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Editorial

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Editorial for Journal of Proteomics and Genomics Research: Second Issue

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The papers in the second issue of JPGR present both sides of this journal: proteomics and genomics research. Additionally, these papers indicate the importance of new methodological approaches and the role of in vivo studies. In general, the scheme: idea > in vitro experiments > in vivo experiments works well if the in vivo model is available (not to mention a good, better, great idea).

In the laboratory of Dr. E.I.Chen (the paper of A.Koller and colleagues) 15N SILAC (Stable Isotope Labeling with Amino acid in Cell culture) mice were generated and mass spectrometry-based quantitative proteomic analysis with tissue-matched labeled peptides was performed. At the end, what is important for the researches to know is that 15N SILAC mouse tissues could serve as a global reference for MS quantification in comparison to the label-free method, which has a number of limitations. In addition, these mice can provide a renewable source of labeled peptides for quantitative analysis of human proteins from tissue, in case that no appropriate cell lines exist.

In the paper by D.S. Phelps and colleagues the humanized transgenic mice with surfactant protein A (SP-A) knockout and expressing human SP-A1 or SP-A2 were created. This allowed the authors to show that in vivo SP-A1 and SP-A2 are able to change the proteomic profile of alveolar macrophages (AM) in a different way: protein expression in SP-A2 transgenic mice was similar to the Wild Type but different in SP-A1 mice. They speculated that the AM function is dependent on the relative amounts of SP-A1 and SP-A2.

The paper W.J. Fu and colleagues is an example of bioinformatics. The authors developed a new two-stage model for maternal-fetal genotype (MFG) incompatibility. This model was tested in simulation and case-control experiments, and allowed to identify a single nucleotide polymorphism (SNP) in the IGF2R gene with marked allelic effect as well as SNP in the IGF1 gene with a significant MFG incompatibility. These data may find an application in genetic research.

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