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Keynote Forum

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Baolin Zhang

Food and Drug Administration, USA

Glycosylation of therapeutic proteins: Functions and analytical innovation

Glycosylation is a critical quality attribute of therapeutic glycoproteins, including monoclonal antibodies (mAbs), which can directly affect product safety and efficacy. However, the complexity of protein glycosylation poses a daunting analytical challenge. The current methods for glycan analysis (e.g., mass spectrometry) consist of laborious enzymatic digestion protocols and analyses of the resulting free glycans and aglycosylated proteins. This presentation describes an innovative lectin-based microarray approach for high throughput glycan analysis of native proteins. Case studies of commercial therapeutic glycoproteins will be discussed to highlight the applications of the lectin microarray platforms for the characterization of biotechnology products.

Biography

Baolin Zhang is a Senior Investigator and Review Team Leader in the Office of Biotechnology Products of the Center for Drug Evaluation and Research (CDER) at the US Food and Drug Administration (FDA). He has 15 years of FDA experience regulating biotechnology drug product applications, including monoclonal antibodies and biosimilars. He also directs a research program on advancing analytics for biotechnology products. He has published over 80 original studies in high profile journals and presented at numerous scientific and regulatory conferences. He has received numerous awards for excellence in scientific achievement and for mentoring junior scientists including FDA Excellence in Laboratory Science and Excellence in Leadership.

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Chien-Hsun Huang

Fudan University, China

Reconstruction of evolutionary history of several plant families using bioinformatics as a framework for comparative studies

Bioinformatics is getting vital in the genomic era with the advance of sequencing techniques leading to large amounts of datasets generated around the world. Similarly is the emerging importance of the comparative studies, instead of focusing on understanding one particular model species in previous days, to find the mechanisms basal and universal to most of the species as well as the ones specified to a few organisms. However, a well-resolved and robust phylogeny is required for many of the comparative studies to make assumptions as well as possible. Thus, we focus on resolving the phylogeny of angiosperms, hoping to provide a framework for comparative studies in plants. Using large numbers of transcriptomic datasets, we selected hundreds of low-copy or single-copy nuclear genes to reconstruct the phylogeny of several angiosperm families such as *Asteraceae, Rosaceae* and *Brassicaceae*. In these studies, we first provide a solid relationship among members of these families by using different approaches to confirm the results, and then reconstruct the history of morphological characters or gene/genome duplications based on the model phylogeny. We have found repeated and nested whole-genome duplications in *Asteraceae*, and also reveal the evolutionary history of fruit type in *Rosaceae*. Furthermore, we especially focus on and anticipate providing a solid framework and sufficient information for *Brassicaceae* to be used as a model family in plant biology.

Biography

Chien-Hsun Huang is an Associate Researcher in Fudan University, China. He has received his PhD degree of Plant Biology in the Institute of Plant Biology, Department of Life Sciences, National Taiwan University and started to study plant evolution in Bioinformatics as Post-doctorate. He accumulated his experiences in molecular biology, biochemistry and bioinformatics. He has involved in several government-granted projects of NSFC.

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