

# Proteomic Analyses on an Ancient Egyptian Cheese and Biomolecular Evidence of Brucellosis

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**ABSTRACT:** The material analyzed in this study is probably the most ancient archeological solid residue of cheese ever found to date. The sample was collected during the Saqqara Cairo University excavations in the tomb of Ptahmes dated to XIX dynasty (El-Aguizy, O. *Bulletin de l'Institut Française d'Archéologie Orientale (BIFAO)* 2010, 110, 13–34 (ref 1); Staring, N. *Bulletin de Institut Français d'Archéologie Orientale (BIFAO)* 2015, 114, 455–518 (ref 2)). Our biomolecular proteomic characterization of this archeological sample shows that the constituting material was a dairy product obtained by mixing sheep/goat and cow milk. The interactions for thousands of years with the strong alkaline environment of the incorporating soil rich in sodium carbonate and the desertic conditions did not prevent the identification of specific peptide markers which showed high stability under these stressing conditions. Moreover, the presence of *Brucella melitensis* has been attested by specific peptide providing a reasonable direct biomolecular evidence of the presence of this infection in the Ramesside period for which only indirect paleopathological evidence has been so far provided (Pappas, G.; Papadimitriou P. *Int. J. Antimicrob. Agents* 2007, 30, 29–31 (ref 3); Bourke, J. B. *Medical History* 1971, 15 (4), 363–375 (ref 4)). Finally, it is worth noting that, although proteomic approaches are successfully and regularly used to characterize modern biological samples (D'Ambrosio, C.; Arena, S.; Salzano, A. M.; Renzone, G.; Ledda, L.; and Scaloni, A. *Proteomics* 2008 8, 3657–3666 (ref 5)), their application in ancient materials is still at an early stage of progress, only few results being reported about ancient food samples (Yang, Y.; Shevchenko, A.; Knaust, A.; Abuduresule, I.; Li, W.; Hu, X.; Wang, C.; Shevchenko, A. *J. Archaeol. Sci.* 2014, 45, 178–186 (ref 6)). In the absence of previous relevant evidence of cheese production and/or use, this study, undoubtedly has a clear added value in different fields of knowledge ranging from archaeometry, anthropology, archeology, medicine history to the forensic sciences.



The tomb of Ptahmes, mayor of Memphis and high-ranking official under the Pharaohs Sethi I and Ramses II (1290–1213 B.C.) of the XIX dynasty was rediscovered in 2010 after a part of it was revealed in 1885 and lost under the sands at the end of the 19th century.<sup>7–17</sup> Now the site is just partially excavated and published.<sup>1,2,18,19</sup> It is located in the south of the Causeway of the Pharaoh Unas which yields a number of tombs dated to the New Kingdom. The sample in this study was discovered during the excavation procedures of Cairo University in the season 2013–2014. While cleaning the sand around the southern outer wall of the tomb, in a corner formed from the difference in width between the forecourt and the second court, in an area corresponding to one of the lateral storehouses, a big number of broken jars were found. One of these contained a solidified whitish mass, while a canvas fabric which might have covered it or used for its preservation was found in one of the fragments of the jar. (Figure 1). The characteristic of the canvas made it unsuitable for containing liquid or, in general, non solid-materials. The sample

(PTAH\_1) was accurately collected in order to avoid any kind of contamination.

A first investigation was performed in order to study the microscopic structure of the sample. In Figure 2 the SEM (FEDSEM LEO Supra 55VP with Zeiss GEMINI column) image shows the heterogeneity of the material that contains both crystalline and amorphous species. The crystals were analyzed by Bruker D5005 X-ray diffractometer, and the primary compound was sodium carbonate in the *trona* phase.<sup>20,21</sup> The origin of this specie is clearly driven by the extensive presence of this salt in the surrounding area where the rare but present rainfalls induce periodic cycles of solubilization, diffusion, and recrystallization of the sodium carbonate. Such a highly alkaline environment reacted with almost all the fats present in the solid residue causing

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**Figure 1.** Jar and canvas discovered inside the tomb of Ptahmes, Mayor of Memphis during the XIX dynasty (photos by the authors).

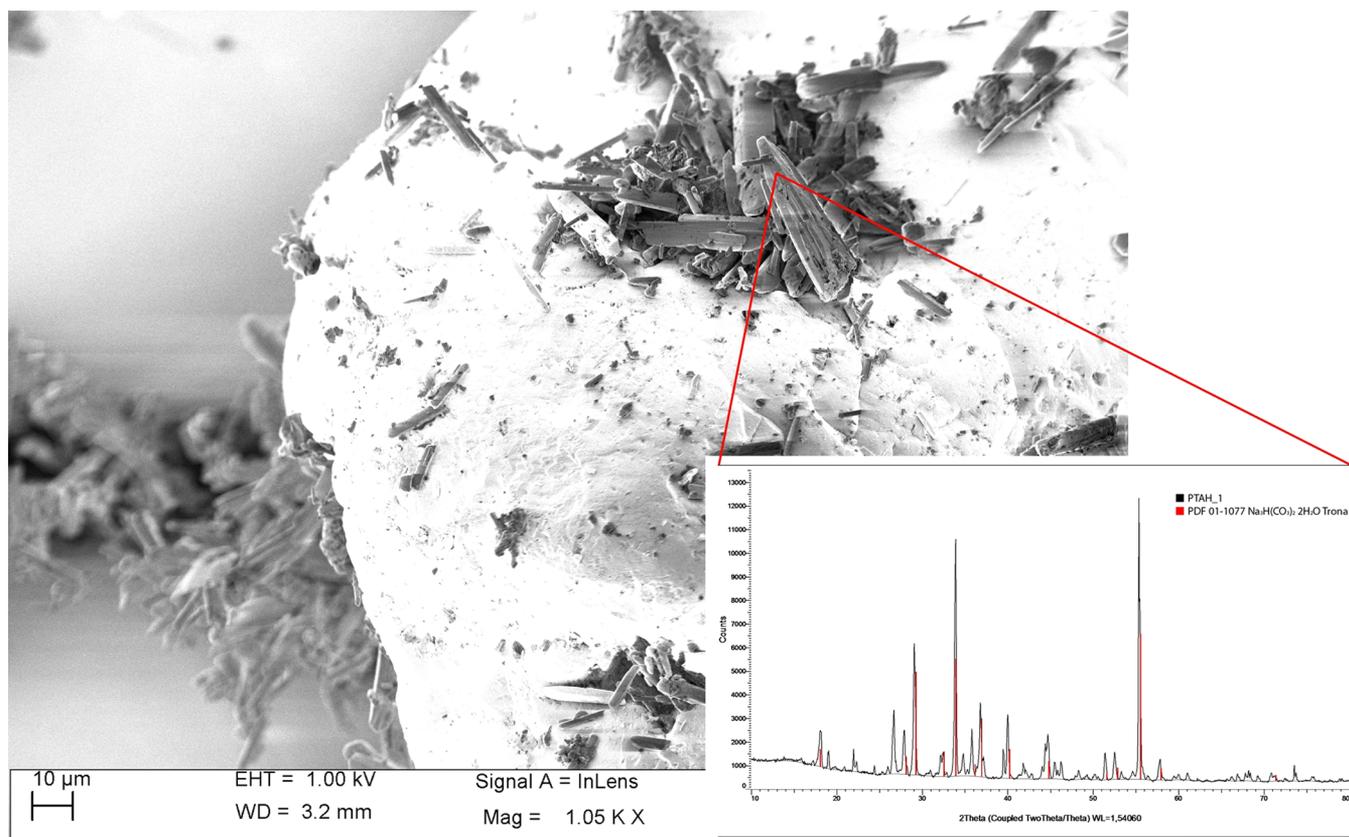
saponification. For this reason, a proteomic analysis was found to be more suitable for the recognition of the nature of the sample.

In order to analyze the amorphous components, the samples were dissolved in aqueous 0.1% trifluoroacetic acid (TFA) at a concentration of 1 mg/mL (pH 2.6). The protein concentration, determined using the fluorometric assay, was 170  $\mu\text{g}/\text{mL}$ . The sample was desalted and purified from nonprotein contaminants using the PlusOne 2-D Clean-Up kit (GE Healthcare Life Sciences) according to the manufacturer's

recommendations and dissolved in 20 mM ammonium bicarbonate (pH 8.3) at a concentration of 1 mg/mL and then reduced, alkylated, and digested with porcine trypsin as previously reported.<sup>22</sup> The resulting solution was diluted 1:2 in 5% aqueous formic acid (FA) and analyzed by UHPLC/high-resolution nanoESI-MS/MS.

Mass spectrometry data were acquired on an Orbitrap Fusion Tribrid (Q-OT-qIT) mass spectrometer (Thermo-Fisher Scientific, Bremen, Germany) equipped with a Thermo-Fisher Scientific Dionex UltiMate 3000 RSLC nano system (Sunnyvale, CA), as previously described.<sup>23</sup> LC/MS/MS data were analyzed and searched against the comprehensive (all species) UniProt protein sequences database (April 2017 release, containing 554 241 entries)<sup>24</sup> using integrated PEAKS de novo sequencing software (v. 7.0, Bioinformatics Solutions Inc., Waterloo, ON, Canada) and Mascot algorithm (Matrix Science, London, U.K., version 2.5.1), as previously reported.<sup>22</sup> Peptide spectral matches (PSM) were validated using a Target Decoy PSM Validator node based on  $q$ -values at a 0.1% false discovery rate (FDR). Proteins that contained the same peptides and could not be differentiated based on MS/MS analysis alone were grouped to satisfy the principles of parsimony.

Proteomic analysis allowed the characterization of about 500 peptides coming from more than 90 proteins with different organism origin. Most of them were from human and represented a background that comprised keratins, skin, and saliva-associated proteins probably due to contamination. Taking into account that sample PTAH\_1 was supposed to be an ancient dairy product, it is important to note that nine peptides were from *Bovidae* milk proteins (cow, sheep, goat, or



**Figure 2.** SEM image and XRD of the sample PTAH\_1 and PDF reference of the trona phase.<sup>20,21</sup>

Table 1. Selected proteins present in the sample PTAH\_1 and identified by database search of MS data (details in the text)

proteins	protein coverage (%)	protein score (%)	peptide score <sup>a</sup> (%)	supporting peptides ( <i>species</i> )	monoisotopic <i>m/z</i> ( <i>z</i> )		
					measured	calculated	$\Delta m$ (ppm)
$\alpha_{s1}$ -casein	20	98.8	99.9	FVVAPFPEVFR (sheep; goat)	654.3610 (2+)	654.3610	0
				YLGYLEQLLR (sheep; goat; cow; buffalo)	634.3561 (2+)	634.3559	0.3
				YIQKEDVPSER (sheep; goat)	455.2332 (3+)	455.2333	-0.2
				YNVPQLEIVPK (sheep; goat)	650.3688 (3+)	650.3690	-0.3
$\beta$ -casein	9	59.5	97.5	YPVEPFTESQSLTLTDVEK (sheep; goat)	1092.0400 (2+)	1092.0414	-1.3
$\kappa$ -casein	5	61.6	99.8	YIPIQYVLSR (sheep; goat; cow; buffalo)	626.3585 (2+)	626.3584	0.2
lysozyme	8	61.7	99.9	STDYGIFQINSR (cow)	700.8441 (2+)	700.8439	0.3
serum albumin	5	81.7	98.0	KVPQVSTPTLVEVSR (cow)	547.3174 (3+)	547.3174	0
				LFTFHADICTLPDTEK <sup>b</sup> (cow)	636.6456 (3+)	636.6451	0.8
protein RecA	2	55.6	94.5	IGSIKER ( <i>Brucella melitensis</i> biotype 1)	401.7428 (2+)	401.7427	0.2

<sup>a</sup>Percentage confidence score is used to reflect the probability that this peptide-spectrum match is correct. The percentage score is calculated in accordance with the empirical calculation used in PeptideProphet.<sup>28</sup> <sup>b</sup>Cysteine residue is carbamidomethylated.

buffalo). Six of them were from caseins ( $\alpha_{s1}$ -,  $\beta$ -, and  $\kappa$ -), whereas the remaining three peptides belong to two proteins (i.e., lysozyme and serum albumin) typically present in the whey fraction of milk and milk-derived foods<sup>25–27</sup> (Table 1). In detail, four peptides, FVVAPFPEVFR, YIQKEDVPSER, YLGYLEQLLR, and YNVPQLEIVPK allowed the identification of an  $\alpha_{s1}$ -casein; all these peptides are common to the ovine (UniProt Accession No. P18626) and caprine (Accession No. P04653)  $\alpha_{s1}$ -casein. On the other hand, the sequence YLGYLEQLLR is also related to the cow (Accession No. P02662) and water buffalo (Accession No. 062823) species.  $\beta$ -casein was identified by the characterization of the peptide YPVEPFTESQSLTLTDVEK, a sequence trait common to sheep (Accession No. P11839) and goat (Accession No. P33048) species. Finally, the peptide YIPIQYVLSR, shared between sheep (Accession No. P02669), goat (Accession No. P02670), cow (Accession No. P02668), and water buffalo (Accession No. P11840) species, allowed the identification of a  $\kappa$ -casein. As above-reported, three peptides were markers of two cow proteins normally present in milk and dairy products. In detail, cow milk lysozyme (Accession No. Q6B411) was identified by the characterization of the peptide STDYGIFQINSR; cow serum albumin (Accession No. P02769) was identified by the characterization of peptides KVPQVSTPTLVEVSR and LFTFHADICTLPDTEK.

Albumin, which occurs in many body tissues and secretions, is not synthesized in the mammary gland but it is presumed to enter the milk by leaky junctions between the mammary epithelial cells or by uptake with other components such as immunoglobulins. Lysozyme, another protein that is typically found in milk whey fraction, is an enzyme belonging to the glycoside hydrolases and it is known to be a natural antimicrobial agent.

Altogether, these data confidently suggested that the investigated archeological organic sample represents a cheese-like product obtained using bovine milk mixed with milk from ovine (goat or sheep).

Among the hundreds peptides identified in the ancient sample, no proteins or peptides from *Lactobacillus kefirifaciens* and other lactic acid bacteria (usual microbial signature characteristic for kefir or kefir-like fermentation<sup>6</sup>) were found. Moreover, the sequence IGSIKER (see Table 1) allowed the identification of a protein (Accession No. P65975) from

*Brucella melitensis* biotype 1. It is interesting to note that *Brucella melitensis* is the main cause of brucellosis in human and represents a natural pathogen for sheep and goats.<sup>29</sup>

It should be noted that this amino acid trait is common to proteins from other bacteria, such as a hypothetical protein from *Coxiella burnetii* (e.g., NCBI Accession No. WP\_098953193) another Gram-negative bacterium that mostly affect ruminants.<sup>30</sup> On the light of this evidence it is not possible to exclude *a priori* that this peptide could be related to *Coxiella burnetii*. However, it should be noted that if the peptide IGSIKER arises from the protein RecA of *Brucella melitensis*, it represents a theoretical tryptic fragment generated by two specific cleavages at the level of the Arg<sup>238</sup>-Ile<sup>239</sup> and Arg<sup>245</sup>-Asp<sup>246</sup> bonds. On the contrary, the peptide IGSIKER may be generated from a hypothetical protein of *Coxiella burnetii* if we hypothesized an unspecific tryptic cleavage at the Thr<sup>292</sup>-Ile<sup>293</sup> bond. Taking into account that less of 5% (corresponding to about 25 peptides) of all the identified peptides was generated by unspecific tryptic cleavages and in order to satisfy the principles of parsimony (i.e., Occam's razor), the sequence IGSIKER may be reasonably related to the *Brucella melitensis*.

In conclusion, even if very ancient kefir or milk or dairy residues, coming from North African,<sup>31</sup> Chinese,<sup>6,27</sup> and European<sup>32</sup> excavations have been found and analyzed, the present sample represent the oldest solid cheese so far discovered (3200 BP).

The results here obtained show how proteomic investigation of ancient materials may provide valuable contributions for their characterization. In particular, the present work evidences the capability of these approaches in order to identify not only the milk components preserved in the ancient dairy material but also the unambiguous detection of different milk species employed in ancient cheese manufacturing.

Moreover, up until now, only indirect signs of Brucellosis have been discovered on Egyptian archeological pelvic and hip bones such as sacroiliitis, spondylitis, and osteoarticular lesions dated 750 B.C.<sup>3,33,34</sup> Therefore, the identification of a peptide sequence which may be related to the *Brucella melitensis* in our investigation could represent the first biomolecular direct evidence of this disease during the pharaonic period, even if it requires additional investigations in order to be exhaustively and conclusively confirmed.

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### Author Contributions

E.C. conceived and planned the project. E.C. and E.G. wrote the paper. E.G., S.F., V.C., and R.S. performed the analytical work and data analysis, and O.E.-A. and M.A. directed the excavations procedures and sampling of archeological materials. All authors read and approved the final manuscript.

### Notes

The authors declare no competing financial interest.

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