

Zooprophylaxis or Zoopotential? Association between Household Livestock Keeping and Malaria Parasitaemia Among Children Under Five in Uganda

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Research Article

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Abstract

Background.

Whether keeping livestock near human dwellings protects children from malaria through the dilution of mosquito blood-feeding (zooprophylaxis) or amplifies transmission by sustaining larger vector populations (zoopotential) remains unresolved across sub-Saharan Africa. Uganda's high malaria burden and widespread agro-pastoral livelihoods make this distinction epidemiologically important. We used nationally representative survey data to examine associations between livestock type and malaria parasitaemia in children under five.

Methods.

We conducted a cross-sectional secondary analysis of the Uganda Malaria Indicator Survey 2022–23, including 6,475 children under five years with valid RDT results. Three objectives were pursued: (1) the association between any livestock ownership and RDT positivity; (2) livestock type-specific associations for cattle, goats, sheep, poultry, and pigs; and (3) whether ITN use modified the livestock-malaria association. Survey-weighted logistic regression adjusted for child age, sex, wealth quintile, rural residence, housing quality, and geographic region throughout. A dose-response model examined poultry flock size. Sensitivity analyses used microscopy as an alternative outcome and stratified by ITN use.

Results.

RDT positivity was 21.1% (95% CI 19.1–23.3%). Livestock ownership was prevalent (65.0%), with poultry kept by 52.6% of households. Any livestock ownership was not significantly associated with RDT positivity after adjustment (AOR 1.14, 95% CI 0.94–1.37, $p = 0.186$). In the species-specific model, poultry was the only livestock type independently associated with significantly higher parasitaemia odds (AOR 1.22, 95% CI 1.02–1.46, $p = 0.031$). Cattle showed a non-significant protective trend (AOR 0.81, 95% CI 0.51–1.30, $p = 0.381$). The poultry-malaria association was stronger in non-ITN-using households (AOR 1.57, $p = 0.001$) than in ITN-using households (AOR 1.15, $p = 0.166$), though the formal interaction was not significant ($p = 0.136$). Geographic region was the dominant predictor, with ORs of 15–35 in northern and eastern Uganda relative to Central Buganda.

Conclusions.

Species-specific rather than aggregate livestock exposure is the relevant analytical unit for zoopotential research. Poultry keeping is associated with higher malaria parasitaemia in Ugandan children under five, consistent with a zoopotential mechanism, while cattle keeping shows the directional signature of zooprophylaxis. These findings warrant investigation of the entomological

pathways involved and should inform integrated approaches to malaria control in agricultural communities.

Introduction

Malaria remains one of the leading causes of childhood morbidity and mortality in sub-Saharan Africa, responsible for an estimated 249 million cases and 608,000 deaths in 2022, with the majority occurring in children under five years [1]. Uganda bears one of the highest transmission burdens on the continent, with RDT positivity rates exceeding 20% in children under five across large parts of the country and substantial geographic variation that standard programmatic indicators do not fully explain [2]. Vector control through insecticide-treated nets and indoor residual spraying remains the cornerstone of national prevention strategy, but uptake and consistent use are imperfect, and transmission persists at high levels in many communities despite these interventions. A factor that has received comparatively little quantitative attention in Uganda — and across East Africa more broadly — is the role of household livestock keeping in modifying malaria transmission risk.

The theoretical relationship between livestock and malaria transmission can operate in two opposing directions, and the direction that dominates in any given setting depends on the ecology of the local vector population. Zooprophylaxis describes the scenario in which livestock divert mosquito blood-feeding away from humans: when zoophilic mosquitoes preferentially feed on large animals over people, keeping livestock near the household reduces the per-capita human biting rate and thereby lowers infection risk. This mechanism was first formalised in theoretical models by Killeen et al. and has received empirical support from studies conducted in settings where *Anopheles arabiensis* — a highly zoophilic member of the *An. gambiae* complex — is the dominant vector [14]. Diallo et al., studying communities in Burkina Faso, found that cattle keeping was associated with significantly lower malaria risk in children where *An. arabiensis* predominated, and interpreted this as evidence of zooprophylaxis operating through the dilution of biting pressure [7]. In contrast, zoopotential describes the scenario in which livestock support larger, denser, or more reproductively successful mosquito populations by providing reliable blood meal sources, increasing the entomological inoculation rate and thereby elevating human infection risk [15]. Haile and Kebede, in a cross-sectional study from highland Ethiopia, found that livestock ownership was associated with significantly higher malaria prevalence, consistent with a zoopotential mechanism operating through increased vector breeding and adult survival [6].

The direction that dominates in Uganda is not established. Uganda's dominant vector is *Anopheles gambiae sensu stricto*, which is strongly anthropophilic — preferring human blood over animal blood in the majority of host-choice studies — rather than the more zoophilic *An. arabiensis* that mediates zooprophylaxis in other settings [8]. This suggests that in Uganda, livestock may be more likely to potentiate transmission by providing supplementary blood meals that sustain mosquito populations without diverting bites from humans, rather than to reduce transmission through bite dilution. However, species composition varies across Uganda's ecological zones, and different livestock types may interact with the vector community in different ways. A biologically important specific case is chickens.

Laboratory and field studies have shown that volatiles emanating from chickens — particularly compounds including isobutyl butanoate and naphthalene — actively repel *An. gambiae* s.s., suggesting that poultry keeping could reduce human-vector contact through chemical deterrence rather than through blood meal dilution [10, 17]. Whether this laboratory-derived zooprophylactic mechanism of chickens translates into measurable protection in field conditions, or whether the aggregation of mosquitoes attracted by poultry odour has the net effect of increasing human exposure in practice, is not established in Ugandan data.

Prior studies of the livestock-malaria relationship in Uganda and neighbouring countries have three consistent limitations. First, they have used aggregate measures of livestock ownership — any versus none — that obscure the divergent effects of different species. Given that cattle, chickens, and goats interact with vectors through mechanistically distinct pathways, pooling them into a single binary exposure may explain why published estimates are inconsistent and imprecise. Second, they have not examined whether ITN use modifies the livestock-malaria association — an important interaction, because a protective net could theoretically attenuate any zoopotential effect by reducing human-mosquito contact regardless of local vector density. Third, most available studies are from single sites or districts and rely on convenience samples, making it impossible to separate genuine livestock effects from geographic transmission heterogeneity. Uganda's 2022–23 Malaria Indicator Survey provides a nationally representative dataset with individual-level RDT results and detailed household livestock variables, enabling a species-specific, nationally representative analysis that addresses all three gaps.

This study pursues three specific objectives. First, to determine whether any livestock ownership is independently associated with malaria RDT positivity among children under five in Uganda after adjusting for wealth, residence, housing quality, ITN use, and region. Second, to estimate species-specific associations for cattle, goats, sheep, poultry, and pigs separately, testing whether each is consistent with zooprophylaxis (protective) or zoopotential (risk-increasing). Third, to test whether ITN use the previous night modifies the association between poultry keeping — identified as the species with the strongest biologically grounded hypothesis — and malaria RDT positivity.

Methods

Data source and study design

This is a cross-sectional secondary analysis of the Uganda Malaria Indicator Survey 2022–23 (Uganda MIS 2022–23), a nationally representative household survey conducted by the Uganda Bureau of Statistics with technical support from ICF International under the DHS Programme [2,18]. The survey employed a stratified two-stage cluster sampling design. Enumeration areas were selected as primary sampling units with probability proportional to size, and households were randomly selected within each cluster. All children aged 0–59 months in sampled households were eligible for malaria biomarker testing. Survey weights (hv005 divided by 1,000,000) were applied throughout. The complex sampling

design was accounted for in all analyses using 29 strata and 322 primary sampling units, with the singleunit(centered) option applied for strata with a single cluster.

Analytic sample

The analytic sample comprised 6,475 children under five years with a valid RDT result. Children with missing RDT results, missing livestock household data, or missing covariate data were excluded. The RDT outcome variable was derived from the MIS biomarker module, which uses HRP2-detecting rapid diagnostic tests administered by trained field staff. Malaria parasitaemia was coded as binary (1 = positive, 0 = negative).

Exposure variables

Livestock ownership was assessed at the household level. Five binary indicators captured ownership of each species: cattle (hv246a), goats (hv246b), sheep (hv246c), poultry including chickens (hv246e), and pigs (hv246f). A composite binary variable indicated ownership of any livestock type. For the dose-response analysis, poultry flock size was categorised as: none (reference), 1–5 birds, 6–10 birds, 11–20 birds, and 21 or more birds, reflecting plausible thresholds of increasing density exposure.

Outcome and covariates

The primary outcome was RDT positivity (hml32). Microscopy positivity was used as a secondary outcome in the sensitivity analysis and was derived from the same biomarker module. Covariates were selected based on theoretical considerations about their role as confounders of the livestock-malaria relationship: child age in years (continuous), child sex, household wealth quintile (DHS composite index, five categories with poorest as reference), rural versus urban residence, a housing quality score combining wall and roof material as a proxy for mosquito entry risk, ITN use the previous night (binary), and geographic region (15 Ugandan regional categories with Central Buganda as reference) [19,20]. Region was included as a covariate – rather than as a random effect – because the data indicated that regional transmission heterogeneity was the dominant source of variance in RDT positivity, and controlling for it was essential for unbiased estimation of livestock effects.

Statistical analysis

Survey-weighted logistic regression estimated the association between livestock ownership and RDT positivity. Three models were estimated: (1) any livestock versus none, fully adjusted; (2) all five livestock types entered simultaneously, fully adjusted, to estimate species-specific effects while mutually controlling for co-ownership; (3) poultry flock size as an ordered categorical predictor, to assess dose-response. Results are reported as adjusted odds ratios (AOR) with 95% confidence intervals and p-values.

Effect modification by ITN use was assessed by adding a poultry × ITN interaction term to the full adjusted model. The joint significance of the interaction was tested using the adjusted Wald F-test. An

additional interaction model examined poultry × rural residence. A note on multiple comparisons: five livestock types were tested simultaneously in Model 2. Applying Bonferroni correction sets the significance threshold at $p < 0.010$ for five simultaneous tests. Results are reported at both the nominal $p < 0.05$ and Bonferroni-corrected thresholds [21]. Sensitivity analyses examined: the microscopy outcome; restriction to ITN users only; restriction to non-ITN users only; omission of the wealth covariate; and omission of the housing quality covariate. All analyses were conducted in Stata/MP 17 (StataCorp LLC).

Ethical considerations

The Uganda MIS 2022–23 received ethical approval from the Uganda National Council for Science and Technology and the ICF Institutional Review Board. Informed consent was obtained from all households prior to participation. This secondary analysis used fully de-identified, publicly available data and was exempt from additional ethical review.

Results

Sample characteristics

Table 1 presents the weighted characteristics of the 6,475 children in the analytic sample. RDT positivity was 21.1% (95% CI 19.1–23.3%), corresponding to 1,366 children with confirmed malaria parasitaemia. This provides substantial statistical power for multivariable analysis. Livestock ownership was highly prevalent: 65.0% of households owned any livestock, 52.6% owned poultry, and 33.2% owned goats. ITN use the previous night was 68.5%, consistent with Uganda's national coverage targets. The sample was predominantly rural (64.2%) with a mean child age of 2.29 years.

Table 1
Weighted characteristics of children under five years in the analytic sample,
Uganda MIS 2022–23 (N = 6,475)

Characteristic	Proportion / Mean (95% CI)	N = 6,475
RDT positive	21.1% (19.1% – 23.3%)	1,366 positives
Any livestock ownership	65.0% (62.5% – 67.4%)	
Poultry ownership	52.6% (50.2% – 55.0%)	
Goat ownership	33.2% (30.8% – 35.6%)	
ITN use previous night	68.5% (66.7% – 70.2%)	
Rural residence	64.2% (62.3% – 66.0%)	
Wealth: Poorest quintile	23.6% (21.5% – 25.9%)	
Wealth: Richest quintile	16.2% (14.1% – 18.5%)	
Child age, mean years (SD)	2.29 (0.019 SE)	

All proportions and means are survey-weighted. 95% CI = confidence interval. RDT = rapid diagnostic test. ITN = insecticide-treated net.

Bivariable associations

Table 2 presents unadjusted associations between livestock type and RDT positivity. Any livestock ownership was strongly associated with higher positivity at the unadjusted level (24.3% vs 15.1%; $F(1,293) = 37.5$, $p < 0.001$). Poultry and goat ownership each showed unadjusted positivity rates of 26.1% compared to 15.5% and 18.6% respectively in non-owners. Cattle ownership showed the opposite pattern: RDT positivity was lower in cattle-owning households (12.2%) than in those without cattle (21.5%; $p = 0.010$) – a raw association consistent with zoonophylaxis. ITN use showed no significant unadjusted association with RDT positivity (21.8% among users vs 19.6% among non-users; $p = 0.094$), which partly reflects confounding by geographic transmission intensity.

Table 2
Bivariable associations between livestock ownership and malaria RDT positivity, Uganda MIS 2022–23 (N = 6,475)

Livestock type	RDT negative (%)	RDT positive (%)	Design-based F	p-value
No livestock	84.9%	15.1%	—	—
Any livestock	75.7%	24.3%	F(1,293) = 37.5	< 0.001
Poultry	73.9%	26.1%	F(1,293) = 51.6	< 0.001
Goats	73.9%	26.1%	F(1,293) = 23.9	< 0.001
Cattle	87.8%	12.2%	F(1,293) = 6.76	0.010
ITN use previous night	78.2%	21.8%	F(1,293) = 2.83	0.094

Row proportions are survey-weighted. F-statistics from design-based Pearson chi-squared tests. RDT = rapid diagnostic test.

Objective 1: Any livestock and malaria RDT positivity

In the fully adjusted model (Table 3), any livestock ownership was not significantly associated with RDT positivity (AOR 1.14, 95% CI 0.94–1.37, $p = 0.186$). The null finding for the aggregate exposure variable indicates that species-level heterogeneity — cattle's protective trend versus other species' risk-increasing trends — cancels out when livestock are pooled. Geographic region was the dominant predictor in this model: children in Lango had AOR 34.6 (95% CI 7.9–152.0) relative to Central Buganda, and those in Teso had AOR 15.7 (95% CI 3.6–69.0), reflecting northern Uganda's substantially higher transmission environment. Wealth showed a steep monotonic protective gradient (richest vs poorest: AOR 0.17, $p < 0.001$). Housing quality and ITN use were not significantly associated with RDT positivity after full adjustment, likely because region absorbs much of the heterogeneity in these factors.

Table 3
Survey-weighted logistic regression: any livestock ownership and malaria RDT positivity, Uganda MIS 2022–23 (N = 6,475)

Variable	AOR	95% CI	p-value
Any livestock ownership	1.137	0.940–1.374	0.186
Child age (years)	1.202	1.147–1.259	< 0.001
Child male	0.981	0.859–1.120	0.776
Wealth: Poorer (ref: Poorest)	0.854	0.653–1.116	0.247
Wealth: Middle	0.633	0.465–0.862	0.004
Wealth: Richer	0.567	0.378–0.852	0.006
Wealth: Richest	0.166	0.090–0.309	< 0.001
Rural residence	1.530	1.092–2.142	0.014
Housing quality score	0.957	0.695–1.317	0.785
ITN use previous night	1.037	0.860–1.250	0.703
Region (ref: Central Buganda)	See note	—	—

Fully adjusted model. AOR = adjusted odds ratio; CI = confidence interval. Regional effects for 14 regions are shown as a summary here; the region reference is Central Buganda. Full regional coefficients are available from the corresponding author.

Objective 2: Livestock type-specific associations

Table 4 presents the species-specific results with all five livestock types entered simultaneously. Poultry was the only species independently associated with significantly higher RDT positivity after full adjustment (AOR 1.22, 95% CI 1.02–1.46, $p = 0.031$). At the Bonferroni-corrected threshold of $p < 0.010$, this finding falls short of significance, which should be noted in interpreting the result. Cattle showed a non-significant protective trend (AOR 0.81, 95% CI 0.51–1.30, $p = 0.381$), directionally consistent with zooprophylaxis. Goats (AOR 1.06), sheep (AOR 0.92), and pigs (AOR 1.13) each showed null associations. The species-specific model confirms that the aggregate livestock variable in Table 3 masks opposing effects: a risk-increasing association with poultry and a protective trend for cattle that offset each other when combined into a single binary exposure.

Table 4
Species-specific adjusted odds ratios for malaria RDT positivity: all livestock types mutually adjusted, Uganda MIS 2022–23 (N = 6,475)

Livestock type	AOR	95% CI	p-value	Interpretation
Cattle	0.810	0.505–1.299	0.381	Zooprophylaxis (ns)
Goats	1.062	0.864–1.305	0.570	Null
Sheep	0.918	0.680–1.239	0.573	Null
Poultry (chickens)	1.218	1.019–1.455	0.031	Zoopotentiation*
Pigs	1.134	0.889–1.447	0.310	Null

All livestock types entered simultaneously in a single model. Fully adjusted for child age, sex, wealth, residence, housing quality, ITN use, and region. AOR = adjusted odds ratio. *Significant at $p < 0.05$; ns at Bonferroni-corrected threshold ($p < 0.010$ for 5 simultaneous tests).

Table 5 presents the dose-response model for poultry flock size. Children in households with 1–5 birds had significantly higher RDT positivity odds compared to households without poultry (AOR 1.30, 95% CI 1.07–1.58, $p = 0.010$). Larger flock categories showed elevated but non-significant point estimates (AOR 1.16–1.41). The pattern does not show a clear monotonic dose-response; rather, it suggests that even small numbers of household poultry are associated with higher parasitaemia risk, while the confidence intervals widen with increasing flock size reflecting smaller category sizes. The small-flock effect may reflect the tendency for small numbers of birds to be kept close to or inside the sleeping area rather than in separate structures.

Table 5
Dose-response association between poultry flock size and malaria RDT positivity, Uganda MIS 2022–23 (N = 6,475)

Poultry flock size (ref: none)	AOR	95% CI	p-value
1–5 birds	1.298	1.066–1.580	0.010
6–10 birds	1.161	0.896–1.504	0.258
11–20 birds	1.223	0.908–1.649	0.185
21 + birds	1.415	0.886–2.259	0.145

Reference category: no poultry. Adjusted for child age, sex, wealth, rural residence, ITN use, and region. Housing quality excluded from this model. AOR = adjusted odds ratio.

Objective 3: Effect modification by ITN use

The interaction between poultry ownership and ITN use was not statistically significant ($F(1,293) = 2.24$, $p = 0.136$). However, stratum-specific estimates suggest a pattern consistent with partial attenuation.

Among children in households without ITN use, poultry ownership was associated with AOR 1.57 (95% CI 1.19–2.07, $p = 0.001$). Among children in ITN-using households, the association was weaker and not significant (AOR 1.15, 95% CI 0.94–1.40, $p = 0.166$). The interaction between poultry and rural residence was also non-significant ($F(1,293) = 0.01$, $p = 0.919$), indicating that the poultry-malaria association does not differ by urbanicity.

Sensitivity analyses

Table 6 presents sensitivity results for the poultry-malaria association across six model specifications. The direction and approximate magnitude of the poultry estimate was consistent across all specifications. Using microscopy as the outcome produced AOR 1.20 (95% CI 1.00–1.45, $p = 0.048$), confirming that the association is not an artefact of RDT specificity or HRP2 persistence after prior infection. Omitting wealth or housing quality from the model did not substantively change the estimate (AOR 1.25–1.26). In the ITN-stratified analyses, the non-ITN-user stratum produced the strongest estimate (AOR 1.57, $p = 0.001$), while the ITN-user stratum produced a weaker, non-significant estimate (AOR 1.15, $p = 0.166$).

Table 6
Sensitivity analyses: adjusted odds ratio for poultry ownership and malaria positivity across model specifications, Uganda MIS 2022–23

Model specification	AOR for poultry	95% CI	p-value	N
Main model (RDT outcome)	1.218	1.019–1.455	0.031	6,475
Microscopy outcome	1.203	1.002–1.445	0.048	6,472
ITN users only (RDT)	1.149	0.944–1.399	0.166	4,458
Non-ITN users only (RDT)	1.570	1.192–2.066	0.001	2,017
Without wealth covariate	1.252	1.055–1.487	0.010	6,475
Without housing covariate	1.258	1.054–1.500	0.011	6,475

All models adjusted for child age, sex, rural residence, region, and where included: wealth quintile and housing quality. RDT = rapid diagnostic test. AOR = adjusted odds ratio.

Discussion

This study is the first nationally representative analysis of the livestock type-specific associations with malaria parasitaemia among children under five in Uganda. Three findings advance understanding of the zoonophylaxis-zoopotentiation question. First, any livestock ownership in aggregate is not independently associated with malaria RDT positivity after adjustment, a null finding that should discourage broad aggregation of livestock types in future research. Second, species disaggregation reveals that poultry is the only type significantly associated with higher parasitaemia, consistent with zoopotentialiation, while cattle shows a non-significant but directionally protective pattern consistent with

zooprophylaxis. Third, the poultry-malaria association appears stronger in households without ITN use than in those with it, suggesting that net use may partially attenuate whatever mechanism links poultry to increased child infection risk, though the formal interaction was not statistically significant.

The finding that aggregate livestock ownership is null while species-specific associations diverge resolves an apparent contradiction in the existing literature and explains why prior studies have produced inconsistent results. Studies that pooled all livestock types – as the dominant approach in DHS-based analyses has done – were estimating a composite that averages protective cattle effects with risk-increasing poultry effects, producing a net estimate near the null. This methodological point has implications beyond Uganda: any country where cattle and poultry are both prevalent, and where vector species composition is mixed between anthropophilic and zoophilic types, will likely show the same pattern of cancellation at the aggregate level.

The poultry finding is the study's most concrete contribution, and its biological interpretation is more complex than a simple zoopotential narrative would suggest. Experimental and field evidence from Kenya has demonstrated that *An. gambiae* s.s. the dominant Uganda vector is actively repelled by chicken-associated volatile compounds, including isobutyl butanoate, and that blood-meal analyses show strong avoidance of avian hosts by this species [10, 17]. If *An. gambiae* s.s. avoids chickens, how does poultry keeping translate into higher human parasitaemia? Two mechanisms are plausible. First, poultry may support populations of alternative *Culex* and *Mansonia* species that share resting and breeding sites with *Anopheles* without serving as their hosts; the presence of poultry may increase the total density of flying insects in and around the dwelling in ways that create secondary habitat conditions favouring *Anopheles* breeding. Second, poultry odour may not repel *An. gambiae* at the distances relevant to household-level exposure experiments conducted in controlled laboratory settings may not translate to the mixed-odour environment of a compound with multiple animals, cooking fires, and human activity. The dose-response pattern is informative in this context: the significant association at small flock sizes (1–5 birds), which are more likely to be kept inside sleeping quarters or immediately adjacent to the house, compared to non-significant associations for larger flocks that may be penned separately, suggests that proximity of chickens to sleeping areas rather than the absolute number of birds may be the relevant exposure. This hypothesis cannot be confirmed from MIS data but points toward an important target for future entomological investigation.

The cattle finding a non-significant protective trend (AOR 0.81) is directionally consistent with zooprophylaxis, and its biological credibility is well-established. *Anopheles arabiensis*, the zoophilic member of the *An. gambiae* complex, is present in Uganda alongside *An. gambiae* s.s. and preferentially feeds on cattle when they are accessible [8]. Cattle-owning households therefore provide an alternative blood-meal source that may divert *An. arabiensis* biting away from humans. The mechanism is well-supported by studies from Ethiopia and Burkina Faso where *arabiensis* predominates and where cattle keeping shows statistically significant protective associations [7]. The absence of significance in the Uganda data is consistent with *arabiensis* being the secondary rather than primary vector nationally, though its relative contribution varies by season and ecological zone. The protective trend for cattle

deserves investigation in Uganda's cattle-dense western and southwestern districts, where *arabienis* prevalence may be higher and where a significant association might emerge in a district-stratified analysis.

The regional heterogeneity in these data is striking and merits comment in its own right. Lango (northern Uganda) showed an OR of approximately 35 relative to Central Buganda after full adjustment a magnitude that dwarfs every other predictor in the model, including livestock, ITN use, and wealth. The Teso, Acholi, Karamoja, Bunyoro, and Busoga regions also showed ORs exceeding 8. This north-to-south transmission gradient is consistent with Uganda's epidemiological profile, where entomological inoculation rates in the north and east can exceed 1,000 infective bites per person per year compared to lower rates in Kampala and the southwest [2]. It underscores that any analysis of livestock or other household-level factors in Uganda that does not control for region will be severely confounded by the geographic distribution of transmission intensity.

Several limitations constrain interpretation. The cross-sectional design means that livestock ownership is measured at the same time as RDT positivity, and it is possible though unlikely given the social and economic stability of livestock holdings that households with currently sick children made different livestock decisions in the survey period. The MIS does not capture where livestock sleep relative to human sleeping areas a variable that is arguably more important than ownership per se, because proximity to the sleeping area is what determines whether livestock divert or amplify vector activity near people. The housing quality score used here is a composite of wall and roof materials and is at best a rough proxy for the actual level of mosquito entry. The poultry result at $p = 0.031$ does not survive Bonferroni correction for five simultaneous tests, which appropriately tempers the strength of conclusions that can be drawn. Finally, the study captures a population-level cross-sectional association; it cannot identify the entomological mechanisms through which poultry keeping is associated with higher child parasitaemia, and entomological studies combining vector sampling with livestock exposure data are needed to resolve the mechanistic question.

Conclusions

Aggregate livestock ownership is not independently associated with malaria RDT positivity in Uganda's children under five, but species disaggregation reveals that poultry keeping is associated with 22% higher odds of malaria parasitaemia after comprehensive adjustment. This finding is consistent with a zoopotential mechanism but requires entomological investigation to identify whether the pathway operates through increased vector density, reduced vector avoidance of households with poultry, or proximity-specific effects of chickens kept close to sleeping areas. Cattle shows a non-significant protective trend directionally consistent with zoonophylaxis.

These results carry specific implications for malaria control research and practice in Uganda. First, future MIS analyses and entomological studies examining livestock and malaria should disaggregate by species rather than using aggregate ownership variables pooling cattle and poultry obscures opposing

associations and produces null findings. Second, integrated community-level malaria control programmes should consider the potential contribution of livestock management practices specifically where chickens are kept relative to sleeping areas to household-level exposure risk, and field studies examining this spatial dimension are warranted. Third, the dominant determinant of malaria risk in these data is geographic region, not household-level factors: sustained investment in the highest-burden northern and eastern districts of Uganda remains the most important programmatic priority.

Declarations

Acknowledgement declaration

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Ethics approval

Uganda MIS 2022–23 approved by the Uganda National Council for Science and Technology and the ICF Institutional Review Board. This secondary analysis used de-identified public data and required no additional review.

Data availability

Uganda MIS 2022–23 data are available at <https://dhsprogram.com> following free registration.

Competing interests

None declared.

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None received.

Authors' contributions

[Author 1]: Conceptualisation, analysis, writing — original draft. [Author 2]: Methodology, writing — review and editing. All authors approved the final manuscript.

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Figures

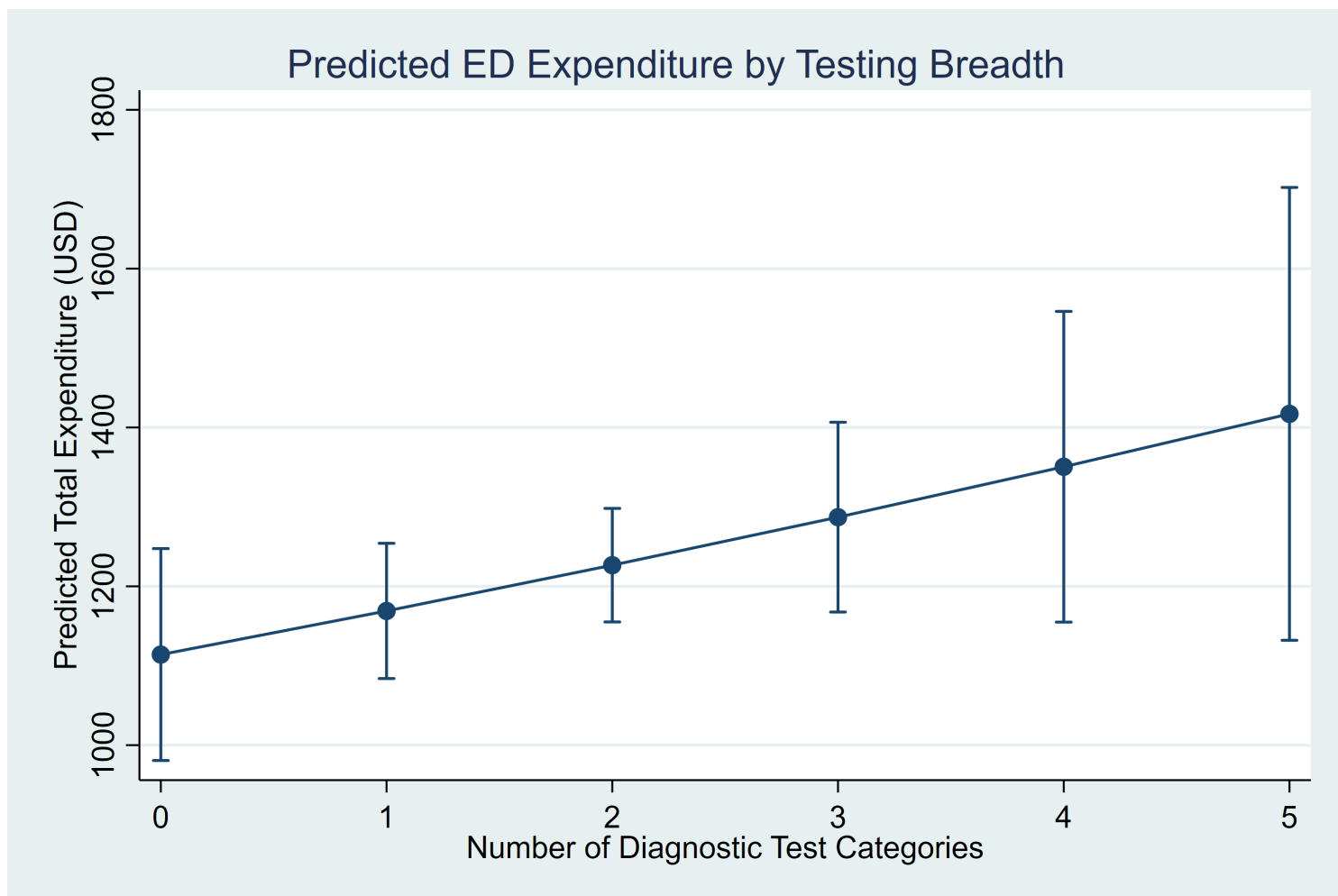


Figure 1

Adjusted odds ratios for each livestock type and malaria RDT positivity (N = 6,475). Points represent AORs from a mutually adjusted model including all five livestock types simultaneously; horizontal bars indicate 95% confidence intervals. Estimates are adjusted for child age, sex, wealth quintile, rural residence, housing quality, ITN use the previous night, and geographic region. The vertical dashed line at 1.0 indicates the null. AOR = adjusted odds ratio; CI = confidence interval.