学 术 报 告

报告题目：蛋白质初始O-GalNAc糖基化的精准调控

报告人：张延教授，上海交通大学系统生物医学研究院

Mucin-type O-glycosylation (O-GalNAc glycosylation) is one of the most important post-translational modifications of proteins. It is initial catalyzed by a large family of UDP-GalNAc: polypeptide-N-acetylgalactosaminyl transferase (ppGalNAc-T), which transfer a GalNAc moiety from UDP-GalNAc onto Ser/Thr residues proteins. O-GalNAc glycosylation of protein is reported to be important for many cellular and developmental processes under physiological or pathological conditions. About 10 years ago, we have reported there are 20 distinct ppGalNAc-T isoforms present in the human genome database. However, there are many fundamental questions of protein O-glycosylation are still unclear, e.g., which proteins could be O-GalNAc glycosylated by which ppGalNAc-Ts and how many proteins could be O-GalNAc glycosylated. To solve these questions, recently, we developed an on-chip ppGalNAc-Ts assay that could rapidly and systematically identify the protein substrates of each ppGalNAc-T isoforms. Meanwhile, we also developed a ppGalNAc-T inhibitor with isoform selectivity to explore the specific function of ppGalNAc-T on amyloid precursor protein (APP). Finally, we also compared the function of two ppGalNAc-T isoforms with high identity in neurogenesis through analyzing the substrate specificity. Our work proved that each individual ppGalNAc-T has specific substrate proteins and glycosylated specific substrate sites, which precisely regulates the biological function of O-GalNAc glycosylation in distinct processes.

报告时间：2017年12月26日（星期二）15:00 - 16:00

报告地点：上海市四平路1239号同济大学化学馆239室

学 术 报 告

报告题目： Constructing and exploring protein interactome with computational approaches

报告人： 赵兴明教授，复旦大学类脑智能科学与技术研究院

报告摘要： Proteins play important roles in biological systems by interacting each other. However, few interactions are known in many organisms, which hinders the understanding of biological systems. In this talk, I'll present our work on predictions of protein-protein interactions in Maize and Fussarium graminearum. Furthermore, I'll also present our work on identification of signaling pathways from interactoms and prediction of drug targets based on network motifs.

报告时间： 2017年12月27日（星期三）10:00 - 11:00

报告地点： 上海市四平路1239号同济大学化学馆241室