Novel loci associated with plasma immunoglobulin G *N*-glycosylation identified by a multivariate analysis

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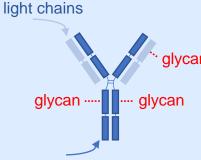


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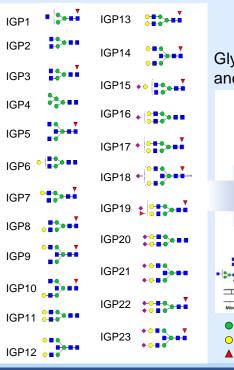
Introduction

IgG structure



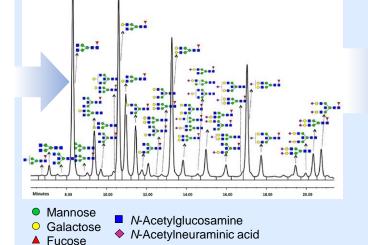
heavy chains

Glycans attached to IgG



- All IgG molecules are <u>N-glycosylated</u>
- N-glycosylation of IgG influences its effector functions and plays a regulatory role in the immune system
- Changes in IgG *N*-glycosylation pattern are associated with different diseases
- Studying the genetic control of IgG glycosylation helps to uncover molecules and pathways regulating IgG *N*-glycome composition
- Previous genome-wide association studies (GWAS) identified and replicated 22 genetic loci associated with plasma IgG *N*-glycosylation

Glycans attached to IgG can be released and measured by UPLC. IGP1-23 correspond to peaks



Study aim

The aim of our study was to identify novel loci associated with plasma IgG *N*-glycosylation traits.

Our aim was achieved by applying a multivariate approach to the largest currently available dataset linking genotypes with IgG glycan measurements.

Methods

- We used GWAS summary statistics for plasma IgG *N*-glycosylation traits obtained in the study by Klarić et al., 2020 (*Science Advances,* PMID:32128391) for European-ancestry cohorts with a total sample size of 8,090 individuals
- We grouped 23 glycan traits into 9 groups based on their general structural and chemical properties and performed a multivariate analysis

Groups of N-glycosylation traits

- 1) N-glycosylation: IGP1, IGP2, IGP3, IGP4, IGP5, IGP6, IGP7, IGP8, IGP9, IGP10, IGP11, IGP12, IGP13, IGP14, IGP15, IGP16, IGP17, IGP18, IGP19, IGP20, IGP21, IGP22, IGP23
- 2) Monogalactosylation: IGP6, IGP7, IGP8, IGP9, IGP10, IGP15
- 3) Digalactosylation: IGP11, IGP12, IGP13, IGP14, IGP16, IGP17, IGP18, IGP20, IGP21, IGP22, IGP23
- 4) Galactosylation: IGP6, IGP7, IGP8, IGP9, IGP10, IGP11, IGP12, IGP13, IGP14, IGP15, IGP16, IGP17, IGP18, IGP20, IGP21, IGP22, IGP23
- 5) Monosialylation: IGP15, IGP16, IGP17, IGP18
- 6) Disialylation: IGP20, IGP21, IGP22, IGP23
- 7) Sialylation: IGP15, IGP16, IGP17, IGP18, IGP20, IGP21, IGP22, IGP23
- 8) Fucosylation: IGP1, IGP3, IGP5, IGP7, IGP8, IGP9, IGP10, IGP13, IGP14, IGP15, IGP17, IGP18, IGP22, IGP23
- 9) BisectingGlcNAc: IGP5, IGP9, IGP10, IGP12, IGP14, IGP18, IGP23

<u>Results</u>

- We identified a total of 32 loci associated with at least one group of IgG *N*-glycosylation traits with *P*-value < 5.6e-09 (5e-08/9)
- Median number of trait groups associated with the identified loci was 6 (range 1-9)
- 6 loci have not been reported in previous IgG N-glycome genetic studies

Six novel loci associated with IgG *N*-glycosylation trait groups identified by the multivariate analysis

Lead SNP	Chr: position (GRCh37.p13)	Effective/ reference allele	EAF*	Top trait group**	P-value	N [#]	Number of traits groups§	Nearest gene(s)
rs12049042	1:246288812	C/T	1.3%	Galactosylation	1.20e-09	4,417	1	SMYD3
rs11895615	2:26113120	C/T	70.3%	BisectingGlcNAc	5.69e-10	8,024	1	ASXL2
rs1372288	3:142901537	C/T	23.3%	N-glycosylation	8.73e-11	8,090	2	CHST2, SLC9A9
rs12635457	3:196203979	A/G	63.6%	N-glycosylation	1.61e-13	8,016	1	RNF168
rs479844	11:65551957	A/G	42.0%	N-glycosylation	1.97e-13	8,089	3	OVOL1
rs4561508	17:16848750	C/T	89.5%	N-glycosylation	1.38e-10	8,002	2	TNFRSF13B

* Effective allele frequency

** Trait group most significantly associated with the locus

[#] Number of subjects in a multivariate analysis

§ Total number of trait groups associated with the locus

Conclusion

Our results significantly expand the number of identified IgG *N*-glycomeassociated loci and demonstrate the efficacy of the multivariate analysis methods in investigating the genetic architecture of complex traits

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