Microarray assessment of N-glycan-specific IgE and IgG profiles associated with Schistosoma mansoni infection in rural and urban Uganda

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Core β-1,2-xylose and α-1,3-fucose are antigenic motifs on schistosome N-glycans, as well as prominent IgE targets on some plant and insect glycoproteins. To map the association of schistosome infection with responses to these motifs, we assessed plasma IgE and IgG reactivity using microarray technology among Ugandans from rural Schistosoma mansoni (Sm)-endemic islands (n = 209), and from proximate urban communities with lower Sm exposure (n = 62). IgE and IgG responses to core β-1,2-xylose and α-1,3-fucose modified N-glycans were higher in rural versus urban participants. Among rural participants, IgE and IgG to core β-1,2-xylose were positively associated with Sm infection and concentration peaks coincided with the infection intensity peak in early adolescence. Responses to core α-1,3-fucose were elevated regardless of Sm infection status and peaked before the infection peak. Among urban participants, Sm infection intensity was predominantly light and positively associated with responses to both motifs. Principal component and hierarchical cluster analysis reduced the data to a set of variables that captured core β-1,2-xylose- and α-1,3-fucose-specific responses, and confirmed associations with Sm and the rural environment. Responses to core β-1,2-xylose and α-1,3-fucose have distinctive relationships with Sm infection and intensity that should further be explored for associations with protective immunity, and cross-reactivity with other exposures.

Schistosomiasis is second only to malaria as a parasitic cause of human morbidity, with over 230 million infections globally, the majority of which occur in tropical and subtropical sub-Saharan Africa1–3. Despite important strides in coverage of anthelminthic treatment, reductions in infection prevalence have only been modest4–6, and the long struggle for a vaccine breakthrough continues7. The host immunological response to Schistosoma infection is shaped to a significant extent by schistosome surface-exposed and secreted glycans and glycoproteins.

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For example, anti-glycan antibody responses dominate the host humoral response to schistosome larvae and eggs\(^8\)–\(^10\) and \textit{Schistosoma} soluble egg antigen (SEA)-mediated Th2-polarisation profoundly relies on glycosylation\(^11\),\(^12\). In a mouse model for periovular granuloma formation, periodate treatment of SEA-coated beads inhibited their granulomogenic activity\(^13\), further demonstrating the functional relevance of glycan-specific responses in \textit{Schistosoma}-mediated immunity and pathology. A better understanding of the human immune response to the \textit{Schistosoma} glycome may be beneficial to the current drive towards identification of better \textit{Schistosoma} diagnostic markers and potent vaccine candidates\(^14\)–\(^18\).

Current insights into the \textit{Schistosoma} glycome, the most characterised among parasites, have been particularly aided by mass spectrometry-based (MS) studies\(^19\)–\(^21\). Analysis of asparagine (N)-linked glycans expressed by schistosomes reveals two standout, non-mammalian substitutions\(^22\),\(^23\) on the trimannosyl-chitobiose core (Man\(_3\)GlcNAc\(_2\), conserved in all eukaryotes): an \(\alpha\)-1,3-fucose (\(\alpha\)3Fuc) linked to the asparagine-linked N-acetylglucosamine (GlcNAc) of the chitobiose component and a \(\beta\)-1,2-xylose (\(\beta\)2Xyl) linked to the \(\beta\)-mannose of the trimannosyl component\(^24\) (Fig. 1). These substitutions are also found on nematode glycans from \textit{Haemonchus contortus} and \textit{Caenorhabditis elegans}\(^25\)–\(^28\), and on invertebrate\(^29\),\(^30\) and plant glycans\(^31\)–\(^33\), but have so far not been detected on glycans from other helminths prevalent in the tropics\(^19\). Detailed MS studies have neither detected core \(\beta\)2Xyl nor core \(\alpha\)3Fuc modified N-glycans in adult schistosome worms but both are present in miracidia and eggs, while cercariae express core \(\beta\)2Xyl but no \(\alpha\)3Fuc on the core GlcNAc\(^34\). Other common alterations to the schistosome Man\(_3\)GlcNAc\(_2\) core include addition of antennae composed of GalNAc\(_\beta\)1-4GlcNAc (LacdiNAc, LDN), GalNAc\(_\beta\)1-4(Fuc\(\alpha\)1-3)GlcNAc (fucosylated LacdiNAc, LDN-F) and Gal\(_\beta\)1-4(Fuc\(\alpha\)1-3)GlcNAc (Lewis X, LeX) units. These antennary modifications are expressed in schistosomes (at all developmental stages, albeit with varying surface expression patterns)\(^34\) but are rare in mammals\(^35\), and occur variably in other helminth species\(^39\).

Core \(\beta\)2Xyl and \(\alpha\)3Fuc modified schistosome egg N-glycoproteins induce potent Th2-type cellular responses\(^36\). In plants, core \(\beta\)2Xyl and \(\alpha\)3Fuc may be the most common N-glycan epitopes targeted by human IgE\(^37\),\(^38\). It is plausible that N-glycan core substitutions play a major role in the glycan-dependent host response to chronic schistosomiasis. For example, most N-glycans on the SEA-derived glycoprotein omega-1 carry \(\alpha\)3Fuc motifs in combination with terminal LeX units\(^39\). Omega-1 drives both immunoregulatory\(^40\) and Th2 responses\(^41\), the latter in a glycan-dependent manner\(^42\). Kappa-5, another major component of the Th2-polarising SEA\(^42\), expresses glycans modified with both core \(\beta\)2Xyl and core \(\alpha\)3Fuc\(^43\). Whether protective immunity against \textit{Schistosoma} infection and reinfection (long associated with host IgE responses\(^44\),\(^45\)) can be credited to these epitopes will require further investigations in animal and human studies.

The advent of glycan microarray technology enabled serum/plasma profiling of antibodies raised to a wide repertoire of N-glycan variants during schistosome infections. This technology has been employed in a small number of human studies. Recently, in Ghana, sera from a few \textit{S. haematobium}\(^\text{infected schoolchildren showed elevated IgE responses to core 32Xyl modified N-glycans on a synthetic glycan microarray}^46\), and in sera from a small cohort of \textit{Schistosoma mansoni} (Sm)-infected children and adults near Lake Albert, Uganda, IgG1-4 subclass responses to core \(\beta\)2Xyl and \(\alpha\)3Fuc motifs were examined using the same array\(^47\). Two other human studies employing shotgun microarrays constructed of complex native schistosome N-glycans showed strong anti-glycan IgG and IgM responses against a wider range of N-glycans during schistosome infections\(^48\),\(^49\). A better understanding of population-level immune responses to \textit{Schistosoma} glycans is important for research and clinical applications, and requires larger, well-defined immuno-epidemiological studies in endemic settings.

**Figure 1.** Non-mammalian carbohydrate substitutions on the N-glycan core. Non-mammalian monosaccharide substitutions are denoted by blue brackets. \(\pm\) implies that motifs in brackets are present or absent in different species. Figure drawn using GlycoWorkbench software, version 2.1 (European Carbohydrates Database Project).
Fishing villages in the Lake Victoria islands of Koome, Uganda, have a high prevalence of S. mansoni, and have been surveyed as part of a portfolio of studies on helminth infections and allergy-related outcomes in Uganda. This setting provided a unique opportunity, within the context of a well-characterised large study, to correlate epidemiological trends pertaining to S. mansoni infection (and intensity) with microarray-detected plasma IgE and IgG responses to N-glycans with and without core α-1,3-fucosylation and/or β-1,2-xylosylation. Plasma from residents of nearby mainland urban communities with lower S. mansoni exposure enabled us to make rural-urban comparisons of anti-glycan antibody responses.

Methods
Study design and population. Individuals included in the current investigation were randomly selected using a Stata program (StataCorp, College Station, USA) from participants of two cross-sectional surveys in rural and urban Uganda, who had a sufficient volume of stored plasma. The rural survey was the outcome survey (year three, September 2015–August 2016) of the Lake Victoria Island Intervention Study on Worms and Allergy-related diseases (LaVIISWA; ISRCTN47196031), a cluster-randomised trial of community-based standard versus intensive anthelmintic intervention in 26 S. mansoni-endemic fishing villages of Koome islands (Lake Victoria, Uganda). The trial description and survey results after three years of intervention have been published briefly, standard intervention included annual, community-based, mass drug administration of praziquantel; intensive intervention included quarterly praziquantel. The urban survey (September 2016–September 2017) was conducted in the 24 sub-wards of Entebbe municipality, an area with lower helminth exposure, located on the northern shores of Lake Victoria (approximately 35 km from Koome). It was designed to collect data from an urban setting for comparison with the S. mansoni-endemic rural survey.

In both surveys, intestinal helminth infections were assessed using the Kato-Katz (KK) method on a single stool sample (prepared on two slides, read by different technicians). The remaining sample was stored at −80°C and later investigated for S. mansoni, Necator americanus and Strongyloides stercoralis infections using multiplex real-time PCR. Mid-stream urine was also assessed for S. haematobium circulating cathodic antigen (CCA) using a point-of-care test (Rapid Medical Diagnostics, Pretoria, South Africa). Schistosoma haematobium is not present in the surveyed areas. Blood samples were processed to obtain plasma for immunological measurements, including N-glycan-specific IgE and IgG by microarray (detailed below) and Schistosoma egg [SEA]- and adult worm [SWA] antigen-specific IgE, IgG4 and IgG by ELISA (Supplementary Material).

The research ethics committees of the Uganda Virus Research Institute and the London School of Hygiene and Tropical Medicine, and the Uganda National Council for Science and Technology approved this work. All methods were performed in accordance with guidelines and regulations of these committees. Informed consent was obtained from all participants and/or their legal guardians and assent from children aged ≥8 years.

Microarray detection of N-glycan-specific IgE and IgG. Immunoglobulin E and G responses to 135 chemically synthesised glycans with and without core α-1,3-fucosylation and, or, β-1,2-xylosylation (Supplementary Fig. S1) were assessed using a non-commercial microarray. Fluorescently-labeled bovine serum albumin (BSA) was included as an array printing control. Microarray construction procedures have been described in detail elsewhere, as follows: Nexterion H N-hydroxysuccinimide-coated microarray slides (Schott AG, Mainz, Germany) (pre-blocked with 50 mM ethanolamine in 50 mM sodium borate buffer pH 9.0, and stored at −20°C) were thawed at room temperature (RT) and covered with silicone gaskets to create seven wells with printed microarrays per slide. Each microarray was incubated with 300 μl of a 1:30 plasma dilution in 1% BSA - 0.01% Tween20 for one hour at RT while shaking. After sequential washes with PBS-0.05% Tween20 and PBS, the slides were incubated for 30 minutes at RT in the dark with PromoFluor 647-labelled anti-human IgE (diluted 1/150 in PBS-0.01% Tween20) and Cy3-labelled anti-human IgG (diluted 1/1000 in PBS-0.01% Tween20), while shaking. After a final wash with PBS-0.05% Tween20, PBS and deionised water, sequentially, the slides were dried and kept in the dark until scanning. The slides were scanned for fluorescence at a 10 μm resolution with a G25655BA scanner (Agilent Technologies, CA, USA) using 633 nm and 532 nm lasers for detection of reactivity to glycan-specific IgE and IgG, respectively.

Data analysis. Using GenePix Pro 7.0 software (Molecular Devices, CA, USA), a spot-finding algorithm was used to align and re-size fluorescence spots in the microarray images, without setting a composite pixel intensity threshold. Data on median fluorescence intensity (MFI) for each spot and the local background were then exported to Microsoft Excel software, where background MFI subtraction was done for each glycan structure, averaged over four spots. Further processing of IgG and IgE MFIs in Excel was done as described by Oyelaran et al., and Amoah et al., respectively, to yield log-transformed values.

Graphical representations of antibody responses and further data analyses were done using Stata 13.1 (College Station, Texas, USA), R (R foundation for Statistical Computing, Vienna, Austria) via the RStudio interface (version 1.1.383, RStudio, Inc. Boston, USA) and GraphPad Prism (version 6.0c, Fay Avenue, La Jolla, CA, USA). Schistosoma mansoni infection and the rural-urban environment were the main exposures of interest: we compared anti-glycan antibody responses between S. mansoni infected and uninfected participants separately in the rural and urban survey, and thereafter between rural and urban participants. Initial analyses considered each anti-glycan antibody response independently, while further analyses combined antibody responses to reduce the dimensionality of the outcome data, as detailed below.

Rural-urban differences in S. mansoni infection and Schistosoma-specific antibodies were assessed using survey design-based logistic and linear regression, respectively. Most log-transformed anti-glycan IgE responses maintained a skewed distribution. Therefore, Mann-Whitney tests were used to assess differences in individual glycan structure-specific antibody responses between S. mansoni infected and uninfected participants and between rural and urban areas.
and urban participants. Most log2-transformed anti-glycan IgG responses were normally distributed and were assessed using unpaired t-tests. The Kruskal-Wallis (IgE responses) and one-way ANOVA test (IgG responses) were also conducted to assess differences along the infection intensity gradient. Since many of the anti-glycan antibody responses were correlated, the above tests were conducted within a Monte Carlo simulation approach based on 1000 permutations, to generate empirical p-values corrected for multiple testing.

Results

Characteristics of the rural and urban survey participants included in this analysis are presented in Table 1. Rural participants were, on average, older [median age (IQR) 22 (5, 37)] than urban participants [median age (IQR) 21 (5, 37)] (p < 0.001). A significantly higher percentage of rural, compared to urban participants, were infected with Sm (KK, p = 0.0002; PCR, p < 0.001; CCA, p = 0.015). Furthermore, median levels of total IgE (p < 0.001) and SEA- and SWA-specific IgE (p < 0.001), IgG4 (p = 0.001) and IgG (p = 0.002 and p < 0.001, respectively) were higher among rural compared to urban participants.

We recently reported that community-based intensive versus standard anthelminthic intervention in the rural survey reduced Sm infection intensity but had no effect on the overall Sm prevalence (measured using the urine CCA test)42. The current analysis found no evidence of an effect of intensive versus standard treatment on total IgE, SEA- or SWA-specific antibodies, or on antibody reactivity to any of the N-glycans on the microarray. Therefore, data from the rural survey were not stratified by trial treatment arm in the further analyses presented herein.

### Associations between S. mansoni infection and IgE and IgG responses to individual core α-1,2-xylosylated and core α-1,3-fucosylated N-glycans.

In the rural survey, IgE and IgG responses to the 32Xyl modified Man\(\beta\)GlcNAc2 core (G34) were significantly higher among Sm infected (KK and/or PCR, and CCA positive), compared to uninfected individuals, and were positively associated with Sm infection intensity but had no effect on the overall Sm prevalence (measured using the urine CCA test)42. The current analysis found no evidence of an effect of intensive versus standard treatment on total IgE, SEA- or SWA-specific antibodies, or on antibody reactivity to any of the N-glycans on the microarray. Therefore, data from the rural survey were not stratified by trial treatment arm in the further analyses presented herein.

### Table 1. Study participants: Schistosoma mansoni and Schistosoma-specific antibodies.

| Characteristic                                      | Rural (n = 209) | Urban (n = 62) | p value |
|-----------------------------------------------------|-----------------|----------------|---------|
| Age in years, median (IQR)                          | 22 (5, 37)      | 21 (5, 18)    | <0.001* |
| Male sex, n/N (%)                                   | 97/209 (44.3)   | 18/62 (29.0)  | 0.163*  |
| Helminth infections, n/N (%)*                       |                 |               |         |
| S. mansoni (single KK)                              | 54/197 (27.5)   | 2/3 (66.7)    | <0.001* |
| S. mansoni intensity (KK)                           | 4/197 (2.1)     | 0/3 (0.0)     |         |
| Uninfected (0 eggs/g)                               | 143/197 (65.5)  | 118/199 (66.0)| 0.002*  |
| Light (0–99 eggs/g)                                 | 29/197 (17.2)   | 54/196 (27.5)| 0.002*  |
| Moderate (100–399 eggs/g)                           | 14/197 (10.2)   | 118/199 (66.0)|        |
| Heavy (≥400 egg/g)                                  | 11/197 (6.0)    | 0/3 (0.0)     |         |
| S. mansoni (PCR)                                    | 118/199 (66.0)  | 32/62 (51.6)  | 0.001*  |
| S. mansoni (urine CCA)                              | 6/48 (12.5)     | 0/3 (0.0)     |         |
| Any nematode infection§                             | 118/199 (66.0)  | 32/62 (51.6)  | 0.001*  |
| Total IgE (kU/L), median (IQR)                      | 548.4 (404.4, 666.9) | 103.3 (63.8, 146.5) | <0.001* |
| Schistosoma egg and worm-specific antibody levels, (µg/ml), median (IQR) | | |
| SEA-specific IgE                                    | 4.2 (2.6, 6.6)  | 2.2 (1.4, 3.6)| <0.001* |
| SWA-specific IgE                                    | 3.9 (2.4, 5.9)  | 2.1 (1.3, 3.1)| <0.001* |
| SEA-specific IgG4                                   | 161.0 (45.9, 663.8)| 8.8 (0.0, 48.4)| 0.001*  |
| SWA-specific IgG4                                   | 71.6 (39.5, 188.1)| 32.1 (7.8, 57.9)| 0.001*  |
| SEA-specific IgG                                    | 1687.3 (848.1, 2727.7)| 730.7 (527.4, 1413.4)| 0.002*  |
| SWA-specific IgG                                    | 1432.4 (845.8, 1941.6)| 804.5 (572.7, 1313.1)| <0.001* |

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IgE PC1, but not PC2, were higher among those glycans with antennae constructed of LDN-F (G90) and LeX (G89) units (Fig. S3).

### Principal component analysis of anti-glycan antibody responses.

Antibody responses to individual core modified N-glycans were strongly correlated. Principal component analysis (PCA) was conducted to summarise these responses, and to evaluate to what extent the resultant principal components (PCs) were associated with *S. mansoni* infection.

Scatterplots of PC1 and PC2 loadings are shown in Fig. 4. In the rural survey, the first two IgE and IgG PCs each accounted for 37% of the total variance in the data (IgE: PC1 28.2%, PC2 8.8%; IgG: PC1 27.7%, PC2 9.7%). Principal component 1 was characterized by responses to core β2Xyl and/or α3Fuc modified glycans while PC2 was characterized by responses to non-xylosylated and non-fucosylated glycans (Fig. 4, panel a and b). Scores for IgE PC1, but not PC2, were higher among *Sm* infected (KK or PCR) compared to uninfected individuals.
p = 0.028, age- and sex-adjusted p = 0.167). Similarly, IgG PC1 scores were higher among Sm infected (KK or PCR) compared to uninfected individuals (crude p = 0.009, adjusted p = 0.027). There were no differences in PC scores between CCA+ and CCA− individuals.

In the urban survey, the first two IgE and IgG PCs accounted for 31% and 35% of the total variance, respectively (IgE: PC1 19.4%, PC2 11.5%; IgG: PC1 24.2%, PC2 10.6%). Interestingly, most IgE responses to glycans carrying core β2Xyl without α3Fuc clustered with non-xylosylated and non-fucosylated glycans in PC2 while responses to glycans carrying both core β2Xyl and α3Fuc and those carrying core α3Fuc without β2Xyl clustered together in PC1 (Fig. 4, panel c). Akin to the rural survey, scores for IgE and IgG PC1 were higher among Sm infected compared to uninfected urban individuals.

Scores for PC1 were positively associated with SW A- and SEA-specific IgE and IgG in both surveys, while PC2 scores were inversely associated with the same Schistosoma-specific antibodies (Table S1).

In addition to PCA, we conducted HCA to further identify groups of anti-glycan IgE and IgG responses that might be jointly elicited in Sm infected versus uninfected individuals. Figure S4 shows clusters of IgE and IgG responses in the rural and urban surveys, and the dominant core substitutions on the glycans in these clusters. Generally, antibody clusters comprising core β2Xyl modified glycans were positively associated with Sm infection and intensity in both surveys (Table S2).

Rural-urban comparisons of anti-glycan antibody responses. Immunoglobulin E responses to individual core β2Xyl and/or α3Fuc modified glycans were higher among rural compared to urban participants, as exemplified in Fig. 5a. Principal component analysis of data combined from both surveys yielded distinct groups of anti-glycan responses (Fig. 5b,f): PC1 was characterized by responses to core β2Xyl and/or α3Fuc modified glycans while PC2 was characterized by responses to non-xylosylated and non-fucosylated glycans. Scores for IgE PC1 (Fig. 5c), but not PC2 (Fig. 5d), were higher among rural compared to urban individuals (p = 0.002). Differences in IgG PC1 scores were not statistically significant. However, IgG PC2 scores were lower among rural compared to urban individuals (p = 0.013).

Further assessment by HCA showed that clusters that comprised IgE responses to core β2Xyl and/or α3Fuc modified glycans (IgE-C1, IgE-C2 and IgE-C4; Fig. S5) were positively associated with the rural setting (Table S4), while IgE-C3 (characterised by very low responses, raised against non-xylosylated and non-fucosylated glycans) was positively associated with the urban setting. Immunoglobulin G response clusters were generally similar between rural and urban settings, except for IgG-C7 which comprised responses to non-xylosylated and non-fucosylated glycans and was positively associated with the urban setting.
By studying rural *S. mansoni*-endemic Ugandan fishing communities and a proximate urban community, we have dissected antibody responses to core β2Xyl and α3Fuc modified N-glycans. Antibody responses to the core modified glycans were higher in the rural communities compared to a proximate urban community. In the urban community, IgE and IgG to both core β2Xyl and core α3Fuc were positively associated with *S. mansoni* infection. In the rural communities, IgE and IgG to core β2Xyl were strongly positively associated with *S. mansoni* infection while reactivity to core α3Fuc was elevated in both *S. mansoni* infected and uninfected individuals. In the rural communities the concentration of antibodies to core α3Fuc modified N-glycans peaked ahead of the peak of *S. mansoni* infection intensity, while the peak of antibodies to N-glycans with only core β2Xyl coincided with it.

The positive association between current *S. mansoni* infection and IgE and IgG reactivity to N-glycans carrying only core α3Fuc in the urban, but not the rural communities, might reflect universal exposure to infection, and persistence of light infection despite treatment, in the rural setting. Core α3Fuc is abundant on N-glycans from *S. mansoni* eggs but is not expressed by cercarial and adult worm N-glycans. It is plausible that responses to core α3Fuc persist after active infection in high *S. mansoni* exposure rural settings: in mice, eggs and hepatic granulomas persist long after clearance of worms. Another explanation for elevated responses to core α3Fuc in the rural communities, regardless of *S. mansoni* infection status, is cross-reactivity. Core α-1,3-fucosylation and β-1,2-xylosylation are also present on certain plant and insect glycoproteins, hence similar core α3Fuc responses in both *S. mansoni* infected and uninfected individuals may also be explained by an exposure other than schistosomes, more prevalent in the rural than the urban setting, that carries core α3Fuc. The observation that antibodies to core β2Xyl were significantly higher among *S. mansoni* infected individuals in both urban and rural settings implies a dominant role for core β2Xyl (compared to core α3Fuc) in *S. mansoni*-specific humoral immunity, shown here for the first time. It also appears that
responses only to core β2Xyl are more responsive to change in Sm exposure: core β2Xyl is abundant on cercarial N-glycans despite being absent in adult worms.

The prominent contribution of core β2Xyl and α3Fuc to cross-reactivity between schistosomes and other environmental exposures such as pollen, hymenoptera venom and vegetable foods22,37,38 is a caveat against the use of core modified glycans in schistosome diagnostic tests. Cross-reactivity with other helminth infections might also occur, but only a few other helminth species25–28, none of which are prevalent in humans in our survey settings, have so far been demonstrated to express glycans with core β2Xyl and α3Fuc motifs. More extensive glycomic studies of other helminths in our survey settings (S. stercoralis, hookworm, T. trichiura, A. lumbricoides, M. perstans) are warranted. However, we did not find any significant associations between these infections and IgE or IgG reactivity to core modified glycans.

Our observations that IgE and IgG reactivity to N-glycans modified with antennae carrying LDNF and LeX units were associated with Sm infection in both surveys are consistent with previous studies in animal models and in humans49,66. No associations were observed with responses to glycans carrying unsubstituted LDN units.

Principal component analysis indicated strong correlations between antibody responses to β-1,2-xylosylated and α-1,3-fucosylated glycans in both surveys. Core β2Xyl and α3Fuc epitopes can be found on similar Sm antigens, where they may be expressed on the same glycoproteins and glycans (such as those expressed by SEA)19, inducing analogous immune responses36. Non-xylosylated and non-fucosylated glycans with antennae constructed of LDN, LDN-F or LeX units may be expressed on the same Sm antigens as glycans with core β2Xyl and α3Fuc motifs. Furthermore, these terminal antennary substitutions can occur on the same glycans as core β2Xyl and α3Fuc19,39,43. However, PCA showed that responses to non-core-substituted glycans with LDN, LDN-F or LeX units did not cluster with core β2Xyl/α3Fuc substituted glycans. Temporal changes in expression of glycans on Sm antigens have been reported20,34; it is possible that these two groups of glycans are expressed at varying magnitudes during Sm antigen maturation. Positive associations between Sm infection and
the first principal component (representing responses to core β3Xyl and α3Fuc) reflect the important role of these core substitutions in the glycan-dependent host response to Sm. To further evaluate their contribution to the host immune response to Sm, it will be important to compare their antibody reactivity with that of other highly antigenic terminal motifs absent from glycans on the array used in this study, such as multi-fucosylated LDN motifs59. It is important to note that while IgG is abundantly detected to many schistosome glycans, and is triggered by Sm infection, only to core β3Xyl and α3Fuc modified glycans is IgE abundantly detected66,67.

Notably in the urban survey, PCA showed that IgE responses to core β3Xyl modified glycans clustered with responses to non-xylosylated and non-fucosylated glycans (Fig. 4c), and IgG responses to core β3Xyl and α3Fuc separated out less distinctly (Fig. 4d) than in the rural survey. The observed β3Xyl clustering patterns may be attributed to the greater intensity of repeated exposure to schistosome cercariae (core β3Xyl) and sustained egg deposition (core β3Xyl and α3Fuc) among rural compared to urban participants. In other words, rural-urban differences in antibody responses to core modified glycans may be indicative of differences in the intensity of Sm infection and/or degree of exposure between the two settings. However, this study did not have sufficient power to assess statistical interactions between the rural and the urban setting. Rural-urban differences in antibody responses to core modified glycans may also be explained by exposures other than schistosomes (mentioned above), perhaps more prevalent in the rural than the urban setting; however, this is unlikely as we observed strong associations between Sm infection and reactivity to core modified N-glycans, particularly to those carrying core β3Xyl. It is also noteworthy that urban survey participants were significantly younger than rural participants; however, this disparity did not seem to influence the observed rural-urban differences in anti-glycan responses, as observed from test statistics before and after adjusting for age.

One of the key challenges in schistosomiasis vaccine development is the risk of allergic (IgE) sensitisation to candidate vaccine antigens60. Glycans are attractive vaccine candidates because they are generally considered to be benign as allergenic determinants69.70. There are a few known exceptions, such as the galactose-α1,3-galactose (α1,3-gal) epitope (found in non-primate mammalian proteins, and shown to elicit severe allergy71), so assessment for any associations between IgE to antigenic Sm glycans and allergy-related phenomena are important. The case for consideration of core modified Sm glycans as Schistosoma vaccine candidates will also need definite proof for an association between reactivity to core modified glycans and protection from Sm infection/re-infection. Our data suggests that a protective role, if any, is more plausible for core β3Xyl than core α3Fuc: in the rural survey, antibody responses to core α3Fuc (G73 and G37, Fig. 3c,d) peaked in childhood, prior to the Sm infection peak in early adolescence, while responses to core β3Xyl (G34) coincided with the Sm infection peak (preceding the more ‘protected’ period in adulthood). However, concrete evidence is required from further population and mechanistic studies exploring the role of Sm N-glycans in protective immunity. For example, it may be important to assess antibodies to these core modifications (and other antigenic terminal motifs) in re-infection study cohorts evaluating the immunological characteristics of individuals who are Sm-resistant following anthelmintic treatment.

In conclusion, we provide an immuno-epidemiological description of IgE and IgG responses to N-glycans in rural and urban Uganda, highlighting the significance of core β3Xyl and core α3Fuc to the glycan-dependent host immune response during chronic schistosomiasis. Moreover, our data imply that IgE and IgG responses to core β3Xyl and α3Fuc modified N-glycans have distinctive relationships with Sm infection and intensity, which may reflect their different contributions towards protective immunity against Sm that need to be further explored using mechanistic animal and human studies.

Data Availability

The datasets generated during and/or analysed during the current study are available from the corresponding author on reasonable request.

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Author Contributions
G.N., C.H.H., M.Y., A.M.E., R.v.R. and A.v.D. contributed to the conception and experimental design of the study. A.M.E., R.E.S. and M.N. led the field and clinic procedures. S.S. and N.C.R. constructed the synthetic microarrays. G.N. conducted the microarray antibody binding experiments. G.N., J.N., J.K. and I.N. participated in establishing and conducting all other immunological and parasitological experiments. G.N. analysed the data with important contributions from E.L.W. and A.v.D. G.N. wrote the manuscript, with all authors contributing to the interpretation of the results, and revision and approval of the final manuscript. G.N. is the guarantor of the article.
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