

Complementary Insights into Multiple Sclerosis by Mass Spectrometry-Based N-Glycomics of Total Serum and IgG

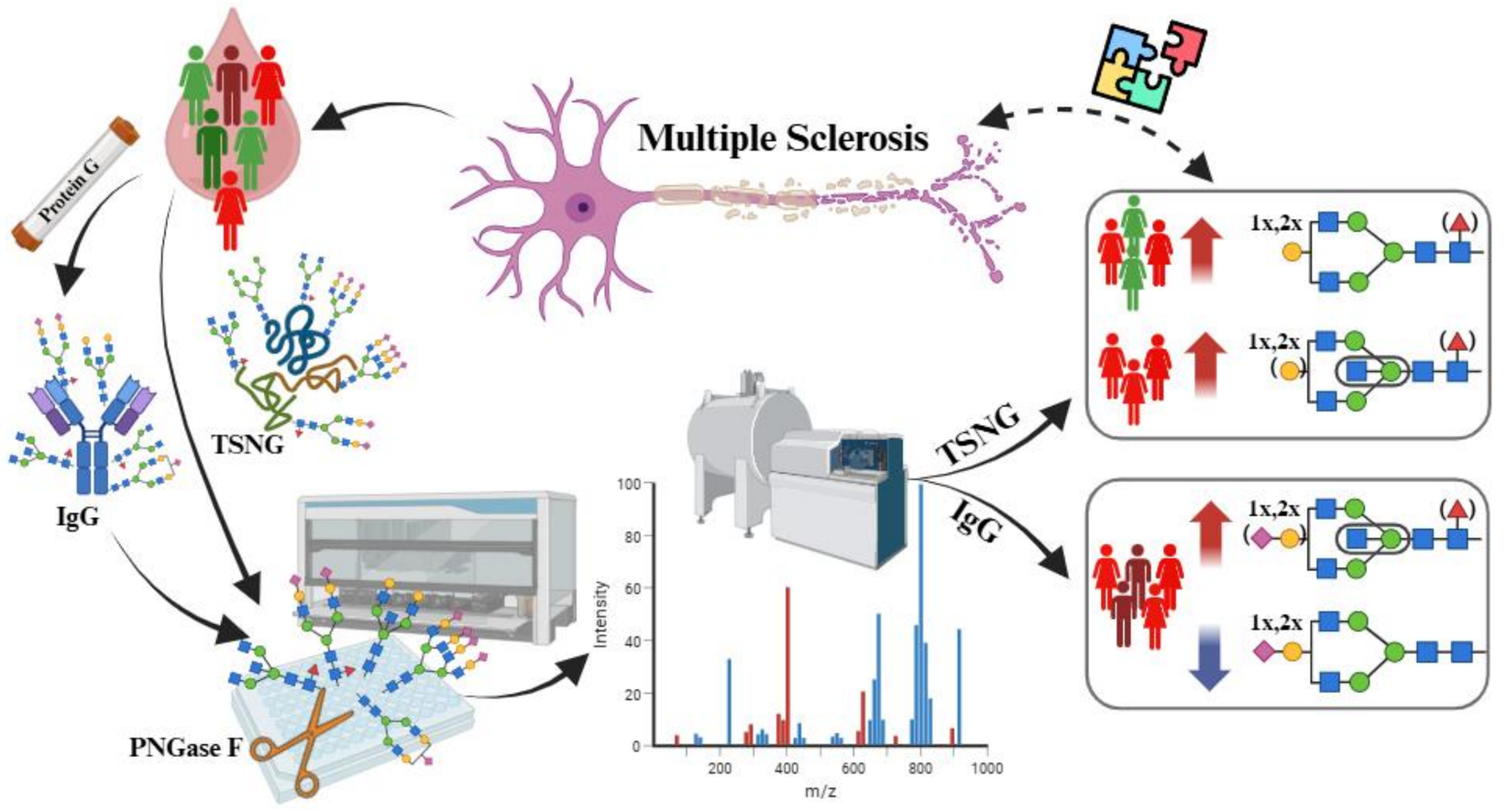
Dalma Dojcsák[1]; Marco Bladergroen[2]; Wenjun Wang[2]; Oleg A. Mayboroda[2]; Csaba Váradi[3]; Tamás Pongrácz[2,4]; Manfred Wuhrer[2]

[1]Advanced Materials and Intelligent Technologies Higher Education and Industrial Cooperation Centre, University of Miskolc, Hungary;
[2] Center for Proteomics and Metabolomics, Leiden University Medical Center, Leiden, The Netherlands
[3]Institute of Chemistry, Faculty of Materials Science and Engineering, University of Miskolc, 3515 Miskolc, Hungary
[4] Department of Clinical Sciences, Karolinska Institutet Danderyd Hospital, Stockholm, Sweden

INTRODUCTION

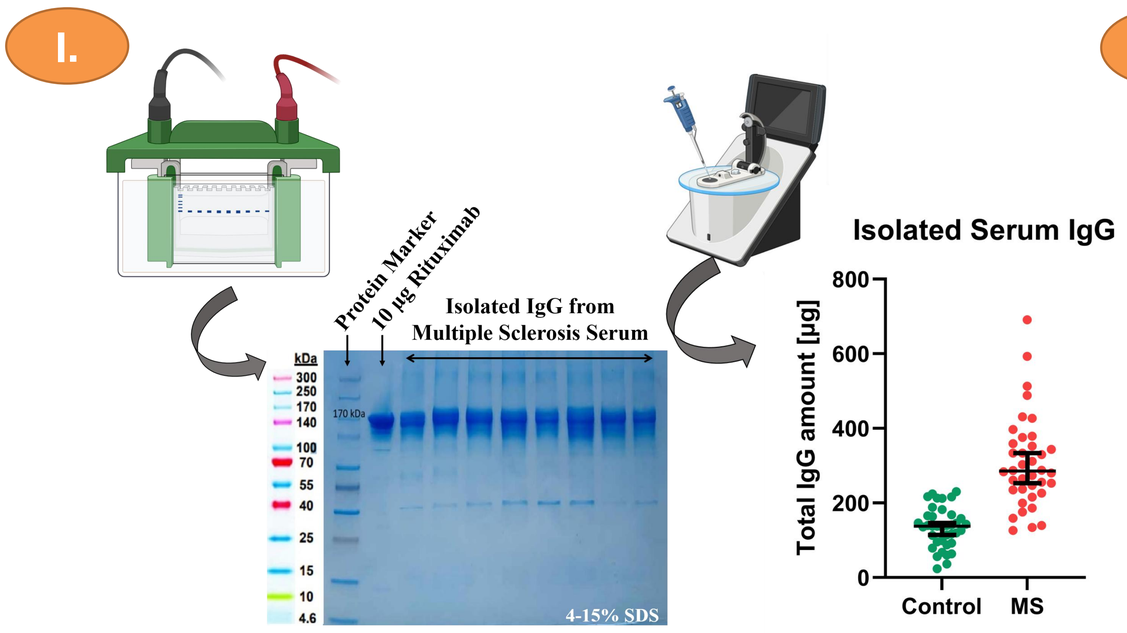
Recent advances in **glycomics** have highlighted the potential of serum protein-derived N-glycans as **biomarkers**. The immunoglobulin G (IgG) is particularly interested, as its N-glycosylation profile is closely associated with **immune regulation** and undergoes alterations in chronic inflammatory diseases, including **multiple sclerosis** (MS). MS is a chronic inflammatory and neurodegenerative disorder and previous glycomic investigations have primarily focused on cerebrospinal fluid-derived IgG, while the influence of demographic factors and potential confounders has received relatively limited attention. **In this study**, we performed a comprehensive **mass spectrometry-based characterization** of total serum N-glycome (**TSNG**) and **IgG N-glycosylation** profiles in 38 MS patients receiving disease-modifying therapies and 38 age- and sex-matched healthy controls. Furthermore, **complementary analytical platforms** were employed to assess the consistency of glycomic alterations and explore the additional information provided by orthogonal analytical approaches.

METHODOLOGY

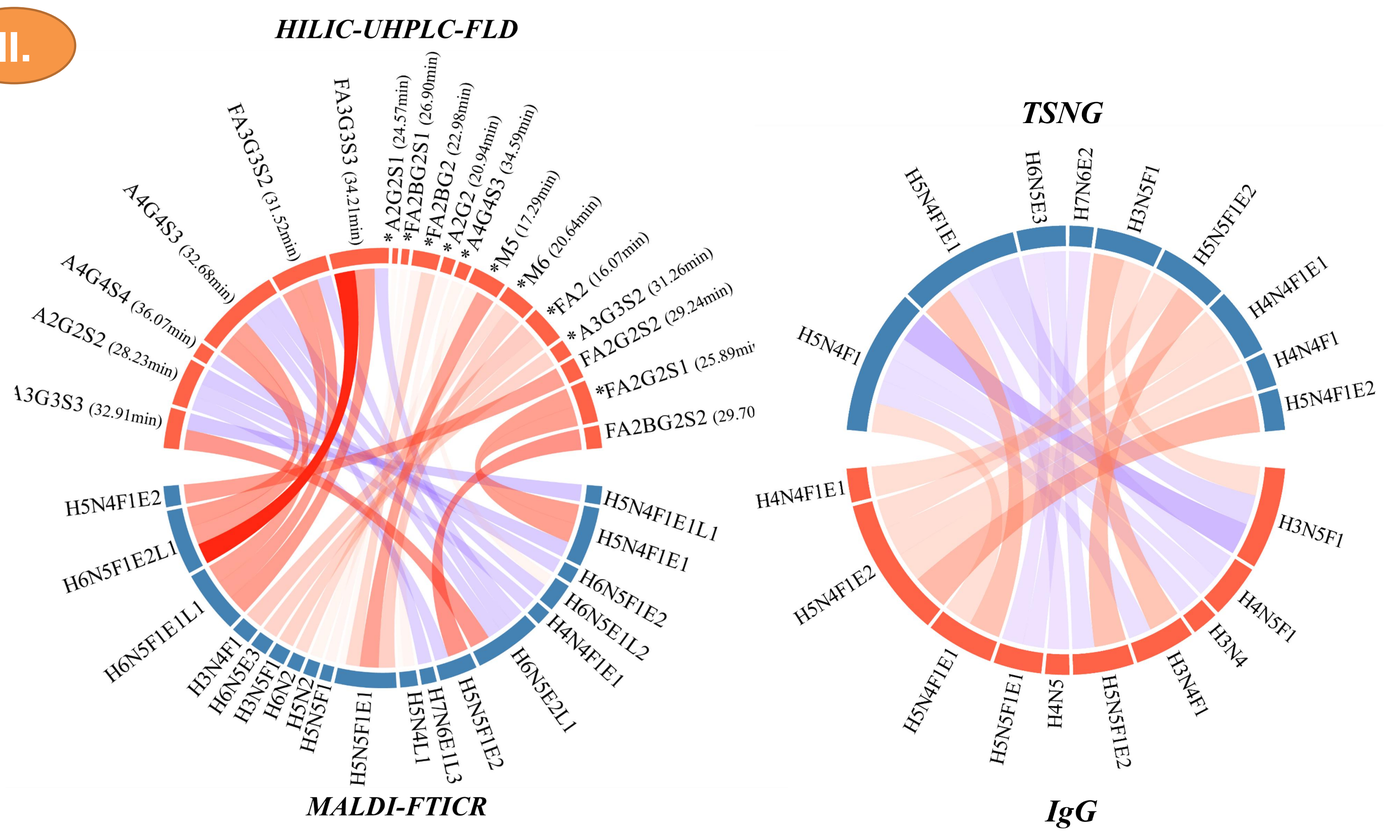


RESULTS OF MULTIPLE SCLEROSIS SPECIFIC N-GLYCOSYLATION

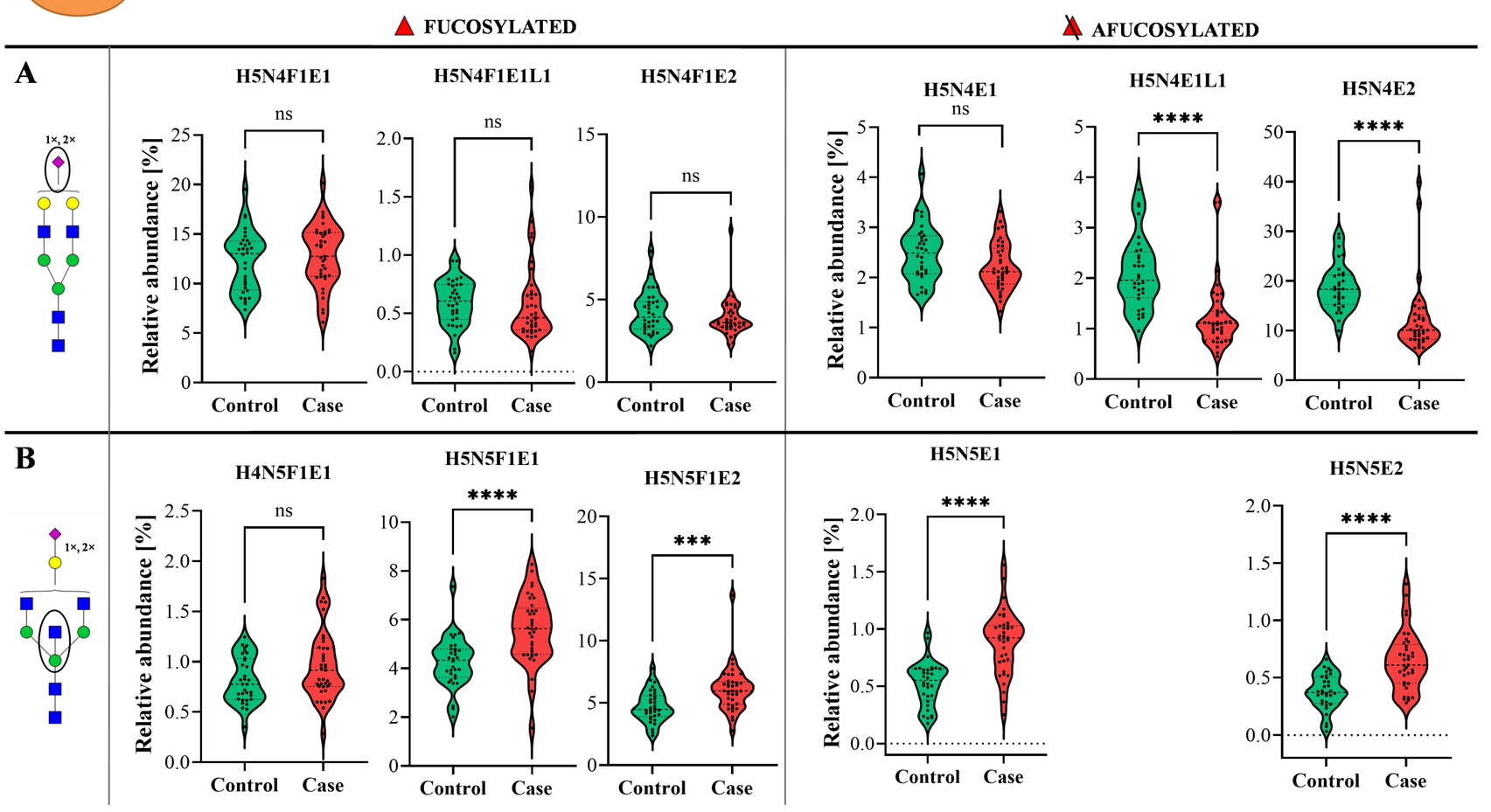
I.



II.



III.



CONCLUSIONS

- IgG N-glycosylation: Decreased sialylation of afucosylated glycans and increased bisecting GlcNAc structures.
- Increased bisection: The most discriminative feature in TSNG analysis.
- Distinct glycosylation patterns: IgG reflected primarily disease-associated changes, while TSNG showed stronger sex-associated variation.
- Complementary approaches: Combining IgG-specific and total serum N-glycomic analyses provides a more comprehensive understanding of glycosylation alterations in multiple sclerosis.

ACKNOWLEDGEMENT

This research was supported by the framework of the 2020-1.1.6-JÖVŐ-479 2021-00009 project.