

**[Supplementary material]**

**The earliest water buffalo in the Caucasus: shifting animals and people in the medieval Islamic world**

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**Table S1. Peptide markers used in the identification of indeterminate bone fragments (Buckley *et al.* 2009; Welker *et al.* 2016; Brown *et al.* 2021).**

Sample #	ID	COL1a1 508–519	COL1a2 978–990	COL1a2 978–990	COL1a2 484–498	COL1a2 502–519	COL1a2 292–309	COL1a2 793–816	COL1a2 454–483	COL1a1 586–618	COL1a1 586–618	COL1a2 757–789	COL1a2 757–789
AEB01 T1 (372) (AH01)	Failed												
AEB01 T1 (372) ZIP 1967 (AH02)	Bos/bison	1105.7		1208.8	1427.9		1649	2131.1		2853.7			3033.5
AEB01 T1 (372) ZID 1968 (AH 03)	Bos/bison	1105.7		1208.8	1427.9		1649	2131.1		2853.6			
AEB01 T1 (20) ZID 411 DA-AEB- 0518-01	Failed												
AEB01 T1 (20) ZID 412 DA-AEB- 0518-02	Bos/bison	1105.6		1208.7	1427.7			2131.1		2853.6	2869.4		
AEB01 T1 (20) ZID 413 DA-AEB- 0518-03	Bos/bison	1105.7		1208.8	1427.7			2131.2		2853.6	2869.6		
AEB01 T1 (20) ZID 414 DA-AEB- 0518-04	Water buffalo	1105.7		1208.8	1455.8					2853.7			

AEB01 T1 (20) ZID 415 DA-AEB- 0518-05	Bos/bison	1105.7		1208.8	1427.9	2131.4	2853.7
AEB01 T1 (20) ZID 416 DA-AEB- 0518-06	Water buffalo			1208.8	1456.0	2131.4	2853.8
AEB01 T1 (20) ZID 417 DA-AEB- 0518-08	Bos/bison	1105.8	1193.0	1208.9	1428.1	2131.5	3018
AEB01 T1 (20) ZID 418 DA-AEB- 0518-09	Bos/bison	1105.9	1193.0	1209.0	1428.1		

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## Methodology

Fragments of the indeterminate Bovid sp. long bones were selected for ZooMS analysis to determine species identification. Bovid sp. elements which were not fragmented were not selected in this initial study in order to preserve their morphology. Since sampling was initially conducted in 2018, a non-destructive ZooMS method has been published and may provide a way to revisit these Bovid sp. specimens in the future (McGrath *et al.* 2019; Martisius *et al.* 2020). Zooarchaeology by Mass Spectrometry (ZooMS) is a form of peptide mass fingerprinting which is used to assign a taxonomic identification to digested proteins, specifically collagen extracted from bone (Buckley *et al.* 2009), leather, ivory, and parchment (Fiddymment *et al.* 2015; Coutu *et al.* 2016; Ebsen *et al.* 2019). The method is most reliable in assigning a genus or family level identification but, in some instances, has been successful in making species-specific determinations. Bos and Bison for instance, cannot be separated using ZooMS as the resulting spectra and the peptide markers used for taxonomic identification are identical. The differentiation between Bos/bison and *Bubalus bubalis* collagen is made on the basis of a single marker, COL1A1T38 known as marker B. Bos/bison carry a mass-to-charge ( $m/z$ ) value of 1427 for their B marker whereas *Bubalus bubalis* carry a  $m/z$  value of 1455 (Buckley *et al.* 2009; Welker *et al.* 2016).

Samples were demineralised in 0.6M hydrochloric acid (HCl) for 18 hours. The HCl was removed and the sample was rinsed three times in 50mM ammonium bicarbonate (AmBic). After rinsing, the sample was incubated at 65°C for an hour in 100µl of 50mM AmBic. 50µl of the resulting supernatant was treated with trypsin (Pierce™ Trypsin Protease, Thermo Scientific) at 37°C for 18 hours. Following digestion, the samples were subjected to C18 cleanup (Pierce™ C18 Tips, Thermo Scientific), mixed with a matrix solution of  $\alpha$ -cyano-4-hydroxycinnamic of 10mg/mL in 50% acetonitrile (ACN)/0.1% trifluoroacetic acid (TFA) and allowed to co-crystallise. All samples were analysed in triplicate using an Autoflex MALDI-TOF (Bruker Daltonics, Bremen). The resulting mass spectra were screened for diagnostic markers using the FlexAnalysis and mMass software (Niedermeyer & Strohaln 2012) and compared against a reference library (Buckley *et al.* 2009; Welker *et al.* 2016). Samples were also analysed alongside multiple blanks which all returned negative results and were determined to be empty.

**Table S2. Zooarchaeological metrical data for *Bos taurus*, and possible *Bubalus bubalis* from Bardha'a, compared against a *Bubalus bubalis* specimen from Munich Zoo.**

Unique Z												
Site	ID	Phase	ID	GL	GLI	GLC	Bp	Dp	SD	Bd	BT	HTC
AEB01	1541	5	<i>Bos taurus</i>							58.69	57.47	25.91
AEB01	3184	5	<i>Bos taurus</i>							60.41	58.27	25.66
AEB01	3535	4	<i>Bos taurus</i>							66.87	66.44	29.6
AEB01	3536	4	<i>Bos taurus</i>							67.06	59.27	29.62
AEB01	1006	6	<i>Bos taurus</i>							67.56	64.53	27.44
AEB01	575	7	<i>Bos taurus</i>							70.07	67.22	31.17
AEB01	2105	10	Bovid sp.							72.08	68.25	30.63
AEB01	1817	8	Bovid sp.							73.86	67.49	33.78
AEB01	1925	8	<i>Bos taurus</i>							75.18	73.56	34.29
AEB01	412	3	Bos/bison*							77.72	75.32	31.02
AEB01	1968	10	Bos/bison*				92.04	84.78		89.8	87.12	38.7
AEB01	293	6	Bovid sp.							91.06	85.66	37.41
AEB01	411	3	<i>Bubalus bubalis</i> *							94.81	79.82	39.02
MunichZoo												
(male)	2	0	<i>Bubalus bubalis</i> (ref)							102.5	88.5	57.2
AEB01	418	3	Bos/bison*									
AEB01	577	7	<i>Bos taurus</i>				40.64	52.29				

\* Sent for ZooMS analysis and confirmed to genus/species. Note that Munich Zoo specimen originates from the Staatssammlung für Anthropologie und Paläoanatomie. The specimen number for this is listed under the ‘ZID’ column.

**Table S3. Zooarchaeological identification of *Bubalus bubalis* and *Bos taurus* from the excavations of Bardha‘a by chronological phase.**

	<b>Phase</b>	<b><i>Bos</i></b>	<b>Probable <i>Bubalus</i></b>	<b>Total</b>	<b>% Bos of</b>	<b>% Bubalus of</b>	<b>% Bos of phase</b>	<b>% Bubalus of</b>
<b>Phase</b>	<b>NISP</b>	<b><i>taurus</i></b>	<b><i>bubalis</i></b>	<b>bovids</b>	<b>bovids</b>	<b>bovids</b>	<b>total</b>	<b>phase total</b>
3	234	65	4	69	94	6	28	2
4	509	103	5	108	95	5	20	1
5	460	70	3	73	96	4	15	1
6	891	134	10	144	93	7	15	1
7	550	80	6	86	93	7	15	1
8	394	41	11	52	79	21	10	3
9	246	25	3	28	89	11	10	1
10	232	37	5	42	88	12	16	2

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