Robust experimental and observational data implicate inflammation as a fundamental driver in the pathogenesis of atherosclerotic cardiovascular disease (CVD).1 Chronic inflammatory diseases provide unique opportunities to gain insight into mechanisms of accelerated atherogenesis in broader populations. Patients with diseases such as psoriasis and rheumatoid arthritis that are characterized by chronically higher levels of systemic inflammation also have substantially elevated risk of CVD, and this risk is lower when these patients are treated with anti-inflammatory medications. For example, studies of patients with psoriasis, a chronic inflammatory skin disorder, have suggested a 25% reduction in CVD risk with the use of disease modifying agents that suppress systemic inflammation.2 In these populations, traditional risk assessment tools often underestimate the true burden of cardiovascular risk, at least in part because of inadequately capturing the magnitude of inflammatory risk. Hence, there is a need for more reliable inflammatory risk assessment tools.

An important avenue of research that addresses this gap comes from recent technical advances in high-performance metabolomics profiling, both nuclear magnetic resonance spectroscopy and mass spectrometry technologies that now allow the identification and quantification of systemic inflammation through protein glycosylation signatures. Regulated enzymatic glycosylation involves the post-translational modification of proteins by attaching oligosaccharide (sugar) moieties and is an important step in regulating protein folding, localization, function, and stability. The significance of these glycosylated attachments is exemplified by their role in modulating numerous biological processes, including cell trafficking, signal transduction, regulation of metabolism, and host–pathogen recognition. As they reflect more downstream protein phenotypes, characterizing the human glycome has received increasing interest as a novel tool to identify markers and potential mediators of disease pathogenesis.3,4

Most secreted proteins undergo N-linkage of glycans to the amide side chains of specific asparagine residues, creating bi-, tri-, and tetra-antennary glycan branches (Figure). From the mobile N-acetyl methyl protons of a subset of glycan moieties and is an important step in regulating protein folding, localization, function, and stability. The significance of these glycosylated attachments is exemplified by their role in modulating numerous biological processes, including cell trafficking, signal transduction, regulation of metabolism, and host–pathogen recognition. As they reflect more downstream protein phenotypes, characterizing the human glycome has received increasing interest as a novel tool to identify markers and potential mediators of disease pathogenesis.

The measured amplitude (size) of the GlycA signal, therefore, serves as a potential composite marker of systemic inflammation sensing the levels and glycosylation states of multiple inflammatory blood proteins. Indeed, we and others have observed that the GlycA signal is associated with longitudinal risk of CVD,6–10 diabetes mellitus,3,11 and mortality6,12,13 (both cardiovascular and cancer mortality), in multiple diverse cohorts. Through its putatively summative nature, a potential advantage of GlycA in clinical practice is that it may be less prone to day-to-day fluctuations that could complicate clinical use of an individual biomarker.5 Indeed, the intraclass correlation coefficient of variation of 4.3% over short-term repeated assessments for this signal has been observed to be lower than that for other inflammatory biomarkers.5 Furthermore, this summative property could imply that GlycA is more likely to provide broader, more integrative profiling of multiple inflammatory pathways, better reflecting the extent of systemic inflammation. GlycA has been correlated with multiple cytokines from various inflammatory pathways, and a relationship with neutrophil activity (through inference form coexpression-based network analysis) has been proposed.14 In addition, in several of the outcome studies mentioned above,6,8,9,11 comparing patterns of risk associations for GlycA with those for other inflammatory biomarkers supports overlap in the risks captured. In these studies, incremental adjustment for these correlated inflammatory markers in many instances attenuates the magnitude of risk associations. In some contexts, the effect of inclusion of other inflammatory markers in risk models accounts for most or all of the observed risk, whereas in other contexts risk persists despite mutual adjustment.

With this mechanistic and observational background in mind, Joshi et al15 sought to better understand the relationship between GlycA and CVD among 2 well-phenotyped case-control cohorts of patients with psoriasis. Strengths of their
study include detailed profiling of vascular inflammation by 18-F fluorodeoxyglucose positron emission tomography/computed tomography and coronary artery disease burden by coronary computed tomographic angiography. Cross-sectional associations between GlycA and these measures demonstrated robust relationships in this population. Notably, these associations remained significant after adjusting for traditional markers of CVD risk, including another marker of systemic inflammation, hsCRP. The observations were strengthened by the finding of a dose-dependent relationship between GlycA level and severity of psoriasis. Intriguingly, anti-inflammatory agents used to treat psoriasis by inhibiting tumor necrosis factor (antitumor necrosis factor) led to the reductions in GlycA and vascular inflammation; however, even after therapeutic
reduction in systemic inflammation, the relationship between GlycA and vascular inflammation persisted.

The findings have several important implications. First, compelling evidence is provided that GlycA is a robust blood biomarker of inflammation-related CVD risk in this population and may outperform other traditional risk markers. Second, as previous studies have suggested, examination of correlations and patterns of risk associations after adjustment for other inflammatory biomarkers supports the hypothesis that GlycA captures summative risk related to multiple inflammatory pathways. Finally, and perhaps of greatest interest, the observation that GlycA is a marker of antitumor necrosis factor therapy suggests that this biomarker could be used as a marker of treatment response and CVD risk among individuals receiving systemic anti-inflammatory therapies—potentially even beyond only those with psoriasis. By comparison, HMG-CoA reductase inhibitors (statins) reduce high-sensitivity C-reactive protein levels by ≈20% to 30% but do not result in clinically meaningful reductions in GlycA. Future prospective studies will be needed to further evaluate this, including in ongoing, large-scale clinical trials that are investigating systemic anti-inflammatory therapies among broader, nonrheumatologic populations to reduce residual risk of CVD. The performance of GlycA in reflecting the effects of nonpharmacological lifestyle interventions to reduce inflammation and CVD risk also warrants further study.

In conclusion, the study by Joshi et al13 provides significant insight into the markers and mechanisms of atherosclerosis in a well-phenotyped high-risk population with psoriasis, with plausible implications for atherosclerosis prediction and treatment in broader populations. By studying patients with more extreme phenotypes—as has been undertaken for evaluating lipid-related risk pathways—we gain deeper insight into the mechanisms of atherosclerosis risk. More fundamentally, the findings support ongoing efforts, founded in biological understanding, to develop innovative, metabolomics-based targeted biomarkers that push the frontier of precision cardiovascular diagnostics.

Disclosures

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