Spatial clustering of Giardia duodenalis assemblages and sub-assemblages with environmental and anthropozoonotic factors in Busia, Western Kenya

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Abstract

Background: Giardiasis is a common intestinal disease caused by the protozoan parasite Giardia duodenalis. The transmission of giardiasis is influenced by a complex interplay of environmental hazards such as contaminated water sources, markets, and/or roads or pathways including anthropozoonotic domestic animal-related factors and accessibility to healthcare. However, the risk factors of acquiring G. duodenalis including its assemblages and sub-assemblages have not been previously mapped in high burden populations in rural Africa. To mitigate transmission in rural African settings with special reference to Kenya, it is important to map out the clustering of the disease occurrence in relation to risk factors. Accordingly, this study evaluated geospatial clustering of G. duodenalis assemblages and sub-assemblages, in relation with environmental and domestic animal-related factors in Busia County, a rural setting of Western Kenya.

Methods: In this cross-sectional study, 147 human stools were microscopically and molecularly analyzed by polymerase chain reaction (PCR) for G. duodenalis infection. A total of 88 human stool specimens positive for G. duodenalis deoxyribonucleic acid were genotyped at the glutamate dehydrogenase (gdh) and triose-phosphate isomerase (tpi) loci using PCR-restriction fragment length polymorphism (PCR-RFLP). Data on human and livestock population densities were obtained from the Kenya National Bureau of Statistics and incorporated into the geospatial analyses to explore their relationship with infection patterns. Distances from households to the nearest market, stream and/or river, road and/or pathway, and health facility were calculated and linked to geospatial clustering with the disease.

Results: Overall, 59.9% of the human stool samples were positive for giardiasis in the sampled population. Geospatial clustering analyses indicated that giardiasis clustered with residing near a market (adjusted; aOR, 1.73), stream and/or river water source (aOR, 1.16), road (aOR, 1.74), an area with larger cattle (aOR, 1.83) or poultry (aOR, 1.36) densities (all $P < 0.05$). Likewise, assemblage A (aOR, 1.14 and 1.06) and sub-assemblage AII (aOR, 1.51 and 1.62) clustered with residing near stream and/or river water sources, and in localities with larger cattle density, respectively (all $P < 0.05$). Conversely, assemblage B (aOR, 1.87; 1.46; and 2.98) clustered with distance to the road, including cattle and poultry densities ($P < 0.05$ to $P < 0.01$). Furthermore, sub-assemblages BIII (aOR, 2.04 and 1.22) clustered with distance to the road and cattle densities, while BIV (aOR, 1.62) clustered with poultry densities ($P < 0.05$ to $P < 0.01$).

Conclusion: Giardia duodenalis assemblage A and B including sub-assemblages AII, BIII, and BIV infections cluster differentially with residence at the nearest stream and/or river water source, market or road or within areas with larger cattle or poultry densities. In contrast, the absence of such environmental and domestic animal-related risk factors may represent areas that are relatively less affected by giardiasis. While we did not explicitly designate "low-risk" zones, the spatial clustering patterns suggest that environments with limited human-animal-environmental interface pressures are less conducive to giardiasis transmission.

Keywords: Giardia duodenalis assemblages; Giardiasis; Spatial clustering; Sub-assemblages.