

Copyright is owned by the Author of the thesis. Permission is given for a copy to be downloaded by an individual for the purpose of research and private study only. The thesis may not be reproduced elsewhere without the permission of the Author.

DEVELOPMENT OF METHODS FOR

CAPILLARY ISOELECTRIC

FOCUSING OF

DAIRY PROTEINS

A THESIS PRESENTED IN FULFILMENT OF THE

REQUIREMENTS FOR THE DEGREE OF

MASTER OF SCIENCE IN CHEMISTRY

AT MASSEY UNIVERSITY,

NEW ZEALAND

LEYTON WILLIAM GAPPER

January 2006

Abstract

Capillary Isoelectric Focusing (CIEF) is a high-resolution technique which can be applied to the separation and characterisation of complex biological mixtures such as dairy proteins. Although dairy proteins are commonly analysed by traditional gel electrophoresis techniques including 2-Dimensional PAGE, CIEF offers the advantages of reduced analysis times, the ability to handle smaller sample volumes and increased sensitivity with improved separation efficiencies.

Several methods for capillary isoelectric focusing of dairy proteins have been developed herein. For the analysis of soluble whey proteins methods that can be used with either UV or mass spectrometry (MS) detection have been set up. For MS detection a coaxial sheath flow interface in conjunction with electrospray ionisation has been utilised. For analysis of the inherently insoluble casein proteins with UV detection denaturing and reducing agents have been introduced into the system. Results have shown very close similarities to those obtained by IEF gels.

Acknowledgements

I would like to thank my wonderful supervisors Dr Kate Palmano and Professor Dave Harding for their hard work in helping me with every step of this thesis.

In addition I would like to thank Mark Ward for giving me the opportunity under his management to undertake this thesis. I would like to acknowledge the following managers who have allowed me to work on this thesis during time in their section: Nick Robinson and Steve Holroyd.

Bertram Fong requires a large amount of thanks for numerous hours helping me with ideas throughout the thesis, trouble shooting and generally being a great friend. Thank you to the following people who have taught me techniques or added ideas: Don Otter, Carmen Norris, and Debbie Husband.

Thanks to other people who have worked in the laboratory in particular Therese Considine, Yacine Hemar, Skelte Anema, Dave Elgar, Sophia Stathopoulos and all the other staff in the Level 2 South wing laboratory at Fonterra Innovation throughout the time of my thesis.

My family require a special acknowledgement. With out the support of my Mother Linda, Father Brian and Brother Nigel this thesis would have been a lot harder, I have drawn inspiration from you all to keep me motivated to finish the thesis. This document is dedicated to all 3 of you and one last special person,...

Janina, Thank you for your love and compassion, and your patience for me to do the thesis as it has meant sacrificing many hours together.

Contents

Abstract	i	
Acknowledgements ii		
Contents	iii	
List of Abbreviations	xiv	
1 Overview	1	
 2 Literature Review 2.1 Composition of Bovine Milk 2.2 Introduction to Capillary Electrophoresis 2.3 Capillary Zone Electrophoresis 2.4 Micellar Electrokinetic Chromatography 2.5 Capillary Isotachophoresis 2.6 Capillary Electrochromatography 2.7 Capillary Isoelectric Focusing 2.8 Recent Reviews on CE of Large Biomolecules 2.9 CE of Dairy Proteins 2.9.1 Analysis of Casein 2.9.2 Whey Protein Separation 2.10 CE-MS 13 2.10.1 Coaxial Sheath-flow Interface 2.10.2 Sheathless Interface 2.11.1 CZE-MS 2.11.2 CIEF-MS 2.11.3 CITP-MS 2.11.4 MEKC-MS 2.11.5 CEC-MS 2.11.6 CGE-MS 	3 5 7 7 8 8 9 9 10 13 14 15 16 16 16 16 17 17 18 18	
 3 Experimental Conditions 3.1 Chemicals 3.2 Sample and Buffer Preparations for CIEF Experiments 3.2.1 Whey Basic Protein Fraction 3.2.2 Whey Protein from Skim Milk 3.2.3 Casein Protein from Skim Milk 3.2.4 Standards 	20 20 21 21 21 21 21 22	

		3.2.5	Buffers	22
	3.3	CIEF-U	V Experiments	22
	3.4	CIEF-U	V in a non-denatured system	23
	3.5	CIEF-U	V in a denatured system	24
	3.6	CIEF-M	IS Experiments	25
	3.7	Infusior	n MS experiments	27
	3.8	CZE of	Whey Proteins	27
	3.9	CZE of	Casein	27
		3.9.1	Buffers	27
		3.9.2	Sample Preparation	28
		3.9.3	CZE Parameters	28
	3.10	Flatbed	IEF gel preparation	29
		3.10.1	IEF Sample preparation	29
		3.10.2	Skim Milk	29
		3.10.3	Standards	29
		3.10.4	Whey Basic Fraction	30
	3.11	Flatbed	IEF gel running conditions	30
	3.12	Focusir	ıg	30
	3.13	IEF gel	staining	30
		3.13.1	Coomassie Blue R-250 Stain	30
		3.13.2	Coomassie De-Stain	31
		3.13.3	Staining Procedure	31
	3.14	2-Dime	nsional Gel Electrophoresis Experiments	31
		3.14.1	Buffers	31
		3.14.2	Sample Preparation	32
		3.14.3	IEF Focusing	32
		3.14.4	Second Dimension SDS-PAGE	32
	Resu	ults		34
	4.1	CIEF-U	V Water Soluble Method	34
		4.1.1	Method development protocol	34
		4.1.2	Protein Concentration	34
		4.1.3	Buffer Choice	37
		4.1.4	Column Choice, Length & Internal Diameter	40
		4.1.5	Detection Choice and Wavelength Selection	48
		4.1.6	Ampholyte Choice	50
		4.1.7	Focusing Times	56
		4.1.8	Mobilisation Techniques	58
		4.1.9	Changes in Voltage	60
\$.		4.1.10	Temperature Effects	64
		4.1.11	Addition of Surfactants	67
		4.1.12	Linearity of Standards	67
		4.1.13	Method Repeatability	69
		4.1.14	Applications of the CIEF-UV Method	72
	4.2	Insolub	le Dairy Proteins with UV detection	81
	4.3	MS Infu	ision Experiments	82

4

	4.4	CIEF-MS Detection	84
		4.4.1 Method Development	84
		4.4.2 CIEF-MS Applications	88
	4.5	Flat Bed IEF Gels	91
	4.6	PAGE 2D Gels	92
	4.7	CZE of Dairy Proteins and Peptides	95
		4.7.1 Whey Proteins	95
		4.7.2 Casein	95
	4.8	Comparison of Methods	96
		4.8.1 CIEF to CZE Methods	96
		4.8.2 CIEF to Gel Methods	98
		4.8.3 CIEF-MS to 2D-PAGE-MS	99
5	Con	clusions	101
6	Futu	ıre Work	103
7	Refe	erences	104
Арр	endix	1 CIEF literature	116
Арр	endix	2 Results of Infusion MS experiments	124
Арр	endix	3 Results of MS infusion of basic protein fraction samples	144
Appendix 4 Publications			150

Table of Figures

Figure 1 Ger	neral Schematic overview of a CE instrument including	
	cathode, anode, capillary, high voltage power supply.	
	detector and data acquisition.	5
Figure 2 Sch	ematic of the Finnigan coaxial sheath-flow CE-MS interface	-
0	as used in this research.	15
Figure 3 A ty	pical electropherogram (Black) with current trace (Red) of	
- ·	whey protein from skim milk, with internal pl markers added.	
	The sample was run on a 30 cm MicroSoly Zero flow column	1
	at 12 kV. Focusing was performed for 6 minutes followed by	•
	pressure mobilisation at 0.1 psi. Anode comprised 20 mM	
	phosphoric acid and cathode buffer comprised 20 mM	
	sodium hydroxide, Ampholytes used were Beckman 3-10 at	
	2% (v/v) concentration. Tryp = trypsinopen. Mb-B =	
	myoglobin basic, Mb-A = myoglobin acidic, CA = carbonic	
	anhydrase I, β -lac-B = β -lactoglobulin-B, β -lac-A = β -	
	lactoglobulin-A, α -Lac = α -lactalbumin. TI = trypsin inhibitor.	
	AM = amyloglucosidase. Detection was UV at 280 nm.	36
Figure 4 Con	nparison of buffer types. Electropherograms of skim milk	
-	whey protein with internal standards. Samples were ran in	
	an identical manner to that in Figure 3 except bottom trace	
	(Red) represents run with 1 % acetic acid at the anode and	
	1 % ammonia at the cathode. Peak 1 = trypsinogen, peak 2	
	= myoglobin, peak 3 = carbonic anhydrase, peak 4 = β -	
	lactoglobulin-B, peak 5 = β -lactoglobulin-A, peak 6 = α -	
	lactalbumin, peak 7 = trypsin inhibitor, and peak 8 =	
	amylogiucosidase.	38
Figure 5 Com	nparison of column coatings. Electropherograms of whey	
	proteins from skim milk and internal pl standards run in a	
	manner identical to that in Figure 3 except different columns	
	(30 cm) were used to generate each electropherogram.	
	From the top trace: Black- MicroSolv Zero flow, Red- Bare	
	fused silica, Blue- BGB, Purple- SGE, Maroon- MicroSolv	
	Low flow, Green-Beckman neutral capillary. Peak 1 =	
	trypsinogen, peak 2 = myoglobin, peak 3 = carbonic	
	anhydrase, peak 4 = β -lactoglobulin-B, peak 5 = β -	
	lactoglobulin-A, peak 6 = α -lactalburnin, peak 7 = trypsin	
	inhibitor, and peak 8 = amyloglucosidase.	11
Figure 6 Calif	bration Curves of pl versus migration time for each column	
	type compared in Figure 5. The equation and regression	
 .	values for each column are expressed in Table 5.	14
Figure 7 Com	parison of column length. Electropherograms of skim milk	
	whey proteins and internal pl standards. Both	
	electropherograms run identically to Figure 3 except that the	
	bottom electropherogram was run on a 60 cm column with a	

voltage of 24 kV to be consistent with the 30 cm column. Peak 1 = trypsinogen, peak 2 = myoglobin, peak 3 = carbonic anhydrase, peak 4 = β -lactoglobulin-B, peak 5 = β lactoglobulin-A, peak 6 = α -lactalbumin, peak 7 = trypsin inhibitor, and peak 8 = amyloglucosidase. 46 Figure 8 Electropherograms of whey protein with internal pl standards for capillaries of 75 µm i.d. (top) and 50 µm i.d. (bottom). Note standards are identical to those used in Figure 3 except trypsinogen is replaced with ribonuclease A and amyloglucosidase is replaced with CCK flanking peptide. Peak 1 = ribonuclease A, peak 2 = myoglobin, peak 3 = carbonic anhydrase, peak $4 = \beta$ -lactoglobulin-B, β lactoglobulin-A, and α -lactalbumin peak 5 = trypsin inhibitor, and peak 6 = CCK flanking peptide. 48 Figure 9 Comparison of detector type and wavelength. Samples are whey protein from skim milk run identically to Figure 3. From top to bottom: 214 nm PDA detector, 280 nm PDA detector, 214 nm UV detector, and 280 nm UV detector. 50 Figure 10 Comparison of different ampholyte brands. Each electropherogram represents whey protein from skim milk run on a 60 cm MicroSolv Zero flow column. All samples except that shown in the bottom electropherogram were spiked with β-lac-B. All other instrument settings were the same as those described in Figure 3. From the top: Beckman ampholyte 3-10, Bio-Rad 3-10, Fluka 3-10, Pharmacia 3-10, Sigma 2.5-7. Peak 1 = β-lactoglobulin-B, peak 2 = β -lactoglobulin-A, and peak 3 = α -lactalbumin. 52 Figure 11 Comparison of ampholyte concentration. Electropherograms of whey protein from skim milk showing the effects of different concentrations of ampholytes added to the sample. Top: 2 % (v/v) ampholyte added, Bottom: 0.5 % (v/v) ampholyte added. All other parameters were the same as in Figure 3 except the separation was performed on a 60 cm column. Peak 1 = β -lactoglobulin-B, peak 2 = β -lactoglobulin-A, and peak 3 = α -lactalbumin. 54 Figure 12 Effects of using narrow range ampholytes. Sample is whey basic protein fraction number 2 run identically to the sample in Figure 3 except for the addition of either 2 % (v/v) Bio Lite 7-9 or Fluka 7-9. 56 Figure 13 Electropherograms obtained using different focusing times on the same sample. All samples were run on the same 30 cm MicroSolv Zero flow column with operating parameters and sample identical to those in Figure 3 except for the focusing and mobilisation parameter changes. Peak 1 = trypsinogen, peak 2 = myoglobin, peak 3 = carbonic anhydrase, peak 4 = β -lactoglobulin-B, peak 5 = β -lactoglobulin-A, peak 6 = α - lactalbumin, peak 7 = trypsin inhibitor, and peak 8 = amyloglucosidase.

57

- Figure 14 Mobilisation Techniques. Electropherograms of whey protein from skim milk with internal *pl* markers. Each sample was run identically to that in Figure 3 except different types of mobilisation was used. Top trace = pressure mobilisation at 0.1 psi, middle trace = chemical mobilisation, bottom trace = EOF mobilisation. Peak 1 = trypsinogen, peak 2 = myoglobin, peak 3 = carbonic anhydrase, peak 4 = β lactoglobulin-B, peak 5 = β -lactoglobulin-A, peak 6 = α lactalbumin, peak 7 = trypsin inhibitor, and peak 8 = amyloglucosidase. 59
- Figure 15 Effect of change in voltages across a capillary. Sample and experiment settings were identical to those outlined in Figure 3, except voltage was changed throughout. Peak 1 = trypsinogen, peak 2 = myoglobin, peak 3 = carbonic anhydrase, peak 4 = β -lactoglobulin-B, peak 5 = β lactoglobulin-A, peak 6 = α -lactalbumin, peak 7 = trypsin inhibitor, and peak 8 = amyloglucosidase. 61
- Figure 16 Change in temperature. Electropherograms of whey protein from skim milk with *pl* markers run identically to the sample in Figure 3 except that capillary temperature was altered and ribonuclease *pl* marker was substituted for trypsinogen. From top to bottom: 15, 20, 25, 30, and 35°C. Of particular interest is the disappearance of the α -Lac peak with increasing temperature and differences in the amount of spiking occurring in each electropherogram. Peak 1 = ribonuclease, peak 2 = myoglobin, peak 3 = carbonic anhydrase, peak 4 = β -lactoglobulin-B, peak 5 = β lactoglobulin-A, peak 6 = α -lactalbumin, peak 7 = trypsin inhibitor, and peak 8 = amyloglucosidase. 65
- Figure 17 Differences in the peak areas of whey protein peaks from skim milk at different temperatures for 2 sets of data run identical to Figure 16. Al = α -lactalbumin, BA = β -lactoglobulin-A, and BB = β -lactoglobulin-B. 1 = sample set 1, 2 = sample set 2. 66
- Figure 18 Differences in the percentage areas of the whey protein peaks identified in Figure 16. Percentages were calculated relative to the total area of the whey protein peaks. Samples were analysed identically to those outlined in Figure 16. AL = α lactalbumin, BA = β -lactoglobulin-A, and BB = β lactoglobulin-B. 1 = sample set 1, 2 = sample set 2. 67
- Figure 19 Method reproducibility as shown by 10 electropherograms of whey protein from skim milk with internal *pl* markers run consecutively. Samples were run under identical conditions to those used in Figure 3. Peak 1 = trypsinogen, peak 2 =

myoglobin, peak 3 = carbonic anhydrase, peak 4 = β -	
lactoglobulin-B, peak 5 = β -lactoglobulin-A, peak 6 = α -	
lactalbumin, peak 7 = trypsin inhibitor, and peak 8 =	
amyloglucosidase.	71
Figure 20 Separations achieved for several whey basic protein fraction	
samples. Top trace is the total whey basic protein fraction	
(fraction 1), middle trace is a subfraction of the top trace	
sample (fraction 2) as is the bottom trace (fraction 3). The	
main components of the sample are lactoferrin,	
lactoperoxidase and angiogenins. Each electropherogram	
was generated using the same parameters as used in	
Figure 3.	74
Figure 21 Electropherograms of angiogenin (top), lactogenin (middle), ar	nd
a blank sample (bottom). The angiogenin and lactogenin	
samples are sub fraction samples of the total whey basic	
protein fraction and were found to have a $pl > 9.1$. Samples	3
were run identically to those in Figure 3.	75
Figure 22 Electropherogram of a whey acidic protein fraction from minera	al
acid whey. Sample run identical to the sample in Figure 3.	76
Figure 23 Electropherogram of a GMP fraction (cheese whey acidic	
protein fraction) isolated from a cheese whey retentate.	
Sample run identical to that in Figure 3.	76
Figure 24 Electropherograms of industrial scale samples of	
lactoperoxidase protein. Top trace for reference purposes i	s
a Sigma standard, the following four traces are four differer	nt
prototype products.	77
Figure 25 Analysis of a whey based industrial hydrolysate sample.	
Separation parameters were identical to those used in	
Figure 3. The sample was made at a concentration of 3	
mg/ml (w/v) with 2 % Beckman 3-10 ampholytes added.	78
Figure 26 Electropherograms of bacterial cell lysate "B12" run 4 times	
(each electropherogram off set). Separation conditions wer	е
identical to that in Figure 3.	80
Figure 27 Electropherograms of bacterial cell lysate "X7" (Top and middle	e)
run one after the other. After the second sample was run it	
was noticed that there was a pellet formed at the bottom of	
the sample vial. All samples run using conditions identical t	0
that in Figure 3.	80
Figure 28 Electropherograms of skim milk run under identical conditions	
except the top trace utilised β -mercaptoethanol (BME), whi	le
the bottom trace utilised DTT in the sample buffer.	81
Figure 29 Comparison of different buffers under MS running conditions.	
Samples were whey protein from skim milk with standard p	1
markers. Samples were run identically to those in Figure 3,	
except that a voltage of 10 kV was applied to the 30 cm	
column. Buffers used are outlined in Table 13. Peak 1 =	

trypsinggen, peak 2 = myoglobin, peak 3 = carbonic	
anhydrase, peak 4 = β -lactoglobulin-B, peak 5 = β -	
lactoglobulin-A peak 6 = α -lactalbumin peak 7 = trypsin	
inhibitor and peak 8 = amyloglucosidase	85
Figure 30 TIC of CIEF-MS of whey protein from skim milk spiked with	05
minor whey proteins (BSA_GMP, and PP5) and al marke	arc 87
Figure 31 Representation of molecular weight versus retention time for	:15.07
TIC in Figure 30. Eveny 10 microscope of the MS date w	uie
deconvoluted by Pieworks offware. Proteins were then	ere
identified according to molecular mass with comparison t	
infused standards. Mb B = musclabia basis. Mb A =	0
mused standards. MD-D - myoglobin basic, MD-A =	e
Invoglobili acidic, CA – carbonic annydrase I, p-lac-B = p)-
lactoglobulin-B, p-lac-A = p-lactoglobulin-A, α -Lac = α -	
actaibumin, TT = trypsin innibitor, BSA = bovine serum	
albumin, PP5 = proteose peptone 5, GMP =	~~
giycomacropeptide.	90
Figure 32 IEF flatbed gel of skim milk (SM, left lane) and whey basic	
protein fraction number 1 (right lane).	92
Figure 33 2D PAGE of whey basic protein fraction sample 1.	93
Figure 34 2D PAGE of whey basic protein fraction sample 2.	94
Figure 35 2D PAGE of whey basic protein fraction sample 3.	94
Figure 36 CZE separations of whey proteins from skim milk utilising the	9
method of Kinghorn et al. (1996). The top trace represent	ts
protein standards of the major constituents of whey prote	ins,
α -Lac (peak 1), β -Lac-A (peak 4), β -Lac-B (peak 3) and	
minor component β -Lac-C (peak 2) genetic variant. The	
bottom trace is the response for skim milk showing α-Lac	, β-
Lac-B, and β-Lac-A.	95
Figure 37 CZE separation of milk proteins from skim milk by the metho	d
outlined in section 3.9. The method was similar to that us	ed
by Recio et al., (1997).	96
Figure 38 Comparison of flat bed IEF-PAGE with laser densitometry to	
CIEF-UV using the denaturing CIEF method (Section 3.5). 99
Figure 39 Results of α-Lac standard infused into MS	127
Figure 40 Results of deconvolution of α-Lac	127
Figure 41 Results of amyloglucosidase standard infused into MS	128
Figure 42 Results of deconvolution of amyloglucosidase	128
Figure 43 Results of β-Lac-A standard infused into MS	129
Figure 44 Results of deconvolution of β-Lac-A	129
Figure 45 Results of β-Lac-B standard infused into MS	130
Figure 46 Results of deconvolution of β-Lac-B	130
Figure 47 Results of BSA standard infused into MS	131
Figure 48 Results of deconvolution of BSA	131
Figure 49 Results of carbonic anhydrase standard infused into MS	132
Figure 50 Results of deconvolution of carbonic anhydrase	132

Figure 52 Results of deconvolution of GMP	133
Figure 53 Results of IgG standard infused into MS	134
Figure 54 Results of deconvolution of IgG	134
Figure 55 Results of lactoferrin standard infused into MS	135
Figure 56 Results of deconvolution of lactoferrin	135
Figure 57 Results of lactoperoxidase standard infused into MS	136
Figure 58 Results of deconvolution of lactoperoxidase	136
Figure 59 Results of lactoferrin deglycosylated infused into MS	137
Figure 60 Results of deconvolution of deglycosylated lactoferrin	137
Figure 61 Results of myoglobin standard infused into MS	138
Figure 62 Results of deconvolution of myoglobin	138
Figure 63 Results of PP5 standard infused into MS	139
Figure 64 Results of deconvolution of PP5	139
Figure 65 Results of ribonuclease standard infused into MS	140
Figure 66 Results of deconvolution of Ribonuclease	140
Figure 67 Results of trypsin inhibitor standard infused into MS	141
Figure 68 Results of deconvolution of trypsin inhibitor	141
Figure 69 Results of trypsinogen standard infused into MS	142
Figure 70 Results of deconvolution of trypsinsinogen	142
Figure 71 Results of CCK Peptide standard infused into MS	143
Figure 72 Results of whey basic protein fraction 3 sample infused into M	//S144
Figure 73 Results of deconvolution of whey basic protein fraction 3	145
Figure 74 Results of whey basic protein fraction 2 sample infused into M	//S146
Figure 75 Results of deconvolution of whey basic protein fraction 2	146
Figure 76 Results of whey basic protein fraction 1 sample infused into M	AS147
Figure 77 Results of deconvolution of whey basic protein fraction 1	147
Figure 78 Results of angiogenin sample infused into MS	148
Figure 79 Results of deconvolution of angiogenin sample	148
Figure 80 Results of lactogenin sample infused into MS	149
Figure 81 Results of deconvolution of lactogenin sample	149

Table of Tables

Table 1 Major protein constituents of bovine milk including approximate	
concentration of each protein (depending on time of	
lactation) and genetic variants. From Swaisgood (1986).	4
Table 2 LCQ Mass Spectrometry instrument settings for CIEF-MS	
experiments.	26
Table 3 Literature values for isoelectric points and molecular weights of	
proteins used throughout this research. Typical CIEF	
working concentrations are also included.	35
Table 4 pH values for focusing buffers and mobilisation buffers in CIEF	
experiments.	39
Table 5 Comparison of the electropherograms obtained from using	12025
different 30 cm columns as shown in Figure 5.	43
Table 6 Comparison of column volume (nl) when changing parameters	
such as length or internal diameter. Calculated from CExpe	rt
(Beckman Coulter)	46
Table 7 Comparison of results from the electropherograms shown in	
Figure 7 for differences in column length on the MicroSolv	
Zero Flow capillary and between batches of capillary (For 3	0
cm results)	47
Table 8 Comparisons of focusing times and mobilisation techniques. All	
samples were run on the same 30 cm MicroSoly Zero Flow	
column with instrument parameters identical to those in	
Eigure 3 except for the focusing and mobilization parameter	-
changes	58
Table 9 Comparison of differences in separation for different voltages	00
from data obtained in experiments in Figure 15	63
Table 10 Optimised conditions for CIEE analysis of skim milk whey	00
proteins and p/markers for a Beckman P/ACE CE. The	
ontimised conditions were used on a number of other dainy	
applications for CIEE discussed in later sections	69
Table 11 Analysis of method reproducibility with the results of the average	00
retention time, standard deviation and percentage difference	
for 3 sets of 10 samples run on different days. See text for	C
details	72
Table 12 Results of MS infusion experiments of whey basic protein	12
fraction samples	81
Table 13 Buffer compositions for the electropherograms shown in Figure	04
20 All buffer percentage compositions were in a v/v ratio	86
Table 14 Summary of literature for CIEE with LIV detection. Outlined are	00
applications of samples separated buffers used rupping	
conditions and comments about each reference	116
Table 15 Summary of literature for CIEE with MS detection. Outlined are	110
applications of different types of complex concreted buffer	
applications of unterent types of samples separated, buffer	5

used, running conditions and comments about each reference.

120

Table 16 Results of infusion MS experiments. MS conditions used are
outlined in section 3.7. Deconvolution of mass spectrums
was performed on Bioworks version 3.1. Literature masses
were obtained from Mascot (www.matrixscience.com) web
site. N/A = data not available due to lack of ionisation. Mass
Spectra and deconvoluted data for each standard are
presented in Figure 39 to Figure 70.124

List of Abbreviations

2D	Two Dimensional
a-csn	α-Casein
α-Lac	α-Lactalbumin
Amy	Amyloglucosidase
β-csn	β-Casein
β-Lac	β-Lactoglobulin
β-Lac-A	β-Lactoglobulin-A
β-Lac-B	β-Lactoglobulin-B
BME	β-Mercaptoethanol
BSA	Bovine Scrum Albumin
CA	Carbonic Anhydrase II
ССК	CCK Flanking Peptide
CE	Capillary Electrophoresis
CEC	Capillary Electrochromatography
CGE	Capillary Gel Electrophoresis
CIEF	Capillary Isoelectric Focusing
CITP	Capillary Isotachophoresis
CZE	Capillary Zone Electrophoresis
DNA	Deoxyribosenucleic Acid
DTT	DL-Dithiothreitol
EDTA	Ethylenediaminetetra-Acetic Acid
EOF	Electroosmotic Flow
ESI	Electrospray Ionisation
GMP	Glycomacropeptide
HPLC	High Performance Liquid Chromatography

i.d.	Internal Diameter
IEF	Isoelectric Focusing
Ig	Immunoglobulin
IgG	Immunoglobulin G
к-csn	κ-Casein
kV	Kilo Volt
Lf	Lactoferrin
Lp	Lactoperoxidase
mA	Milli Amps
Mb	Myoglobin
Mb-A	Myoglobin Acidic
Mb-B	Myoglobin Basic
MEKC	Micellar Electrokinetic Chromatography
MFGM	Milk Fat Globule Membrane
mg	Milli Gram
MHEC	Methyl 2-hydroxyethyl cellulose
mL	Milli Litre
MOPS	3-[N-Morpholino]propane-sulfonic acid
MS	Mass Spectrometery
MWCO	Molecular Weight Cut Off
NaOH	Sodium Hydroxide
nL	Nano Litre
PAGE	Polyacrylamide Gel Electrophoresis
PDA	Photo Diode Array
рI	Isoelectric Point (of a protein or peptide)
PP5	Proteose Peptone 5
PSI	Pounds per Square Inch

Rb	Ribonuclease
RNA	Ribosenucleic Acid
RP	Reversed Phase
SDS	Sodium Dodecylsulfate
TCA	Trichloroacetic Acid
TEMED	N,N,N',N'-tetramethylethylenediamine
TI	Trypsin Inhibitor
TIC	Total Ion Count
Tris	Tris(hydroxymethyl)-aminomethane
Тгур	Trypsinogen
μg	Micro Gram
μL	Micro Litre
UV	Ultraviolet
V/cm	Volts per Centimetre (of column length)
v/v	Volume to Volume
v/w	Volume to Weight

1 Overview

Capillary Isoelectric Focusing (CIEF) is a technology that has developed in the last few years and is a technique whereby proteins and peptides are separated according to their isoelectric point (pI); such separations are generally as good as those obtained by flat bed isoelectric focusing (IEF) polyaerylamide gel electrophoresis (PAGE). Advancements in CIEF technology have been led by the requirements of proteomic research for high throughput analysis coupled with limited sample size. Routine methods for CIEF involve ultraviolet (UV) detection, but mass spectrometry (MS) detection is becoming more popular for many research groups. This is analogous to the time consuming method of 2-dimensional IEF/ PAGE in which spots on gels are excised, digested with enzyme, and the digests analyzed by high performance liquid chromatography-MS (HPLC-MS). CIEF-MS has the capability to reduce analysis times considerably and is used for a number of applications. Detection is of intact protein rather than hydrolyzed protein, which saves time on database searches. In recent years the CIEF-UV method that has traditionally only had applications to water soluble protein, has been modified for separation of proteins in denaturing systems. In this way proteins that are inherently insoluble can be separated by CIEF. Currently there is only one CIEF method within the literature that has a dairy application and this is based on the monitoring of glycosylation products of glycomacropeptide (GMP) (Tran et al. 2001).

Over the last few years dairy industries around the world have embarked on largescale proteomic research, with a view to one or more of the following:

- a.) The discovery of low abundance proteins and peptides that may have potential health benefit that could be explored in niche products of the future.
- b.) Understanding expression and co-regulation of milk proteins.
- c.) Acquisition of intellectual property for future strategic use.

The competitive edge of a dairy company is governed partly by the speed in which fundamental research can be translated into a commercial process or product. In this respect it is mandatory to identify new technological areas and analytical techniques that may allow large time and cost savings in the commercialization pipeline. Capillary electrophoresis (CE) is one such analytical tool as it is rapid, has very good detection limits, can be interfaced to MS detection and requires very small sample size.

The aim of this research was to develop new methods in CE analysis that would be applicable to a wide variety of dairy-based samples, and could be used as rapid screening methods for proteomic applications. The CE mode of CIEF was investigated, as sample size in this format is generally 20 times larger than other modes of CE, thus enhancing detection sensitivity, and the method is able to separate proteins and peptides over a wide range of pI values. The method has the additional advantage that pI values can help in the identification of unknown protein. The technique is also very rapid and gives very good comparison to the IEF gel format, making this technology very much cheaper and less labour intensive to use.

Bovine dairy proteins are comprised of two main groups, the casein and the whey proteins. Caseins make up approximately 80 % of dairy protein and typically occur as micelles in milk, being inherently insoluble. Whey proteins on the other hand make up the remaining 20 % of protein and tend to be globular water-soluble proteins, while in addition there is another group of proteins collectively termed the milk fat globule membrane (MFGM) protein that makes up a very small amount (<1 %) of protein in milk. Taking these general properties into consideration the overall aim of this thesis was to develop methods of CIEF for the different types of dairy protein as follows:

- Develop methods using UV detection that are simple to run with minimum preparation and optimized for:
 - The major whey proteins
 - Casein proteins
 - Fractionated protein samples
- Compare these methods to IEF flat bed PAGE
- Develop methods of CIEF-MS for soluble proteins and if possible modify the method for insoluble proteins
- Compare CIEF-MS results to two dimensional PAGE (2D-PAGE) methods
- Compare CIEF methods to already developed CZE methods where applicable