BACKGROUND AND AIMS

Collective prior exposure to non-pathogenic immunogens and infectious agents, including immunomodulatory helminths and anthelminthic treatment, shapes host future immune responses to related and unrelated immunogens. With the widespread rollout of mass drug administration (MDA) across Africa, many populations have now received at least one round of deworming treatment. This raises critical questions about the nature, persistence, and significance of immunological shifts in endemic settings with repeated exposures. Thus, the aim of this proof-of-concept study was to survey and define the exposome, or the collection of immunogens a host has been exposed to, of a helminth-endemic rural Zimbabwean population using a novel peptide microarray approach.

METHODS

Using a bespoke peptide microarray, we determined antigen-specific serum IgM and IgG reactivities of 20 children under five years of age against a variety of B-cell epitopes from 290 immunogens of interest to Zimbabwe, including pathogens, vaccines, allergens, autoantigens, and a variety of parasites.

RESULTS

Data from this microarray revealed broad, heterogenous immunogen recognition early in life. The most frequently recognized exposome constituted viruses, bacteria, fungi, autoantigens, and both micro- and macro-parasites, including helminths, trypanosomes, and plasmodium species.

CONCLUSIONS

This diverse early-life infectome signature may contribute to differential susceptibility to infection severity, vaccine responsiveness, or immune-mediated pathology. Results from the present discovery study provide baseline proof of concept reference values for helminth-endemic under five immune ecologies and should be considered in future public health planning.