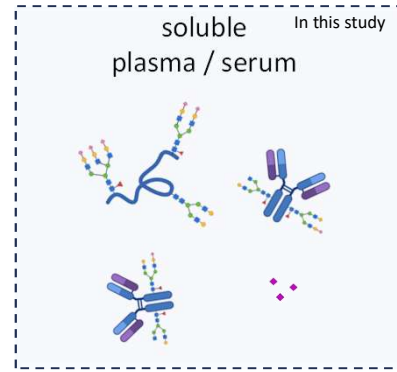
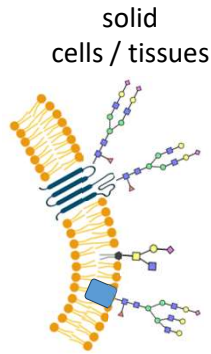
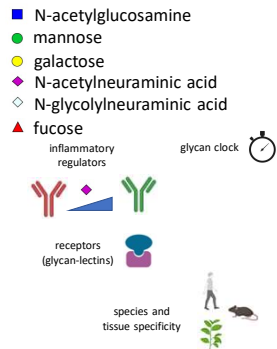


The Sugar Language of Immunology: Glycosylation-Related Biomarkers for Severity Stratification in Post-Infectious Chronic Fatigue Syndrome

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INTRODUCTION

Glycomics represents the **molecular language of cells**, based on **sugar** structures encoded on proteins, lipids, and tissues. Various diseases, including autoimmune disorders and infections, are characterized by **altered glycans**, which contribute to **inflammation**. This study aims to investigate alterations in glycan profiles in the peripheral blood of post-infectious Myalgic Encephalomyelitis/Chronic Fatigue Syndrome (ME/CFS) patients compared to healthy controls.



OBJECTIVES

We aimed to determine whether changes in free sialic acid levels, serum N-glycosylation, and IgG glycosylation patterns in the peripheral blood of ME/CFS patients may serve as potential biomarkers.

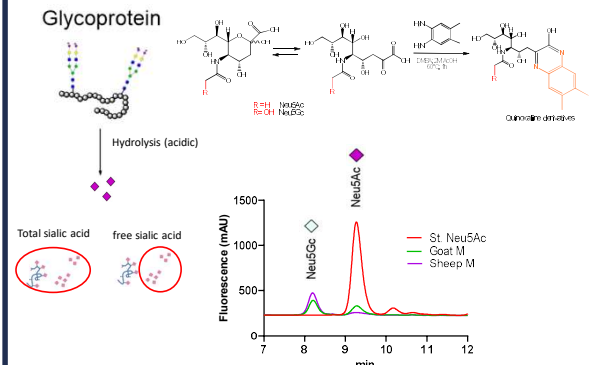
STUDY PARTICIPANTS

description	sample number
post-COVID syndrome	30
COVID convalescent	34
ME/CFS	25
healthy control	31

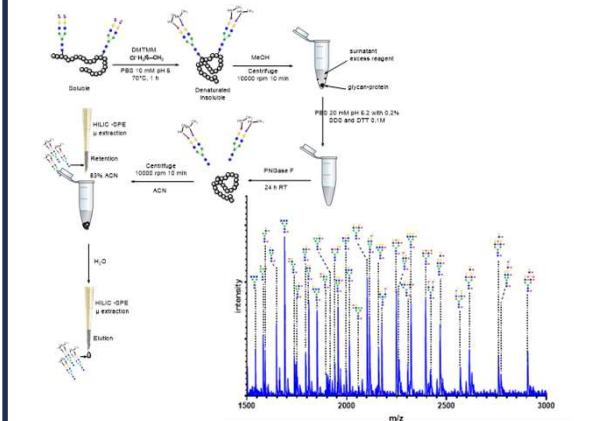


METHODS

Total and free serum **sialic acid** was quantified via HPLC with fluorescence detection.



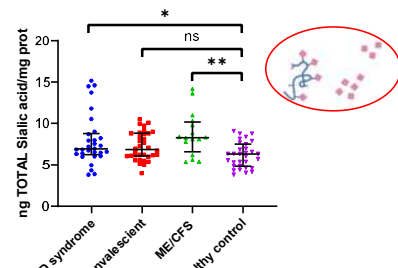
N-Glycan profiles were analyzed by MALDI mass spectrometry previous derivatization, release and SPE microextraction.



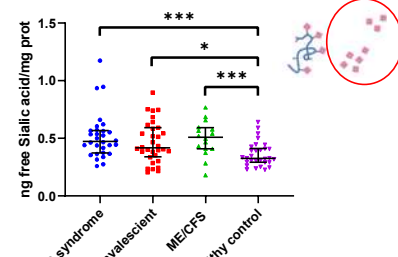
RESULTS

A significant increase in total serum sialic acid was observed in the ME/CFS group compared to the healthy control. The N-glycan profile was characterised by an increased amount of bi- and tri-antennary sialated N-glycans (anti-inflammatory glycans) in the healthy control group compared to the ME/CFS group, on the other hand an increase of pro-inflammatory terminal galactosylated glycans in the ME/CFS group. Analysis of IgG glycosylation required method optimisation to avoid glycan damage during sample preparation, but can provide more accurate and specific information than serum glycan analysis.

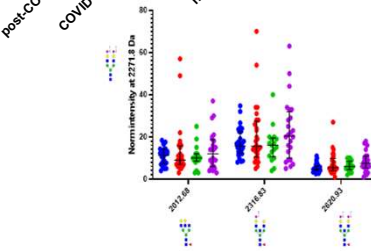
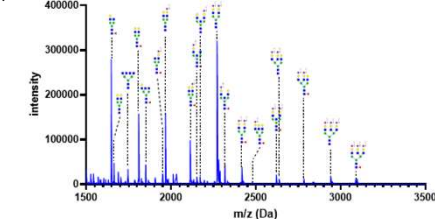
TOTAL Sialic acid concentration



FREE Sialic acid concentration



N-Glycan profile



CONCLUSION

A decrease in sialylated glycans in serum glycans and an increase in total and free serum sialic acid could be due to the cleavage of sialic acid from host tissues caused by pathogenic neuraminidase activity. Targeted glycomics result a powerful approach to decoding immunological signals.

LITERATURE

- Rohrhofer, J., et al., *Immunological Patient Stratification in Myalgic Encephalomyelitis/Chronic Fatigue Syndrome*. Journal of Clinical Medicine, 2024, 13(1): p. 275.
- Ret, D., et al., *DMTMM-mediated methylamidation for MALDI mass spectrometry analysis of N-glycans with structurally conserved sialic acid residues in biological fluids "via directissima"*. Talanta, 2022, 242: p. 123326.

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