Target Peptide Identification for the Mass Spectrometric Detection of Soy Proteins in Food Matrices Lincoln



Shimin Chen¹, Charles Yang², and Melanie Downs¹

¹Food Allergy Research & Resource Program, Department of Food Science and Technology, University of Nebraska-Lincoln, Lincoln, Nebraska, USA ²Thermo Fisher Scientific, San Jose, CA

INTRODUCTION

- Soybeans are one of the "Big eight" allergenic foods in the US, with soy allergies affecting approximately 0.4% of children.¹
- Because of their functional properties and high protein content (~38%), soybeans have been widely used in various food products such as baked foods (e.g. cookies, crackers), beverages, and meat products in the forms of soy flour, soy protein isolates, and soy protein concentrates.
- Mass spectrometry (MS) is playing an increasingly important role in allergen detection and quantification since it has shown better performance in allergen quantification, in some cases, compared with other technologies such as ELISA.
- The objective of the current study was to identify and evaluate target peptides from a variety of soy-derived ingredients for the parallel reaction monitoring ullet(PRM) detection of soy protein in foods.

MATERIALS AND METHODS

Soy ingredients information

Extraction method

OVERVIEW

soy ingredients Selection of target peptides for the soy ingredients

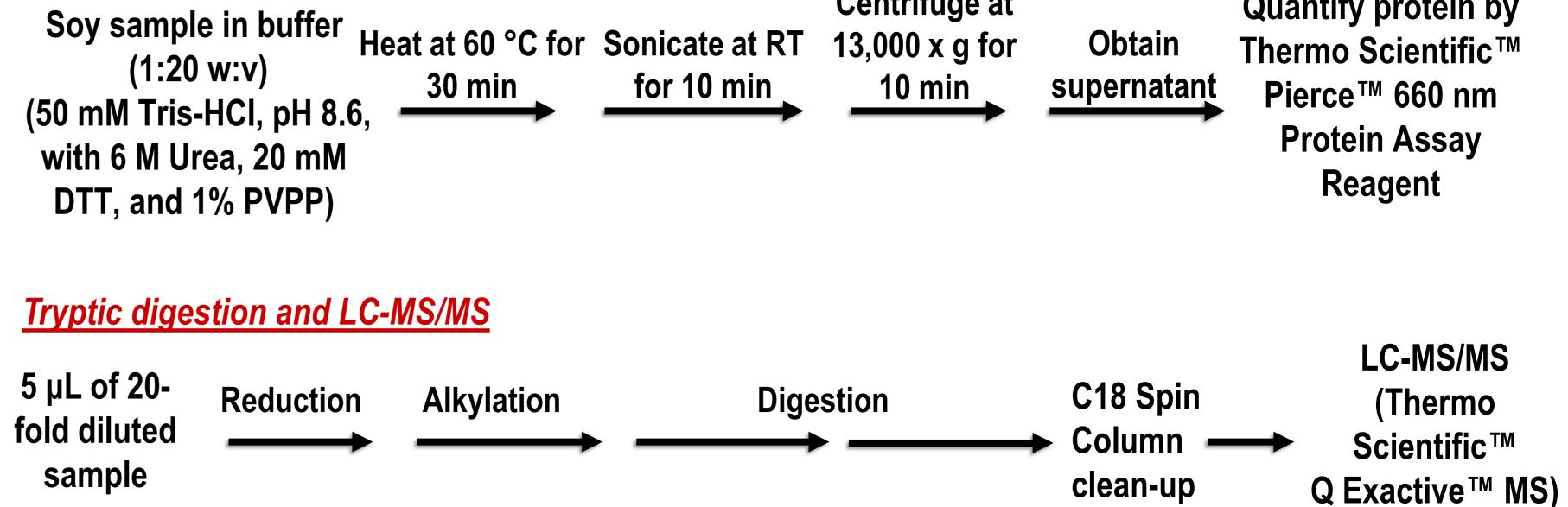
Comparison of protein profiles of six commercial

Comparison of abundance of the selected peptides across six soy ingredients

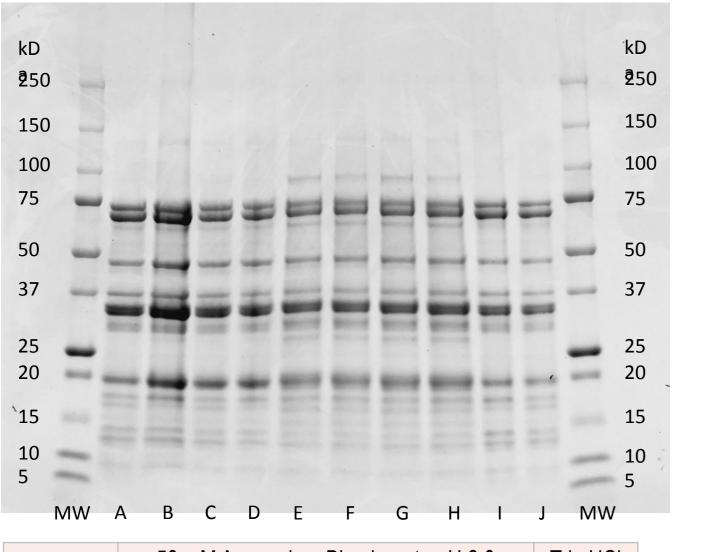
Centrifuge at

Quantify protein by

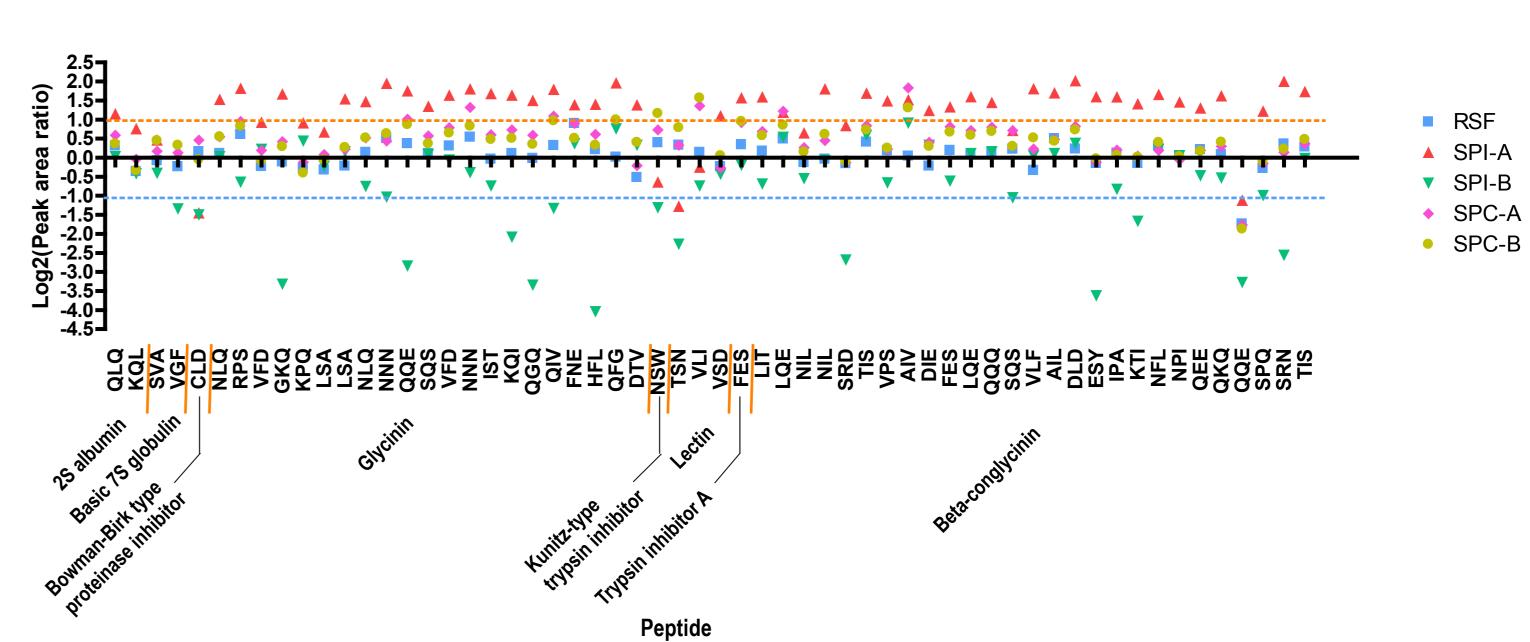
Acronym	Product type	Processing method	Composition
NRSF	Non-roasted soy flour	Minimally heat processed	
RSF	Roasted soy flour	Fully heat treated	
SPI-A	Soy protein isolate		
SPI-B	Soy protein isolate	Hydrolyzed	
SPC-A	Soy protein concentrate		
SPC-B	Soy protein concentrate		
		Protein 📕	at 🔳 Moisture 💻 Other



RESULTS



					0			
kD					• •			kD
250						0	4	250
150) (0		-	-	150
100)		66			-	-	100
75		-		-	-	= '	-	75
50					-			50
37		-			-	=		37
25					-	=.	_	25
20		-	-	-	-	-	-	20
15				in series	10000		-	15
10		-				-	-	10
5								5
ſ	ww к	L	M	N O	Р	Q	MW	



	5	0 mM	Ammo	onium	Bicarbonate pH 8.0				Iris-HCI		
1 M Gu-HCl or 6 M urea	Gu-HCI				Urea			Gu-HCI			
1% (w:v) PVPP	÷	+	-	-	+	+	-	-	÷	+	
20 mM DTT	÷	-	÷	-	+	-	+	-	÷	-	
Buffer	Α	В	С	D	E	F	G	Н		J	

1 M Gu-HCl or 6 M urea	Gu-	HCI		Ur			
1% (w:v) PVPP	-	-	+	+	-	-	PBS
20 mM DTT	+	-	+	-	+	-	
Buffer	Κ	L	Μ	Ν	0	Р	Q

Buffer

50 mM Tris-HCl

6 M Urea

Major protein (258)

No "M" (228)

6-25 aa (180)

High confidence (149)

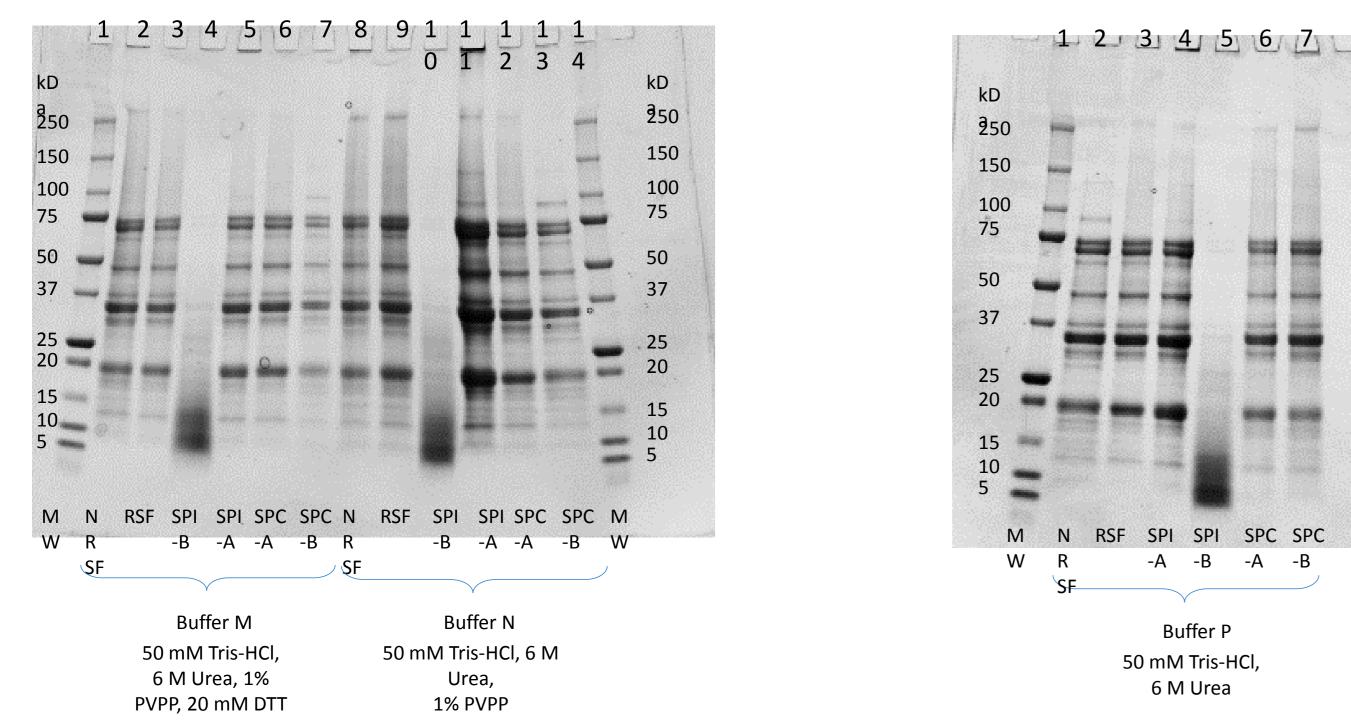
Std<1.5

(124)

Unique,

conserved

Figure 1. SDS-PAGE comparison of protein extraction efficacy from unroasted soy flour



b

Figure 2. SDS-PAGE gel of six commercial soy ingredients with three extraction buffers

Criteria for target	a						
peptides selection:	Protein	Sequence	Contain	Contain	Soy-	number of soy ingredients	Identified as a potential target peptide?
(1) belongs to major seed	FIOLEIN	Sequence	Cysteine?	Methionine?	specific peptide?	can detect the peptide	
storage proteins	2S albumin	ELINLATMCR	Yes	Yes	Yes	6	
•	2S albumin	KQLQGVNLTPCEK	Yes		Yes	6	Yes
(2) does not contain	Basic 7S globulin	LMVFDLAR		Yes	Yes	6	
	Glycinin G2 (A2B1a)	GKQQEEENEGSNILSGFAPEFLK			Yes	<u> </u>	
methionine	β-conglycinin alpha chain	LITLAIPVNKPGR			Yes	6	Yes

All

detectable

peptides

(15332)

Y axis indicates Log₂ (Peak area of the peptide in the specified soy ingredient / peak area of the same peptide in unroasted soy flour), x axis indicates the first three amino acid of each peptide and the protein it belongs to.

Figure 4. Comparison of abundance of selected peptides across six soy ingredients

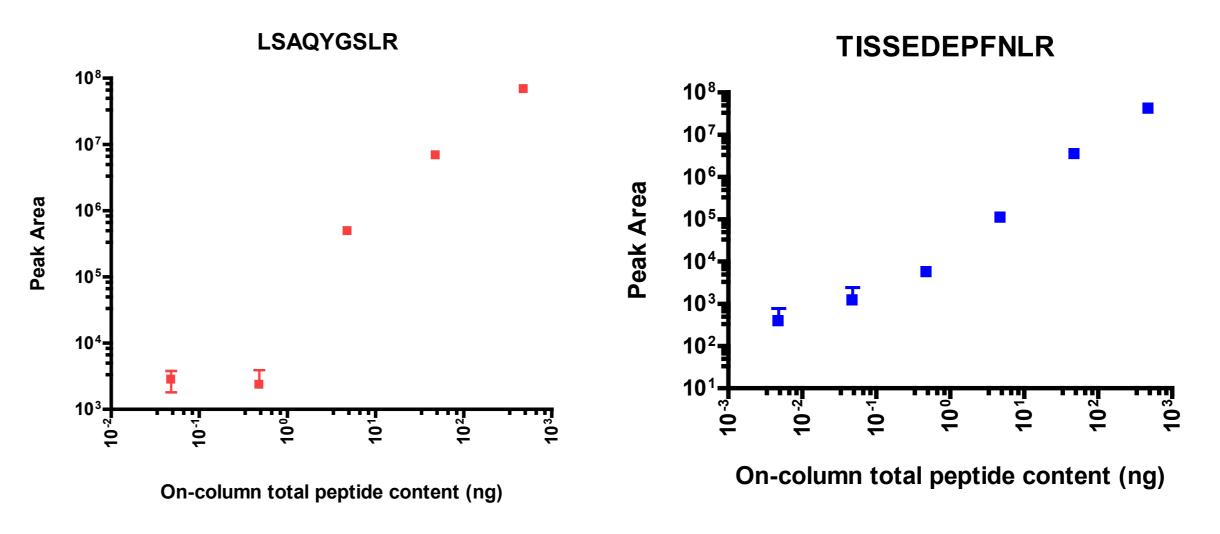


Figure 5. Peptide performance at each level of on-column total peptide content (sample: NRSF, two soy digests with duplicate injections)

CONCLUSIONS

- Buffers M, N, P (50 mM Tris-HCI with 6 M Urea) have shown the optimal extraction effect among all of the buffers.
- The protein profiles of most soy ingredients are very similar to each other except for the SPI-B (soy protein isolate-B), which contains mostly low molecular weight peptides.
- ✤ 57 peptides that satisfy a set of pre-determined criteria were selected for future targeted

MS analysis.

FUTURE STUDIES

- > Optimize extraction and digestion methods for the food matrices test.
- > Evaluate quantitative performance of the selected target peptides.

> Develop a quantitative Parallel Reaction Monitoring (PRM) method using isotopically

labeled internal standards.

Reference:

1. Savage, J. H., Kaeding, A. J., Matsui, E. C. and Wood, R. A. The natural history of soy allergy. J. Allergy Clin. Immunol. 2010, 125, 683-686.

ACKNOWLEDGEMENTS

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of peak area between all soy ingredients is less than 1.5

(5) the standard deviation

(4) high confidence

(3) 6-25 aa

- (6) unique amino acid sequence
- (7) conserved among protein isoforms

(8) have good performance at low concentration

Figure 3. Target peptide selection a. Example of target peptide selection b. Visualization of target peptide identification for soy protein, number of peptides is given in brackets