Contribution ID: **86**   Type: **Poster**

nQuant Enables Precise Quantitative N-Glycomics

Abstract: N-glycosylation, as the most complex post-translational modification of proteins, involves crucial biological functions. It has been demonstrated that aberrant N-glycosylation is directly linked to various human diseases, while mass spectrometry-based N-glycomics still lags behind, limiting the in-depth mining of glycobiological information. Aiming to rectify the bias of the previous quantitative N-glycomics strategies, we developed nQuant, a glycoinformatics tool that enables label-free and isotopic labeling quantification of N-glycomics data obtained via LC-MS/MS, ensuring a low false quantitation rate. nQuant integrates the total signal intensities of N-glycans by considering their mass spectrometric behaviors, including different adducts, charge states, and isotopic distributions, which enables precise quantitative N-glycomics.

Conclusion: Due to the emerging roles of N-glycans in fundamental biological processes and human health, it is important to accurately quantify N-glycans in a systematic manner, a prerequisite for functional studies. In this study, we developed nQuant, a glycoinformatics tool that enables label-free and isotopic labeling quantification of N-glycomics with a low FQR. The key to our design is to automatically integrate different adducts, charge states, and isotopic signals of N-glycans detected by MS. Compared to previous glycoinformatics tools, our design exhibits two major strengths: 1) it enables more precise quantitative N-glycomics through newly developed quantification algorithms, and 2) it includes a calibration algorithm for isotopic labeling quantification. Thus, nQuant proves to be a powerful glycoinformatics tool to understand N-glycome landscapes and dynamics, and it could be used in large-scale glycomics studies.

User consent

yes

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Session Classification: Poster Session 2