

Tissue and Fluid Proteomics

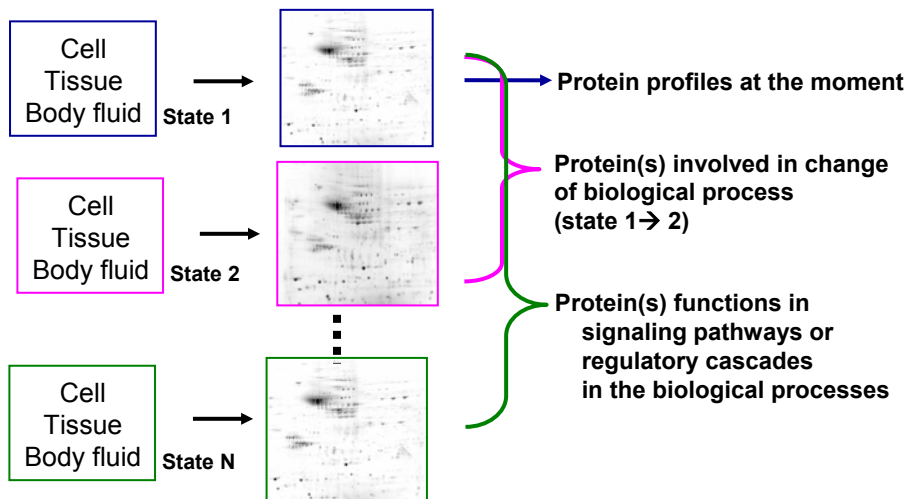
Chao-Cheng (Sam) Wang, Ph.D.

4-6919

ccwang@uab.edu

UAB BMG/PHR 744 - 02/29/08

Proteomics: Picture (s) to Movie



These unique changes of proteins can serve as

- **markers for early detection and predictive purposes**
- **novel targets for drug discovery and therapeutic intervention**

Sample Sources for Proteomic Analysis

- Cell lines.
- Tissue sections.
- Body Fluids:
 - Blood and urine.
 - Fluids from secretion.
 - Fluids in interstitial spaces.

Fluids from Secretion

- Aqueous Humor
 - AH was collected by 27 G needle (150 μ l) from patients w/ or w/o corneal rejection.
 - 2D gel w/ MS ID.
 - Funding et al., Acta Ophthalmol. Scand. (2005) 83, 31-39.
- Saliva
 - Whole saliva or major salivary gland secretions.
 - 2D gel w/o or w/ MS ID; LC-MSⁿ.
 - Proteome database for biomarkers of specific diseases.

Fluids from Secretion

- **Cerebrospinal fluids (CSF)**
 - Fluid surrounding the central nervous system.
 - Total vol ~140 ml, produced at 03-0.4 ml/min.
 - Samples were collected by lumbar puncture (10-12 ml).
 - 2D gel w/ MS ID; LC-MSⁿ
 - Studies of the path-physiological mechanism in front-temporal dementia, Alzheimer's disease
 - Yuan et al. J Chromatogr B , (2005) 815(1-2),179-89. (review)
- **Synovial fluid**
 - A dynamic reservoir for proteins originating from serum, synovial tissue, and cartilage.
 - 2D gel / MS ID and LCⁿ-MSⁿ.
 - Study for biomarkers for Rheumatoid Arthritis.
 - Tilleman et al. Rheumatology (Oxford), (2005) 44,1217-26. (review) .

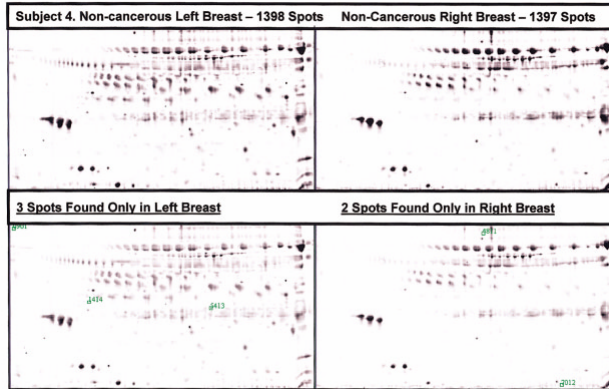
Fluids from Secretion

- **Bronchoalveolar lavage (BAL) fluids**
 - Obtained by washing the epithelial lining of lung with PBS.
 - 2D gel / MS ID and LCⁿ-MSⁿ.
 - Studies of fibrosing interstitial lung diseases, such as sarcoidosis, and allergic asthma.
 - Wattiez et al. J Chromatogr B (2005) 815, 169-178. (review)
- **Nipple aspiration fluid (NAF)/ Ductal lavage fluid**
 - NAF: breast ductal fluid collected by nipple aspiration.
 - Non-invasive way of sample collection.
 - NAF: sample vol: generally ~ 10-20 μ l.
 - 2D gel, SELDI, and chromatography-MSMS.
 - Studies of the early diagnosis of breast cancer.

Review: Human body fluid proteome analysis. Proteomics. 2006 Dec;6(23):6326-53

Protein Profiles of Bilateral Matched Paired NAFs by 2DE-Approach

Non-Cancerous Left Breast Non-Cancerous Right Breast



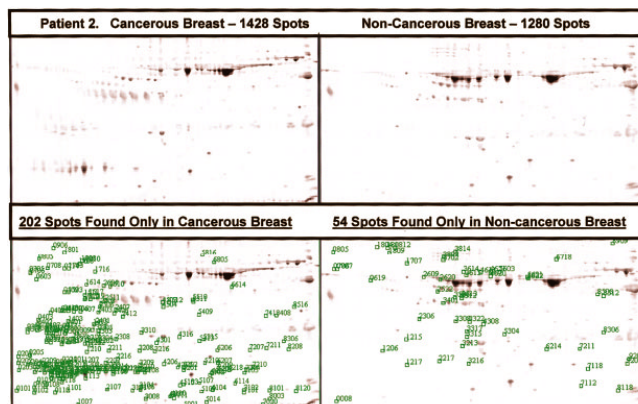
1398 spots
3 spots found only in
Left Breast

1397 spots
2 spots found only in
Right Breast

Kuerer, HM; et al., *Cancer* (2002) 95, 2276-2282.

Protein Profiles of Bilateral Matched Paired NAFs by 2DE-Approach

Cancerous Breast Non-Cancerous Breast



1428 spots
202 spots found only
in Cancerous Breast

1280 spots
54 spots found only in
non-Cancerous Breast

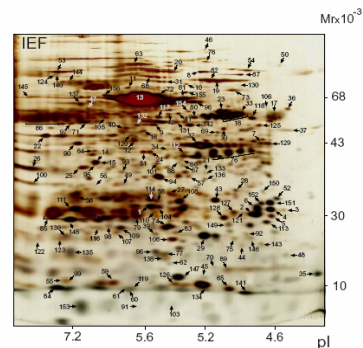
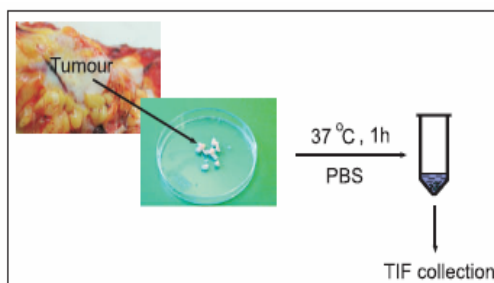
Kuerer et al., *Cancer* (2002) 95, 2276-2282.

Approaches for Sampling from Extra-cellular Space (Interstitial Fluids)

- Tissue perfusion (TIF)
- *In-vivo* sampling from interstitial space with capillary probes (CUF)

Fluids in Interstitial Spaces

Ex-vivo Interstitial fluid collection:

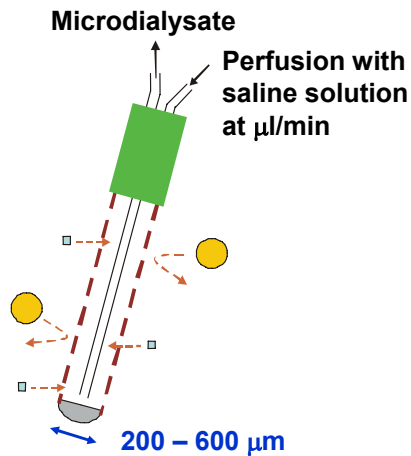


- Complexity of proteins in interstitial space.
- **ex-vivo sampling technique.**
- **Difficulty in obtained samples from the same tissue at different disease stages.**

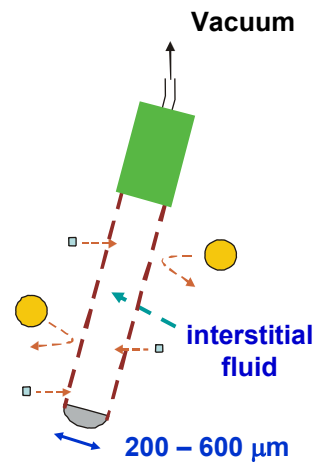
Celis et al., Mol Cell Proteomics. 2004, 327-344.

In-vivo Sampling from Interstitial Space

Microdialysis (MD)



Ultrafiltration (UF)



(small molecules analysis)

Microdialysis vs Ultrafiltration for Proteomic Sampling

Advantage:

- Sampling free drug or metabolites (non-protein-bound) in interstitial fluid at the site of interest.
- Excellent temporal resolution for PK studies from single animal.
- Real *in-vivo* sampling from live, freely-moving animals.

Microdialysis:

diffusion-based technique

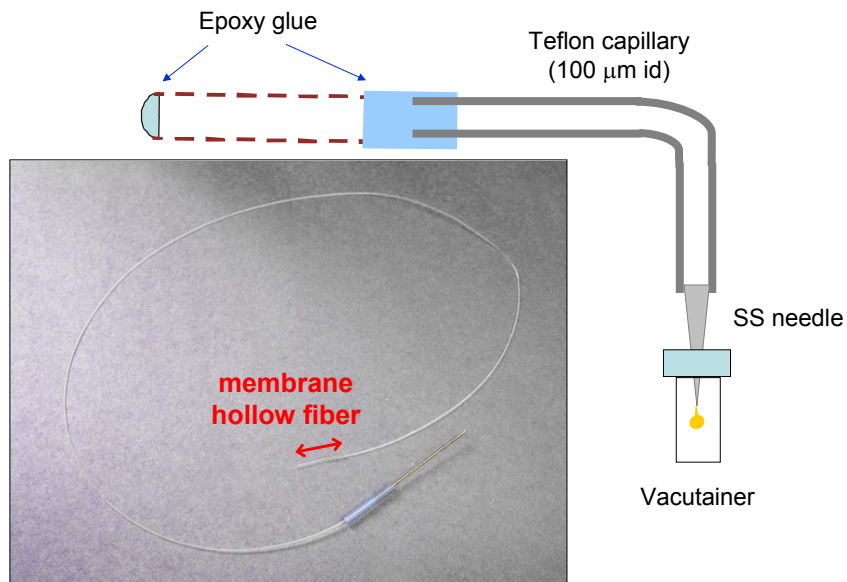
- poor recovery (for peptides and proteins)
- not suitable for long term in-vivo sampling.

Capillary Ultrafiltration:

non-diffusion-based technique

- better & consistent recovery
- suitable for long term sampling (up to 6 month).

Capillary Ultrafiltration Probe



CUF Sampling from Animal Models

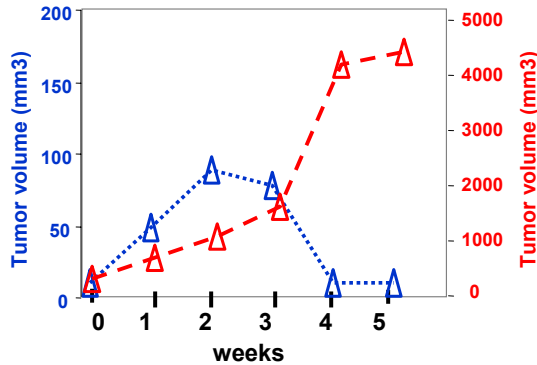
- *In-vivo* UF sampling from interstitial microenvironment in tumor masses at different developing stages.
- Continuous UF sampling from a freely-moving mouse model with chemical-induced Allergic Contact Dermatitis.

Regressive Skin Tumor Model (C2240)

C3H/HeN Mice



Nude mice

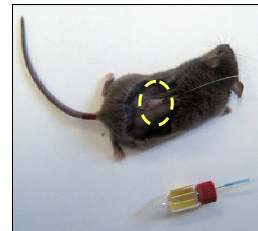


Dynamic interaction
between
Tumor and Host cells

UAB Center of Skin Diseases

CUF Sampling from Regressive Tumor Model

C3H/HeN Mice $\xrightarrow[\text{500,000 cells/50}\mu\text{l Inj s.c. on the back}]{\text{C2240 skin tumor cell}}$
 1. Measure tumor size
 2. Implant CUF probe in tumor masses for IF collection.



- Tumors grew on WK 1, but tumor masses decreased after WK2.
- Interstitial fluid in tumor was collected by a high MWCO probes for 3 hours.

Protein ID through PROWL & SWISS-PROT database

Nano-LC-qTOF MS for peptide sequencing

← tryptic digestion

~2-5 μl of IF collected

Secretomes from Regressive Skin Tumors

Tumors progress at 1st week

1. S100A4 (Metastasis-associated calcium binding protein)
2. Thymosin β 4
3. Thymosin β 10
4. Profilin 1 (dendritic exosomes)
5. beta 1-globin
6. Hemoglobin β 2

Tumors regress at 3rd week

1. Fetuin-A (α -2HS-glycoprotein)
2. Apolipoprotein A-1
3. Alpha-antitrypsin
4. Contrapsin (Trypsin inhibitor)
5. beta 1-globin
6. Hemoglobin β 2

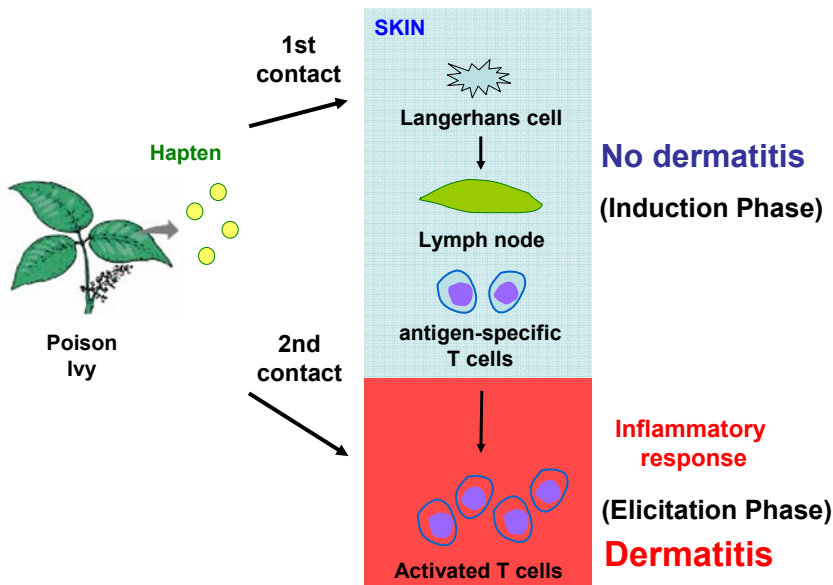
All are secretory proteins

Underline: tumor associated proteins

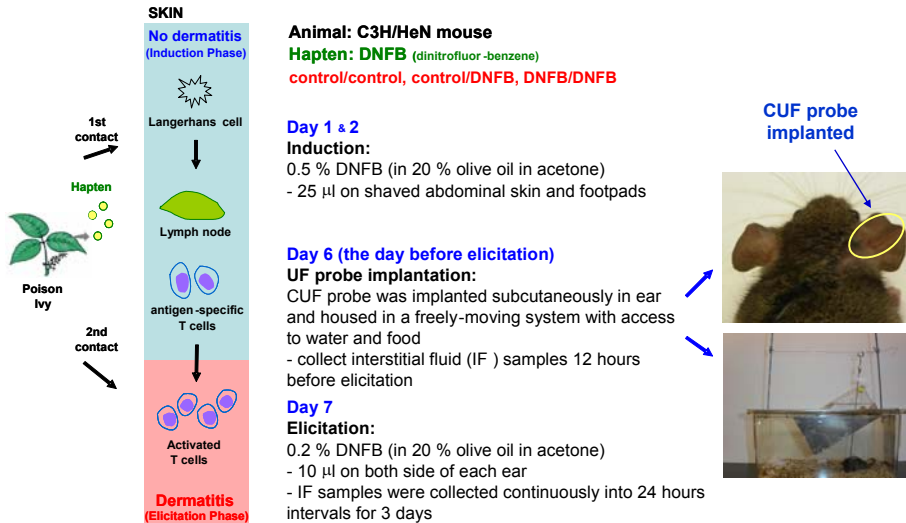
CUF can be used to sample clean interstitial fluid *in-vivo* from animals at different physiological / disease stages

UAB Center of Skin Diseases

Allergic Contact Dermatitis



Dynamic CUF Sampling from ACD Model



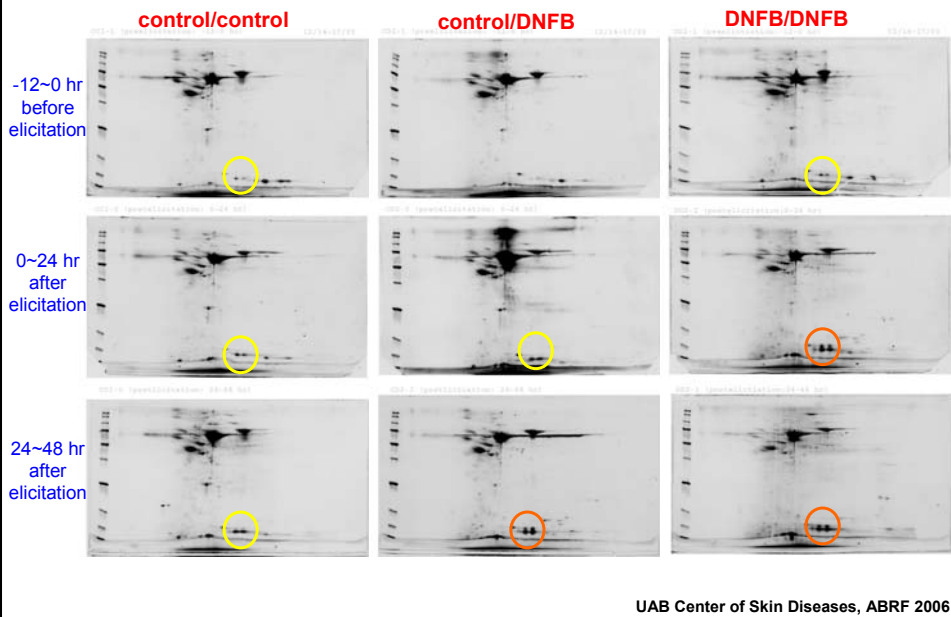
1. Ear thickness were measured daily before and after DNFB elicitation.
2. UF samples were processed with 2DE cleanup kit and analyzed with 75 µl protein load on 3-10 IEF/ 12.5% SDS gel / Sypro staining.

Ear Swelling of ACD Model

	CC-1	CD-1	CD-2	DD-1	DD-2
24 hrs after elicitation	0/1	0/2	0/2	4/-	7/10
48 hrs after elicitation	0/2	0/0	1/2	7/-	5/5

1. Left ear / Right ear (with Probes), unit: 0.01 mm.

2DE Analysis of IFs from different ACD Stages



Protein ID of IFs from different ACD Stages

Protein	Mass	MS	MOWSE
Cp protein	121074	MALDI	126
Gsn protein	80712	MALDI	114
Plasminogen	90723	MALDI	88
transferrin	76628	MALDI	140
albumin 1	68678	MALDI	167
vitamin D-binding protein	53051	MALDI	82
kininogen 1	47868	MALDI	74
Serpina1a protein	45593	MALDI	103
apolipoprotein A-IV	44545	MALDI	168
gamma-actin	40992	MALDI	135
apolipoprotein A-I	30569	MALDI	118
trophoblast specific protein beta	13802	MALDI	66
vitamin D-binding protein	53085	Q-TOF	
Calgranulin B	12909	Q-TOF	

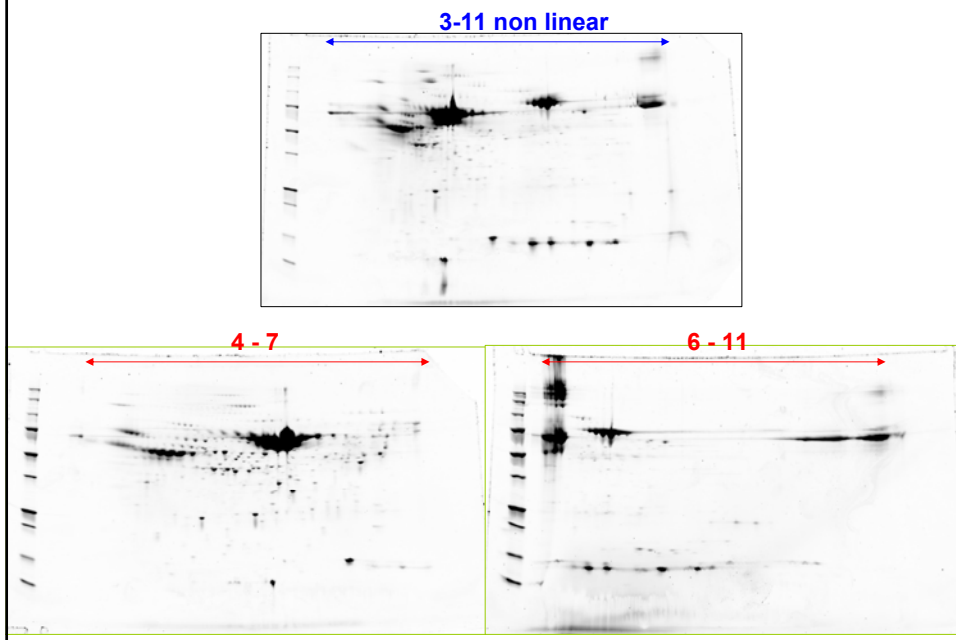
* This protein list only represents spots observed in most of 9 gels.
Detail analysis of differences between gels is not shown.

UAB Center of Skin Diseases, ABRF 2006

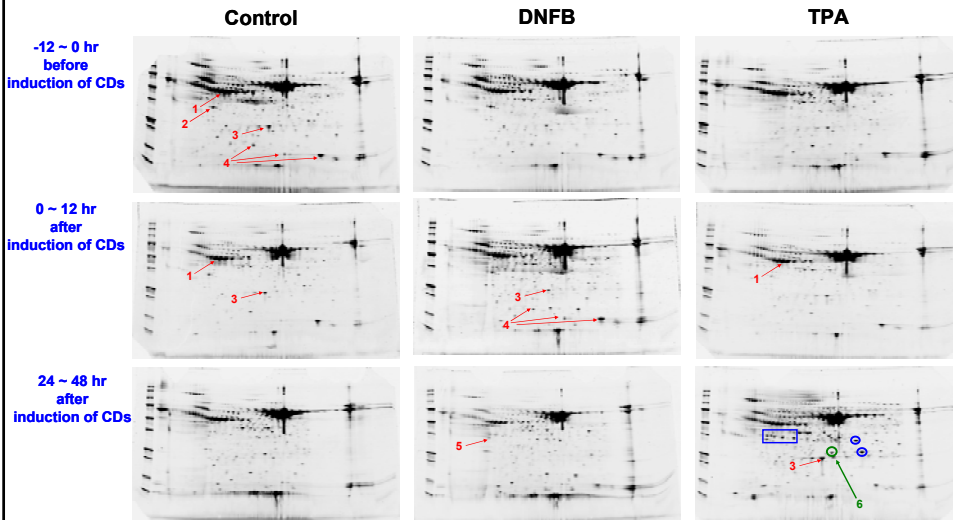
CUF for Proteomics Analysis of Interstitial Microenvironments

- We have evaluated the use of Capillary Ultrafiltration for proteomic study in interstitial microenvironments by providing both in-vivo and dynamic sampling.
- Challenges in analyzing CUF samples by 2DE:
 - **Salty matrix:** may not be a problem; desalt cleanup may lose proteins.
 - **Albumin:** albumin depletion assay: insufficient, protein loss.
 - **Sample size:** increase collection area (multiple probes or longer probes) and longer collection time (lost of temporal resolution).
 - **Quantitative analysis:** DIGE will help.

2DE Analysis of CUFs



2DE Analysis of CUFs from different CD Stages

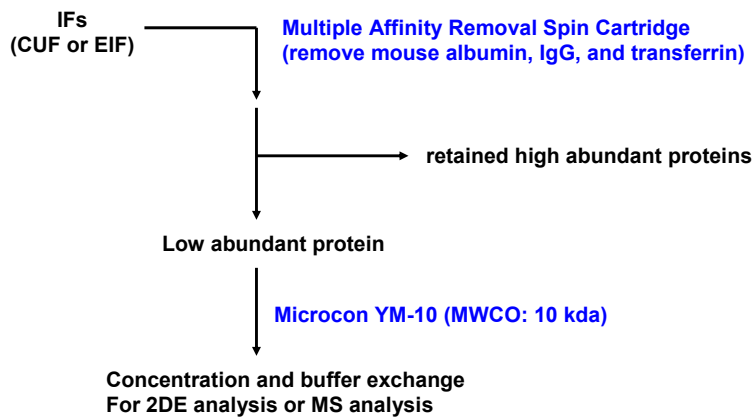


60 μ g, IEF: 4-7, 10-20 % SDS PAGE, Sypro Ruby staining

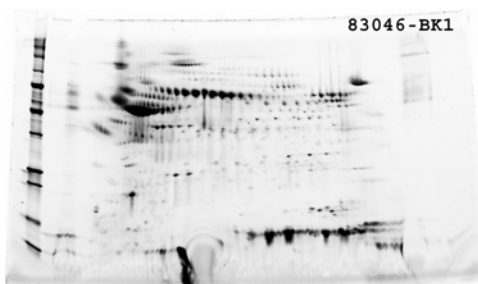
Protein ID of IFs from different ACD Stages

Protein	Mass	MS	MOWSE	Spot
Cp Protein	121074	MALDI	126	
Gsn Protein	80712	MALDI	114	
Plasminogen	90723	MALDI	88	
Transferrin	76628	MALDI	140	
Albumin	68678	MALDI	167	
Vitamin D-binding protein	53051	MALDI	82	
Kininogen 1	47868	MALDI	74	
Serpina1a protein	45593	MALDI	103	
Apolipoprotein A-IV	44545	MALDI	168	
gamma-actin	40992	MALDI	135	
Apolipoprotein A-I,	30569	MALDI	118	
trophoblast specific protein-beta	13802	MALDI	66	
Vitamin D-binding protein	53085	Q-TOF		
Calgranulin B	12909	Q-TOF		
transthyretin	15766	MALDI	103	4
Apolipoprotein A-I, precursor	30358	MALDI	96	2
Apolipoprotein A-I	23008	MALDI	131	3
serine (or cysteine) proteinase inhibitor, clade A, member 1d	45969	MALDI	89	1
Serum amyloid P-component precursor	26230	MALDI	130	6
complement component c3d	33442	MALDI	74	5

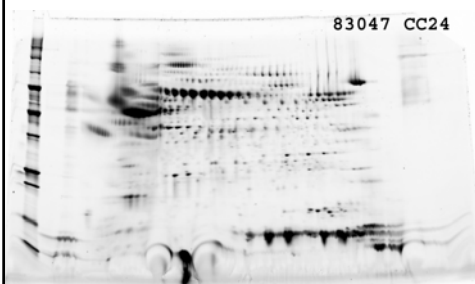
Sample Prep for Proteomic Analysis of IFs



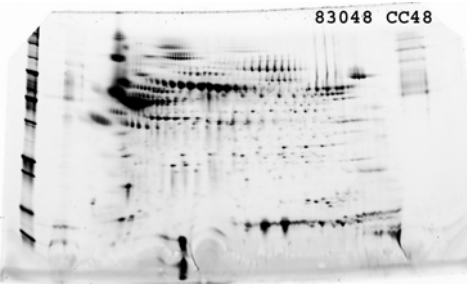
2DE Analysis of CUFs from different CD Stages



Pooled BK CUF collected -12-0 hr before treatment

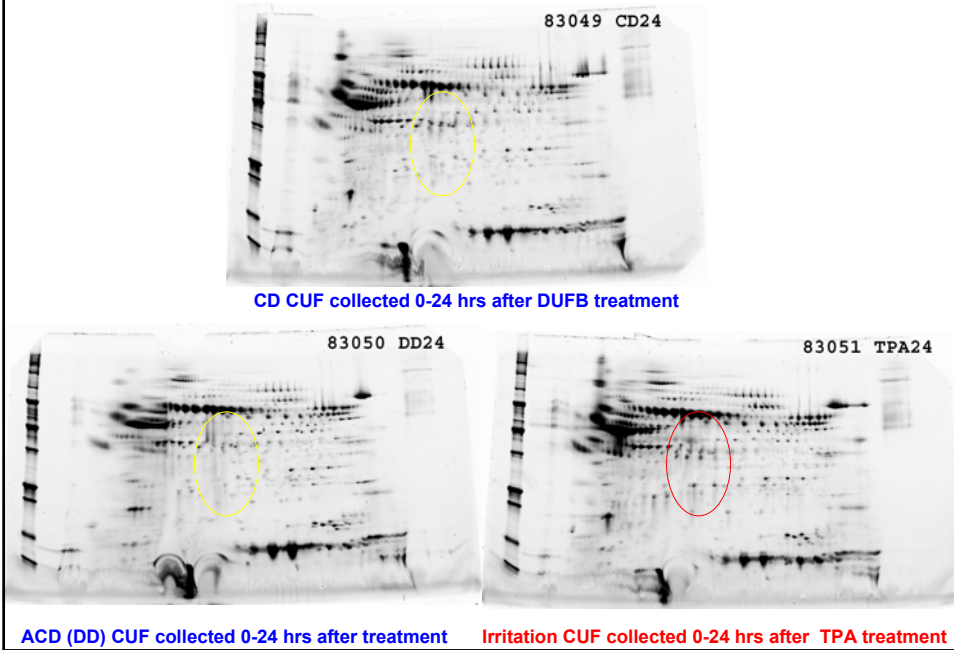


CC CUF collected 0-24 hrs after treatment

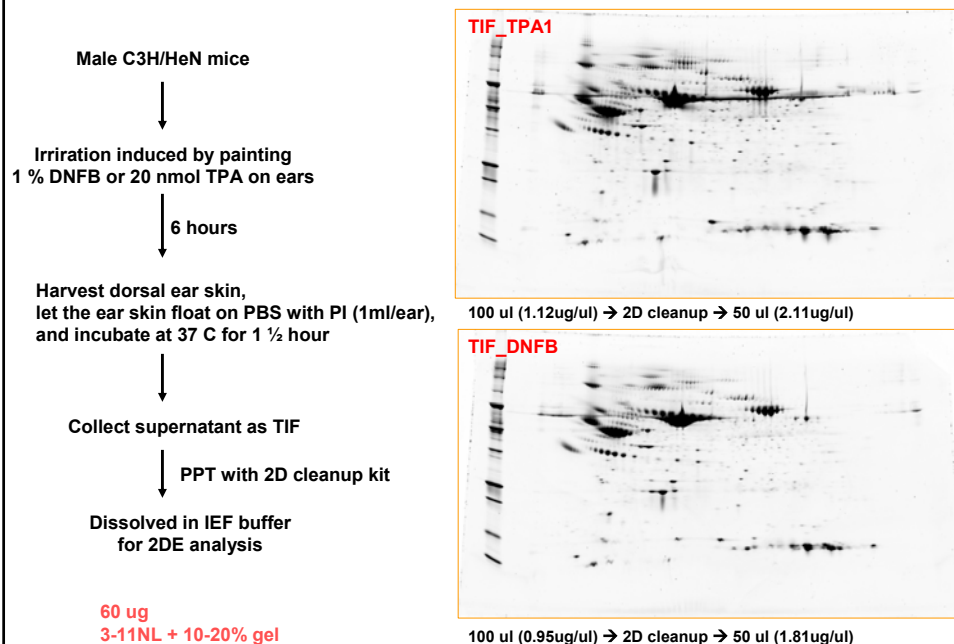


CC CUF collected 24-48 hrs after treatment

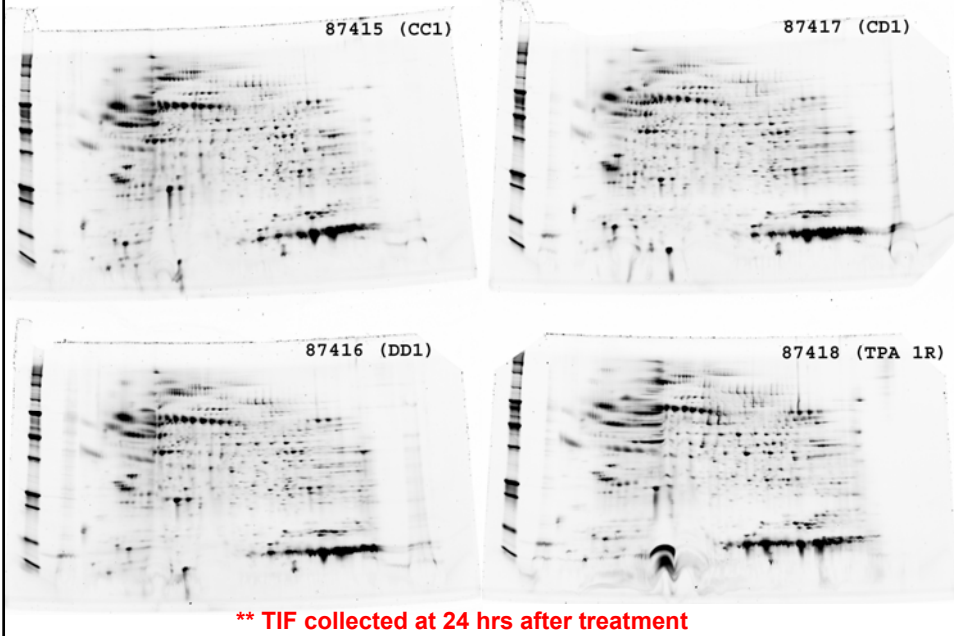
2DE Analysis of CUFs from different CD Stages



2DE Analysis of TIFs from TPA or DNFB Irritated Ear

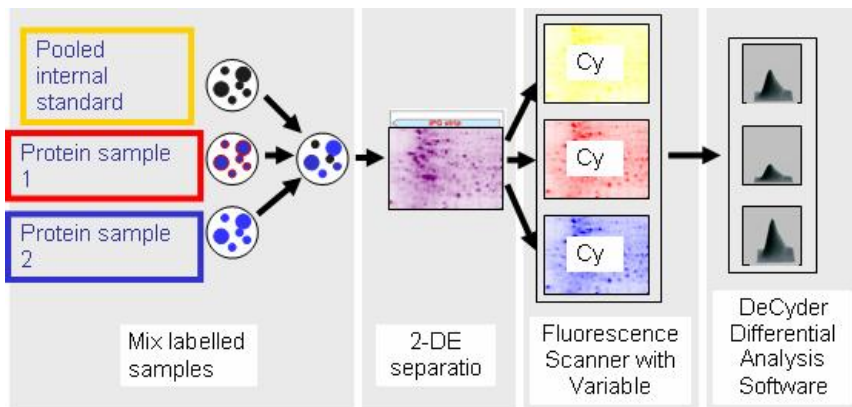


2DE Analysis of TIFs Collected from TPA- Irritated or DNFB-CHS Ear



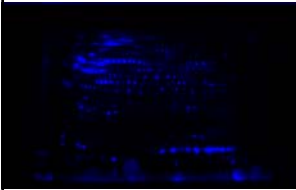
Quantitative Proteomics

- Gel_based approach:
 - Difference gel electrophoresis (DIGE)

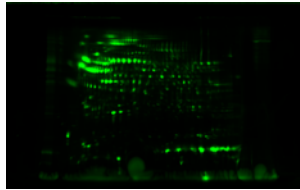


DIGE of TIF samples

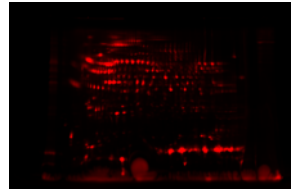
Cy2-pooled standard



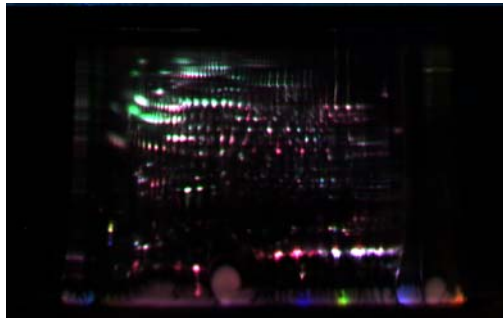
Cy3-TIF DD



Cy5-TIF TPA



- 10 µg/ Cy dye labeled samples
- limited cy dye labeling (0.5%)
- 30 mg/gel
- IEF: 3-11 NL; 10-20% SDS PAGE



Gel 2 (84174, DD-TPA) Cy2 Cy3 Cy5 Overlay

Summary

- The use of Capillary Ultrafiltration for proteomic study in interstitial microenvironments by providing both in-vivo and dynamic sampling.
- Challenges in analyzing UF samples by 2DE:
 - **Salty matrix:** may not be a problem; desalt cleanup may lose proteins.
 - **Albumin:** depletion kit from Sigma did not work well.
 - **Sample size:** increase collection area (multiple probes) and longer collection time (lost of temporal resolution).
 - **One shot deal:** DIGE will help.
- Other Multi-dimensional approaches may be more suitable for analysis of IF samples.