Reports from University of Arizona, Environmental Health Sciences Center Add New Data to Research in Peptides and Proteins
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Research findings, 'Identification of chemical-adducted proteins in urine by multi-dimensional protein identification technology (LC/LC-MS/MS),' are discussed in a new report. According to recent research published in the journal Methods In Molecular Biology, "Recent technological advancements in mass spectrometry facilitate the detection of chemical-induced posttranslational modifications (PTMs) that may alter cell signaling pathways or alter the structure and function of the modified proteins. To identify such protein adducts (Kleiner et al., Chem Res Toxicol 11:1283-1290, 1998), multi-dimensional protein identification technology (MuDPIT) has been utilized."

"MuDPIT was first described by Link et al. as a new technique useful for protein identification from a complex mixture of proteins (Link et al., Nat Biotechnol 17:676-682, 1999). MuDPIT utilizes two different HPLC columns to further enhance peptide separation, increasing the number of peptide hits and protein coverage. The technology is extremely useful for proteomes, such as the urine proteome, samples from immunoprecipitations, and 1D gel bands resolved from a tissue homogenate or lysate. In particular, MuDPIT has enhanced the field of adduct hunting for adducted peptides, since it is more capable of identifying lesser abundant peptides, such as those that are adducted, than the more standard LC-MS/MS," wrote M.T. Labenski and colleagues, University of
Arizona, Environmental Health Sciences Center (see also ).

The researchers concluded: "The site-specific identification of covalently adducted proteins is a prerequisite for understanding the biological significance of chemical-induced PTMs and the subsequent toxicological response they elicit."

Labenski and colleagues published their study in Methods In Molecular Biology (Identification of chemical-adducted proteins in urine by multi-dimensional protein identification technology (LC/LC-MS/MS). Methods In Molecular Biology, 2011;691():339-47).

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