Mass Spectrometry & Proteomics in Botanicals Research

Monday, September 9

7:45 am	Registration and continental breakfast
8:15 am	Dr. Stephen Barnes, Course Director, and Dr. Helen Kim, Co- Course Director: Welcome to UAB and course objectives
	 Purdue-UAB Botanicals Center for Age-Related Disease Mass spectrometry as a versatile technique, suitable for many types of biological molecules
	Identification and quantification of active substances in hetapiagle is assential for systematic research.
	 botanicals is essential for systematic research The role of proteomics in botanicals research
	The core of procedures in comments research
8:45 am	Introduction to proteomics methodologies (Dr. Helen Kim)
	• 2DE vs MUDPIT vs chips
9:00 am	Elements of 2D-proteomics (Dr. Helen Kim)
	Sample preparation
	IEF sample buffer recipe
	 How to reduce protein complexity
9:30 am	Break
10:00 am	Sample preparation and electrospray ionization (<i>Dr. Stephen Barnes</i>)
	What is electrospray ionization?ESI vs. HN-APCI
	 Sample preparation and importance of desalting MS of polyphenols and peptides

10:30 am MS-MS analysis of peptides (*Mr. Marion Kirk*)

- Selection of parent ion
- Advantage of doubly charged ions
- Principal sites of cleavage (b and y ions)
- Other cleavages

11:00 am Qualitative LC-MS and MS-MS of polyphenols (*Dr. Jeevan Prasain*)

- *LC-MS* with isocratic or gradient elution
- Fragmentation of parent molecular ions
- Selection of ions for Multiple reaction ion monitoring

11:30 am Principles of nanoelectrospray ionization and high sensitivity analysis (*Dr. Sam Wang*)

- Concentration rules in ESI
- Advantages of nanoflow
- *Miniaturizing sample absorption*
- Application to polyphenols

12:00 pm **Lunch**

Afternoon sessions (1 - 5 pm) involve going in turn to each of the stations in groups of 3-4. Following the break, revisit stations 1-4 depending on interest. Also visit in small groups Stations 5 and 6. Drs. Barnes and Kim will be available for informal discussions during this period. Posters concerning botanical research projects will be shown in room 637.

Station 1 Running 2D-gels (*Mr. Heath McCorkle*)

- *Rehydration of 1st D gels*
- Starting the 1st D strip.
- Laying the 1st D strip on top of the 2nd D gel

Station 2 Demonstration of Q-TOF-MS-MS of peptides (*Mr. Marion Kirk*)

Station 3 LC-MS-MS of polyphenol-containing samples (*Mr. Ray Moore*)

Station 4 Demonstration of analysis of microdialysate (*Dr. Sam Wang*)

3:15 - 3:30 pm

Break

Station 5 Demonstration of gel scanning and protein spot selection (*Mr. Heath McCorkle*)

Station 6 Informal discussions (*Dr. Stephen Barnes and Dr. Helen Kim*)

- Student/postdoc poster presentations
- Selection of instruments to purchase
- Problem solving

Tuesday, September 10

8:00 am **Continental breakfast**

8:15 am MALDI-TOF analysis (*Dr. Stephen Barnes*)

- Principles of MALDI and TOF-MS
- Large molecules
- Peptides
- Non-protein samples

8:45 am Peptide mass fingerprinting (*Mr. Landon Wilson*)

- Preparation of sample clean protein/gel spot
- Choice of peptidase
- Spotting and sample purity
- De-isotoping MALDI spectra
- MASCOT

9:15 am Bioinformatics (*Dr. Stephen Barnes and Dr. Helen Kim*)

- *So, I've discovered a protein what next?*
- NCBI Entrez/Swiss Protein
- 2DE databases
- Blink
- SCOP

9:45 am **Break**

The morning session (10 am -12 pm) involves going in turn to each of the stations in groups of 3-4.

Station 1/2 Quantitative analysis of polyphenols (*Mr. Ray Moore and Mr. Kenneth Jones*) – in lab and at various computer stations

Station 3/4 MALDI analysis of 2D-gel spots (*Mr. Landon Wilson and graduate students*)

12:00 pm **Lunch**

The afternoon session (1-3 pm) involves going in turn to each of the stations in groups of 3-4.

Station 1 Image analysis of 2D-gel (Mr. Kiran Sarikonda)

Station 2-4 Use of informatics (*Dr. Stephen Barnes and graduate students*)

Further opportunities to try all techniques in analysis of polyphenols and proteins, and to ask questions