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# Spatial distribution of and socio-ecological risk factors for strongyloidiasis in Australia

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## SUMMARY

*Introduction:* Strongyloidiasis, caused by the soil-transmitted helminth Strongyloides stercoralis, remains a neglected public health issue in Australia, particularly among remote Aboriginal and Torres Strait Islander communities. This study aimed to map the spatial distribution of strongyloidiasis and investigate associated socioecological factors to identify high-risk areas and guide targeted interventions in Australia.
*Methods:* We used data from a previous nationwide pathology data survey conducted between 2012 and 2016, which included 81,131 individuals across 332 statistical area level 3 (SA3) regions in Australia. Socio-ecological and environmental variables were extracted from publicly available online sources to explore their relationship with strongyloidiasis. Spatial patterns were analysed using Global Moran's I and Getis-Ord statistic to identify clusters of high and low disease prevalence. Bayesian spatial modelling was applied to investigate whether socio-climatic factors explain the spatial distribution of strongyloidiasis in Australia.
*Results:* The predicted prevalence map showed substantial spatial heterogeneity of strongyloidiasis, with the highest prevalence identified in regions of the Northern Territory, northern Queensland, and northern Western Australia. Bayesian geospatial analysis indicated significant positive associations between strongyloidiasis prevalence and higher temperature (β: 0.080; 95% Credible Interval [CrI]: 0.043, 0.117) and higher soil pH (β: 0.231; 95% CrI: 0.038, 0.425). Conversely, a higher Socio-Economic Indexes for Areas

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*Abbreviations:* ABS, Australian Bureau of Statistics; CrI, Credible Interval; ELISAs, Enzyme-Linked Immunosorbent Assays; GEE, Google Earth Engine; IRSD, Index of Relative Socio-economic Disadvantage; MDA, Mass Drug Administration; NTD, Neglected Tropical Disease; NDVI, Normalised Difference Vegetation Index; SEIFA, Socio-Economic Indexes for Areas; STH, Soil-Transmitted Helminths; VIF, Variance Inflation Factors; WASH, Water, Sanitation, and Hygiene; WHO, World Health Organization

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(SEIFA) score, that is, areas with generally higher socio-economic status, was negatively associated with the strongyloidiasis prevalence (β: −0.107; 95% CrI: −0.179, −0.036).

*Conclusion:* Our findings reveal significant geographical variation in strongyloidiasis prevalence across Australia, with high prevalence observed in northern Queensland, the Northern Territory, and northern Western Australia, where climatic factors, soil characteristics, and socioeconomic conditions can shape the spatial distribution of the disease. Geographically tailored strategies targeting high prevalence areas are essential for effective prevention and control.

## Introduction

Strongyloidiasis, a chronic infection primarily caused by the parasitic nematode *Strongyloides stercoralis*, remains a significant yet neglected tropical disease (NTD).[1] Globally, an estimated 300–600 million people are infected with *S. stercoralis,* and its distribution is highly heterogeneous.[2,3] The disease is endemic throughout tropical and subtropical regions worldwide, predominantly in resource-limited countries.[4,5] Pockets of continued transmission are found among underserved and socioeconomically marginalised communities in some high-income nations, including the United States, Central Europe, and Australia.[6–8] The South-East Asia, African, and Western Pacific Regions account for 76.1% of global strongyloidiasis cases,[2] with estimated prevalence rates of 12.1%, 10.3%, and 7.1% respectively.[2] However, the epidemiological features are likely underreported due to diagnostic challenges.[9,10]

In Australia, strongyloidiasis is recognised as a significant public health concern, disproportionately affecting remote Aboriginal and Torres Strait Islander communities. Despite Australia's high Human Development Index (HDI) score, socioeconomic disadvantage and limited access to healthcare services, which are frequently found in geographically isolated areas, have contributed to conditions that favour the transmission and persistence of strongyloidiasis.[11–13] The prevalence of strongyloidiasis is also higher among returned travellers, Vietnam veterans and ex-prisoners of war, and immigrants from endemic areas, including refugees or asylum seekers.[14,15]

The geographical distribution of endemic *Strongyloides* acquisition is influenced by a range of individual, population, and environmental factors. Prior studies have shown that occupation-related activities such as agricultural or outdoor labour,[16] walking barefoot,[5] and poor water, sanitation, and hygiene (WASH) practices[17,18] are associated with an increased risk of strongyloidiasis. Additionally, ecological factors such as temperature, humidity,[19,20] soil carbon content, and soil pH[21,22] facilitate the transmission, growth, and development of free-living stages of the worm. The parasite has a unique ability for autoinfection, enabling lifelong infection. Strongyloidiasis presents with a wide clinical spectrum, from asymptomatic chronic infection to rapidly progressive, life-threatening disease. The initial signs of infection are induced by allergic reaction to the migration of infective larvae through the skin, lungs, and to the gut. These may include rash at the site of skin penetration, cough (Loeffler's syndrome), and mild gastrointestinal symptoms.[23] In immunocompetent individuals, around 50% of chronic cases show persistent or recurrent symptoms.[24] If symptoms are reported, they are typically mild and nonspecific, including urticaria, intermittent abdominal pain, diarrhoea, or chronic or recurrent respiratory symptoms,[25] frequently remaining unrecognised for years without targeted testing. Hyperinfection and disseminated disease occur in immunosuppressed individuals such as those on corticosteroid therapy or with Human T-cell Lymphotropic Virus Type 1 (HTLV-1) co-infection, and characterised by uncontrolled parasite replication and dissemination to organs such as the brain and liver.[26–28] Case-fatality rates exceed 60%,[29,30] and severe disease is often complicated by secondary bacterial sepsis, meningitis, pneumonia, and multiorgan failure. A systematic review reported that 41% of *Streptococcus gallolyticus* meningitis cases were associated with *S. stercoralis* infection, highlighting the role of bacterial translocation in severe disease.[31] In Australia, fatal outcomes have occurred in patients who were not screened for *S. stercoralis* before immunosuppressive therapy, despite clear risk factors such as origin from endemic areas or unexplained eosinophilia,[10,32] and guidelines that recommend screening prior to immunosuppression.[33]

The burden of strongyloidiasis has remained persistent due to limited emphasis on the parasite in public health programmes. Existing mass deworming programmes for soil-transmitted helminth (STH) in school-age children utilise anthelminthic drugs albendazole or mebendazole, which respectively have poor efficacy against strongyloidiasis or are administered in insufficient dosage.[34] However, a single dose of ivermectin proves highly effective for uncomplicated chronic infection, making it the preferred option for preventive chemotherapy.[26] In addition, given the high prevalence of strongyloidiasis among adults, an effective control strategy is likely to require a community-wide ivermectin-based mass drug administration (MDA).[16] The World Health Organization (WHO) has developed a road map from 2021 to 2030 to guide global strategies for NTDs, which includes a specific goal to address strongyloidiasis.[35] In addition, the WHO released its first guideline on the public health control of the disease in 2024,[36] recommending a single dose of ivermectin as preventive chemotherapy in endemic areas with ≥5% prevalence in school-aged children or ≥10% in the general population. Effective and sustainable control of strongyloidiasis requires accurate diagnostics, epidemiological monitoring, targeted delivery of multicomponent interventions, and ongoing surveillance, particularly in high-risk populations.

Understanding the spatial patterns and socio-ecological drivers of strongyloidiasis is key for effective control, yet detailed knowledge of its geographic variation across Australia is still limited due to the absence of consistent data collection methods and surveillance systems. A previous study[8] focused on mapping the disease's proportion across the country; it did not describe socioeconomic and environmental factors or the use of advanced spatial analysis techniques. Geospatial analysis offers a powerful tool to visualise disease distribution, detect disease clusters, and elucidate socioecological risk factors that underpin the spatial patterns of infection. Thus, a more advanced spatial modelling approach can better inform control strategies in endemic and non-endemic areas and direct resources to where they are most required. Such evidence is clinically relevant, informing targeted screening and early intervention in high-risk populations. This study aimed to investigate the spatial distribution of strongyloidiasis prevalence across Australia, identify areas with significantly higher disease prevalence, and highlight the socio-ecological drivers contributing to these spatial patterns.

## Methods

### *Data sources*

This geospatial analytics study utilised pathology laboratory data on strongyloidiasis collected across Australia between 2012 and 2016 and aggregated at the Statistical Area Level 3 (SA3). Data were obtained from a previous study that retrospectively reviewed nationwide pathology records from six laboratories in Australia[8] that perform diagnostic serological testing of patients for *Strongyloides* infection.

A total of 81,131 individuals who underwent serology testing represented by either their first *Strongyloides*-positive test or their first test if they never had a positive *Strongyloides* test (negatives) were included in the final analysis, aggregated at the SA3 level. Three enzyme-linked immunosorbent assays (ELISAs) were employed across the laboratories: the Bordier ELISA using *S. ratti* somatic infective larval antigens, an inhouse ELISA also based on *S. ratti* infective larval antigens, and the In Vitro Diagnostic (IVD) ELISA using *S. stercoralis* infective larval antigens. Further methodological details are available online.[8]

The SA3 data included in the pathology records cover diverse ecological zones, climatic conditions, and varying socioeconomic contexts across Australia, enabling a comprehensive analysis of environmental and socio-ecological determinants of strongyloidiasis prevalence. Socioeconomic and environmental covariates data were extracted from multiple publicly available sources at a spatial resolution of 1 km$^2$. Population density and Socio-Economic Indexes for Areas (SEIFA) data were obtained from the Australian Bureau of Statistics (ABS). Environmental data were also retrieved from publicly available datasets hosted on Google Earth Engine (GEE), a cloud-based platform for remote sensing and geographical big data analysis.[37] GEE provides an extensive library of satellite imagery and climate datasets, including data from sensors like Landsat and Sentinel. It supports analyses at global to local scales, with daily updates enabling diverse applications and instant data access.[38] Details of data sources for each variable are summarised in Table 1. The geographical distribution of these variables across Australia is displayed in Fig. 1. Moreover, a polygon shapefile for the Australian administrative boundaries at the SA3 was obtained from the ABS database.

### *Variable selection*

Candidate covariates were selected based on national representativeness, high spatial resolution, and previous evidence of associations with strongyloidiasis or other STH infections. Raster values of the covariates were extracted at each SA3 level based on corresponding geographic coordinates. To address potential multicollinearity, variance inflation factors (VIF) were computed for all candidate variables. Covariates with VIF exceeding six were considered collinear and excluded from the final analysis to improve model stability and interpretability. A two-stage variable selection process was employed to construct a parsimonious predictive model. Initially, each covariate was evaluated independently using Bayesian geospatial bivariable regression. Only covariates demonstrating significant associations with strongyloidiasis prevalence in the bivariable analysis were retained for inclusion in the multivariable model. Accordingly, population density, precipitation, temperature, elevation, soil pH, NDVI, Soil clay content, soil sand content, and SEIFA score were included in the final model.

### *Geospatial analysis*

The global Moran's I and Getis-Ord statistical tests were applied to identify clusters of high prevalence of strongyloidiasis. Moran's I assessed the presence, strength, and direction of spatial autocorrelation and tested the assumption of spatial independence in the spatial pattern analysis. The Getis-Ord statistic identified local clusters of strongyloidiasis prevalence.

Bayesian areal-level spatial analysis with a logistic regression framework was also used to estimate a predicted prevalence of strongyloidiasis at the SA3 area level. The outcome variable was defined as the number of positive cases out of the total number of tested population, assumed to follow a binomial distribution. The model included various socio-environmental factors as fixed effects, while spatial autocorrelation was constructed using the Besag-York-Mollié (BYM) model. This spatial component captured spatially structured and unstructured random effects, with neighbourhood relationships defined based on Queen's contiguity among SA3 regions. The model was constructed as follows:

$\mathrm{Y_j} \sim \mathrm{Binomial}\,(\mathrm{n_j}, \mathrm{p_j})$; Where $n$ is the total number of participants and $p$ is the predicted prevalence of strongyloidiasis at location $j$. The prevalence at each location is then related to a linear predictor via a logit link function, whereby:

$$logit\,(p_j) = \alpha + \Sigma_{Z=1}^{Z} \beta_Z X_{Z,j} + u_j + v_j$$

where $\alpha$ is the intercept, $\beta$ denotes the matrix of covariate coefficients, X is a design matrix of z covariates, $u_j$ represents the spatially structured random effect based on Queen's adjacency and $v_j$ represents the spatially unstructured random effect.

For the spatial random field parameters, we used a default prior distribution constructed by the Integrated Nested Laplace Approximation (INLA) approach in R (version 4.2.3). Multiple iterations were performed to fully characterise the posterior distribution, and the predicted prevalence of strongyloidiasis was estimated by combining spatially varying fixed effects with spatial random effects. The intercept was included in the linear predictor, and results were back-transformed from the logit scale to the prevalence scale, producing spatial maps that describe the estimated prevalence at all prediction locations.

### *Model selection*

The conditional predictive ordinates (CPO) and the probability integral transform (PIT) statistics were computed for model validation. Various models with different combinations of covariates were constructed and compared, with the best-fitting model selected based on the lowest Watanabe-Akaike Information Criterion (WAIC)

**Table 1**
Summary of data sources used for outcome and socioecological variables.

| Variables | Data sources |
|---|---|
| **Strongyloidiasis prevalence data** | The number of strongyloidiasis cases and tested population number were obtained from a previously published study[8] that retrospectively reviewed nationwide pathology records. |
| **SEIFA** | Socio-Economic Indexes for Areas (2016) are sourced from the ABS, providing an aggregated measure of socioeconomic conditions.[39] |
| **Precipitation** | Annual precipitation was obtained from the CHIRPS dataset at a spatial resolution of 1 km for the period 2012–2016.[40] |
| **Temperature** | Annual mean temperature between 2012 and 2016 derived from the WorldClim v2.1 dataset at a spatial resolution of 1 km.[41] |
| **Altitude** | Digital Elevation Model from the Shuttle Radar Topography Mission (SRTM) dataset.[42] |
| **Population density** | Population estimates from the ABS, calculated as the number of people per square kilometre.[39] |
| **Soil PH at 10 cm** | Obtained from the SoilGrids global gridded soil information database.[43] |
| **Soil clay content at 5 cm** | Obtained from the SoilGrids global gridded soil information database.[43] |
| **Soil sand content** | Obtained from the SoilGrids global gridded soil information database.[43] |
| **Normalised Difference Vegetation Index (NDVI)** | Average annual NDVI composite obtained from the MODIS Terra Vegetation Indices product (MOD13Q1).[44] |

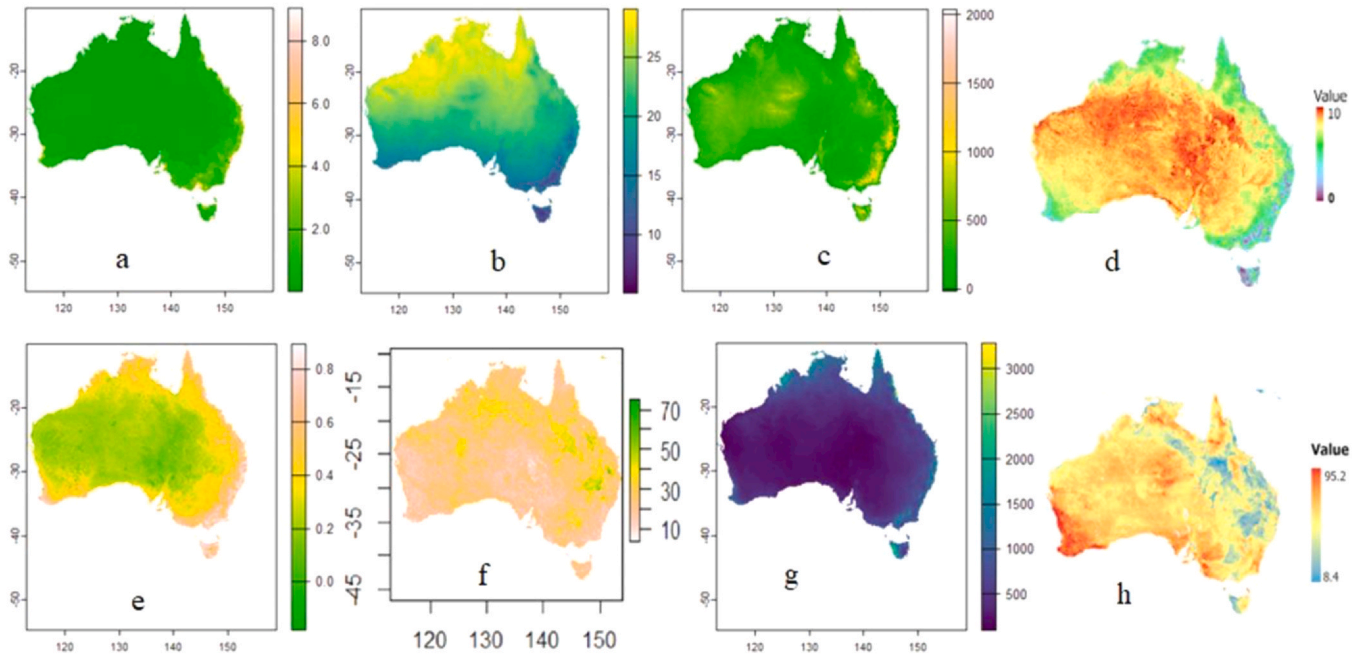

**Fig. 1.** Geographical distributions of socioenvironmental covariates in Australia: a) Population density 2016 (persons/km²), b) Average mean annual temperature (2012–2016) (°C), c) Elevation(m), d) Soil pH value, e) Average NDVI (2012–2016), f) Soil clay content (%), g) Average mean annual precipitation (2016–2016) (mm/yr), and h) Soil sand content (%).

score. Data management, analysis, and mapping were performed using R (version 4.2.3).

### *Ethical consideration*

This study used only publicly available, de-identified data and did not involve direct participation of human subjects. An ethics waiver was granted by the QIMR Berghofer Human Research Ethics Committee (HREC).

## Results

In total, we included 332 georeferenced clusters with 81,131 samples.

### *Spatial clustering of strongyloidiasis in Australia*

The global Moran's I statistic for strongyloidiasis prevalence was 0.28 ($p < 0.001$), demonstrating significant positive spatial autocorrelation across the study. The Getis-Ord statistical analysis identified significant high-risk clustering of strongyloidiasis in the Northern Territory, northern Queensland, and parts of northern Western Australia. In contrast, the southern parts of the country, including Tasmania and the southern regions of Western and South Australia showed low values or a lack of clustering (Fig. 2).

Fig. 3 shows the structured spatial effect estimated from the Bayesian BYM model for the prevalence of strongyloidiasis in Australia, highlighting strong positive spatial effects in northern Queensland and the Northern Territory (Fig. 3).

### *Predicted prevalence of strongyloidiasis in Australia*

The estimated prevalence of strongyloidiasis showed spatial variations, with higher predicted prevalence observed in the Northern Territory (26.9%), northern Queensland (reaching up to 37.8%), and northern Western Australia (22.2%). In contrast, southern Australia, including Tasmania and the southwestern region of Western Australia, showed a low predicted prevalence, remaining below 3% (Fig. 4).

Table 2 presents the Bayesian multivariable regression model of socioecological level factors associated with the prevalence of strongyloidiasis in Australia. Temperature was positively associated with the spatial distribution of strongyloidiasis (β: 0.080; 95% CrI: 0.043, 0.117). Similarly, soil pH was positively associated with the prevalence of strongyloidiasis (β: 0.231; 95% CrI: 0.038, 0.425). However, the Index of Relative Socio-economic Disadvantage (IRSD) score was negatively associated with the spatial distribution of strongyloidiasis prevalence (β: −0.107; 95% CrI: −0.179, −0.036) (Table 2).

## Discussion

This study presents one of the first geospatial analyses of strongyloidiasis in Australia. We found substantial spatial variation and identified key socio-climatic factors associated with the distribution of strongyloidiasis.

Our study identified high-risk areas for strongyloidiasis in the Northern Territory, northern Queensland, and northern Western Australia. These patterns are consistent with previous literature indicating that strongyloidiasis is endemic in warm tropical and socioeconomically disadvantaged regions.[12,45] A study in the Northern Territory found that 40.3% of adult patients across four clinics in remote North East Arnhem Land tested positive for strongyloidiasis with prevalence rates ranging from 34.1% to 51.2%.[12] A complex interplay of environmental, socio-economic, and health system barriers influences the high prevalence of strongyloidiasis in these areas. Many remote Aboriginal and Torres Strait Islander communities face significant challenges related to housing conditions, limited healthcare access, and inadequate environmental health infrastructure, such as safe drinking water, functional toilets, and access to public laundries.[46,47] These findings further reinforce the urgent need to address social determinants of health, including housing, sanitation facilities, and access to culturally appropriate healthcare services to help reduce the burden of strongyloidiasis.

While our model highlights areas with increased environmental risk of local transmission, considerable disease burden also exists from

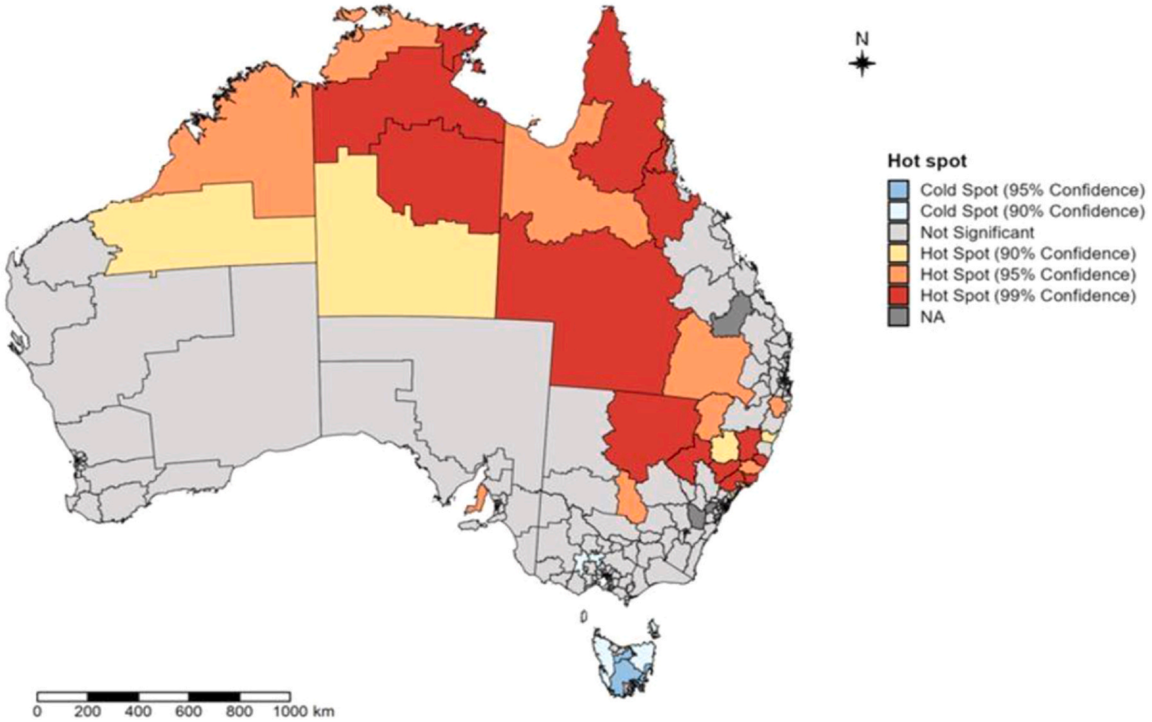

**Fig. 2.** Spatial clustering of strongyloidiasis prevalence based on Getis-Ord statistical analysis, 2012–2016.

imported cases in metropolitan areas such as Sydney and Melbourne. These areas do not appear as high-risk areas in the model because of less favourable environmental conditions for transmission, yet they are home to large migrant and refugee populations who may have acquired infection in endemic countries. Seroprevalence rates of 20–42% have been reported among refugees and immigrants in Australia.[48,49] High case numbers in these metropolitan areas likely reflect the result of screening and diagnosis based on symptoms, rather than ongoing local transmission.

*Strongyloides stercoralis* has a global distribution, with cases increasingly recognised in otherwise non-endemic settings due to migration, travel, and in military veterans.[50] With rising corticosteroid use and

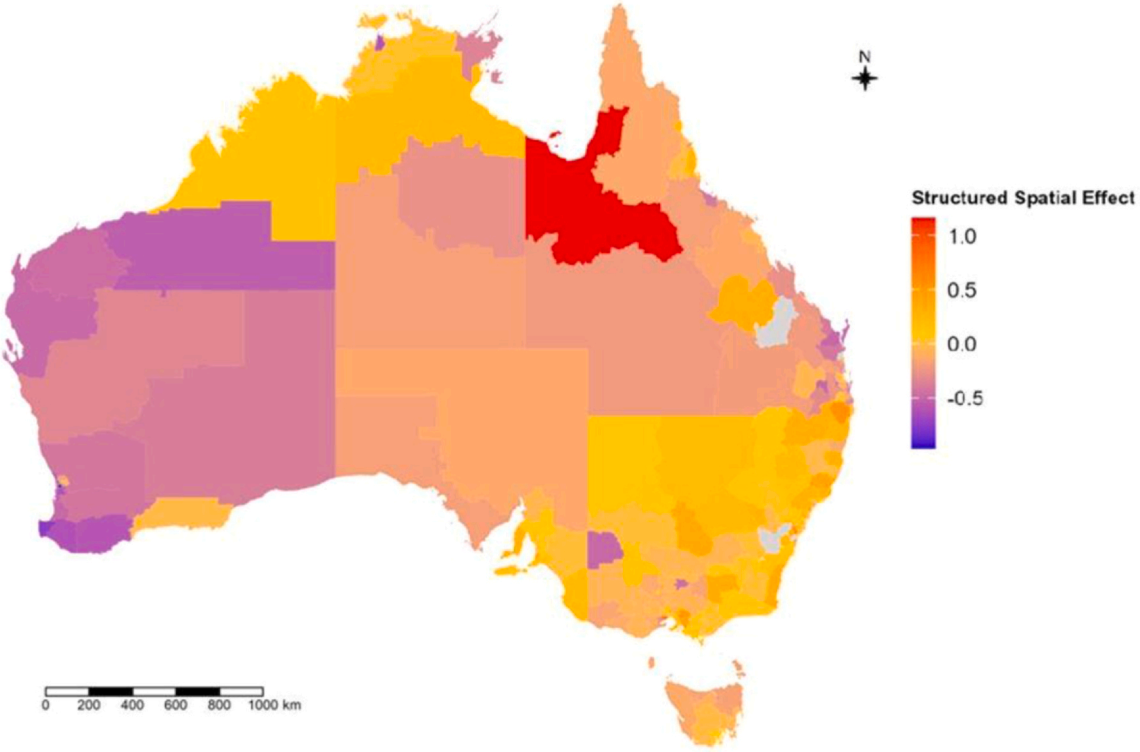

**Fig. 3.** Structured spatial effects of strongyloidiasis estimated using the INLA model. Grey areas represent missing data.

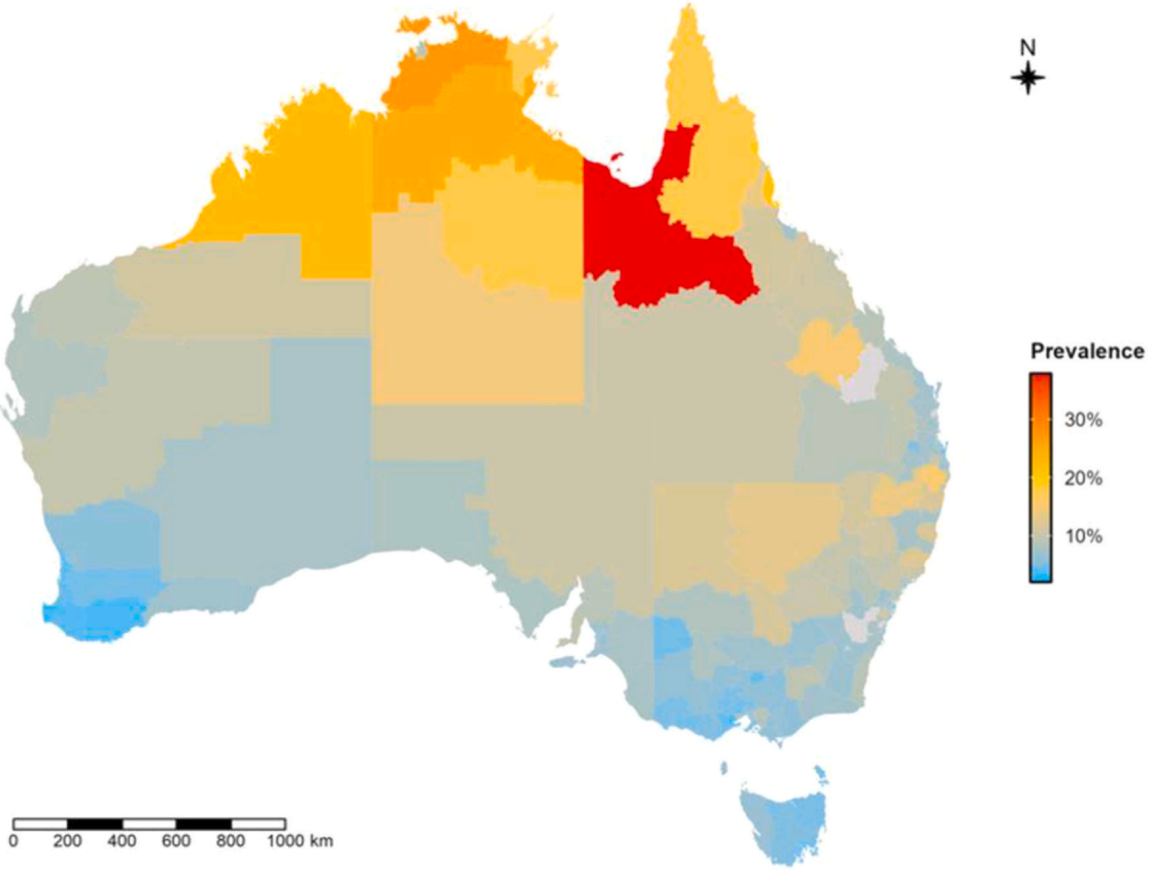

**Fig. 4.** Predicted mean prevalence of strongyloidiasis in Australia from 2012 to 2016. Socioecological level factors associated with spatial clustering of strongyloidiasis.

**Table 2**
Regression coefficient mean and 95% CrIs of socioclimatic factors considered in a Bayesian spatial model for strongyloidiasis prevalence in Australia.

| Socioclimatic variables | Regression coefficient mean 95% CrIs |
|---|---|
| **Elevation** | 0.095 (−0.008, 0.198) |
| **Precipitation** | 0.109 (−0.027, 0.244) |
| **Temperature** | 0.080 (0.043, 0.117)* |
| **Soil clay content at 5 cm** | −0.009 (−0.034, 0.016) |
| **Soil pH at 10 cm** | 0.231 (0.038, 0.425)* |
| **Soil sand content** | −0.003 (−0.009, 0.003) |
| **NDVI** | 0.590 (−0.445, 1.624) |
| **SEIFA (IRSD score)** | −0.107 (−0.179, −0.036)* |
| **Population density (people/km$^2$)** | −0.041 (−0.092, 0.011) |
| **Intercept** | −5.149 (−6.863, −3.435) |

NDVI, Normalised Difference Vegetation Index.

[*] Statistically significant covariates at p-value < 0.05.

limited clinical awareness in high-income countries,[33] *S. stercoralis* is likely to become an increasing clinical concern. In a systematic review of 244 cases (171 with hyperinfection and 73 with confirmed systemic disease), Buonfrate et al.[30] reported corticosteroid exposure in 67% of patients. Early detection in at-risk individuals is crucial to prevent complications.[10] Clinicians should be alert to the possibility of chronic strongyloidiasis in individuals who have lived in or travelled to endemic areas and remain aware of the risk of hyperinfection and dissemination. Although the true incidence of severe strongyloidiasis among immunosuppressed individuals is uncertain, it is likely underestimated, as many cases are overlooked or misdiagnosed as community-acquired sepsis or meningitis. Most reported cases occur in those receiving corticosteroids, organ transplants, or co-infected with HTLV-1. Notably, in Central Australia, 63.6% of patients with complicated strongyloidiasis were HTLV-1 seropositive, and most cases were fatal.[51] In such a situation, presumptive ivermectin treatment may be justified even in the absence of positive test results or overt clinical symptoms.[52]

Effective national control should not overlook urban areas and requires integration of routine screening into migrant and refugee health programmes, regardless of time since arrival. Screening should also be prioritised for individuals from endemic regions starting immunosuppressive therapy or with haematological malignancies, who are at high risk of severe disease.

Like many NTDs, strongyloidiasis is more prevalent in settings of socioeconomic disadvantage and poor sanitation.[4] Understanding socioeconomic and environmental factors is important for designing effective and integrated control measures and reducing the impact of strongyloidiasis on vulnerable populations. In this study, the IRSD score showed an inverse association with the spatial distribution of strongyloidiasis prevalence, indicating that greater socioeconomic disadvantage is related to a higher disease burden. Previous studies in Australia found that low socioeconomic status increases the risk of strongyloidiasis and disproportionately affects remote Aboriginal and Torres Strait Islander communities.[53,54] Socioeconomic status may be explained by various factors, with socioeconomic inequalities being a primary contributor to inadequate sanitation and hygiene practices.[55] The parasite's lifecycle and mode of transmission further reinforce the notion that inadequate sanitation facilities create conditions favourable to infectious and parasitic diseases.[56,57] Moreover, limited access to healthcare services in lower-income populations further exacerbates the disease burden. Intersectoral collaboration among health services, government, and environmental agencies is essential for eliminating strongyloidiasis.

Environmental factors such as temperature and soil pH play a key role in shaping disease transmission, underscoring the need for targeted public health and health promotion interventions in high-risk areas. Consistent with previous studies,[58,59] our findings indicate a strong positive association between temperature and the spatial distribution of strongyloidiasis, supporting the well-established understanding that warm climates facilitate the development and survival of *S. stercoralis* larvae in soil. High soil temperatures contribute to the parasite's lifecycle by accelerating larval maturation, increasing the survival of free-living adults, and increasing human exposure, especially in regions where individuals may walk barefoot or engage in outdoor activities.[59,60] The infective larvae can survive in moist soil for several weeks when the temperature is optimal, typically between 29 °C and 30 °C.[61] This highlights the role of environmental suitability in sustaining transmission and underlines the need for interventions tailored to climatic risk profiles. Globally, rising temperatures associated with climate change are expected to expand the geographic and seasonal suitability for *S. stercoralis* development.[62,63] In Australia, a projected temperature increase of approximately 1.7–2.4 °C under a 2 °C global warming scenario[64] is likely to increase the future disease burden. Therefore, policymakers, researchers, and local stakeholders need to work together to prioritise targeted control and prevention strategies in endemic regions, predict future transmission dynamics, and develop adaptive intervention measures to mitigate the public health risks of strongyloidiasis in the context of climate change. Aligning deworming and community-based interventions with warmer periods, particularly in northern Australia, may further enhance the effectiveness of prevention efforts.

Our analysis also identified increasing (i.e., more alkaline) soil pH as a significant environmental factor positively associated with the spatial distribution of strongyloidiasis. Although the biological mechanisms linking soil pH and strongyloidiasis variability are not fully understood, some previous studies have also suggested that more neutral to slightly alkaline soil conditions may support the survival of larvae.[65] In contrast, other studies[20,66] have suggested that neutral to slightly alkaline soils may not provide optimal conditions for strongyloidiasis and other STH transmission. This discrepancy highlights the need for further investigation to understand the role of soil pH in the spatial distribution of strongyloidiasis prevalence.

Our study has some strengths and limitations. We integrated high-resolution satellite imaging data with a Bayesian spatial analysis to improve the accuracy and reliability of our findings. Social and environmental factors were included in the model. However, using SA3-level estimates, rather than finer resolutions like SA1 or SA2, may reduce the ability to capture localised variation effectively. This study used de-identified, aggregated data from only six laboratories in Australia, without details on testing indications or risk group classification. As a result, the findings may not accurately reflect the true population-level prevalence of strongyloidiasis. In addition, some important variables, such as age, ethnicity, Indigenous status, WASH, and behavioural factors, were not included due to data unavailability, which might better explain spatial variation. Lastly, the 2012–2016 data from six laboratories may be considered outdated, and we were unable to include individual-level studies due to the limited evidence available in Australia. Therefore, future research should prioritise more recently available strongyloidiasis data at the SA1 or SA2 spatial scale to identify localised high-risk areas in Australia. Spatiotemporal analysis using recent data could also provide evidence on temporal trends and spatial patterns, facilitating the implementation of targeted public health interventions.

## Conclusion

There is substantial spatial heterogeneity in the prevalence of strongyloidiasis across Australia, which is significantly associated with socioeconomic status, temperature, and soil pH. Environmental management strategies, including improved access to sanitation facilities and healthcare, may therefore interrupt the transmission of strongyloidiasis. Establishing mechanisms and policy interventions for the nationwide surveillance and mandatory reporting of strongyloidiasis cases would enable more accurate data collection to inform prevention strategies and reduce the morbidity and mortality associated with *S. stercoralis.* Furthermore, large-scale studies are needed to inform targeted policies and enhance health systems in high-risk areas, particularly in remote Aboriginal and Torres Strait Islander communities, who remain disproportionately at risk.

## Funding

None.

## Author contributions

FW and DJG conceived the idea for the study. FW, DJG, JS, SJB, KAA, RB, WP, BAB, CG, SM, and MW contributed to the study design. All authors contributed to outcome measures. FW, KAA, JS, and DJG contributed to the statistical analysis. FW, KAA, and DJG drafted the manuscript. All authors critically revised the manuscript for important intellectual content, reviewed the draft, and approved the final submission.

## Data availability

The strongyloidiasis case and testing data were obtained from a previously published study based on retrospective analysis of nationwide pathology records. Aggregated data at the SA3 level are available within that publication. All other datasets used in the analyses are publicly accessible from their original sources, as detailed in Table 1 of this manuscript.

## Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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