Introduction

Childhood anaemia is a severe public health problem in sub-Saharan Africa (SSA) affecting 67% or 83.5 million children in the region. Anaemia in children is associated with an increased risk of death, and may impair cognitive development, growth and immune function.

Anaemia has a multifactorial aetiology and the major contributors include non-infectious (malnutrition, inherited haemoglobinopathies) and infectious causes.

Infectious causes include: malaria, untagenial schistosomiasis, soil-transmitted helminthiasis (STH, caused by Ascaris lumbricoides, Trichuris trichiura and hookworms), among others.

The prevalence of anaemia has been used as a measurable indicator for parasite control programme evaluation purposes because it reflects the aim of the control policy which is to control morbidity caused by these infections.

The development of maps indicating the geographical risk profile of anaemia can help identify communities most in need and, if based on information on the major aetiologies of anaemia, allows an assessment of the risk of anaemia due to different causes.

It is important to evaluate the relationship between an ecological approach and a complementary individual-level approach to modelling, by building spatial anaemia models using different modeling approaches.

Using data from a recently, sub-national parasitological survey conducted in a meso-endemic area of Angola (Dande municipality in Bengo province), we built Bayesian geostatistical models of malaria (PIPRA), S. haematobium, Ascaris lumbricoides and Trichuris trichiura and predict small-scale spatial variation in these infections.

The predictions and their associated uncertainty were used as inputs for a model of anaemia prevalence to predict small-scale spatial variation of anaemia.

Aims

1. quantify the role of factors associated with the geographical variation of anaemia in children aged ≤15 years,
2. determine the geographical distribution of anaemia using an individual-level modeling approach and
3. produce the first high-resolution, local-scale anaemia risk map.

Results 1. Dataset for analysis

Table 1. Characteristics of children aged ≤15 years included in the analysis by anaemia (Hb<11.0 g/dL) status.

Results 2. Geographical variation in parasite infections

Table 2. Spatial effects and population attributable fractions of chronic malnutrition and parasite infections on anaemia, in children aged ≤15 years in Dande province in Angola (95% credible interval).

Results 3. Spatial models of anaemia (Table 2 & Fig 3)

Table 2. Spatial effects and population attributable fractions of chronic malnutrition and parasite infections on anaemia, in children aged ≤15 years in Dande province in Angola (95% credible interval).

Discussion

The predictive map of anaemia (Fig. 3), based on an ecological approach (mapped outputs from spatial models of malaria, S. haematobium and STH), identifies the clusters of high anaemia risk and indicates that anaemia control should be prioritised to inland rural communities within the high endemicity areas (prevalence >8%).

The areas associated with lower anaemia risk are inland rural areas between Western province and Kwanza Sul province of central Angola.

Malaria, malnutrition and S. haematobium play a central role in anaemia burden in this region of Angola; almost 16% of anaemia cases in children aged ≤15 years could have been averted in 2010 by eliminating malaria in the population, 12% by eliminating malnutrition and 9.7% by eliminating schistosomiasis.

Materials and Methods

Data source:

Parasitological, Hb, questionnaire (age, sex, literacy, occupation, access to healthcare and history of previous treatment) and antropometric data were obtained from a baseline community-based cross-sectional survey conducted during May-August 2010 in three of five communes (Castro Malabub and Ucua) in Dande municipality, Bengo Province, Angola, which is a part of a Demographic Surveillance System (DSS) maintained by the CSA Project (Centre for Health Research in Angola).

Household information on type of flooring, ceiling and water, sanitation and hygiene (WASH) indicators was obtained from the ISA DSS database.

A total of 972 households, distributed in 36 hamlets were selected. Study participants included 960 mothers or caregivers (mean age 33.8 years, range 16-80 years) and 2,375 children (mean age 5.9 years, range 6 months-15 years).

Electrical data for land surface temperature and rainfall for a 1 km × 1 km grid cell resolution were obtained from the WorldClim database and the distance to lakes, rivers and irrigation canals was extracted for each sector in a geographical information system (GIS). The geographical centre of the sector was linked to the environmental data to obtain values of the environmental variables using the spatial overlay procedure in the GIS.

Data analysis framework:

Multimodels of for each parasite infection built using the environmental variables as covariates and investigated residual spatial variation using semivariograms. This assessment revealed considerable residual spatial clustering which justified modeling of second-order spatial variation using model-based geostatistics (MGB).

The following analyses were conducted in two phases (Fig 1):

- In Phase 1, we investigated the geographical variation of parasite infections in children aged ≤15 years using MGB.
- In Phase 2, we evaluated the impact of imprecise measurement of parasite infections on their effect sizes in relation to anaemia. Estimated PAF of anaemia due to malnutrition and parasite infections.

Results 4. Risk of anaemia attributable to malnutrition and parasite infections

Using Model 1, the estimated risk of anaemia in children aged ≤15 years attributable to malnutrition and parasite infections. PAF estimates represent the fraction of total anaemia risk in the population that was caused by each aetiological factor, or alternatively, would not have occurred if the aetiological factor was eliminated, assuming the effects of other covariates (e.g., environmental variables) remain unchanged.

Conclusions

The rails of the clusters of malaria, S. haematobium infection, schistosomiasis and trichuriasis were 24 km, 22 km, 26 km and 27 km respectively.