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1 **Characterization of the major whey proteins from milk of Mediterranean water**
2 **buffalo (*Bubalus bubalis*)**

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21

1 **Abstract**

2 In this work, the whey protein fractions from 120 Mediterranean water buffalo individual milks
3 were analysed by microchip electrophoresis (MCE), reverse-phase high-performance liquid
4 chromatography (RP-HPLC) and mass spectrometry (ESI-MS). Validation procedures were carried
5 out for both MCE and HPLC. The chromatographic analysis allowed the complete separation of the
6 whey protein fractions, resulting in a well-defined peak structure; the adopted RP-HPLC and ESI-
7 MS protocols provided identification of β -lactoglobulin (18,266 Da), α -lactoalbumin (14,236 Da)
8 and serum albumin (66,397 Da). The calculated mean concentrations were 4.04 g/l, 2.45 g/l and
9 0.35 g/l, respectively.

10

11 **Keywords**

12 Water buffalo milk, Whey proteins, Microchip electrophoresis, Reverse-phase high-performance,
13 liquid chromatography, Mass spectrometry

14

1 **1. Introduction**

2 Whey is a biological fluid derived from milk. It is rich in proteins and peptides which play a crucial
3 role in the innate immunity of the progeny (Zimecki & Kruzel, 2007). The protein components of
4 whey include serum albumin (SA), α -lactalbumin (α -LA), β -lactoglobulin (β -LG) and
5 immunoglobulins (Fox, 1989). Besides, the minor proteins include lactoferrin, lactoperoxidase and
6 lysozyme, which have important antimicrobial and carrier functions (Marshall, 2004; Parodi, 2007).
7 The primary structures are known for β -lactoglobulin and α -lactalbumin; their genetic properties
8 and factors responsible for quantitative variability in their expression, are reported in the literature
9 (Farrell et al., 2004). The physicochemical characterization of whey proteins can be achieved by a
10 combination of electrophoretic, chromatographic and spectroscopic methods (Andreotti, Trivellone,
11 & Motta, 2006; Bonfatti, Grigoletto, Cecchinato, Gallo, & Carnier, 2008; Bonizzi, Buffoni, &
12 Feligini, 2009; Bordin, Cordeiro Raposo, de la Calle, & Rodriguez, 2001; Bramanti, Sortino, Onor,
13 Beni, & Raspi, 2003; D'Ambrosio et al., 2008; Elgar et al., 2000; El-Zahar et al., 2004; Vallejo-
14 Cordoba, González-Córdova, & Olguin-Arredondo, 2008). On the other hand, recent advances in
15 chip-based separation of proteins (microchip electrophoresis, MCE) have provided an easier system
16 than conventional gel electrophoresis with higher throughput (Anema, 2009). Despite cow milk
17 proteins having been extensively studied, there still is a substantial lack of characterization, and
18 particularly of quantitative information, about whey proteins from water buffalo. Several studies on
19 whey proteins have determined the primary structures of genetic variants of β -LG (Vohra, Kumar
20 Bhattacharya, Dayal, Kumar, & Sharma, 2006) and α -LA (Chianese et al., 2004; Fan, Li, & Wu,
21 2000; Ramesha, Khosravinia, Gowda, & Rao, 2008). Even after these reports, quantitative data
22 about whey proteins from Mediterranean water buffalo (the milk of which is mostly used to produce
23 the highly-valued PDO Mozzarella cheese) are evidently unavailable. Milk protein content can be
24 influenced by physiological and nutritional factors, but several studies have indicated that genetic
25 context plays the most important role in the control of milk composition (Martin, Szymanowska,
26 Zwierchowski, & Leroux, 2002). The main goal of this work was to obtain new data on the quali-

1 quantitative composition of the major whey proteins in Mediterranean water buffalo milk, useful for
2 animal selection purposes. An additional aim of this work was to test the performance of the MCE
3 technique for the routine analysis of water buffalo whey proteins.

4

5 **2. Materials and methods**

6

7 *2.1. Materials and reagents*

8 Commercial purified whey proteins, β -LG (purity 80%), α -LA (purity 85%), SA (purity 98%) from
9 bovine milk, and trifluoroacetic acid (TFA) were supplied by Sigma–Aldrich (St. Louis, MO, USA).
10 HPLC-grade water and acetonitrile were purchased from VWR International (West Chester, PA,
11 USA). MCE of whey protein was performed using the Bioanalyzer Protein 80 kit (Agilent
12 Technologies, Waldbronn, Germany) that contains chips and proprietary reagents (sieving gel
13 matrix, protein dye concentrate solution, marker protein buffer solution and protein molecular mass
14 ladder solution). All the other chemicals were purchased from Bio-Rad (Hercules, CA, USA).

15

16 *2.2. Standard solutions*

17 Individual mother solutions of whey proteins were prepared by weighing 45 mg of β -LG, 17 mg of
18 α -LA or 23 mg of SA and dissolving the weighed amounts in 4 ml, 4 ml and 25 ml of water,
19 respectively. Equal volumes of the individual mother solutions (1.5 ml each) were combined to
20 obtain a mixed standard solution. Aliquots of 200 μ l, 400 μ l, 600 μ l, 800 μ l and 1 ml were diluted to
21 the volume of 1.2 ml with water in order to obtain a set of diluted standards; these were used to
22 construct six-level calibration curves along with the undiluted mixed standard solution itself. The
23 final concentrations of this set of standards, corrected for the purity degrees of each protein, are
24 shown in Table 1.

25

26 *2.3. Milk sampling*

1 Individual milk samples from 120 Mediterranean water buffaloes (genus *Bubalus*, species *Bubalus*
2 *bubalis*) were collected at four farm sites in the Campania region (southern Italy). The animals were
3 from different breeding stocks. All samples were collected from animals at 120 d post partum. After
4 collection, samples were immediately frozen and kept at -20 °C until analysis. Prior to
5 determinations, milk was thawed overnight at 4 °C and the whey was obtained by centrifugation of
6 raw milk (8 ml) at 57,438 g for 90 min at 4 °C.

7

8 *2.4 Microchip electrophoretic analysis (MCE)*

9 A subset of 40 randomly chosen individual whey samples was analyzed by microchip
10 electrophoresis (MCE). The analyses were performed using an Agilent 2100 Expert Bioanalyzer,
11 operated by the 2100 Expert software, in conjunction with Agilent Protein 80 series II kits. The kit
12 reagents were prepared according to the manufacturer's instructions. In brief, the required gel-dye
13 mix was prepared by mixing 600 µl of spin-filtered sieving matrix with 25 µl of dye, whereas the
14 destaining solution was spin-filtered sieving matrix without any addition. To obtain reducing
15 conditions, a 3.5% (by volume) solution of β-mercaptoethanol was added to the kit sample buffer.
16 Two hundred microlitres of whey samples were diluted with 400 µl of water and filtered through a
17 0.45 µm-pore cellulose membrane (Phenomenex, Torrance, CA, USA), then prepared as follows.
18 Four microlitres of diluted samples were mixed with 2 µl of Protein 80 denaturing solution in 0.5 ml
19 tubes and heated at 95 °C for 5 min. After cooling at room temperature for 5 min, and shortly
20 spinning tubes at 11,000g for 30 s at 4 °C, the resulting solutions were further diluted with 84 µl of
21 water, vortexed and loaded onto the chips. All chips were loaded with two samples, in two repeats
22 each, and the full set of calibration standards. The instrumental operational parameters for the MCE
23 analysis, i.e. electrode programme, chip temperature and fluorescence detection, were set by the
24 Bioanalyzer software (which also allowed electrophoretogram acquisition and processing) upon
25 user's specification of the utilized kit.

26

1 *2.5. Reversed phase-high-performance liquid chromatography*

2 Whey samples were prepared by diluting 200 µl of ultracentrifuged whey with 400 µl of HPLC-
3 grade water. The diluted samples were filtered through a 0.45 µm-pore cellulose membrane and
4 directly analyzed in two repeats per sample. The chromatographic equipment consisted of a Waters
5 system (Waters, Milford, MA, USA), including two pumps (model 515, Waters), a manual injector
6 (Rheodyne, Cotati, CA, USA) equipped with a 20 µl loop, and a UV detector (model 2487, Waters).
7 The chromatographic separation was performed in reversed-phase mode, using a Jupiter C4 column
8 (250 x 4.6 mm, 300 Å-sized pores, 5 µm-sized particles; Phenomenex) maintained at 30 °C.
9 Gradient elution and peak detection were performed according to Enne et al. (2005).
10 Chromatograms were acquired and processed by the Empower 2 software (Waters).

11 12 *2.6. Mass spectrometry and chromatographic analysis of whey proteins*

13 The determination of the molecular mass of the chromatographic peaks was carried out on an
14 Agilent 1100 series HPLC chromatographer (Agilent, Santa Clara, CA, USA) combined with a
15 Micromass Q-TOF mass spectrometer (Waters), which was equipped with a nanospray source and
16 operated by the Mass-links version 4.1 (Waters) software. The chromatographic separation
17 conditions were as described above. Experiments were run using positive ion detection, applying a
18 capillary voltage of 2–5 kV and a cone voltage of 30–35 V; the capillary temperature was set at
19 220 °C. Determinations were carried out on two buffalo samples and one standard solution and
20 were repeated twice each.

21 22 *2.7. Quantification of whey proteins*

23 Whey proteins in samples were quantified by HPLC through the construction of calibration curves
24 by the external standard method. The calibration was performed by analyzing each mixed standard
25 in 10 repeats and calculating a linear regression of mean peak areas over concentration, in order to
26 obtain a six-level, 60-points calibration curve for each whey protein. Validation was performed as

1 follows: to estimate repeatability, a standard solution corresponding to the level 3 of the calibration
2 curves was analyzed, in 10 repeats, on the same analytical day; repeatability was expressed as the
3 relative standard deviation of peak times and areas over this dataset. Ruggedness (intermediate
4 precision) was estimated by repeating the same set of analyses for 3 days and calculating the overall
5 relative standard deviation for retention times and peak areas. Accuracy was evaluated by recovery
6 assays. Briefly, a bovine whey sample was subdivided into four 10 ml aliquots; one was taken as
7 blank and known amounts of commercial whey proteins were added to the other three, as follows.
8 The first aliquot was fortified with 4 mg of SA, 8 mg of α -LA and 20 mg of β -LG; the second one
9 was with 5 mg of SA, 10 mg of α -LA and 25 mg of β -LG, and the third one was with 6 mg of SA,
10 12 mg of α -LA and 30 mg of β -LG. The four aliquots were diluted, as above, and analyzed in
11 triplicate; the recovery rate was determined for each protein as the ratio between the peak area due
12 to the addition (i.e. the differences between the fortified aliquots and the blank) and the peak area
13 predicted by the calibration curves for the same addition, taking into account the purity degree of
14 the commercial whey proteins. Student's t-tests were applied to check whether the recovery rates
15 were significantly different from 100%. In order to test the performance of MCE, quantification of
16 whey protein in a 40-sample subset was also done, using the same set of standards as adopted for
17 HPLC. The electrophoretic quantification was calibrated by loading the set of standards onto each
18 chip, along with samples (two samples in two repeats per chip); the chip-specific calibration curves
19 obtained on each run were then used to quantitate the samples loaded onto the same chip only. The
20 MCE protocol was submitted to validation according to the same procedure as adopted for HPLC.
21 Statistical analysis was performed by means of the instrumentation software and of the R language
22 for statistical computing, version 2.8.1 (R Development Core Team, 2008).

23

24 **3. Results and discussion**

25 *3.1. Electrophoretic characterization of whey fractions*

1 Electrophoretic separation of water buffalo whey samples was performed by the MCE technique;
2 the aim was to obtain protein separation and quantification. This technique allowed very fast
3 separation of the major whey proteins as the run time was about 3 min per chip well. The resolution
4 achieved by this method enabled the complete separation of the three major whey proteins (Fig. 1).
5 The electrophoretograms are characterized by three major peaks and a number of lesser peaks,
6 possibly corresponding to minor whey proteins or degradation products. Overall, the separation
7 performance of MCE appeared very similar to traditional SDS–PAGE, which also indicated a slight
8 difference in SA migration between standards and samples. This small variation, however, did not
9 interfere with protein identification through sizing. Such features make MCE a convenient
10 alternative to SDS–PAGE (Goetz et al., 2004) with considerably higher throughput. Protein
11 quantification over a 40-sample subset was performed on a per-chip basis by loading the standards
12 onto each chip and using the software “calibrated quantification” feature to quantitate the samples
13 loaded onto the same chip, so that chip-specific calibration curves (Table 1) were used. The
14 corresponding results are shown in Table 2. The instrumental response showed nearly linear
15 behaviour, leading to average r^2 coefficients of 0.95 for α -LA, 0.94 for β -LG and 0.93 for SA over
16 all the chip runs. The mean values of buffalo α -LA, β -LG and SA concentrations indicated a
17 higher mean concentration of α -LA and β -LG than the literature data obtained for bovine whey
18 proteins by both HPLC (Farrell et al., 2004) and MCE (Anema, 2009); however, a high variability
19 (up to 39% for SA) was observed in the MCE results over the 40 analyzed samples.

20

21 *3.2. Identification of whey protein by chromatographic analysis and mass spectrometry*

22 The described RP-HPLC protocol allowed effective resolution of the individual whey proteins in
23 about 24 min with good precision of the retention times, thus allowing a reliable recognition of the
24 chromatographic peaks associated with SA, α -LA and β -LG proteins in the buffalo whey (Fig. 2).
25 In order to achieve an unambiguous identification of whey proteins from water buffalo samples, the
26 molecular masses of the chromatographic peaks, separated by the HPLC protocol, were determined

1 by ESI-MS. The results were: 66,397 Da for peak 1, 14,236 Da for peak 2 and 18,266 Da for peak 3,
2 corresponding to SA, α -LA and β -LG, respectively. As expected, the main difference between
3 standards and samples was represented by the β -LG which exhibits genetic polymorphism in cow
4 whereas it is genetically invariant in Mediterranean water buffalo. Besides, genetic polymorphisms,
5 at the β -LG locus, have been observed in Asian riverine buffalo (Vohra et al., 2006). Furthermore,
6 water buffalo α -LA exhibited a secondary small peak eluting before the major one, as shown in Fig.
7 2 (referred to as peak 2s). The presence of a minor additional peak may arise because of
8 glycosylation: in fact, several differently glycosylated forms of bovine α -LA have been described
9 by Slangen and Visser (1999). In addition, calcium ion loss at low pH, leading to a conformational
10 change with different folding and hydrophobicity, has been observed in human α -LA (Håkansson et
11 al., 2000) and subsequently confirmed in cow (Expósito & Recio, 2006). The molecular mass
12 measured for peak 2s (16,663 Da) is in accordance with the results reported by Slangen et al. (1999),
13 thus supporting the glycosylation scenario. The glycosylated alpha-lactalbumin was detected in all
14 whey samples. A further peak occurring in buffalo samples only and eluting after β -LG, as first
15 reported in Resmini, Pellegrino, Andreini, and Prati (1989), was also detected in all samples and
16 considered as the buffalo-specific Bx compound (referred to as peak 5 in Fig. 2); this peak was not
17 quantified but only characterized by its migration time (24.64 min with standard deviation of 0.22
18 min) and molecular mass (18,447 Da).

19

20 *3.3. Quantification of water buffalo whey proteins*

21 Protein quantification of 120 individual whey samples was performed by HPLC through the
22 external standard calibration method. The standards were analyzed at six concentration levels, in ten
23 repeats each, and the mean total peak areas generated by each protein were calibrated over
24 concentration by linear regression, yielding the equations and the corresponding statistical
25 parameters summarized in Table 3. The set of mixed standard solutions was designed to reflect the
26 commonly known proportions between the whey proteins in milk while ensuring suitable

1 concentration ranges for their simultaneous quantification. The instrument response was linear over
2 the chosen concentration range for all the proteins with r^2 coefficients of at least 0.998 and a
3 satisfactory prediction uncertainty (RSD less than 2.4% for all the proteins). The quantitative results
4 achieved for the three major whey proteins are shown in Table 4. Compared to the literature data on
5 bovine whey proteins, Mediterranean water buffalo showed, on average, higher concentrations of α -
6 LA, whereas β -LG and SA were very close to the values reported for cow milk. The quantitative
7 variability over the sampled buffaloes, as determined by HPLC, was in the range 17–27%, for all
8 three whey proteins. No data on the absolute quantification of water buffalo whey proteins by
9 HPLC or other techniques were found in the literature to draw a comparison. Farm-wise mean
10 protein concentrations were calculated and one-way ANOVA was used to test the presence of
11 significant differences between farms ($\alpha = 0.05$). The results indicated that the farm-wise groupings
12 were significant for all the proteins. One farm, referred to as “farm1” (means \pm SD: α -LA = $2.82 \pm$
13 0.69 g/l; β -LG = 4.92 ± 1.01 g/l; SA = 0.43 ± 0.13 g/l) featured several significant differences with
14 respect to the others. In particular, “farm1” showed significantly higher α -LA concentration than
15 did “farm2” (2.33 ± 0.41 g/l) and “farm4” (2.43 ± 0.44 g/l), significantly higher SA concentration
16 than “farm3” (0.32 ± 0.09 g/l) and “farm4” (0.34 ± 0.08 g/l) and, most interestingly, significantly
17 higher β -LG concentration than all the other farms (“farm2” = 4.12 ± 0.58 g/l; “farm3” = $3.81 \pm$
18 0.60 g/l; “farm4” = 3.96 ± 0.67 g/l). No significant differences not involving “farm1” were
19 observed, suggesting that the milk production from this farm is influenced by site-specific factors
20 (for example, genealogy of animals).

21

22 *3.4. Validation of HPLC and MCE protocols*

23 The performances of the HPLC protocol were tested in terms of precision and accuracy. The results
24 of the validation procedure are reported in Table 5. The method showed repeatability and
25 ruggedness of retention times below 1.5%, thus enabling a straightforward recognition of protein
26 peaks. The chromatographic results featured satisfactory and nearly uniform repeatability and

1 ruggedness of chromatographic areas (the former at levels below 2.4% and the latter not exceeding
2 3.6%) for all the peaks, indicating that the method offers acceptable quantification precision.
3 Accuracy was evaluated by means of recovery assays. The protocol achieved recovery rates close to
4 100% for all the whey proteins with acceptable standard deviations (8.8% or less), so that none
5 significantly differed from the theoretical expectation (for $\alpha = 0.05$). The same validation scheme
6 was applied to MCE, leading to the results shown in Table 5. The repeatability and ruggedness of
7 migration times were satisfactory, whereas the same parameters calculated for peak areas were in
8 the range of roughly 7–11%, depending on the protein. The observed repeatability and ruggedness
9 of the MCE separation are in accordance with those reported by Anema (2009) for α -LA and β -LG
10 and by Goetz et al. (2004) for SA, respectively. On the other hand, the recovery assays performed
11 by MCE led to recovery rates quite distant from 100% (up to 183% in the case of SA); in spite of
12 this, the Student's t-test did not indicate significant differences from the theoretical expectation (for
13 $\alpha = 0.05$) because of the large associated standard deviations. It is interesting to note that the former
14 are calculated on a single chip (repeatability) or using 30 repeats over 3 chips (ruggedness),
15 respectively. On the other hand, as no more than 10 analyses can be run on a single chip, the
16 recovery assays could only be performed using several chips because the calibration standards had
17 to be loaded on every run. Therefore, the exceedingly large standard deviations and distances from
18 100% observed in the MCE recovery assays can only be due to between-chip variation. This, of
19 course, implies that chips are scarcely comparable to each other, thus limiting the use of MCE as a
20 quantitative technique. The validation procedures highlighted substantial dissimilarities between
21 HPLC and MCE; the two methods are not strictly comparable, either by separation principle or by
22 separation and quantification performances. In particular, MCE does not feature the same
23 quantification reliability as does HPLC because of its larger standard deviations, thus allowing the
24 occurrence of discrepancies in the quantification of samples, such as those observed in the case of
25 β -LG (Tables 2 and 4).

1 **4. Conclusions**

2 In this study, the Mediterranean water buffalo whey proteins were analyzed to achieve reliable
3 identification and quantification of the α -LA, β -LG and SA by using a RP-HPLC method; well-
4 established techniques, such as gradient reverse-phase HPLC and electrospray ionization mass
5 spectrometry, were exploited. The analytical findings indicate that α -LA is, on average, more
6 abundant in water buffalo than in cow, whereas β -LG and SA show similar mean values. The
7 proteins did not show heterogeneity in chromatograms although a peak corresponding to
8 glycosylated α -LA was observed in buffalo samples. The results we report address the lack of data
9 concerning the Mediterranean water buffalo whey protein profile, as no previous data are available
10 in the literature.

11 In addition, as the obtained data are based upon the analysis of a suitable number of animals, this
12 research represents novel information that can be applied to the definition of selection schemes for
13 buffalo. In particular, the analysis of the protein concentrations, by farm, allowed us to identify one
14 site producing milk with significantly higher levels of whey proteins than the others. Furthermore,
15 we tested the ability of the microchip electrophoresis (MCE) to rapidly separate and characterize
16 whey proteins. The key operational advantage of MCE is its speed of analysis, representing a
17 significant and convenient improvement over traditional techniques, such as SDS-PAGE. The
18 higher throughput and the ability to consistently estimate molecular mass make MCE a suitable
19 technique for rapid screening of large sample sets and for routine protein sizing.

20

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7

1 **Table 1**

2 Composition of the whey protein concentration standards

Standard level	Final protein concentration [g/l]		
	SA [purity 98%]	α -LA [purity 85%]	β -LG [purity 80%]
1	0.05	0.20	0.50
2	0.10	0.40	1.00
3	0.15	0.60	1.50
4	0.20	0.80	2.00
5	0.25	1.00	2.50
6	0.30	1.20	3.00

3

4

1 **Table 2**

2 Mean concentration of whey proteins in water buffalo samples, as determined by MCE.

Peak	Whey protein	Migration time mean \pm SD, n = 40 [s]	Concentration mean \pm SD, n = 40 [g/l]
1	α -LA	21.86 \pm 0.05	2.20 \pm 0.88
2	β -LG	24.28 \pm 0.04	4.6 \pm 1.5
3	SA	39.60 \pm 0.04	0.40 \pm 0.15

3

4

1 **Table 3**

2 HPLC Calibration curves.

Whey protein	Equation ^a	RSD ^b [%]	r ²	Standard errors	
				Slope	Intercept
SA	$y = 3.64 * 10^7 x - 1.14 * 10^5$	1.91	0.999	$5.73 * 10^5$	$1.11 * 10^5$
α-LA	$y = 3.65 * 10^7 x + 7.17 * 10^5$	2.06	0.999	$6.25 * 10^5$	$4.87 * 10^5$
β-LG	$y = 3.02 * 10^7 x + 3.06 * 10^5$	2.36	0.998	$6.03 * 10^5$	$1.17 * 10^6$

3

4 ^a y: peak area; x: analyte concentration expressed as g/l.

5 ^b All the curves consist of 6 data points, each taken as the mean of 10 repeats.

6

7

1 **Table 4**

2 Concentration of whey proteins in water buffalo samples.

Peak	Whey protein	Rt mean \pm SD [min]	Concentration mean \pm SD, [g/l]	Cow (literature data ^a) [g/l]
1	SA	15.64 \pm 0.047	0.35 \pm 0.10	0.4
2	α -LA	18.26 \pm 0.0067	2.45 \pm 0.45	0.6–1.7
3	β -LG	22.73 \pm 0.0056	4.04 \pm 0.72	2–4

3

4 ^a Farrell et al., 2004.

5

1 **Table 5**

2 Validation of the HPLC and MCE protocols using bovine standards: precision and accuracy.

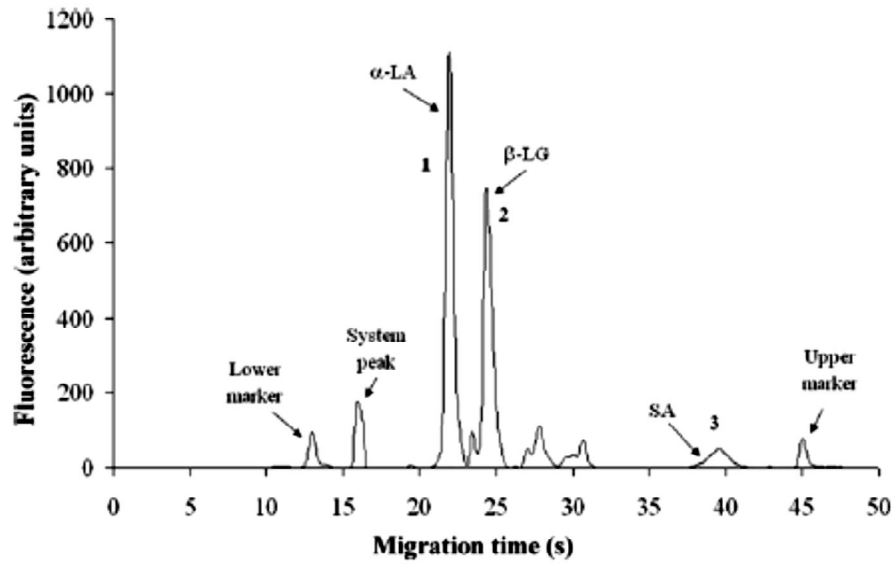
	Peak time RSD (%)		Peak area RSD (%)		Quantitation accuracy		
	Repeatability	Ruggedness	Repeatability	Ruggedness	Recovery rate (%)	RSD (%)	<i>t</i> -test ($t_{0.05,2} = 4.30$)
<i>HPLC</i>							
SA	0.31	1.31	2.31	2.80	99.8	5.46	0.047
α -LA	0.037	1.20	2.35	3.18	109.6	3.90	4.252
β -LG	0.025 ^a 0.034 ^b	0.82 ^a 0.73 ^b	2.06 ^a 2.07 ^b	3.04 ^a 3.58 ^b	97.1	8.80	0.562
<i>MCE</i>							
SA	0.09	0.92	11.3	11.9	183	36	4.039
α -LA	0.23	0.25	7.16	6.85	130	46	1.111
β -LG	0.18	0.21	6.91	9.04	140	65	1.058

3

4 ^a First peak in elution order.5 ^b Second peak in elution order.

6

1 **Fig. 1.** MCE electrophoretogram (emitted fluorescence vs. migration time) of whey from
2 Mediterranean water buffalo individual milk obtained by MCE using an Agilent 2100 Bioanalyzer
3 in combination with a Protein 80 kit. Mass markers and system peaks are also indicated.



4

5

1 Fig. 2. Chromatogram of whey from Mediterranean water buffalo individual milk. Peak 2s is a
2 secondary α -lactalbumin peak observed in buffalo samples, which is considered a glycoform of α -
3 LA based on its molecular mass. Column: Phenomenex Jupiter C4 (250 mm x 4.6 mm, 300 Å pores,
4 5 μ m particles); detection: UV, $\lambda = 205$ nm; mobile phase: water containing 0.1% trifluoroacetic
5 acid (TFA)/acetonitrile containing 0.1% TFA (refer to Section 2.5 for elution gradient details).

