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Abstract Title: Changes in Serum IgA Glycosylation Caused by Sickle Cell Anemia

Immunoglobulin A (IgA), as the principal antibody class in the secretions that cover mucosal surfaces, acts as an important first line of defense in the human body. IgA, an important serum immunoglobulin, mediates a variety of protective functions through interaction with specific receptors and immune mediators. IgA is heavily glycosylated, containing up to ten O-glycosylation and four N-glycosylation sites. IgA glycans have been shown to interact with bacterial surface receptors, thereby inhibiting attachment of several species of bacteria to mucosal surfaces. A key mediator of IgA effector function is CD89. IgA molecules clustered on the surface of a pathogenic target can trigger various elimination processes through engagement of CD89 present on neutrophils, monocytes, eosinophils and some macrophages and dendritic cells.

Sickle cell disease (SCD), a chronic inflammatory disease, has been associated with changes in glycosylation and increases in serum immunoglobulins, including IgA. Here we investigated the expression and glycosylation status of serum IgA in sickle cell patients.

IgA samples were isolated from healthy human plasma (n = 7) and patients with sickle cell disease (n = 8) using Jacalin affinity spin columns. IgA glycan expression was investigated using lectin microarrays and western blotting. Preliminary results from both lectin array and western blotting showed that expression of IgA glycan structures differ in regard to core 1 and sialic acid between healthy people and those with sickle cell disease. These changes were reflected in significant differences seen in binding of Jacalin and ABL (specific to core 1, sialylated and asialyl) and SNA, SSA, and TJA-I lectins (specific to sialic acid) to IgA samples. These differences are blood-type specific, especially between O- and A-type blood groups.

The data indicates that sickle cell disease effects glycosylation of IgA, which can then result in increased inflammation and possibly decreased clearing of pathogenic bacteria from the body.

Future directions will include the identification of O-glycan and N-glycan structures on healthy and SCD IgA from O and A-type blood groups by mass spectrometry, as well as increased sample numbers for the methods already used.