contamination. The acquired MS/MS spectra were transformed in *mzData*(.XML) format and used for protein identification with a licensed version of MASCOT software (www.matrixscience.com) version 2.4.0.

Data handling. Preliminary data obtained by nanoLC-MSMS analysis were used to query the SwissProt database 2012_08 (537505 sequences; 190795142 residues), without any taxonomy restriction. Mascot search parameters were: trypsin as enzyme; 3, as allowed number of missed cleavage; 10 ppm MS tolerance and 0.6 Da MSMS tolerance; peptide charge from +2 to +3. No fixed chemical modification was inserted, but possible oxidation of methionine and the formation of pyroglutamic acid from glutamine residues at the N-terminal position of peptides were considered as variable modification. As soon as collagen proteins were identified, a new identification run was carried out, with the insertion of hydroxylation on Lysine and Proline as variable modifications, since more confident identifications are commonly obtained with these proteins by taking into consideration their extensive post-translational modifications [8]. Individual ion score threshold provided by software to evaluate the quality of matches in MSMS data was 41. Spectra with score of <20, having low quality were rejected. Error tolerant searches were also carried out for each sample using as variable modifications proline and lysine hydroxylation to allow for single amino acid substitutions, enzyme non-specificity, as well as to check for unexpected modifications potentially induced by aging.

Bone samples. A set of four bovid size II and III [9] and one equine (*Equus quagga*) bone samples from Sibudu, layer MOD, were selected for the analysis (identifications by

Ina Plug, catalogue nos. 86, 91,1117, 1120, and 69). Approximately 3 mg of bone powder from each sample was weighed into a 1.5 mL microtube and demineralised, to get the highest sequence coverage possible for these reference collagens,with extensive incubation in 400 µl 0.5 M EDTA pH 8 at 4°C for 24 h. Insoluble pellets were then extensively washed with MilliQ water, and then submerged in 200 µl ammonium bicarbonate 10 mM pH 8.0, and trypsin digested in heterogeneous phase as described above for the MOD flake.

Table C. Identification of the proteins in the MOD sample from Sibudu by overnight trypsin digestion in heterogeneous phase and LCMSMS analysis^a. Proteins were identified searching UniprotSprot database, without any taxonomy restriction, with MS/MS Ion search Mascot software (Matrix Science).

Identified protein (Accession number)	Total score ^a	Sequence coverage (%)	Individual ion score	Matched sequence (Oxidation of methionine, hydroxylation of proline and lysine, pyro-Glu formation at Gln at the N-terminus of peptides were inserted as variable modifications).
Collagen alpha-1(I) chain (P02453)	832	40	20	GAPGPAGPK + Hydroxy (P)
			26	GAAGLPGPK+ Hydroxy (P)
			34	GPAGPQGPR
			27	GFSGLDGAK
			44	GSEGPQGV
			26	GFPGADGVAGPK + Hydroxy (P)
			33	GADGAPGKDGVR
			29	GVQGPAGPR + Hydroxy (P)
			28	GQAGVMGFPGPK+ Oxidation (M); Hydroxy (K)
			40	GLTGSPGSPGPDGK+ 2 Hydroxy (P)
			24	GFPGLPGSPGEPGK + Hydroxy (P)
			26	GPSGPQGPSGPPGPK + Hydroxy (P)
			24	GETGPAGPAGPIGPVGAR
			21	GSPGEAGRPGEAGLPGAK + Hydroxy (K); 2 Hydroxy (P)
			20	EGAPGAEGSPGRDGSPGAK + Hydroxy (K); 2 Hydroxy (P)
			22	GPPGPMGPPGLAGPPGESGR + Oxidation (M); 2 Hydroxy (P)
			36	GEPGPTGIQPPGPAGEEGK + 2 Hydroxy (P)
			31	SGDRGETGPAGPAGPIGPVGAR
			36	GEPGPTGIQPPGPAGEEGKR + 2 Hydroxy (P)
41	GDRGETGPAGPPGAPGAPGAPVGPAGK + 4 Hydroxy (P)			
26	GAPGDRGEPGPPGPAGFAGPPGADGQPGAK+ 4 Hydroxy (P)			
58	GFSGLQPPGPPGSPGEGQPSGASGPAGPR + 3 Hydroxy (P)			
29	GLTGPIGPPGPAGAPGDKGEAGPSGPAGPTGAR + Hydroxy (K); Hydroxy (P)			
Collagen alpha-2(I) chain (P02465)	575	24	35	GLPGADGR + Hydroxy (P)
			21	GATGPAGVR
			26	GVVGPQGAR
			46	VGAPGPAGAR+ Hydroxy (P)
			24	GEPGNIGFPGPK + 2 Hydroxy (P)
			36	GPAGPSGPAKDGVR
			32	GIPGEFGLPGPAGAR + 2 Hydroxy (P)
			21	GDGGPPGATGFPGAAGR + 2 Hydroxy (P)
			25	GAAGLPGVAGAPGLPGR+ 3 Hydroxy (P)
			35	GPPGESGAAGPTGPIGSR + Hydroxy (P)
			30	GSTGEIGPAGPPGPPGLR + 2 Hydroxy (P)
			20	EGPVGLPGIDRPGPIGPAGAR+ 2 Hydroxy (P)
65	GLPGVAGSVGEPGLGIAGPPGAR + 3 Hydroxy (P)			

Alpha-S1-casein (P02662)	249	33	40 20 31 24 59	EDVPSEK YLGYLEQLLR FFVAPFPEVFGK VPQLEIVPNSAEER HQGLPQEVLNENLLR
Alpha-S2-casein (P02663)	160	23	34 30 28 28	TKVIPYVR FALPQYLK NAVPIPTLNR ALNEINQFYQK
Beta-casein (P02666)	99	12	24 25 21	VLPVPQK AVPYPQR VLPVPQKAVPYPQR
Kappa-casein (P02668)	47	14	24 23	YIPIQYVLSR SPAQILQWQVLSNTVPAK

Proteins were identified searching UniprotSprot database with MSMS Ion search Mascot software (Matrix Science) without any taxonomy restriction, with oxidation on Met, hydroxylation on Lys and Pro as variable modifications. Individual ion score above the significance threshold (>41) indicate identity or extensive homology ($p < 0.05$). Only peptides with individual ion scores >20 were considered for identification purposes. Only proteins identified with at least two peptides were considered as significant.

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1  MKLLILTCLVAVALARPKHPKIKHQGLPQEVLNENLLRFFVAPFPEVFGKEKVNEL----- 55  P02662  CASA1_BOVIN
1  MRLILITCLVAVALARPKLPLRYPERLQNPSE-----SSEPIPLESREEYMNGMNRQRN 54  P47710  CASA1_HUMAN
1  MKLLILTCLVAVALARPKHPINHRGLSPEVPNENLLRFFVAPFPEVFRKENINEL----- 55  P18626  CASA1_CAPHI
1  MKLLILTCLVAVALARPKHPKIKHQGLSSEVLNENLLRFFVAPFPEVFRKENINEL----- 55  P04653  CASA1_SHEEP

*:***** *:.: : : *: * : * :

56  -----SKDIGSESTEDQAMEDIKQMEAESISSSEEIVPNSVEQKHIQEDVPSERY 106  P02662  CASA1_BOVIN
55  ILREKQTDEIKDTRNESTQNCVVAEPEKMESSISSSSEEMS-----L 96  P47710  CASA1_HUMAN
56  -----SKDIGSESTEDQAMEDAKQMKAGSSSSSEEIVPNSAEQKYIQKEDVPSERY 106  P18626  CASA1_CAPHI
56  -----SKDIGSESIEDQAMEDAKQMKAGSSSSSEEIVPNSAEQKYIQKEDVPSERY 106  P04653  CASA1_SHEEP

** .** :: .: : ::*: *****:

107 LGYLEQLLRLKKYKVPQLEIVPNSAEERLHSMKEGIHAQQKEPMIGVNQELAYFYPELFR 166  P02662  CASA1_BOVIN
97  SKCAEQFCRLNEYNQQLQ--AAHAQEQIRRMNENSH-----VQVPFQ 137  P47710  CASA1_HUMAN
107  LGYLEQLLRLLKKYNVPQLEIVPKSAEEQLHSMKEGNPAHQKQPMIAVNQELAYFYPLFR 166  P18626  CASA1_CAPHI
107  LGYLEQLLRLLKKYNVPQLEIVPKSAEEQLHSMKEGNPAHQKQPMIAVNQELAYFYPLFR 166  P04653  CASA1_SHEEP

**: **:*: *: *: *: *: *: *:

167  QFYQLDAYPSGAWYYVPLGTQYTDAPSFSDIPNPIGSENSEKTT-MPLW 214  P02662  CASA1_BOVIN
138  QLNQLAAYPYAVWYYPQ-IMQYVPFPPFSDISNPTAHENYEKNNVMLQW 185  P47710  CASA1_HUMAN
167  QFYQLDAYPSGAWYYLPLGTQYTDAPSFSDIPNPIGSENSGKTT-MPLW 214  P18626  CASA1_CAPHI
167  QFYQLDAYPSGAWYYLPLGTQYTDAPSFSDIPNPIGSENSGKIT-MPLW 214  P04653  CASA1_SHEEP

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Fig. F. Alignment of Alpha-S1-casein sequences from cattle (*Bos taurus*, P02662), human (*Homo sapiens*, P47710), goat (*Capra hircus*, P18626), and sheep (*Ovis aries*, P04653). Highlighted in grey and bold are the matched sequences.

Fig. G . Alignment of the matched peptides in the MOD flake to the Collagen alpha-1(I) chain from *Bos taurus* (P02453) and *Equus asinus* (B9VR88). Peptides identified in the MOD flake sample were manually aligned over the automatically generated alignment (CLUSTAL O(1.2.0) multiple sequence alignment, of the two collagen alpha-1(I) chain from *Bos taurus* (P02453) and *Equus asinus* (B9VR88). Peptides from MOD flake are reported in bold. An * (asterisk) indicates positions which have a single, fully conserved residue; : (colon) indicates conservation between groups of strongly similar properties; . (period) indicates conservation between groups of weakly similar properties. Under the alignment, peptides matched in samples from bones of some Bovids and *Equus quagga* remains recovered from Sibudu layer MOD, are reported. Underlined sequences are those identified in the error tolerant database search and the modified residue is indicated in red. Numbering refers to the precursor polypeptide chain while only the sequence of the mature protein is reported.

MOD flake

P02453 *Bos taurus* QLSYGYDEKSTGISVPGPM 180
 B9VR88 *Equus asinus* QLSYGYDEKSAGISVPGPM 180
 *****:*****

#86 Bovid STGISVPGPM
 #69 *Equus quagga*
 #1120 Bovid
 #1117 Bovid STGISVPGPM
 #91 Bovid

MOD flake

P02453 *Bos taurus* GPSGPRGLPGPPGAPGPGQGFQGGPPGEPGEPGASGPMGPRGPPGPPGKNGDDGEAGKPGRP 240
 B9VR88 *Equus asinus* GPSGPRGLPGPPGAPGPGQGFQGGPPGEPGEPGASGPMGPRGPPGPPGKNGDDGEAGKPGRP 240

#86 Bovid GPSGPRGLPGPPGAPGPGQGFQGGPPGEPGEPGASGPMGPRGPPGPPGKNGDDGEAGKPGRP
 #69 *Equus quagga* GPPGPPGKNGDDGEAGKPGRP
 #1120 Bovid GPPGPPGK
 #1117 Bovid GPSGPRGLPGPPGAPGPGQGFQGGPPGEPGEPGASGPMGPRGPPGPPGKNGDDGEAGKPGRP
 #91 Bovid GPPGPPGK

MOD flake

GFSGLDGAK

P02453 *Bos taurus* GERGPPGPQGARGLPGTAGLPGMKGHRGFSGLDGAKGDAGPAGPKGEPGSPGENGAPGQM 300
 B9VR88 *Equus asinus* GERGPPGPQGARGLPGTAGLPGMKGHRGFSGLDGAKGDAGPAGPKGEPGSPGENGAPGQM 300

#86 Bovid GERGPPGPQGARGLPGTAGLPGMK GFSGLDGAKGDAGPAGPKGEPGSPGENGAPGQM
 #69 *Equus quagga* GERGPPGPQGAR GEPGSPGENGAPGQM
 #1120 Bovid GPPGPQGAR GFSGLDGAKGDAGPAGPKGEPGSPGENGAPGQM
 #1117 Bovid GERGPPGPQGARGLPGTAGLPGMK GFSGLDGAKGDAGPAGPKGEPGSPGENGAPGQM
 #91 Bovid GPPGPQGAR

MOD flake

P02453 *Bos taurus* GPRGLPGERGRPGAPGPAGARGNDGATGAAGPPGPTGPAGPPGFPGAVGAKGEGGPQGR 360
 B9VR88 *Equus asinus* GPRGLPGERGRPGAPGPAGARGNDGATGAAGPPGPTGPAGPPGFPGAVGAKGEGGPQGR 360

#86 Bovid GPRGLPGERGRPGAPGPAGARGNDGATGAAGPPGPTGPAGPPGFPGAVGAK
 #69 *Equus quagga* GPRGLPGERGRPGAPGPAGARGNDGATGAAGPPGPTGPAGPPGFPGAVGAKGEGGPQGR
 #1120 Bovid GPRGLPGERGRPGAPGPAGARGNDGATGAAGPPGPTGPAGPPGFPGAVGAK
 #1117 Bovid GPRGLPGERGRPGAPGPAGARGNDGATGAAGPPGPTGPAGPPGFPGAVGAK
 #91 Bovid GRPGAPGPAGARGNDGATGAAGPPGPTGPAGPPGFPGAVGAK

MOD flake	GSEGPQGVR	GFPARGPSGPQ	
P02453 <i>Bos taurus</i>	GSEGPQGVRRGEPGPPGAGAGPAGNPGADGQPGAKGANGAPGIAGAPGFPARGPSGPQ		420
B9VR88 <i>Equus asinus</i>	GSEGPQGVRRGEPGPPGAGAGPAGNPGADGQPGAKGANGAPGIAGAPGFPARGPSGPQ		420

#86 Bovid	GSEGPQGVRRGEPGPPGAGAGPAGNPGADGQPGAKGANGAPGIAGAPGFPARGPSGPQ		
#69 <i>Equus quagga</i>	GSEGPQGVRRGEPGPPGAGAGPAGNPGADGQPGAKGANGAPGIAGAPGFPARGPSGPQ		
#1120 Bovid	GSEGPQGVRRGEPGPPGAGAGPAGNPGADGQPGAKGANGAPGIAGAPGFPARGPSGPQ		
#1117 Bovid	GSEGPQGVRRGEPGPPGAGAGPAGNPGADGQPGAKGANGAPGIAGAPGFPARGPSGPQ		
#91 Bovid	GSEGPQGVRRGEPGPPGAGAGPAGNPGADGQPGAKGANGAPGIAGAPGFPARGPSGPQ		
MOD flake	GPSGPPGPK	GEPGTGIQPPGPAGEEGR	
P02453 <i>Bos taurus</i>	GPSGPPGPKGNSGEPGAPGSKGDTGAKGEPGTGIQPPGPAGEEGRGARGEPGAGLP		480
B9VR88 <i>Equus asinus</i>	GPSGPPGPKGNSGEPGAPGSKGDTGAKGEPGTGIQPPGPAGEEGRGARGEPGAGLP		480

#86 Bovid	GPSGPPGPKGNSGEPGAPGSKGDTGAKGEPGTGIQPPGPAGEEGRGARGEPGAGLP		
#69 <i>Equus quagga</i>	GPSGPPGPK	GEPGTGIQPPGPAGEEGR	GEPGTGLP
#1120 Bovid	GPSGPPGPKGNSGEPGAPGSKGDTGAK		GEPGAGLP
#1117 Bovid	GPSGPPGPK	GDTGAKGEPGTGIQPPGPAGEEGR	GEPGAGLP
#91 Bovid	GPSGPPGPKGNSGEPGAPGSKGDTGAKGEPGTGIQPPGPAGEEGR		GEPGTGLP
MOD flake	GFPAGDVAGPK	GAPGAPGKSPGEAGRPGEAGLPAGKLT	
P02453 <i>Bos taurus</i>	GPPGERGGPGRGFPAGDVAGPKGAPGAPGKSPGEAGRPGEAGLPAGKLT		540
B9VR88 <i>Equus asinus</i>	GPPGERGGPGRGFPAGDVAGPKGAPGAPGKSPGEAGRPGEAGLPAGKLT		540

#86 Bovid	GPPGER	GFPAGDVAGPK	GAPGAPGKSPGEAGRPGEAGLPAGKLT
#69 <i>Equus quagga</i>	GPPGER	GFPAGDVAGPK	GAPGAPGKSPGEAGRPGEAGLPAGKLT
#1120 Bovid	GPPGER	GFPAGDVAGPK	GAPGAPGKSPGEAGRPGEAGLPAGKLT
#1117 Bovid	GPPGER	GFPAGDVAGPK	GAPGAPGKSPGEAGRPGEAGLPAGKLT
#91 Bovid	GPPGER	GFPAGDVAGPK	GAPGAPGKSPGEAGRPGEAGLPAGKLT
MOD flake	GSPGSPGDGK	GQAGVMGFPGPK	
P02453 <i>Bos taurus</i>	GSPGSPGDGKTGPPGAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGERGVP		600
B9VR88 <i>Equus asinus</i>	GSPGSPGDGKTGPPGAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGERGVP		600

#86 Bovid	GSPGSPGDGKTGPPGAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEPGK	GVP	
#69 <i>Equus quagga</i>	GSPGSPGDGK	GQAGVMGFPGPKGAAGEPGK	GVP
#1120 Bovid	GSPGSPGDGKTGPPGAGQDGRPGPPGPPGARGQAGVMGFPGPK		
#1117 Bovid	GSPGSPGDGKTGPPGAGQDGRPGPPGPPGARGQAGVMGFPGPK	GVP	
#91 Bovid	GSPGSPGDGKTGPPGAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGERGVP		
MOD flake			
P02453 <i>Bos taurus</i>	GPPGAVGPAGKDGEAGAQQPPGAPGAGERGEQQPAGSPGFQGLPGPAGPPGEAGKPGEQ		660
B9VR88 <i>Equus asinus</i>	GPPGAVGPAGKDGEAGAQQPPGAPGAGERGEQQPAGSPGFQGLPGPAGPPGESGKPGEQ		660

#86 Bovid	GPPGAVGPAGKDGEAGAQQPPGAPGAGERGEQQPAGSPGFQGLPGPAGPPGEAGKPGEQ		
#69 <i>Equus quagga</i>	GPPGAVGPAGKDGEAGAQQPPGAPGAGER		
#1120 Bovid	GPPGAVGPAGK		
#1117 Bovid	GPPGAVGPAGKDGEAGAQQPPGAPGAGERGEQQPAGSPGFQGLPGPAGPPGEAGKPGEQ		
#91 Bovid	GPPGAVGPAGKDGEAGAQQPPGAPGAGER		

MOD flake GVQPPGPAGPR

P02453 *Bos taurus* GVPGDLGAPGPSGARGERGFPPGERGVQPPGPAGPRGANGAPGNDGAKGDAGAPGAPGSQ 720
 B9VR88 *Equus asinus* GVPGDLGAPGPSGARGERGFPPGERGVQPPGPAGPRGNSGAPGNDGAKGDAGAPGAPGSQ 720
 *****:*****

#86 Bovid GVPGDLGAPGPSGAR GFPPGERGVQPPGPAGPRGNSGAPGNDGAKGDAGAPGAPGSQ
 #69 *Equus quagga* GVQPPGPAGPR GDAGAPGAPGSQ
 #1120 Bovid GFPPGERGVQPPGPAGPR GDAGAPGAPGSQ
 #1117 Bovid GVPGDLGAPGPSGAR GFPPGERGVQPPGPAGPR GDAGAPGAPGSQ
 #91 Bovid GFPPGERGVQPPGPAGPR

MOD flake GAAGLPGPK GADGAPGKDGVRGLTGP IGP PPAGAPGDK

P02453 *Bos taurus* GAPGLQGMPGERGAAGLPGPKGDRGDAGPKGADGAPGKDGVRGLTGP IGP PPAGAPGDK 780
 B9VR88 *Equus asinus* GAPGLQGMPGERGAAGLPGPKGDRGDAGPKGADGSPKDGVRGLTGP IGP PPAGAPGDK 780
 *****:*****

#86 Bovid GAPGLQGMPGER GLTGP IGP PPAGAPGDK
 #69 *Equus quagga* GAPGLQGMPGERGAAGLPGPK GLTGP IGP PPAGAPGDK
 #1120 Bovid GAPGLQGMPGER GADGAPGKDGVR
 #1117 Bovid GAPGLQGMPGERGAAGLPGPKGDR GLTGP IGP PPAGAPGDK
 #91 Bovid GAAGLPGPK GADGAPGKDGVRGLTGP IGP PPAGAPGDK

MOD flake GEAGPSGPAGPTGARGAPDRGEPGPPGAGFAGPPGADGQPGAK

P02453 *Bos taurus* GEAGPSGPAGPTGARGAPDRGEPGPPGAGFAGPPGADGQPGAKGEPGDAGAKGDAGPP 840
 B9VR88 *Equus asinus* GETGPSGPAGPTGARGAPDRGEPGPPGAGFAGPPGADGQPGAKGEPGDAGAKGDAGPP 840
 :***

#86 Bovid GEAGPSGPAGPTGARGAPDRGEPGPPGAGFAGPPGADGQPGAKGEPGDAGAKGDAGPP
 #69 *Equus quagga* GETGPSGPAGPTGAR GEPGPPGAGFAGPPGADGQPGAK GDAGPP
 #1120 Bovid
 #1117 Bovid GEAGPSGPAGPTGARGAPDRGEPGPPGAGFAGPPGADGQPGAK GDAGPP
 #91 Bovid GEAGPSGPAGPTGARGAPDRGEPGPPGAGFAGPPGADGQPGAKGEPGDAGAKGDAGPP

MOD flake

P02453 *Bos taurus* GPAGPAGPPGPIGNVGAPGPKGARGSAGPPGATGFPGAAGRVGPPGPSGNAGPPGPPGPA 900
 B9VR88 *Equus asinus* GPAGPAGPPGPIGSVGAPGPKGARGSAGPPGATGFPGAAGRVGPPGPSGNAGPPGPPGPV 900
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#86 Bovid GPAGPAGPPGPIGNVGAPGPK GSAGPPGATGFPGAAGRVGPPGPSGNAGPPGPPGPA
 #69 *Equus quagga* GPAGPAGPPGPIGSVGAPGPK GSAGPPGATGFPGAAGRVGPPGPSGNAGPPGPPGPV
 #1120 Bovid GSAGPPGATGFPGAAGRVGPPGPSGNAGPPGPPGPA
 #1117 Bovid GPAGPAGPPGPIGNVGAPGPK GSAGPPGATGFPGAAGRVGPPGPSGNAGPPGPPGPA
 #91 Bovid GPAGPAGPPGPIGNVGAPGPKGARGSAGPPGATGFPGAAGRVGPPGPSGNAGPPGPPGPA

MOD flake

P02453 *Bos taurus* GKEGSKGPRGETGPAGRPGEVGP PP GPPGAGEKGPAGADGPAGAPGTPGPQGIAGQRGVV 960
 B9VR88 *Equus asinus* GKEGKGPRGETGPAGRPGEAGPPPPGAGEKGPSGADGPAGAPGTPGPQGIAGQRGVV 960
 **** . ***** . *****:*****

#86 Bovid GK GPRGETGPAGRPGEVGP PP GPPGAGEKGPAGADGPAGAPGTPGPQGIAGQRGVV
 #69 *Equus quagga* GK GETGPAGRPGEAGPPPPGAGEKGPSGADGPAGAPGTPGPQGIAGQRGVV
 #1120 Bovid GK GETGPAGRPGEVGP PP GPPGAGEK GVV
 #1117 Bovid GK GPRGETGPAGRPGEVGP PP GPPGAGEKGPAGADGPAGAPGTPGPQGIAGQRGVV
 #91 Bovid GK GETGPAGRPGEVGP PP GPPGAGEKGPAGADGPAGAPGTPGPQGIAGQRGVV

MOD flake GFPGLPGSPGEPK GPPGPMGPPGLAGPPGESGREGAPGAE

P02453 *Bos taurus* GLPGQRGERGFPLPGPSGEPGKQGPSGASGERGPPGPMGPPGLAGPPGESGREGAPGAE 1020
 B9VR88 *Equus asinus* GLPGQRGERGFPLPGPSGEPGKQGPSGASGERGPPGPMGPPGLAGPPGESGREGSPGAE 1020
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#86 Bovid GLPGQRGERGFPLPGPSGEPGKQGPSGASGERGPPGPMGPPGLAGPPGESGREGAPGAE
 #69 *Equus quagga* GLPGQRGERGFPLPGPSGEPGKQGPSGASGERGPPGPMGPPGLAGPPGESGR
 #1120 Bovid GLPGQR GFPGLPGPSGEPGK EGAPGAE
 #1117 Bovid GLPGQR GFPGLPGPSGEPGKQGPSGASGERGPPGPMGPPGLAGPPGESGREGAPGAE
 #91 Bovid GLPGQRGERGFPLPGPSGEPGK EGAPGAE

MOD flake GSPGRDGSPGAKGDRGETGPAGPPGAPGAPGAPGVPAGKSGDRGETGPAGPAGPIGPV

P02453 *Bos taurus* GSPGRDGSPGAKGDRGETGPAGPPGAPGAPGAPGVPAGKSGDRGETGPAGPAGPIGPV 1080
 B9VR88 *Equus asinus* GSPGRDGSPGPKGDRGETGPAGPPGAPGAPGAPGVPAGKSGDRGEAGPAGPAGPIGPV 1080
 ***** *****:*****

#86 Bovid GSPGR GDRGETGPAGPPGAPGAPGAPGVPAGKSGDRGETGPAGPAGPIGPV
 #69 *Equus quagga* GETGPAGPPGAPGAPGAPGVPAGKSGDRGEAGPAGPAGPIGPV
 #1120 Bovid GSPGRDGSPGAK GETGPAGPPGAPGAPGVPAGK GETGPAGPAGVGPV
 #1117 Bovid GSPGR GDRGETGPAGPPGAPGAPGAPGVPAGKSGDRGETGPAGPAGPIGPV
 #91 Bovid GSPGRDGSPGAKGDRGETGPAGPPGAPGAPGAPGVPAGKSGDRGETGPAGPAGPIGPV

MOD flake GAR GFSGLQGPPPPGSPGEQGPSGASGPAGPR

P02453 *Bos taurus* GARGPAGPQGPGRGDKGETGEQDRIKGRGFSGLQGPPPPGSPGEQGPSGASGPAGPR 1140
 B9VR88 *Equus asinus* GARGPAGPQGPGRGDKGETGEQDRIKGRGFSGLQGPPPPGSPGEQGPSGASGPAGPR 1140

#86 Bovid GARGPAGPQGPR GFSGLQGPPPPGSPGEQGPSGASGPAGPR
 #69 *Equus quagga* GARGPAGPQGPR GPPGSPGEQGPSGASGPAGPR
 #1120 Bovid GAR
 #1117 Bovid GARGPAGPQGPR GFSGLQGPPPPGSPGEQGPSGASGPAGPR
 #91 Bovid GARGPAGPQGPGRDK

MOD flake

P02453 *Bos taurus* GPPGSAGSPGKDGLNGLPGPIGPPGPRGRTGDAGPAGPPGPPGPPGPPGPPSGGYDLSFL 1200
 B9VR88 *Equus asinus* GPPGSAGAPGKDGLNGLPGPIGPPGPRGRTGDAGPVPAGPPGPPGPPGPPGPPSAGFDLSFL 1200
 *****:*****.*****.*****:***

#86 Bovid GPPGSAGSPGKDGLNGLPGPIGPPGPR
 #69 *Equus quagga*
 #1120 Bovid
 #1117 Bovid GPPGSAGSPGKDGLNGLPGPIGPPGPR
 #91 Bovid DGLNGLPGPIGPPGPR

MOD flake

P02453 *Bos taurus* PQQPQEKAHDGGRYR 1260
 B9VR88 *Equus asinus* PQQPQEKSHDGGRYR 1260
 *****:*****

#86 Bovid
 #69 *Equus quagga*
 #1120 Bovid
 #1117 Bovid
 #91 Bovid

Fig. H. Alignment of the matched peptides in the MOD flake to the Collagen alpha-2(I) chain from *Bos taurus* (P02465) and *Equus asinus* (B9VR89). Peptides identified in the MOD flake sample were manually aligned over the automatically generated alignment (CLUSTAL O(1.2.0) multiple sequence alignment, of the two collagen alpha-2(I) chain from *Bos taurus* (P02465) and *Equus asinus* (B9VR89). Peptides from MOD flake are reported in bold. An * (asterisk) indicates positions which have a single, fully conserved residue; : (colon) indicates conservation between groups of strongly similar properties; . (period) indicates conservation between groups of weakly similar properties. Under the alignment, peptides matched in samples from bones of some Bovids and *Equus quagga* remains recovered from Sibudu layer MOD, are reported. Underlined sequences are those identified in the error tolerant database search and the modified residue is indicated in red. Numbering refers to the precursor polypeptide chain while only the sequence of the mature protein is reported. X stands for either Ile or Leu that cannot be distinguished as substitution since are isobaric.

MOD flake		<u>GPPGASGAPGPQGF</u> X <u>GPPGEPGE</u>	
P02465 <i>Bos taurus</i>		QFDAKGGGPGMGLMGRGPPGASGAPGPQGFQGGPPGEPGE	120
B9VR89 <i>Equus asinus</i>		QFDAKGGGPGMGLMGRGPPGASGAPGPQGFQGGPAGEPGE	120

#86 Bovid		GPPGASGAPGPQGFQGGPPGEPGE	
#69 <i>Equus quagga</i>			
#1120 Bovid			
#1117 Bovid		GPPGASGAPGPQGFQGGPPGEPGE	
#91 Bovid			
MOD flake	<u>PGQTGPAGAR</u>	<u>GVVGPQGAR</u>	
P02465 <i>Bos taurus</i>	PGQTGPAGARGPPGPPGKAGEDGHPGKPRPGERGVVGPQGARGFPPTPLPGFKGIRGH		180
B9VR89 <i>Equus asinus</i>	PGQTGPAGARGPPGPPGKAGEDGHPGKPRPGERGVVGPQGARGFPPTPLPGFKGIRGH		180

#86 Bovid	PGQTGPAGARGPPGPPGK	GVVGPQGARGFPPTPLPGFK	GH
#69 <i>Equus quagga</i>	GPPGPPGK	GVVGPQGARGFPPTPLPGFK	
#1120 Bovid	GPPGPPGK	GVVGPQGAR	
#1117 Bovid	PGQTGPAGARGPPGPPGKAGEDGHPGKPRPGERGVVGPQGARGFPPTPLPGFK		
#91 Bovid	GPPGPPGK	GVVGPQGAR	
MOD flake		<u>VGAPGPAGAR</u>	
P02465 <i>Bos taurus</i>	NGLDGLKGQPGAPGVKGEPEGAPGENTPGQTGARGLPGERGRVGPAGPAGARGSDGSVGP		240
B9VR89 <i>Equus asinus</i>	KGLDGLKGQPGAPGVKGEPEGAPGENTPGQAGARGLPGERGRVGPAGPAGARGSDGSVGP		240
	:*****		
#86 Bovid	NGLDGLKGQPGAPGVKGEPEGAPGENTPGQTGARGLPGER	VGAPGPAGARGSDGSVGP	
#69 <i>Equus quagga</i>	GQPGAPGVK	GLPGER	VGAPGPAGARGSDGSVGP
#1120 Bovid		GLPGER	VGAPGPAGAR
#1117 Bovid	GQPGAPGVKGEPEGAPGENTPGQTGARGLPGER	VGAPGPAGARGSDGSVGP	
#91 Bovid		VGAPGPAGAR	
MOD flake			
P02465 <i>Bos taurus</i>	VGPAGPIGSAGPPGFPAGPDKGELGPNPAGPAGPRGEVGLPGLSGVPVPPGNPGA		300
B9VR89 <i>Equus asinus</i>	VGPAGPIGSAGPPGFPAGPDKGELGPNPAGPAGPRGEVGLPGLSGVPVPPGNPGA		300

#86 Bovid	VGPAGPIGSAGPPGFPAGPDKGELGPNPAGPAGPRGEVGLPGLSGVPVPPGNPGA		
#69 <i>Equus quagga</i>	VGPAGPIGSAGPPGFPAGPDKGELGPNPAGPAGPRGEVGLPGLSGVPVPPGNPGA		
#1120 Bovid			
#1117 Bovid	VGPAGPIGSAGPPGFPAGPDKGELGPNPAGPAGPRGEVGLPGLSGVPVPPGNPGA		
#91 Bovid	GELGPNPAGPAGPR		

P02465 *Bos taurus* TGPIGSRGSPGPPGPDGNKGEFVVGAPGTAGPSGSPGLPGERGAAGIPGGKGEKGETGL 660
 B9VR89 *Equus asinus* AGPIGSRGSPGPPGPDGNKGEFVVLGAPGTAGPSGSPGLPGERGAAGIPGGKGEKGETGL 660
 :*****:*****

#86 Bovid TGPIGSRGSPGPPGPDGNKGEFVVGAPGTAGPSGSPGLPGERGAAGIPGGK GETGL
 #69 *Equus quagga* AGPIGSR GAAGIPGGK
 #1120 Bovid TGPIGSR GAAGIPGGK
 #1117 Bovid TGPIGSRGSPGPPGPDGNKGEFVVGAPGTAGPSGSPGLPGERGAAGIPGGKGEKGETGL
 #91 Bovid TGPIGSR GAAGIPGGKGEK

MOD flake

P02465 *Bos taurus* RGDIGSPGRDGARGAPGAI GAPGPAGANGDRGEAGPAGPAGPRGSPGERGEVGPAGP 720
 B9VR89 *Equus asinus* RGEIGNPGRDGARGAPGAVGAPGPAGANGDRGEAGAAGPAGPAGPRGSPGERGEVGPAGP 720
 :*.***:*****

#86 Bovid R GAPGAVGAPGPAGANGDRGEAGPAGXAGPAGPR GEVGPAGP
 #69 *Equus quagga* GEIGNPGRDGARGAPGAVGAPGPAGANGDRGEAGAAGPAGPAGPR GEVGPAGP
 #1120 Bovid
 #1117 Bovid R GAPGAVGAPGPAGANGDRGEAGPAGPAGPAGPR GEVGPAGP
 #91 Bovid GATGAI GAPGPAGANGDRGEAGPAGPAGPAGPR GEVGPAGP

MOD flake

GDGGP

P02465 *Bos taurus* NGFAGPAGAAGQPGAAGKGERGKGPKEGNGPVGPTGPVGAAGPSGPNPAGSRGDGGP 780
 B9VR89 *Equus asinus* NGFAGPAGAAGQPGAAGKGERGKGPKEGNGPVGPTGPVGAAGPSGPNPAGSRGDGGP 780

#86 Bovid NGFAGPAGAAGQPGAAGKGER GPKGENGPVGPPTGPVGAAGPSGPNPAGSRGDGGP
 #69 *Equus quagga* NGFAGPAGAAGQPGAAGKGER GENGPVGPPTGPVGAAGPSGPNPAGSRGDGGP
 #1120 Bovid GDGGP
 #1117 Bovid NGFAGPAGAAGQPGAAGKGER GPKGENGPVGPPTGPVGAAGPSGPNPAGSRGDGGP
 #91 Bovid NGFAGPAGAAGQPGAAGKGER GENGPVGPPTGPVGAAGPSGPNPAGSRGDGGP

MOD flake

PGATGFPGAAGR

P02465 *Bos taurus* PGATGFPGAAGRTPPPGSPGISGPPGPPGAGKEGLRGRDQGPVGRSGETGASGPPGF 840
 B9VR89 *Equus asinus* PGVTGFPGAAGRTPPPGSPGISGPPGPPGAAGKEGLRGRDQGPVGRAGETGASGPPGF 840
 :*.***:*****

#86 Bovid PGATGFPGAAGRTPPPGSPGISGPPGPPGAGKEGLRGRDQGPVGR
 #69 *Equus quagga* PGVTGFPGAAGRTPPPGSPGISGPPGPPGAAGK GDQGPVGRAGETGASGPPGF
 #1120 Bovid PGATGFPGAAGR GDQGPVGR
 #1117 Bovid PGATGFPGAAGRTPPPGSPGISGPPGPPGAGK GDQGPVGR
 #91 Bovid PGATGFPGAAGRTPPPGSPGISGPPGPPGAGK GPRGDQGPVGR

MOD flake

GLPGVAGSVGEPGLGIAGP

P02465 *Bos taurus* VGEKGPSGEPGTAGPPGTPGPQGLL GAPGFLGLPGSRGERGLPGVAGSVGEPGLGIAGP 900
 B9VR89 *Equus asinus* AGEKGPSGEPGTAGPPGTPGPQGLL GAPGILGLPGSRGERGLPGVAGSLGEPGLGIAGP 900

#86 Bovid GPSGEPGTAGPPGTPGPQGLLXPGFLGLPGSR GLPGVAGSVGEPGLGIAGP
 #69 *Equus quagga* AGEK GLPGVAGSLGEPGLGIAGP
 #1120 Bovid
 #1117 Bovid GPSGEPGTAGPPGTPGPQGLLXPGFLGLPGSR GLPGVAGSVGEPGLGIAGP
 #91 Bovid

MOD flake

PGAR

P02465 *Bos taurus* PGARGPPGNVGNPVGAPGEAGRDGNPNDGPPGRDQGPGHKGERGYPNAGPVGAAGA 960
 B9VR89 *Equus asinus* PGARGPPGAVGAPVGNPVGAPGEAGRDGNPNDGPPGRDQGPGHKGERGYPNAGPVGAAGA 960

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#86 Bovid PGARGPPGNVGNPGVNGAPGEAGRDGNPGNDGPPGRDGPQGHK GYPGNAGPVGTAGA
 #69 Equus quagga PGARGPPGAVGAPGVNGAPGEAGR
 #1120 Bovid
 #1117 Bovid PGARGPPGNVGNPGVNGAPGEAGRDGNPGNDGPPGR GYPGNAGPVGTTGA
 #91 Bovid

MOD flake

P02465 Bos taurus PGPQGPVGPVKGHNRRGEPGPAGAVGPAGAVGPRGSPGQGIKGDKEPDKGPRGLPGL 1020
 B9VR89 Equus asinus PGPVGPVGPVKGHNRRGEPGPVGSVGPVAVGPRGSPGQGVKGDKEPDKGPRGLPGL 1020
 :**.*****.**:***.*****:*****:*****:*****:

#86 Bovid PGPQGPVGPVKGHNRRGEPGPAGAVGPAGAVGPRGSPGQGIKGDK GLPGL
 #69 Equus quagga GEPGPVGSVGPVAVGPRGSPGQGV
 #1120 Bovid GEPGPAGAVGPAGAVGPRGSPGQGI
 #1117 Bovid PGPQGPVGPVVK GEPGPAGAVGPAGAVGPRGSPGQGI GLPGL
 #91 Bovid GEPGPAGAVGPAGAVGPRGSPGQGI

MOD flake

GPAGPSGPAGKDGR

P02465 Bos taurus KGHNGLQGLPGLAGHHGDQGAPGAVGPAGPRGAPGSPGAGKDGRIGQPGAVGPAGIRGS 1080
 B9VR89 Equus asinus KGHNGLQGLPGLAGHHGDQGAPGAVGPAGPRGAPGTPGVKDGDRSGQPGTVGPAGVRS 1080
 *****:*****:*****:***.*****.****:*****:***

#86 Bovid KGHNGLQGLPGLAGHHGDQGAPGAVGPAGPRGAPGSPGAGK IGQPGAVGPAGIR
 #69 Equus quagga GPAGPTGVPVK SGQPGTVGPAGVR
 #1120 Bovid GPAGPSGPAGKDGRIGQPGAVGPAGIR
 #1117 Bovid K GPAGPSGPAGKDGRIGQPGAVGPAGIR
 #91 Bovid GPAGPSGPAGK IGQPGAVGPAGIR

MOD flake

P02465 Bos taurus QGSQGPAGPPGPPGPPGPPG 1140
 B9VR89 Equus asinus QGSQGPAGPPGPPGPPGPPG 1140

#86 Bovid
 #69 Equus quagga
 #1120 Bovid
 #1117 Bovid
 #91 Bovid

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