PHYSICIAN-SCIENTIST COMES FULL CIRCLE

From Biomedical Engineering, To Thoracic Medical Oncology, To Building “Wiring Circuits” For Cancer Cells

By Randolph Fillmore

Eric Haura, M.D.

Photography: Ray Reyes
WHAT IS MASS SPECTROMETRY?

Mass spectrometry is an analytical technique and accompanying technology that produces a spectrum of the masses of atoms or molecules in a sample. The spectrum is used to determine the “fingerprint,” or signature of the sample, whether in terms of mass or chemistry.

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of proteins, thus offering more fine-tuning in cells.”

A few years ago, Dr. Haura went to Austria for several months of training in “mass spectrometry,” a complicated and state-of-the-art technology now used for gaining a better understanding of proteins and how they are modified. During that time, the biomedical electrical engineer in him and the researcher/physician in him shook hands.

“Mass spectrometry is one of our most important discovery engines,” Dr. Haura says. “We have to figure out ways to purify different parts of cancer cell protein makeup to better understand how proteins function in cancer. Mass spectrometry does this. It breaks down proteins into their component parts so that we can analyze them and better understand their communication activity. You could say that proteins ‘talk’ to one another, and unraveling the ‘language’ they speak will help open doors to developing more effective, personalized therapies for patients.”

He compares identifying the characteristics of proteins by mass spectrometry to “fishing” to see what protein ends up on the “hook.” For Dr. Haura, discovering the proteins in a tumor and knowing how the proteins are signaling one another is the next giant step for cancer research and developing new personalized therapies.

“For analysis in mass spectrometry, we take a protein, chop it into fine pieces so that we have a long molecule, feed it to the mass spectrometry unit, and out comes a report that helps us build a picture of the protein,” Dr. Haura explains. “We can figure out which proteins stick to other proteins, in other words, which proteins are talking to each other.”

Dr. Haura says his work in proteomics relies heavily on Moffitt’s Proteomics Core, a protein investigation shared resource facility headed by John Koomen, Ph.D. In the lab, a gathering of mass spectrometry units hum loudly, and a busy team of laboratory personnel work with purpose.

Work aided by mass spectrometry is paying off by providing answers to important research questions. In a research paper featured on the cover of the Jan. 13, 2015, issue of Science Signaling, senior author Dr. Haura and colleagues reported a new approach to measure how signaling-associated proteins may have the potential to add to current biomarker tests for drug sensitivity. Prior work with mass spectrometry helped them sort out the characteristics of the proteins involved.

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For Dr. Haura, proteomics is the current frontier for cancer research. He is confident that a better understanding of the role of proteins in cancer will empower clinicians to better predict treatment outcomes, overcome drug resistance and identify biomarkers in the proteins that will help personalize treatments. Along with colleagues, he is beginning to think about how proteomics can better decipher the workings of the immune system related to cancer and develop both new diagnostic and therapeutic strategies.

“When I came to Moffitt in 2000, we could only offer patients traditional chemotherapy, in addition to surgery and radiation therapy,” Dr. Haura recalls. “Soon, a patient coming through the doors at Moffitt will have not only their genome sequenced but also have information gathered on their proteome. This opens the door to treatments designed not only for a patient’s genetic individualism but also built on the proteins that are actually at work in their tumors.”