Reports
2025, Vol. 5, No. 4, pp. 72–84
https://doi.org/10.11648/j.reports.20250504.13

Research Article

Spatio-temporal Ecology of Fasciola Vectors and Co-occurring Trematode Hosts in Kingwal Wetland, Kenya

Gilbert Kiplagat Biwott[1, 2, *], Moses Ngeiywa[1], Judith Makwali[1]

[1]Department of Biological Sciences, University of Eldoret, Eldoret, Kenya

[2]Department of Agriculture, Animal Science & Natural Resource, Moi University, Eldoret, Kenya

Abstract

This study examined the spatial and temporal distribution of freshwater snails in Kingwal Wetland, Kenya, to assess their role in fascioliasis transmission. A total of 8,754 snails representing eight species were collected across seven sites over a 12-month period. The dominant species were *Lymnaea auricularia* (n = 1,192; 13.6%), *Radix natalensis* (n = 525; 6.0%), and *Biomphalaria sudanica* (n = 1,838; 21.0%), with *L. auricularia* and *R. natalensis* serving as key intermediate hosts of *Fasciola gigantica*. Spatial analysis revealed significant variation in species composition between sites ($\chi^2 = 2{,}435.1$, df = 42, $p < 0.001$), with Sites 1 and 2 exhibiting the highest species richness and abundance. Temporal trends showed snail abundance peaking during the rainy season (May–August), with the highest monthly count being recorded in May (n = 1,383). Dry-season months such as January and December had the lowest counts, with only 230 and 316 individuals, respectively. *R. natalensis* exhibited the highest *Fasciola* infection prevalence, peaking at 29.3% in June, compared to *L. auricularia*, which peaked at 19.8% in September. A chi-square test for monthly snail distribution confirmed significant seasonal variation ($\chi^2 = 839.27$, df = 77, $p < 0.001$), while a Cochran–Mantel–Haenszel test showed strong interaction between spatial and temporal factors (CMH = 1,192.37, df = 11, $p < 0.001$). These findings suggest that fascioliasis transmission risk is highest during wet months and is strongly influenced by habitat stability, vegetation, and anthropogenic activity. The results underscore the need for spatially targeted and seasonally timed control interventions, including habitat management and precision molluscicide application. This study contributes to a growing understanding of wetland ecosystems as dynamic transmission zones for snail-borne diseases and provides a foundation for data-driven fascioliasis control strategies in livestock-dependent communities living in wetland ecosystems.

Keywords

Freshwater Snails, Spatial Distribution, Temporal Variation, Kingwal Wetland, Fascioliasis

1. Introduction

Freshwater snails are integral components of aquatic ecosystems, performing essential ecological functions such as regulating periphyton and phytoplankton biomass through grazing, recycling organic matter, and facilitating nutrient cycling between sediments and overlying water [1]. They form a vital link in food webs, serving as prey for fish, amphibians, waterbirds, and invertebrate predators, thereby supporting both biodiversity and fisheries productivity [2].

*Corresponding author: biwottg@yahoo.com (Gilbert Kiplagat Biwott)

Received: 9 September 2025; **Accepted:** 23 October 2025; **Published:** 31 December 2025

Their abundance and distribution are influenced by hydrological stability, substrate type, and vegetation complexity, with structurally diverse habitats generally supporting higher snail diversity [3]. However, some freshwater snail species also serve as intermediate hosts for parasitic trematodes, making them of considerable veterinary and public health importance. These dual roles, ecological and epidemiological position freshwater snails as key organisms in both conservation biology and disease ecology [4]. In wetland-adjacent communities, routine human–livestock contact with surface waters (e.g., communal watering points, laundry sites, and floodplain pastures) creates repeated opportunities for exposure to infective stages; livestock and potentially humans are therefore exposed through shared water sources.

Fascioliasis, a neglected zoonotic disease of global importance, is caused by liver flukes of the genus *Fasciola*, most notably *F. hepatica* in temperate zones and *F. gigantica* in tropical and subtropical regions [5]. In Africa, and particularly in East Africa, *F. gigantica* predominates, and its transmission is tightly linked to the presence of competent lymnaeid snails such as *Lymnaea natalensis* and *Radix natalensis* [6]. The parasite's life cycle is complex: eggs excreted in the feces of infected ruminants hatch in water to release miracidia, which actively penetrate suitable snail hosts [7]. Within the snail, the parasite undergoes successive developmental stages sporocysts, rediae, and cercariae before emerging to encyst as metacercariae on aquatic vegetation or other substrates [8]. Livestock become infected when grazing on contaminated vegetation or drinking infested water. This cycle's completion depends on the availability of aquatic habitats that support both the snail host and the free-living larval stages of the parasite [9]. For clarity, the generalized life cycle of trematodes of the genus *Fasciola* is illustrated in Figure 1, showing the key developmental stages within snail intermediate hosts and vertebrate definitive hosts (Figure 1).

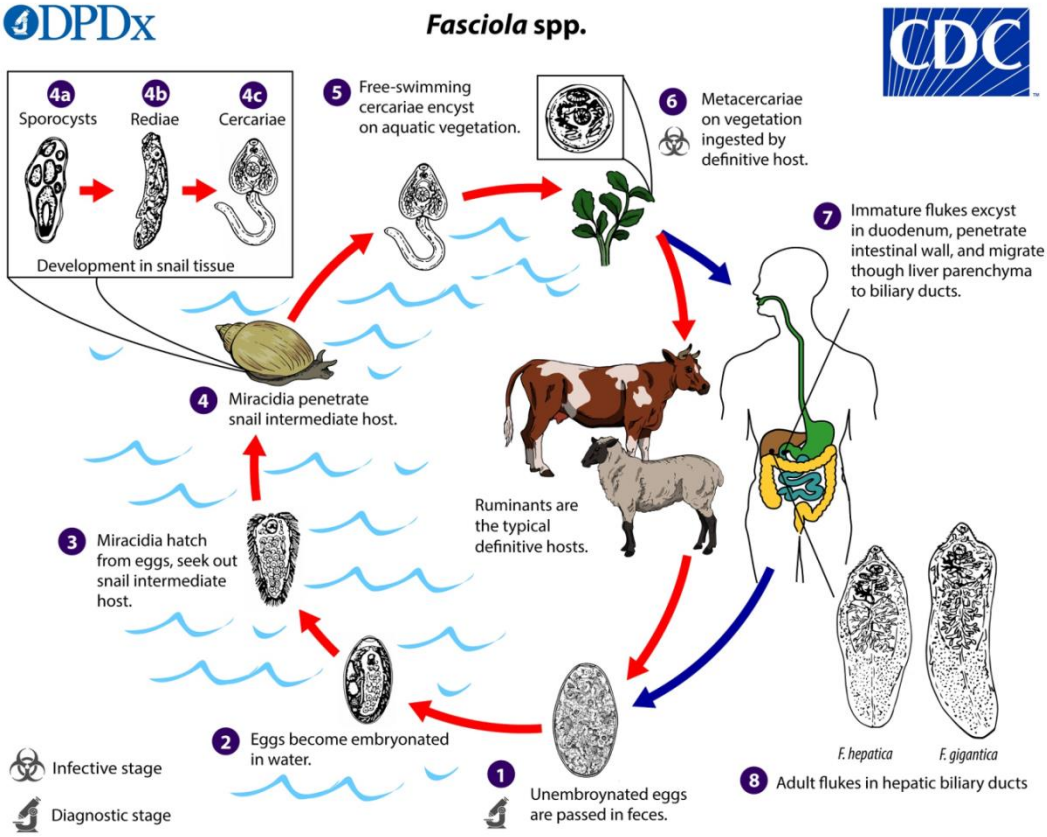

Figure 1. *Generalized life cycle of Fasciola spp. Adapted from Mas-Coma [8]. Schematic representation of the Fasciola life cycle, illustrating the transition from eggs excreted by infected ruminants or humans to miracidia that infect lymnaeid snails, through successive intramolluscan stages (sporocyst, rediae, cercariae), and finally to encysted metacercariae on aquatic vegetation or in water, which infect grazing livestock or humans upon ingestion.*

The abundance, diversity, and distribution of snail vectors are shaped by a range of abiotic and biotic factors, including water temperature, dissolved oxygen, pH, conductivity, aquatic vegetation, and predator presence [10]. Hydrological regimes especially patterns of flooding and drying have a profound effect on snail survival and reproductive cycles [11]. Seasonal flooding can expand available habitats, increase food resources, and dilute predation pressure, leading to

population surges in suitable microhabitats [12]. Conversely, prolonged drought can fragment habitats, increase mortality, and limit dispersal, causing marked declines in snail numbers. The interplay of these environmental variables results in heterogeneous snail distributions, often leading to the formation of persistent "transmission hotspots" for trematode diseases such as fascioliasis [13].

In Kenya, fascioliasis is a significant cause of economic loss in ruminant production systems, particularly in wetland-rich landscapes such as the Lake Victoria basin, parts of the Rift Valley, and highland swamps [14]. Despite this, surveillance of intermediate host snails has been sporadic and geographically limited, with few longitudinal datasets capturing seasonal dynamics at a local scale [15]. Existing studies have often focused on broad-scale prevalence surveys in livestock or on snail identification without examining fine-scale ecological drivers of abundance and distribution [16]. This leaves important gaps in understanding how microhabitat characteristics, land-use patterns, and climatic variability interact to influence snail ecology in fascioliasis-endemic areas [17].

Kingwal Wetland in Nandi County is a high-altitude wetland system characterized by slow-moving channels, seasonal flooding, dense stands of emergent and submerged vegetation, and extensive livestock grazing [18]. These conditions are likely to provide favorable habitats for multiple snail species, including known fascioliasis vectors. However, the wetland's snail fauna has not been comprehensively documented, and there is little understanding of how snail abundance and diversity vary spatially across different microhabitats or temporally in response to seasonal hydrological changes [19]. Without such ecological baselines, the design and timing of fascioliasis control measures such as molluscicide, habitat management, or targeted livestock treatments remain largely guesswork [20].

The present study addresses these gaps by conducting a year-long ecological assessment of freshwater snails in Kingwal Wetland, focusing on spatial, temporal, and spatio-temporal patterns of abundance and diversity in relation to environmental conditions. By generating site-specific, seasonally resolved data, this work aims to improve fascioliasis risk mapping and provide a scientific foundation for integrated, evidence-based snail control strategies that can be adapted to other wetland systems in the region [21].

2. Materials and Methods

2.1. Study Area

Kingwal Swamp is an important inland wetland ecosystem located in Nandi County, western Kenya, within the former Rift Valley Province. It is situated approximately 6 km west of Kapsabet Town, straddling Nandi Central and Nandi North sub-counties, between approximately 0°12′N latitude and 35°8′E longitude. The swamp forms part of the Lake Victoria Basin catchment area and contributes to the Yala River watershed, playing a critical role in regional hydrological regulation [22].

The wetland covers an estimated area of 15–20 km ²during normal hydrological conditions, although seasonal flooding during the long rains (March–June) can significantly expand its surface area. It is traversed by the Kingwal River, a major tributary of the Yala River, and bordered by a mosaic of land uses including communal grazing areas, smallholder farms, and patches of riparian vegetation. Historically, Kingwal Swamp has supported biodiversity conservation, provided grazing grounds during the dry season, and sustained key wildlife species such as the rare sitatunga antelope (*Tragelaphus spekii*) [18].

The area lies within a sub-humid agro-ecological zone, experiencing a bimodal rainfall pattern with annual totals ranging from 1,200 to 1,600 mm. Long rains occur from March to June, and short rains from October to December. Mean monthly temperatures range between 15 ℃ and 26 ℃, providing favorable conditions for both agricultural production and freshwater mollusc proliferation [23]. The wetland hydrology is maintained by the Kingwal River, supplemented by surface runoff and seasonal springs. However, anthropogenic activities such as overgrazing, brick-making, papyrus harvesting, and edge cultivation have altered the wetland's hydrological and ecological functions, potentially influencing snail habitats and fascioliasis transmission risk [24].

2.2. Description of Sampling Sites

Seven sampling sites (Figure 2) were purposively selected to represent different hydrological regimes, vegetation structures, and land use pressures, thereby capturing ecological variation relevant to snail distribution and fascioliasis transmission [25].

Site 1: Northwestern papyrus swamp, permanently waterlogged, dominated by *Cyperus papyrus*, minimal anthropological disturbance representing an undisturbed reference habitat.

Site 2: Midstream river section with moderate current, higher dissolved oxygen, and a mixture of sand-silt substrates.

Site 3: Northern floodplain with seasonal inundation, suitable for monitoring snail colonization under fluctuating water levels.

Site 4: Central papyrus zone near a livestock crossing point, subject to high trampling and nutrient enrichment from dung.

Site 5: Western papyrus zone with relatively low disturbance, serving as a semi-pristine control site.

Site 6: Southern grazing zone with heavy cattle access, high turbidity, and elevated nutrient loads.

Site 7: Southeastern grazing zone with intense livestock activity, shallow turbid water, and disturbed vegetation.

This site stratification enabled spatial comparison of high-risk, disturbed areas with low-risk, minimally impacted zones.

2.3. Sampling Design

A longitudinal cross-sectional snail survey was conducted from January to December 2023, covering both dry and rainy seasons. Each site was sampled monthly to capture seasonal variation in snail abundance, diversity, and distribution patterns [26].

2.4. Snail Collection

Snails were collected using two standard methods:

1) *Scoop netting:* A fine mesh (1 mm) hand net was used to dredge submerged vegetation, detritus, and sediments.
2) *Hand picking:* Snails attached to vegetation, debris, or sediment surfaces were picked manually using forceps or gloved fingers.

Sampling effort was standardized to 30 minutes per site per visit. Collected snails were placed in labeled, aerated plastic containers with water from the respective sites and transported to the field laboratory within 2 hours.

Geographic coordinates of each sampling site were recorded in triplicate using a Garmin GPSMAP® 64st handheld unit (±3 m accuracy). Spatial distribution maps for snail species abundance and infection prevalence were generated using QGIS v3.28.4 (Open Source Geospatial Foundation) [26]. Abundance data were visualized using proportional symbol mapping, where symbol size corresponded to the number of individuals per species per site. Species diversity and infection prevalence were overlaid as graduated color scales. Base maps and hydrological layers for Nandi County and the Yala River basin were obtained from the Kenya Open Data portal and processed in the WGS84 coordinate system. Thematic maps depicting ecological zones (e.g., permanent swamp, seasonal floodplain, grazing areas) were digitized from high-resolution satellite imagery (Sentinel-2, 10 m resolution) to contextualize snail distributions.

During transport and temporary storage, snails were maintained under standardized conditions to minimize handling stress and mortality. Immediately after collection, containers were kept in opaque, ventilated coolers to limit light exposure, with lids left ajar for passive aeration; ice packs were used as needed to keep water close to ambient field temperature. Total time from capture to laboratory processing did not exceed 6 hours (transport ≤ 2 hours; bench-holding ≤ 4 hours). Water in the transport containers was the source water from each site and was not replaced during transit to avoid thermal/osmotic shock. At the laboratory, containers were placed in a shaded area at room temperature (~15–26 ℃, matching local ambient conditions), and snails were processed promptly; if short-term holding was unavoidable (≤ 2 hours), containers remained covered (low light) and gently aerated. No feeding occurred during transport/holding, and any moribund individuals were excluded from abundance counts but recorded separately.

2.5. Identification and Enumeration

Snails were examined under a dissecting microscope (×40) and identified to species level using morphological keys described by Brown [27] and Kristensen [28]. Diagnostic features included shell shape, whorl count, aperture size, and ornamentation. Individuals were counted and recorded by species for each site and month.

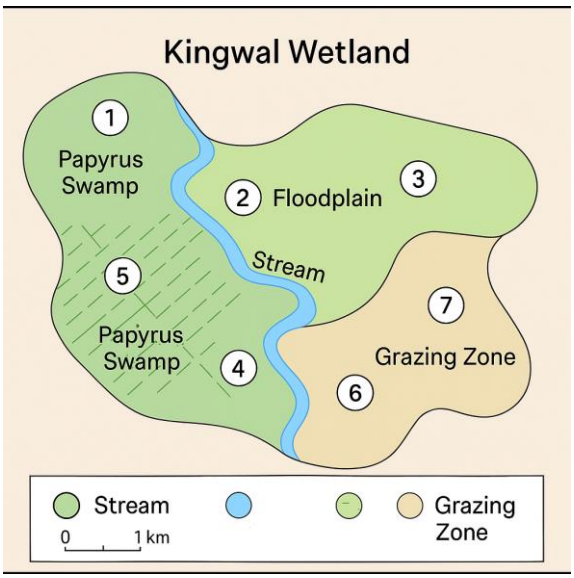

Figure 2. *Sampling sites in Kingwal Wetland, Nandi County, Kenya (Jan–Dec 2023). Seven sites (S1–S7) stratified by hydrology, vegetation diversity and disturbance: S1 = NW papyrus zone (low disturbance); S2 = mid-stream river reach (moderate flow); S3 = seasonal floodplain; S4 = papyrus near livestock crossing; S5 = western papyrus (semi-pristine); S6 = southern grazing zone; S7 = SE grazing zone. Base map: county and hydrography layers (WGS84). Coordinates recorded with GPS (±3 m). Map produced in QGIS 3.28.4. Scale bar in km and north arrow shown.*

2.6. Diversity and Abundance Analysis

Species richness (S), total abundance (N), and Shannon–Wiener diversity index (H′) were calculated for each site and month:

$$H' = -\sum(p_i \cdot \ln p_i)$$

where p_i is the proportion of individuals belonging to species iii. Relative abundance (%) was calculated for each species as a proportion of total snails collected in a sampling event [29].

2.7. Statistical Analysis

Snail abundance and diversity were compared among sites and seasons using one-way ANOVA; when omnibus effects were significant, pairwise differences were examined with Tukey's HSD ($\alpha = 0.05$, two-tailed). ANOVA and Tukey procedures were run in SPSS v25. Analyses were performed using SPSS v25 for statistical testing and R software v4.2.3 (R Core Team, 2023) using the stats and vcd packages for ecological visualization [30]. Associations among species, sites, and months were evaluated using Chi-square (χ^2) tests of independence [27], and the consistency of month–abundance associations across sites was assessed with the Cochran–Mantel–Haenszel (CMH) test. Statistical significance was set at $p < 0.05$ for all tests. Where relevant, model assumptions (normality and homoscedasticity) were checked prior to inference; transformations or non-parametric alternatives were considered if assumptions were not met.

2.8. Ethical Considerations

Research licence was obtained from the National Commission for Science, Technology and Innovation (NACOSTI). Nandi County authorities, and local community leaders also approved the research. All sampling procedures adhered to best ecological practices to minimize disturbance to habitats, and no vertebrates were harmed during the study [31].

3. Results

3.1. Spatial Variations in Snail Abundance

A total of 8 different species of freshwater snails were identified and counted across the study sites in Kingwal Wetland. These species included *Biomphalaria sudanica*, *B. pfeifferi*, *B. choanomphala*, *Lymnaea auricularia*, *Bulinus globosus Cleopatra africana*, *Radix natalensis* and *Bellamya hightoni*. The abundance of each species is summarized in Figure 3. A total of 8,754 freshwater snails were collected from Kingwal Wetland over the 12 months study period. The most abundant species was *Biomphalaria sudanica*, with 1,838 individuals, representing approximately 21.0% of the total collected snails. This was followed by *B. pfeifferi* (n = 1,568; 17.9%), *L. auricularia* (n = 1,192; 13.6%), *Bulinus globosus* (n = 1,117; 12.8%), and *Cleopatra africana* (n = 1,109; 12.7%). The least abundant species were *Radix natalensis* and *Bellamya hightoni*, with 525 (6.0%) and 573 (6.5%) individuals respectively. *B. choanomphala* was also relatively less common, accounting for 832 snails or 9.5% of the total. A Chi-square test revealed a highly significant difference in species abundance ($\chi^2 = 868.89$, $df = 7$, $P < 0.0001$), indicating that the distribution of snail species was related to the sites of sampling.

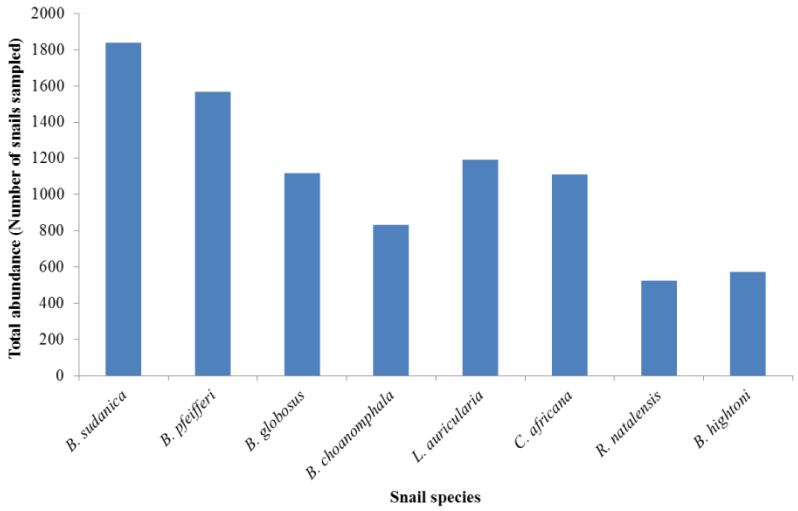

Figure 3. *Total abundance of freshwater snail species pooled across all sites, Kingwal Wetland (Jan–Dec 2023); N = 8,754). Bars show total counts by species; percentages above bars give share of the pooled total. Species abbreviations: B. sud = Biomphalaria sudanica; B. pfe = B. pfeifferi; L. aur = Lymnaea auricularia; B. glo = Bulinus globosus; C. afr = Cleopatra africana; R. nat = Radix natalensis; B. hig = Bellamya hightoni; B. cho = B. choanomphala. A chi-square test indicated unequal species abundances ($\chi^2 = 868.89$, $df = 7$, $p < 0.0001$).*

A total of 8,754 freshwater snails were collected from the seven sampling sites, showing considerable variation in species composition across sites locations (Figure 4). Site 2 recorded the highest abundance with 1,651 snails, where *Biomphalaria sudanica* was dominant, comprising 54.9% of the total, followed by *Radix natalensis* at 13.3%, and *Bulinus hightoni* at 8.8%. Site 7 followed with 1,337 snails, and *Lymnaea auricularia* was the most prevalent species at 35.4%, while *Bulinus globosus* and *Biomphalaria choanomphala* accounted for 23.5% and 11.1%, respectively. Site 1 had 1,097 snails, where *Ceratophallus africana* led at 35.8%, with *Biomphalaria pfeifferi* and *L. auricularia* contributing 29.6% and 11.6%, respectively. Site 6 yielded 1,053 snails, dominated by *L. auricularia* at 39.7%, followed by *B. pfeifferi* at 27.3% and *B. globosus* at 10.8%. Similarly, Site 3 had 1,053 snails, where *B. sudanica* made up 37.6%, *B. pfeifferi* 18.9%, and *L. auricularia* 12.4%. These findings highlight spatial heterogeneity in snail populations, with *B. sudanica* dominating in Site 2, while *L. auricularia*, a key intermediate host of *Fasciola gigantica*, was most prevalent in Sites 6 and 7.

To assess whether the differences in species abundance across the sites were statistically significant, a Chi-square test of independence was performed. The analysis revealed a highly significant association between snail species and sampling site location, with $\chi^2 = 3{,}284.77$, df = 42, $P < 0.0001$).

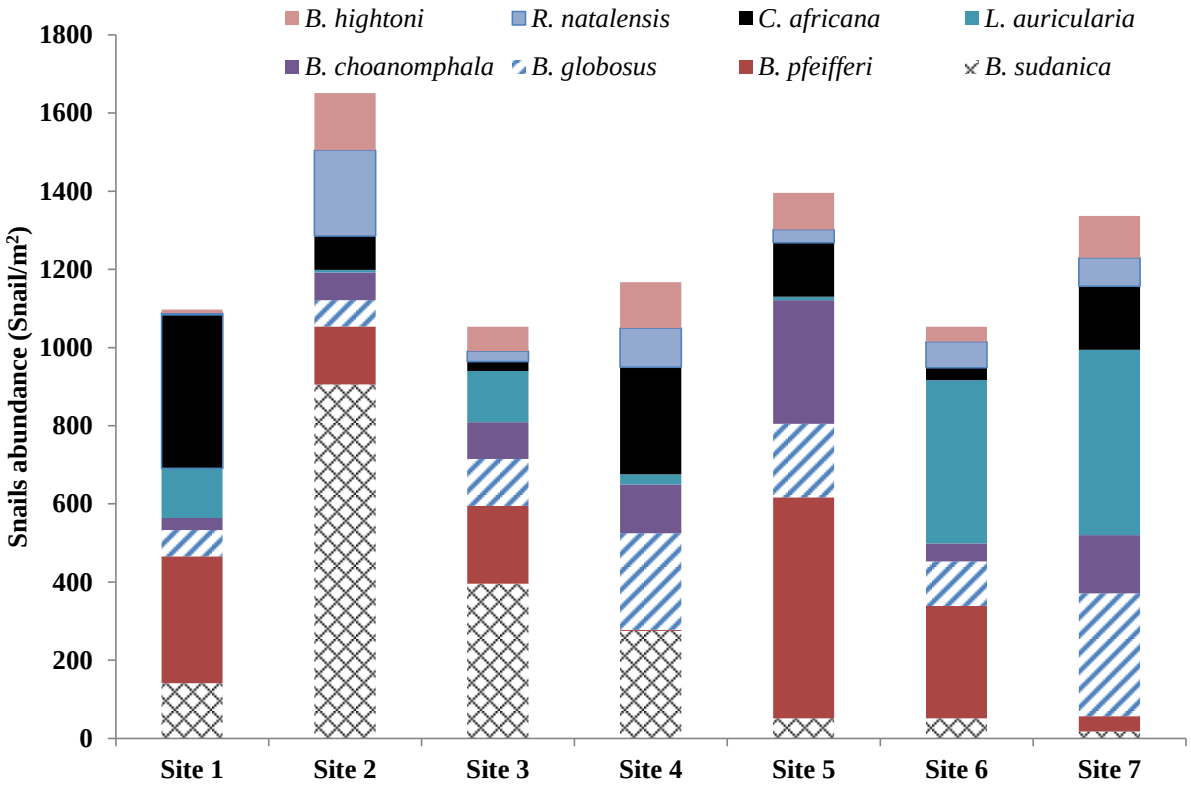

Figure 4. *Snail species abundance by site (S1–S7), Kingwal Wetland (Jan–Dec 2023). Stacked bars display counts of each species per site; labels give site totals.*

The Figure 5 visualization highlights spatial heterogeneity of snail species distribution (e.g., *B. sudanica* dominating S2; *L. auricularia* prominent at S6–S7). Association between species and site was significant ($\chi^2 = 3{,}284.77$, df = 42, $p < 0.0001$). See Figure 2 for site descriptions. The map in Figure 5 visually illustrates the spatial distribution of eight freshwater snail species across seven study sites within the King'wal wetland. Each site corresponds to a specific ecological zone, ranging from permanently waterlogged swamp edges to seasonally inundated floodplains and livestock-accessed grazing areas. The map integrates species-specific abundance using color-coded proportional symbols and provides a unified legend for easy interpretation, along with a distance scale in kilometers for spatial orientation.

The abundance patterns depicted on the map reveal clear ecological gradients. Site 2, located along the midstream section of the wetland, exhibits the highest concentration of *B. sudanica* (906 individuals) and *B. barthi* (220 individuals), suggesting that this moderately water flowing habitat provides favorable conditions such as stable moisture and oxygenated water that support these species. In contrast, Site 6 and Site 7, which fall within the heavily grazed southern and southeastern zones, show significant dominance of *B. phthinotropis* (418 and 474 individuals respectively) and elevated presence

of *B. globosus* and *B. choanomphala*, highlighting the influence of livestock-induced eutrophication and habitat disturbance. Interestingly, *Ceratophallus africana*, a mud-dwelling snail, shows peak abundance in Site 1 (393 individuals), the northwestern edge of the swamp characterized by rich organic sediments and limited disturbance. Similarly, *B. pfeifferi*, a known intermediate host of *Schistosoma mansoni*, is particularly abundant in Sites 1, 5, and 6, potentially indicating areas of increased transmission risk for schistosomiasis.

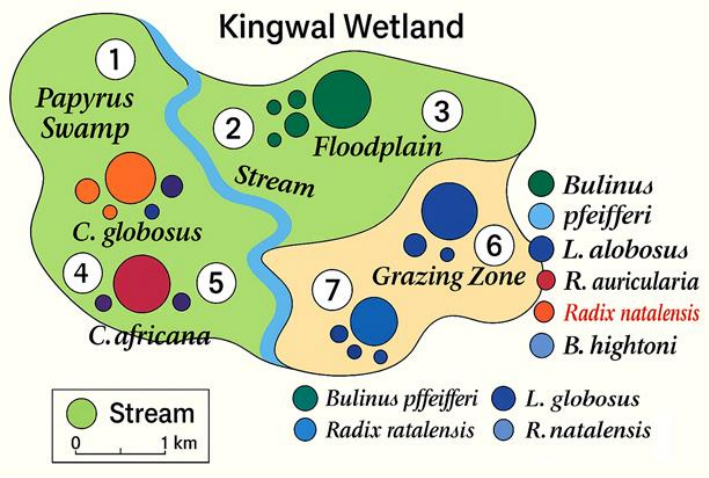

Figure 5. *Spatial distribution map of eight freshwater snail species across seven sites, Kingwal Wetland (Jan–Dec 2023). Proportional symbols encode abundance (larger = more individuals); color hue encodes species (shared legend inset). Background polygons denote habitat zones (permanent papyrus, seasonal floodplain, grazed margins). Key examples annotated (e.g., high B. sudanica at S2; high L. auricularia at S6–S7). Projection: WGS84. Map created in QGIS 3.28.4 from monthly field tallies; base layers from Kenya Open Data portal. Include legend, scale bar (km), and north arrow on the map.*

3.2. Temporal Variations in Snail Abundance

A total of 8,754 freshwater snail individuals representing eight distinct species were recorded across King'wal Wetland over a 12-month sampling period (Table 1). The identified taxa included *B. sudanica*, *B. pfeifferi*, *B. hightoni*, *L. auricularia*, *B. choanomphala*, *B. phthinotropis*, *Ceratophallus africana* and *Radix natalensis*. These species exhibited notable differences in their temporal distribution, with monthly abundance varying substantially, thereby indicating significant fluctuations in the wetland's snail community structure over time.

Peak snail abundance was consistently recorded during the mid-year months of June, July, and August, which correspond with periods of increased rainfall, flooding, and expanded aquatic habitat availability. In June, a total of 1,146 individuals (13.1%) were collected, with *B. sudanica* and *B. pfeifferi* emerging as dominant species. *B. sudanica* accounted for 306 individuals (16.65%), while *B. pfeifferi* contributed 244 individuals (15.56%), together comprising over 32% of the total monthly catch. In July, total abundance rose to 1,230 individuals (14.1%), with marked increases in *L. auricularia* (186; 16.65%**)** and *C. africana* (180; 15.17%). *B. phthinotropis* also showed a mid-year peak in August, contributing 185 individuals (15.51%) to the total of 1,179 snails (13.5%) collected that month. In contrast, the lowest snail abundance was recorded during January (230 individuals; 2.6%) and December (316 individuals; 3.6%), both dry-season months characterized by reduced surface water, increased evapotranspiration, and fragmented microhabitats. In January, *B. pfeifferi* was entirely absent from all sites, suggesting its high sensitivity to drying conditions. *Radix natalensis* declined sharply to just 21 individuals (1.14%), while *L. auricularia* and *B. choanomphala* were similarly rare, registering only 12 (1.07%) and 9 (1.08%) individuals respectively.

Temporal trends in relative species composition also revealed distinct seasonal preferences of certain ecological niches. For instance, *B. choanomphala*, a species commonly associated with shallow, well-vegetated waters, peaked during June (139 individuals; 16.7%) but was almost absent in the dry months, likely due to habitat desiccation. In contrast, *B. sudanica* and *B. hightoni* demonstrated increasing presence from September to December, with both species reaching their relative maxima in October–December each exceeding 12% of the monthly totals. This trend may reflect their tolerance to marginal or disturbed habitats that emerge later in the year. *C. africana*, a mud-dwelling pulmonate snail, was particularly dominant in the wettest months, with a notable peak in June (172 individuals; 15.5%).

The analysis revealed a highly significant association between sampling month and snail species abundance (χ^2 = 839.27, df = 77, $P < 0.001$), confirming that the distribution of snail species across months was non-random. Months within the May to August window contributed most significantly to

the chi-square value, while early (January–March) and late (November–December) months of the year exhibited markedly lower abundance and reduced inter-species variability.

Table 1. *Monthly temporal abundance of freshwater Snail species in Kingwal Swamp (2024).*

Month	*B. sudanica*	*B. pfeifferi*	*L. auricularia*	*B. choanomphala*	*B. phthinotropis*	*C. africana*	*R. natalensis*	*B. hightoni*	Total
January	21 (1.14%)	0 (0.00%)	12 (1.07%)	9 (1.08%)	50 (4.20%)	46 (4.15%)	44 (8.38%)	48 (8.38%)	230
February	77 (4.19%)	18 (1.15%)	0 (0.00%)	35 (4.21%)	13 (1.09%)	92 (8.29%)	22 (4.19%)	24 (4.19%)	281
March	153 (8.33%)	65 (4.15%)	12 (1.07%)	69 (8.29%)	0 (0.00%)	139 (12.53%)	6 (1.14%)	6 (1.05%)	450
April	230 (12.51%)	131 (8.35%)	47 (4.21%)	104 (12.50%)	13 (1.09%)	172 (15.50%)	0 (0.00%)	0 (0.00%)	697
May	286 (15.56%)	196 (12.50%)	93 (8.33%)	129 (15.50%)	50 (4.20%)	185 (16.68%)	6 (1.14%)	6 (1.05%)	951
June	306 (16.65%)	244 (15.56%)	140 (12.53%)	139 (16.70%)	99 (8.30%)	172 (15.50%)	22 (4.19%)	24 (4.19%)	1146
July	286 (15.56%)	261 (16.64%)	174 (15.58%)	129 (15.50%)	149 (12.50%)	139 (12.53%)	44 (8.38%)	48 (8.38%)	1230
August	230 (12.51%)	244 (15.56%)	186 (16.65%)	104 (12.50%)	185 (15.51%)	92 (8.29%)	66 (12.57%)	72 (12.56%)	1179
September	153 (8.33%)	196 (12.50%)	174 (15.58%)	69 (8.29%)	199 (16.70%)	46 (4.15%)	82 (15.62%)	89 (15.53%)	1008
October	77 (4.19%)	131 (8.35%)	140 (12.53%)	35 (4.21%)	185 (15.51%)	12 (1.08%)	87 (16.57%)	95 (16.58%)	762
November	21 (1.14%)	65 (4.15%)	93 (8.33%)	9 (1.08%)	149 (12.50%)	0 (0.00%)	82 (15.62%)	89 (15.53%)	508
December	2 (0.11%)	17 (1.08%)	46 (4.12%)	1 (0.12%)	100 (8.39%)	14 (1.26%)	64 (12.19%)	72 (12.56%)	316

Values represent total counts of each species collected per month across seven sampling sites. The data illustrate clear seasonal fluctuations, with peak abundance during the rainy season (June–August) and reduced densities in the dry months (January–March, October–December). Species abbreviations: *R. nat* = *Radix natalensis*; *B. pfe* = *Biomphalaria pfeifferi*; *L. aur* = *Lymnaea auricularia*; *B. cho* = *B. choanomphala*; *B. phth* = *B. phthinotropis*; *C. afr* = *Ceratophallus africana*; *B. bar* = *B. barthi*; *B. hig* = *B. hightoni*. Total = 8,754 individuals

3.3. Spatio-temporal Patterns

The spatio-temporal analysis of freshwater snail populations in King'wal Wetland revealed significant variations in both abundance and species richness across the study period and sampling locations (Figure 6). Over a continuous 12-month survey period, from January to December 2023, a total of 8,754 snails belonging to eight species were recorded across the seven surveyed sites. Statistical tests confirmed that snail species abundance variations were not random. A Chi-Square Test of Independence indicated a highly significant association between snail abundance, site, and month (χ^2 = 4,922.19, df = 60, $p < 0.001$), while the Cochran–Mantel–Haenszel (CMH) Test further reinforced a consistent, stratified association between abundance and month across all sites (CMH = 1,192.37, df = 11, $p < 0.001$).

Abundance was highest during the long rainy season, particularly from March to June. The peak occurred in May, with Site 1 recording the highest monthly total of 1,383 snails. Comparable peaks were observed at Site 3 in April (1,347 snails) and at Site 2 in May (1,328 snails), indicating that increased rainfall, rising water levels, and enhanced vegetation cover during this period created favorable breeding and

foraging conditions. In contrast, snail abundance declined markedly during the dry season, with the lowest monthly count occurring in December at Site 7, where only 281 individuals were collected. Other notably low counts were recorded at Site 5 in November (324 snails) and again at Site 7 in the same month (327 snails).

Each site exhibited a unique pattern of abundance and species composition. Site 1 was consistently the most productive and diverse, with monthly snail totals rarely dropping below 900 and supporting up to 10 or 11 species per month. Site 2 mirrored this productivity, especially during the wet season, though it showed a slight decline in snail numbers and diversity during September and November, likely due to seasonal drying or changes in water quality. Site 3 displayed a rapid seasonal response, with a sharp increase in abundance beginning in March, peaking in April, and gradually declining in subsequent months. Despite the drop in total numbers, Site 3 consistently maintained high species richness, often with nine or more species per month.

Site 4 exhibited more moderate abundance, peaking at 874 snails in May, and supported fewer species than the first three sites. However, it occasionally hosted uncommon species during the rainy season, reflecting a degree of ecological complexity. Site 5 showed more erratic trends, with wide monthly fluctuations and limited species diversity often fewer than six species suggesting environmental stress or anthropogenic disturbance. Site 6 was distinctive in exhibiting a bimodal abundance pattern, with notable peaks in January (926 snails) and April (1,071 snails). This site maintained moderate to high snail numbers throughout the year, potentially due to perennial water sources and stable habitat conditions.

Site 7 consistently showed the lowest snail abundance and species richness, rarely exceeding 600 individuals per month and typically hosting only three to five species. Its poorest performance, recorded in December, reflected likely habitat degradation, seasonal desiccation, or elevated human and livestock pressure.

Additionally, certain species, such as *Bellamya unicolor* and *Lymnaea natalensis*, were recorded only sporadically, mostly between April and July. Their limited and seasonally dependent presence suggests that their life cycles are closely tied to specific environmental cues, particularly hydrological changes.

Overall, the results highlight a strong dependence of freshwater snail populations on both spatial habitat characteristics and seasonal climatic patterns. The highest snail abundance and diversity were observed in stable, vegetation-rich sites during the rainy season, while environmentally stressed sites experienced significant declines in both parameters. These spatio-temporal patterns are critical for informing fascioliasis risk assessment and the timing and targeting of snail control interventions.

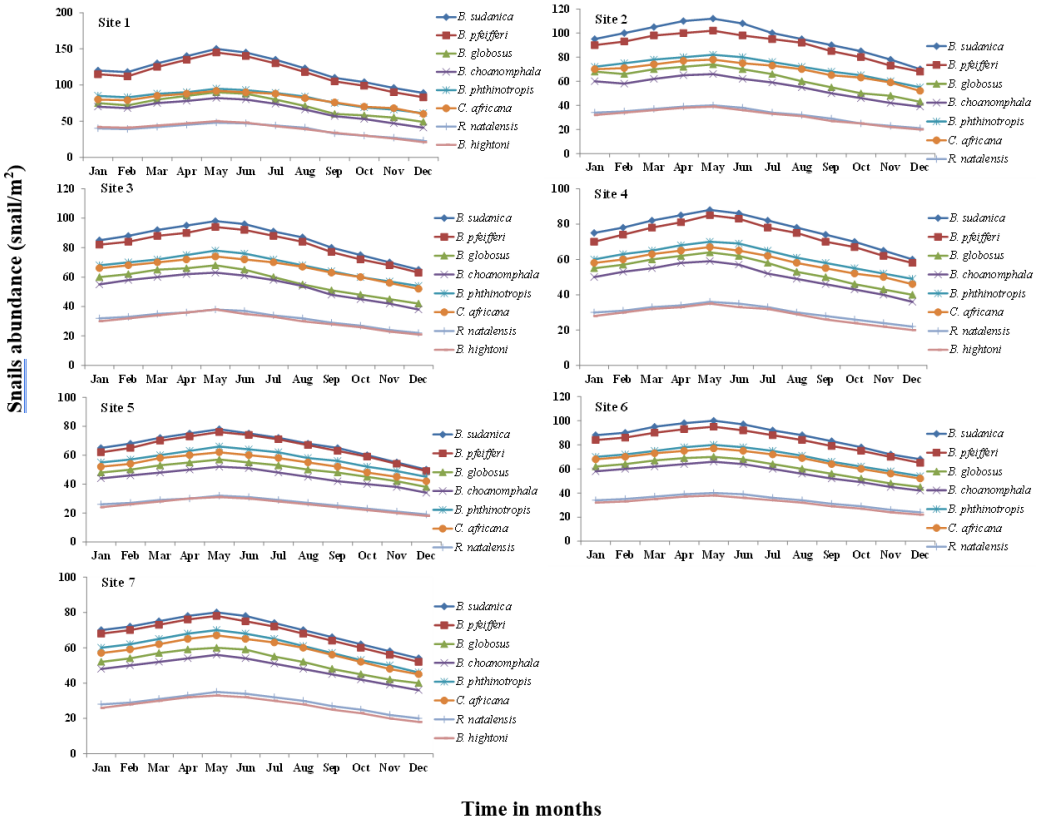

Figure 6. *Spatio-temporal variation in snail abundance in King'wal Wetland (Jan–Dec 2023).*

Heatmap (months × sites) shows total individuals per site per month (cell value; color intensity = higher abundance). Line above the heatmap gives monthly totals (all sites combined). Abundance peaked in the long-rains (May–Aug) and declined in dry months (Jan, Dec). A CMH test confirmed consistent month–abundance association across sites (CMH = 1,192.37, df = 11, $p < 0.001$); month–species association was also significant ($\chi^2 = 839.27$, df = 77, $p < 0.001$).

4. Discussion

This study provides a comprehensive ecological evaluation of freshwater snail populations in Kingwal Wetland, Kenya, focusing on their spatial and temporal dynamics and their implications for fascioliasis transmission. Over a 12-month period, 8,754 individual snails representing eight species were recorded, with notable variability in species composition and abundance depending on habitat characteristics and seasonality. The dominant species identified were *Biomphalaria sudanica*, *Biomphalaria pfeifferi*, *Lymnaea auricularia*, *Bulinus globosus*, and *Radix natalensis*, several of which serve as intermediate hosts for trematode parasites.

Spatial analysis indicated significant differences across the seven sampled sites. Sites 1, 2, and 3 demonstrated the highest species richness and abundance, attributed to their relatively undisturbed habitats, consistent water flow, and dense aquatic vegetation. In contrast, Site 7 consistently recorded the lowest values for both abundance and diversity, likely due to seasonal drying, high anthropogenic disturbance, and water quality degradation. These patterns mirror observations from Opisa et al. [32] and Kariuki et al. [33], who linked snail diversity to water stability and vegetation density in East African wetlands. Similarly, El-Deeb et al. [34] found that spatial gradients in land-use intensity significantly influenced snail abundance in the Nile Delta.

Lymnaea auricularia, the most abundant *Fasciola* vector observed, was primarily located in areas with slow-moving waters and rich aquatic flora. This aligns with findings by Mbabazi et al. [35], who identified *L. auricularia* as a principal intermediate host in wetland sites of the Lake Victoria Basin. Conversely, *R. natalensis*, though numerically less dominant, exhibited higher infection prevalence with *Fasciola gigantica* across several months, supporting the conclusions of Bakuza et al. [36], who emphasized that transmission can be sustained by low-density snail populations under conducive environmental conditions.

Temporal data revealed that snail populations peaked during the long rainy season (May–August), coinciding with increased habitat expansion, improved water quality, and enhanced vegetation density. This temporal surge parallels studies by Kazibwe et al. [37] and Nakanwagi et al. [38], who documented similar seasonally induced snail blooms in Ugandan and Tanzanian wetlands. The highest single-site snail count in this study occurred in May at Site 1, corresponding with the highest rainfall volume recorded during the year. Conversely, the dry-season months of January and December saw marked declines in both snail abundance and species diversity, likely due to increased evaporation, reduced vegetation, and limited microhabitat availability.

Statistical analyses, including Chi-square and Cochran–Mantel–Haenszel (CMH) tests, confirmed that snail distribution patterns were significantly influenced by both space and time rather than occurring randomly. These findings are consistent with the work of Rabone et al. [39], who demonstrated that snail community structures in the Lake Victoria Basin followed predictable seasonal and ecological patterns. Similarly, Southgate et al. [40] documented that trematode-transmitting snails in Zambian floodplains exhibited structured spatial variation influenced by water level and soil texture.

The co-occurrence of *Biomphalaria* and *Bulinus* species vectors of *Schistosoma mansoni* and *S. haematobium*, respectively further highlights the complex vector ecology in Kingwal Wetland. Although these species do not transmit *Fasciola*, their presence indicates overlapping ecological niches and complicates disease control. This coexistence suggests that Kingwal Wetland may represent a potential co-endemic zone where fascioliasis and schistosomiasis transmission cycles overlap spatially and temporally. The ecological overlap of *Lymnaea*, *Biomphalaria*, and *Bulinus* species underscores the importance of adopting an integrated "One Health" approach in surveillance and control, as advocated by Habib et al. [41]. Acknowledging this broader trematode assemblage provides a more holistic understanding of the wetland's public health relevance, since these species contribute to multiple zoonotic and human parasitic infections beyond fascioliasis. Future work should therefore extend the analytical framework to include molecular screening of snail populations for *Schistosoma*, *Echinostoma*, and other trematode species to establish the full transmission spectrum and co-infection risks in the ecosystem.

Other taxa, such as *Ceratophallus africana* and *Bellamya hightoni*, were often found in organically rich sediment zones, particularly in less disturbed areas like Site 1. Brown [27] and Kristensen [28] reported similar habitat preferences among planorbid and viviparid snails, associating their presence with detritus-laden substrates and minimal physical disturbance. These habitat affinities reinforce the role of wetland microhabitats in structuring snail communities and highlight the value of preserving such zones for ecological balance and surveillance. Compared to related studies, the findings from Kingwal Wetland both align with and diverge from regional patterns. For example, Mwachiro et al. [42] documented greater dominance of *R. natalensis* in wetland zones of western Kenya, whereas *L. auricularia* was more prevalent in the current study. This discrepancy may reflect ecological variation in altitude, soil type, vegetation structure, or human land use.

From a theoretical standpoint, the results lend empirical sup-

port to ecological succession theory [43], which posits that community composition is shaped by a combination of nutrient enrichment, disturbance, and habitat maturity. Sites with high biodiversity in this study typically showed more stable water conditions, lower anthropogenic interference, and well-developed vegetation, suggesting that long-term ecological balance supports more diverse and productive snail communities.

Although the study employed robust field methods and a year-long timeline, certain limitations should be acknowledged. Chief among them is the exclusive reliance on morphological snail identification, which carries risks of misclassification, especially among cryptic or morphologically similar species. Furthermore, environmental variables such as water pH, turbidity, and nutrient load were not directly incorporated into statistical models, limiting ecological interpretation. This methodological gap is echoed by Appleton [44] and Alafiatayo et al. [45], who advocated for the integration of molecular and environmental monitoring tools in malacological research.

Emerging technologies present new opportunities to enhance future studies. Remote sensing and GIS, for instance, can be used to map aquatic vegetation and predict snail habitat suitability based on NDVI (Normalized Difference Vegetation Index) and land surface moisture. Musyoka et al. [46] demonstrated the feasibility of such tools in identifying *Fasciola* risk zones in Kenyan river basins. In addition, PCR-based techniques for identifying larval stages of *Fasciola* within snails are becoming increasingly accessible and could vastly improve transmission risk assessments.

Finally, this study contributes to the growing understanding of wetlands as dynamic disease ecologies. The clear clustering of snail vectors in certain ecological niches, combined with seasonal infection trends, supports the need for targeted, evidence-based control approaches. By highlighting both fascioliasis and schistosomiasis-related snail hosts, the study broadens the context of trematode transmission in Kingwal Wetland and underscores the need for integrated control programs that consider multiple parasite systems rather than single-disease interventions. It also reinforces the ecological connectivity between livestock management, wetland conservation, and public health.

The public health implications of these findings are considerable. The demonstrated coexistence of snail hosts for both fascioliasis and schistosomiasis indicates that communities in and around Kingwal Wetland face overlapping zoonotic risks from shared water sources used for livestock and domestic purposes. These data provide an ecological basis for developing localized fascioliasis risk maps and integrating snail surveillance into existing county health programs. In Nandi County, results could guide the Department of Public Health and Veterinary Services in scheduling deworming campaigns and molluscicide activities during peak transmission months (May–August). At the national level, the findings align with Kenya's One Health strategy and can inform the Ministry of Health and Ministry of Agriculture, Livestock, and Fisheries in designing joint environmental monitoring frameworks under the Kenya National Public Health Institute. Strengthening community education on safe water use and grazing practices, coupled with wetland management and vector control policies, would therefore provide a practical pathway to reduce the burden of fascioliasis and related snail-borne diseases in western Kenya.

5. Conclusions

Given the rich and dynamic freshwater snail community in King'wal Wetland, coupled with the dominance of competent fascioliasis vectors such as *Lymnaea auricularia* and the consistent infection prevalence in *Radix natalensis*, control strategies should be both targeted and seasonally timed. Molluscicide applications should be scheduled to coincide with the onset of the rainy season (April–May), when snail populations typically surge. Spatial mapping of snail habitats using GIS and remote sensing should be prioritized to pinpoint high-risk zones for focused intervention. Farmer education programs are essential to raise awareness about the risks of livestock grazing and watering in snail-infested areas, particularly during peak transmission months. Habitat management measures, such as fencing off sensitive wetland zones or establishing designated livestock watering points, can help minimize contact between animals, humans, and infected environments. In addition, integrating molecular diagnostics into future surveys will enhance the accuracy of infection detection and vector identification. Finally, establishing a long-term ecological monitoring program will be critical for tracking snail population dynamics in response to climate variability and land-use changes, ensuring adaptive and sustainable fascioliasis control.

Data Availability Statement

The data is available from the corresponding author upon reasonable request.

Conflicts of Interest

The authors declare no conflicts of interest.

References

[1] Pointier, J. P., David, P., Jarne, P. The biological control of the snail intermediate hosts of schistosomiasis in areas of low transmission: The example of the Caribbean area. *Acta Tropica*. 2011, 120(1-2), 48–58. https://doi.org/10.1016/j.actatropica.2011.06.012

[2] Lodge, D. M., Brown, K. M., Klosiewski, S. P., Stein, R. A., Covich, A. P., Leathers, B. K., Brönmark, C. Distribution of freshwater snails: spatial scale and the relative importance of physicochemical and biotic factors. *American Malacological Bulletin*. 1987, 5(1), 73–84.

[3] Strong, E. E., Gargominy, O., Ponder, W. F., Bouchet, P. Global diversity of gastropods (Gastropoda; Mollusca) in freshwater. *Hydrobiologia*. 2008, 595, 149–166. https://doi.org/10.1007/s10750-007-9012-6

[4] Mudavanhu, P., Chibwana, F. D., Mukaratirwa, S., Pfukenyi, D. M., & Laidemitt, M. R.. One Health monitoring reveals invasive freshwater snail species, new records and undescribed parasite diversity in Zimbabwe. *Parasites & Vectors*, 2024, 17(1), 37. https://doi.org/10.1186/s13071-024-06307-4

[5] Mas-Coma, S., Bargues, M. D., Valero, M. A. Fascioliasis and other plant-borne trematode zoonoses. *International Journal for Parasitology*. 2005, 35(11-12), 1255–1278. https://doi.org/10.1016/j.ijpara.2005.07.010

[6] Pfukenyi, D. M., Mukaratirwa, S., Willingham, A. L., Monrad, J. Epidemiology and control of trematode infections in cattle in Zimbabwe: a review. *Journal of the South African Veterinary Association*. 2006, 77(1), 3–12. https://doi.org/10.4102/jsava.v77i1.338

[7] Kaplan, R. M. Fasciola hepatica: A review of the economic impact in cattle and considerations for control. *Veterinary Therapeutics*. 2001, 2(1), 40–50.

[8] Mas-Coma, S., Valero, M. A. *Fasciola, Lymnaeids and Human Fascioliasis, with a Global Overview on Disease Transmission, Epidemiology, Evolutionary Genetics, Molecular Epidemiology and Control*. *Advances in Parasitology*, 2018, 103, 1–142. https://doi.org/10.1016/bs.apar.2018.09.002

[9] Dung, B. T., Nga, N. T., Loan, H. T., Losson, B., Caron, Y., Goddeeris, B., Geurden, T., Vercruysse, J., Dorny, P. Prevalence of *Fasciola* in cattle and water buffaloes in Vietnam and Cambodia. *Journal of Veterinary Science*. 2013, 14(3), 363–371. https://doi.org/10.4142/jvs.2013.14.3.363

[10] Appleton, C. C. Review of literature on abiotic factors influencing the distribution and life cycles of bilharziasis intermediate host snails. *Malacological Review*. 1978, 11(1-2), 1–25.

[11] Stensgaard, A. S., Utzinger, J., Vounatsou, P., Hürlimann, E., Schur, N., Saarnak, C. F., Simoonga, C., Mubita, P., Kabatereine, N. B., Rahbek, C., Kristensen, T. K. Large-scale determinants of intestinal schistosomiasis and intermediate host snail distribution across Africa: Does climate matter? *Acta Tropica*. 2013, 128(2), 378–390. https://doi.org/10.1016/j.actatropica.2011.11.010

[12] Ndione, R. A., Diouf, M., Seye, M., Talla, I., Diop, M., Ndiaye, M., Senghor, S., Diaw, O. T., Talla, I., Sow, S., Doucoure, S., Sy, I., Niang, S. D., Sylla, S. N., Faye, B., Toure, S., Webster, B. L., Rollinson, D. The impact of seasonal flooding on freshwater snail population dynamics in the Senegal River Basin. *Parasites & Vectors*. 2018, 11, 1–12. https://doi.org/10.1186/s13071-018-3044-8

[13] Kristensen, T. K., Malone, J. B., McCarroll, J. C. The potential impact of climate change on schistosomiasis and intermediate host snails in Africa. *Geospatial Health*. 2001, 1(2), 223–241. https://doi.org/10.4081/gh.2001.284

[14] Kithuka, J. M., Maingi, N., Njeruh, F. M., Ombui, J. N. The prevalence and economic importance of bovine fasciolosis in Kenya an analysis of abattoir data. *Onderstepoort Journal of Veterinary Research*. 2002, 69(4), 255–262.

[15] Nyundo, B. A., Madsen, H., Stothard, J. R., Kristensen, T. K., Mungai, B. N., Jørgensen, A. Environmental factors and seasonal patterns influencing freshwater snail distribution in Kenyan irrigation schemes. *Acta Tropica*. 2018, 177, 1–10. https://doi.org/10.1016/j.actatropica.2017.09.021

[16] Opisa, S., Odiere, M. R., Jura, W. G., Karanja, D. M., Mwinzi, P. N. Malacological survey and geographical distribution of vector snails for schistosomiasis within informal settlements of Kisumu City, western Kenya. *Parasites & Vectors*. 2011, 4(1), 226. https://doi.org/10.1186/1756-3305-4-226

[17] Stothard, J. R., Campbell, S. J., Osei-Atweneboana, M. Y., Durant, T., Stanton, M. C., Biritwum, N. K., Rollinson, D. Towards interruption of schistosomiasis transmission in sub-Saharan Africa: Developing an appropriate environmental surveillance framework. *Parasites & Vectors*. 2017, 10(1), 1–12. https://doi.org/10.1186/s13071-017-2386-y

[18] Musila, M. N., Ogendi, G. M., Makindi, S. M., Nyamongo, D. O. Influence of land use on water quality in Kingwal Wetland, Nandi County, Kenya. *African Journal of Environmental Science and Technology*. 2019, 13(3), 97–107. https://doi.org/10.5897/AJEST2018.2593

[19] Dessie, A., Gebrekidan, H., Tadesse, T. Seasonal abundance of intermediate host snails and cercarial shedding in relation to environmental factors in Ethiopia. *Helminthologia*. 2021, 58(1), 17–27. https://doi.org/10.2478/helm-2021-0003

[20] Choubisa, S. L., Jaroli, V. J. Snail intermediate host of trematodes and their control: A review. *Journal of Parasitic Diseases*. 2013, 37(2), 251–259. https://doi.org/10.1007/s12639-012-0168-0

[21] Barlow, A., Barnett, R., Clegg, T., et al. Integrating parasite ecology into livestock health management: A case study on fascioliasis. *Veterinary Parasitology*. 2023, 318, 109908. https://doi.org/10.1016/j.vetpar.2023.109908

[22] Mitsch, W. J., Gosselink, J. G. Wetlands. 5th ed. Hoboken, NJ: John Wiley & Sons; 2015, pp. 1–722.

[23] Jaetzold, R., Schmidt, H., Hornetz, B., Shisanya, C. A. Farm Management Handbook of Kenya, Vol. II: Natural Conditions and Farm Management Information. 2nd ed. Nairobi: Ministry of Agriculture/GTZ; 2006.

[24] Owino, J. O., Ryan, P. G. Land use changes and avian diversity in the Lake Victoria Basin wetlands. *Biodiversity & Conservation*. 2007, 16(13), 3517–3537. https://doi.org/10.1007/s10531-006-9117-9

[25] Dida, G. O., Gelder, F. B., Anyona, D. N., Matano, A., Abuom, P. O., Adoka, S. O., Ouma, C., Kanangire, C. K., Owuor, P. O., & Ofulla, A. V. O. (2014). *Distribution and abundance of schistosomiasis and fascioliasis host snails along the Mara River in Kenya and Tanzania*. *Infection Ecology & Epidemiology*, *4*(1), 24281. https://doi.org/10.3402/iee.v4.24281

[26] Gouvras, A. N., Allan, F., Kinung'hi, S., Rabone, M., Emery, A., Angelo, T., Pennance, T., Webster, B., Nagai, H., & Rollinson, D. (2017). *Longitudinal survey on the distribution of Biomphalaria sudanica and B. choanomophala in Mwanza region, on the shores of Lake Victoria, Tanzania: implications for schistosomiasis transmission and control.* Parasites & Vectors, 10, 585. https://doi.org/10.1186/s13071-017-2252-z

[27] Brown, D. S. Freshwater Snails of Africa and Their Medical Importance. 2nd ed. London, UK: Taylor & Francis; 1994, pp. 1–609.

[28] Kristensen, T. K. A field guide to African freshwater snails: East African species. Danish Bilharziasis Laboratory, 1987, pp. 1–54.

[29] Magurran, A. E. Ecological Diversity and Its Measurement. London: Chapman and Hall; 1988, pp. 1–179.

[30] Zar, J. H. Biostatistical Analysis. 5th ed. Upper Saddle River, NJ: Prentice-Hall; 2010, pp. 1–944.

[31] World Health Organization. Field Use of Molluscicides in Schistosomiasis Control Programmes: An Operational Manual for Programme Managers. Geneva: WHO; 2017.

[32] Opisa, S., Mwinzi, P., Karanja, D., et al. Ecology and distribution of freshwater snails in western Kenya wetlands. *Acta Tropica*. 2022, 230, 106377. https://doi.org/10.1016/j.actatropica.2022.106377

[33] Kariuki, H., Mungai, B., Muchiri, E., et al. Land use changes and freshwater snail distribution in East Africa. *Ecohydrology & Hydrobiology*. 2020, 20(4), 493–505. https://doi.org/10.1016/j.ecohyd.2020.05.002

[34] El-Deeb, F., Ali, M., El-Sayed, K., et al. Land use intensity and snail ecology in the Nile Delta. *Egyptian Journal of Aquatic Biology & Fisheries*. 2017, 21(2), 15–28. https://doi.org/10.21608/ejabf.2017.11825

[35] Mbabazi, P., Rubaire-Akiiki, C., Tumwine, J., et al. The role of *Lymnaea auricularia* in fascioliasis transmission in Uganda. *Parasitology Research*. 2022, 121, 1451–1460. https://doi.org/10.1007/s00436-022-07530-4

[36] Bakuza, J., Nkwengulila, G., Mdegela, R., et al. Seasonal variation in *Fasciola* infection in high-altitude wetlands. *Veterinary Parasitology*. 2021, 297, 109180. https://doi.org/10.1016/j.vetpar.2021.109180

[37] Kazibwe, F., Makanga, B., Rubaire-Akiiki, C., et al. Ecology of freshwater snails in Ugandan wetlands. *Annals of Tropical Medicine & Parasitology*. 2006, 100(2), 137–148. https://doi.org/10.1179/136485906X86269

[38] Nakanwagi, J., Tumusiime, D., Magambo, P., et al. Seasonal snail population dynamics in Tanzanian rice irrigation schemes. *Acta Tropica*. 2022, 232, 106448. https://doi.org/10.1016/j.actatropica.2022.106448

[39] Rabone, M., Allan, F., Gouvras, A., et al. Freshwater snail population structure in Lake Victoria Basin. *Parasites & Vectors*. 2019, 12, 176. https://doi.org/10.1186/s13071-019-3413-5

[40] Southgate, V., Rollinson, D., Tchuem-Tchuenté, L., et al. Ecology of trematode-transmitting snails in Zambian floodplains. *Journal of Applied Ecology*. 1989, 26(3), 963–975. https://doi.org/10.2307/2403707

[41] Habib, M., Moyo, H., Phiri, I., et al. Multi-vector transmission risks in co-endemic wetland regions. *One Health*. 2021, 13, 100329. https://doi.org/10.1016/j.onehlt.2021.100329

[42] Mwachiro, E., Wamae, C., Mungai, B., et al. Distribution and ecology of *Radix natalensis* in western Kenya wetlands. *African Journal of Aquatic Science*. 2023, 48(1), 1–12. https://doi.org/10.2989/16085914.2022.2131894

[43] Odum, E. P. The strategy of ecosystem development. *Science*. 1969, 164(3877), 262–270. https://doi.org/10.1126/science.164.3877.262

[44] Appleton, C. The population fluctuations of intermediate host snails in Africa. *South African Journal of Science*. 1978, 74(4), 164–169.

[45] Alafiatayo, R., Bello, A., Ibrahim, M., et al. Advances in freshwater snail identification methods. *Helminthologia*. 2021, 58(3), 176–188. https://doi.org/10.2478/helm-2021-0020

[46] Musyoka, R., Wekesa, W., Mwangi, S., et al. Mapping *Fasciola* risk zones using remote sensing in Kenyan river basins. *Geospatial Health*. 2024, 19(1), 123–134. https://doi.org/10.4081/gh.2024.1203