Seasonal variability in faecal bacteria of semiarid rivers in the Serengeti National Park, Tanzania

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Abstract. Humans and livestock are known contributors of faecal waste to surface water. However, little is known about natural fluctuations of faecal bacteria, especially where wildlife may contribute substantial amounts of waste. I tested the hypotheses that ecological factors, including seasonal animal impacts, rainfall and physiochemical water quality, influence the abundance of total coliform (TC) and *Escherichia coli* faecal bacteria in five rivers of the Serengeti National Park, Tanzania. TC and *E. coli* are indicators commonly used to assess water quality and their abundance can be determined quantitatively by using defined-substrate technology. Results demonstrated substantial variation in faecal bacteria across rivers and seasons. In the southern two rivers, faecal bacteria increased significantly during the wet season, compared with dry-season levels, whereas there were few seasonal differences in the northern rivers, suggesting that large populations of resident wildlife in the north dampen the seasonal influence of migratory wildlife. Faecal bacteria were positively related to rainfall and total ammonia/ammonium, and had a negative quadratic relationship with salinity. The present results demonstrated that wildlife in protected regions can be major contributors of faecal bacteria to surface waters, and as demand for water resources increases, pose a significant threat to human health.

Additional keywords: *E. coli*, hippo pool, migration, precipitation, total coliform.

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Introduction

In urbanised watersheds, water quality is affected by point sources of anthropogenic pollution, whereas in rural environments, non-point sources are primarily recognised as contributing to surface-water deterioration (George 1996; Jamieson et al. 2003). Livestock waste deposited in or near rivers results in increased faecal bacteria, especially following precipitation and increased runoff (Buckhouse and Gifford 1976; Belsky et al. 1999; Zhu et al. 2011). The deterioration of surface-water resources because of inputs from human or livestock waste is well documented in northern latitudes (Belsky et al. 1999), but few studies have examined inputs from wildlife, especially in semiarid areas. Natural water bodies in protected areas of temperate systems are assumed to be largely free of bacterial contamination, although detailed analyses have demonstrated that contamination may still be frequent (McDonald et al. 2008). In semiarid savannas, surface-water quality varies spatially and temporally because of seasonal changes in precipitation that drive vegetation growth, wildlife abundance, microbial activity and surface runoff (Ruess and Seagle 1994; Belnap et al. 2005; Shah et al. 2007).

Wildlife can be important generators of organic waste, contributing to the redistribution of nutrients (Augustine et al. 2003; Jacobs et al. 2007). Animal waste deposited in water or carried in runoff contributes to high concentrations of dissolved nitrogen, biochemical oxygen demand and bacterial pollution (Meehan and Platts 1978). Most species of wildlife depend on surface water to survive, especially in arid conditions when vegetation moisture cannot sustain their water requirements (Western 1975; Estes 1992), and the distribution of surface-water resources is an important determinant of suitable habitat for many savanna species (Western 1975; O’Brien et al. 2006; Valeix et al. 2008). Most grazing herbivores seek surface water daily or almost daily during dry seasons, but spend little time in the riparian vegetation because of the potential risks associated with predation (Child and Parris 1971). Although there is very little information about the impact of wildlife on water quality as non-point sources of pollution, one might hypothesise that as the abundance of large mammals such as wildebeest (*Connochaetes taurinus*) and zebra (*Equus burchelli*) increase, animal waste is generated in large amounts, which will increase the abundance of faecal bacteria in the surface water. In addition to seasonally abundant wildlife, some large mammals maintain a close association with surface waters. In East Africa, hippo (*Hippopotamus amphibius*) influences the turbidity, vertical stratification of dissolved oxygen and eutrophication of water resources (Wolanski and Gereta 1999; Mnaya et al. 2006).

I tested the null hypotheses that wildlife density (approximated by total ammonia/ammonium), season, watershed rainfall, dissolved oxygen and water mineralisation do not
significantly affect faecal bacteria in surface waters of the Serengeti National Park. On the basis of previous studies, I expected faecal bacteria to be positively related to wildlife abundance and rainfall, and negatively related to dissolved oxygen. The seasonal abundance of migratory wildlife was expected to heavily influence waste production and as a result, faecal bacteria were expected to increase in the southern watersheds during the wet season and in the northern watershed during the dry season.

Materials and methods
Study area
The Serengeti National Park is in north-western Tanzania, sharing a border with the Maasai Mara Game Reserve in Kenya (Fig. 1). The ecosystem is characterised by a precipitation and soil gradient from south-east to north-west. The southern grasslands are composed of nutrient-rich soils, contributing to highly saline and alkaline conditions. The ecosystem boundaries are defined by the seasonal migration of wildlife, including wildebeest, zebra and Thomson’s gazelle (Gazella thomsonii). In a simplified depiction, the migration spends the wet season in the southern half of the ecosystem and the dry season in the northern half of the ecosystem. Other charismatic species, such as elephant (Loxodonta africana), buffalo (Syncerus caffer) and hippo are also common (Estes 1992). Hippos generally live in groups of up to 150, although groups of 2–15 are most common in the Serengeti.

Although monthly rainfall is heterogeneous, the south-eastern region has a mean annual rainfall of 400 mm and the northern region has a mean annual rainfall of over 1200 mm. High seasonal and spatial heterogeneity in rainfall drives highly variable habitat use (Anderson et al. 2007; Reed et al. 2009). River flows generally peak during the wettest months of March.

Fig. 1. Map of the Serengeti National Park and surrounding areas in northern Tanzania, with main rivers and sample sites identified. + represents sample-site locations along each river.
and April, and discharge decreases when the rains end. As the dry season progresses, soil moisture and surface water are lost to evaporation, and in many instances, rivers cease flowing and pools form in the deepest portions of the river (Fisher et al. 1998). Rainfall was determined at the catchment-basin scale by averaging monthly rainfall from three gauges within each catchment (Fig. 2).

Site determination and sample collection

Sample sites were in the following five rivers across the ecosystem: Mbalageti, Seronera, Nanuki, Naironya and Grumeti. The Mara River was not consistently sampled and was not included in the analysis. Although critical to the northern part of the ecosystem, water quality in the Mara River is affected by landscape-scale factors in Kenya, including deforestation and agriculture, which were not controlled (Gereta et al. 2002). Three water samples were obtained at each of three sites ($n = 3$) within each river in July 2008, April 2009 and June 2009, upstream of all hippo pools. All water samples were obtained with sterile Whirl-Paks (Nasco, Modesto, CA) between 0800 hours and 1200 hours and analysed within 4 h. Stream flow in the sampled rivers originates in the Serengeti National Park, Ngorongoro Conservation Area or in the border regions where there are few permanent human settlements. Diurnal fluctuations in algal growth, dissolved oxygen (DO) and bacterial respiration may have influenced the abundance of bacteria (Wolanski and Gereta 1999). However, consistent sample collection across regions and seasons attempted to minimise such variation. In addition to these samples, single water samples were taken from 12 additional sites along the Seronera River in July 2008, to assess downstream effects.

Additional water samples were collected in 250-mL acid-washed high-density polyethylene bottles for physiochemical analysis. Salinity, DO, and total ammonia and ammonium (NH$_3$) were then measured. Salinity and DO were measured with a YSI multipurpose probe (Yellow Springs Inc., Yellow Springs, OH, USA) and NH$_3$ was measured using a salicylate-cyanurate reaction on filtered (Pall A/E glass-fibre filters, Pall Corporation, Port Washington, NY) samples, following APHA (1995).

Bacterial analysis

Total coliform bacteria (TC) was used as a general indicator of faecal bacteria in surface waters and $E$. coli, which originates from the digestive tract of vertebrate animals, was used as a reliable representative of the coliform group of faecal bacteria (Meehan and Platts 1978; Farnleitner et al. 2010). Faecal contamination was quantified using the QuantiTray-2000 (IDEXX Industries, Westbrook, ME, USA) method as cited in Jagals (2006). Samples of 1-mL volume were diluted with sterile water to 100 mL and incubated with the Colilert-18 (IDEXX Industries, Westbrook, ME, USA) defined colour-changing substrate at 35°C for 18 h. The defined-substrate technology is more precise and versatile for enumerating $E$. coli contamination than is membrane-filter technology (Buckalew et al. 2006). Positive wells were identified visually for the abundance of TC by comparing to a control using a sample blank, and with ultraviolet light for $E$. coli bacteria. The most probable number (mpn) of colony-forming units (cfu) per 100 mL was then calculated on the basis of a standard mpn chart (IDEXX Industries, Westbrook, ME, USA). Sample analysis was completed at the Serengeti Wildlife Research Centre. Quality assurance and control were maintained in the field by taking triplicate samples from each sample site at each time period for analysis. One negative control using only sterile, deionised water was also run with each group of samples analysed.

Data analysis

Before parametric analysis, bacteria, rainfall and salinity data were log$_{10}(x + 1)$ transformed and NH$_3$ data were square-root transformed to meet statistical assumptions. A two-way analysis of variance (ANOVA) was used to determine differences among rivers and between seasons (wet v. dry), and their interaction.
Tukey’s HSD multiple comparisons test was then used to determine individual differences. Relationships between bacteria and environmental parameters were first examined using bivariate plots. Multiple regression analysis was then used to examine the effects of river, salinity, NHT concentration and the previous month’s rainfall on faecal bacteria.

Results and discussion
Spatial and seasonal differences in the concentrations of total coliform bacteria and E. coli
Waste from wildlife was hypothesised to contribute to surface-water pollution and seasonal and spatial fluctuations in the concentration of faecal bacteria were expected to reflect the seasonal patterns of migratory wildlife which dominate the Serengeti fauna. The Serengeti migratory wildlife spends the wet season in the southern grasslands, where the Mbalageti and Seronera rivers are located, and then moves northward at the beginning of the dry season. There was little difference in E. coli concentrations between the two dry seasons in the Grumeti or Naironya rivers, whereas the Mbalageti and Seronera rivers had a greater abundance of E. coli in June 2009 than in July 2008 (Fig. 3). There were significant differences in the concentrations of TC (F4 = 33.1, P < 0.001) and E. coli (F2 = 17.8, P < 0.001) across watersheds, rejecting the hypothesis that concentrations of faecal bacteria are similar in the five rivers of the Serengeti. There were also significant differences between seasons in the concentrations of TC (F1 = 4.81, P = 0.031) and E. coli (F1 = 4.90, P = 0.029), rejecting the hypothesis that the concentrations of faecal bacteria are similar across seasons. River basin and season explained a substantial amount of the variability in TC (r² = 0.63) and E. coli (r² = 0.44) concentrations.

The two-way ANOVA to test the hypothesis that there were significant spatial (river) and seasonal (wet v. dry) effects produced a significant interaction for both TC (F4 = 20.1, P < 0.001) and E. coli (F4 = 5.68, P < 0.001). This was expected based on the prediction that bacteria concentrations during the dry season would increase in northern rivers and decrease in the southern rivers. In the northern three rivers, both TC and E. coli samples had greater ranges and maxima of faecal bacteria in the dry season. Conversely, the southern two rivers had greater ranges and maxima in the wet season.

There was little spatial variability during the dry season, although in 2009, the Nanuki and Naironya rivers had a lower concentration of E. coli than did any of the other rivers. The Mbalageti and Seronera rivers were more contaminated in June 2009 than in July 2008, likely because of the length of time following the departure of migratory wildlife from the southern region as well as differences in monthly rainfall. May in 2009 was a slightly wetter month than that in 2008, increasing surface runoff and the transport of bacteria. Concentrations of E. coli were consistently greater in the Grumeti River than those in the Naironya River; however, this may have reflected the greater abundance of resident herbivores in the Grumeti watershed, or the use of the grazing lands outside of the Serengeti National Park.
Park by Maasai herders near Klein’s Gate in the Grumeti watershed.

During the wet season, concentrations of faecal bacteria increased in the south, whereas the concentration of TC decreased in two of the three northern-most rivers and the concentration of E. coli did not change despite increased rainfall (Fig. 3). This would be expected if migratory wildlife influenced surface-water bacteria. However, the magnitude of change was much less than expected, given the substantial quantities of waste generated in these watersheds over the length of the dry season. The northern woodlands also support year-round populations of gazelles and megafauna that are not always found on the southern plains, dampening any seasonal fluctuations in animal waste production. Rainfall is also more consistent in the northern watersheds, resulting in less variability in the supply of bacteria from overland flow (Collins et al. 2005) and possibly reducing the flush of bacteria in runoff associated with large storm events. These results are consistent with the expectation that migratory herbivores contribute substantially to elevated dung deposition in different watersheds at different periods of the year (Augustine et al. 2003), that dung contributes to surface-water contamination (Buckhouse and Gifford 1976), and that faecal bacteria contribute to seasonal variations in surface-water pollution (Van Donsel et al. 1967). Bacterial survival may also be influenced by seasonal changes in solar radiation (McCambridge and McMeekin 1981), although the extent to which this may influence large spatial differences is not known. It is clear that concentrations of faecal bacteria are not consistent across temporal or spatial scales, and that the seasonal movement of wildlife contributes to fluctuations in microbial water quality. Long-term studies need to be carried out to better quantify the seasonal and spatial variation in the abundance of faecal bacteria.

Ecological factors influencing faecal bacteria

Surface-water quality is directly linked to rainfall; runoff contributes substantially to turbidity and pathogen transport (Atherholt et al. 1998; Dunkell et al. 2011) and increasing soil moisture is known to affect microbial activity (Welter et al. 2005), including mineralisation (Chapin et al. 2002) and nutrient release (Turner and Hygarth 2001). In the Serengeti, there is substantial variability in monthly rainfall, both within and among watersheds. High surface flows during wet months increase erosion and the transport of sediment with bacteria into rivers (Brown et al. 1981; Gereta and Wolanski 1998). In the present study, average rainfall generally increased from south to north, with March being the wettest month (Fig. 2). A correlation analysis tested the hypothesis that the concentrations of faecal bacteria are positively related to rainfall (Fig. 4c). Both TC ($F_{1,108} = 23.2, P < 0.001$) and E. coli ($F_{1,108} = 23.8, P < 0.001$) concentrations showed a positive linear relationship with the previous month’s rainfall (Fig. 4c). This was expected given that many studies have demonstrated a relationship between rainfall and increased runoff from non-point sources of pollution (Atherholt et al. 1998; Kistemann et al. 2002). Surface-water pollution may be more indicative of recent overland flows and not necessarily of recent dung deposition. Thelin and Gifford (1983) demonstrated that faecal bacteria survive for months in dung, despite exposure to solar radiation. However, increased transport of faecal bacteria may be offset by increased stream flows, which could dilute concentrations.

The survival of bacteria in natural waters is also dependent on the physical and chemical conditions, including stream flow, temperature, oxygenation and physiochemical water quality (McFeters and Stuart 1972; Bell et al. 1982). Overall, NH$_4$ and salinity increased from south to north, whereas there was no clear pattern in DO across the Serengeti (Table 1). The variability of each parameter also tended to be higher in the southern than in the northern rivers. The coefficient of variation for rainfall decreased from south to north, being greatest (61.1) for Mbalageti, followed by Seronera (33.8), Nanuki (29.3), Naironya (25.8) and Grumeti (23.2). This may have contributed to the greater variations in physiochemical water quality. Unexpectedly, there were high concentrations of NH$_4$ in the south during the dry season, likely reflecting increased concentrations as a result of reduced base flows and increased evaporation.

Multiple regression analyses tested the importance of watershed, wildlife waste (NH$_4$) and rainfall on the concentrations of faecal bacteria (Table 2). As expected, rainfall, season, NH$_4$ and river basin explained most of the variability in the data for TC ($r^2 = 0.62$) and E. coli ($r^2 = 0.60$). Soil composition is known to vary across the Serengeti (Anderson and Talbot 1965; McNaughton 1988), so it was not surprising that salinity also influenced the abundance of faecal bacteria. Previous studies of freshwater bacteria exposed to salinity described non-linear survival results (Carlucci and Pramer 1960); consequently, I tested the hypothesis that the abundance of faecal bacteria varied quadratically with salinity. This analysis produced a significant negative quadratic relationship between salinity and the concentration of TC ($F_{2,107} = 15.3, P < 0.001$) as well as E. coli ($F_{2,107} = 7.09, P = 0.0013$; Fig. 4f). Painchaud et al. (1995) reported reductions in bacterial growth of 15% and 50% in salinities of 10 and 20, respectively, whereas Mantoura (1987) and Valdés and Albright (1981) described increased mortality of bacteria at low (<3) salinities.

I also tested the hypothesis that animal impact, as approximated by NH$_4$, was positively related to the abundance of faecal bacteria in all samples and found a significant positive linear relationship between NH$_4$ and the concentrations of TC ($F_{1,108} = 76.1, P < 0.001$) and E. coli ($F_{1,108} = 52.7, P < 0.001$; Fig. 4a). This relationship was expected, given the substantial literature that identified herbivores as major contributors to surface-water contamination (Belsky et al. 1999). Additionally, the seasonal migration of ungulates in the Serengeti ecosystem is closely linked to seasonal changes in water quality (Wolanski and Gereta 2001). Fluctuations in DO could also be influencing the survival of faecal bacteria, although DO did not have a clear relationship with either TC ($r^2 = 0.04$) or E. coli ($r^2 = 0.01$) concentration, and was not graphed. The pH of the surface waters may have also contributed to the observed differences in bacteria, because environmental pH has been shown to influence the survival of coliform bacteria (Jameson et al. 2003), although there have been mixed results (Carter et al. 2002). Dryland environments often contain highly saline or alkaline soils that may influence plant, herbivore or water composition (Chhabra 1996; McNaughton 1988; Holdo et al. 2002), and the
The degree to which these influence faecal bacteria in the surface water is not well known. The present data provided some indication that soil mineralisation may influence the survival of faecal bacteria, either on land or in the water.

The influence of hippos on the concentration of faecal bacteria in the Seronera River

In the Seronera River, TC concentration tended to increase from upstream to downstream (Fig. 5). This increase mirrors the general decrease in stream salinity reported by Gereta et al. (2004). Continued inputs of bacteria from runoff into the river are the likely reasons that led to increased coliform concentrations, although *E. coli* concentrations increased only in reaches downstream of hippo pools (shown as arrows on the graph); sample sites following a stream reach without hippo pools resulted in a decrease in *E. coli* bacteria. This suggests that the presence of hippos affects the abundance of faecal bacteria in the immediate reach, but that there is a rapid decline in the concentrations of faecal bacteria, probably by predacious microorganisms (McCambridge and McMeekin 1981). The quantity of increase tended to be consistent upstream of Site 11, whereas Site 12 demonstrated a seven-fold increase. Maximum *E. coli* concentrations were found at Site 12, probably because of the persistence of a large mat of dung and the greatest abundance of hippos in the river. Site 12 was downstream of a hippo pool.
that was consistently occupied by >20 hippos, whereas hippo abundances at Sites 4–6, 8 and 9 remained relatively low (1–9).

Hippos dramatically alter aquatic ecosystems by producing large mats of dung that float in rivers. These mats tend to collect on the surface downstream of hippo pools where river width narrows and flows are constrained by rocks and vegetation. Hippo movement is also likely to affect DO concentrations by stirring the water column (Wolanski and Gereta 1999). Nearly anoxic conditions often persist in semiarid rivers that are heavily eutrophicated by animal dung or when hippos resuspend the highly organic benthic sediment (Gereta and Wolanski 1998; Mnaya et al. 2006). Although wetland vegetation is known to trap sediment and nutrients (Gereta et al. 2004), the present data demonstrated that bacteria might still be carried downstream from large sources of animal waste. Alternatively, behavioural differences of the hippos before sample collection might also explain the unique pattern in *E. coli* concentrations. Hippos feed on land at night and it is difficult to quantify differences in hippo behaviour among different reaches. The development of conservation areas that include riverine habitat with hippo populations should consider their impact on water quality for other users.

Comparisons of contamination with faecal bacteria to other systems

Previously reported concentrations of faecal bacteria in semiarid rivers were similar to those found in the present study. In Australia, Shah et al. (2007) found that an average (± s.e.) mpn of cfu per 100 mL for TC was of 3154 (± 735) from sites with cattle in the watershed, compared with 1947 (± 469) in protected forests. In Wyoming mountain streams, Hussey et al. (1986) found TC concentrations (mpn of cfu per 100 mL) to be between 0 and 316. Animal waste can contain up to 90 000 mpn cfu per 100 mL, so values observed here are not unreasonable in watersheds with substantial waste input (Buckhouse and Gifford 1976). In the US Pacific North-west, the average concentration of faecal coliforms (a subset of TC) of livestock-grazed watersheds ranged from 1 to 78 000 mpn cfu per 100 mL (Jawson et al. 1982). It is likely that extremely high concentrations of faecal

### Table 1. Mean (±s.d.) untransformed physiochemical water-quality parameters (n = 3) for each sampling period and river

<table>
<thead>
<tr>
<th>River and sampling period</th>
<th>DO (mg L⁻¹)</th>
<th>NH₃ (mg L⁻¹)</th>
<th>Salinity (mg L⁻¹)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Grumeti River</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>July 2008</td>
<td>6.94 (1.23)</td>
<td>0.14 (0.09)</td>
<td>300 (100)</td>
</tr>
<tr>
<td>April 2009</td>
<td>7.65 (0.34)</td>
<td>0.28 (0.16)</td>
<td>200 (100)</td>
</tr>
<tr>
<td>June 2009</td>
<td>6.61 (0.60)</td>
<td>0.80 (0.53)</td>
<td>100 (100)</td>
</tr>
<tr>
<td>Naironya River</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>July 2008</td>
<td>7.06 (1.21)</td>
<td>0.08 (0.03)</td>
<td>700 (500)</td>
</tr>
<tr>
<td>April 2009</td>
<td>6.54 (0.47)</td>
<td>0.30 (0.23)</td>
<td>200 (100)</td>
</tr>
<tr>
<td>June 2009</td>
<td>6.97 (0.17)</td>
<td>0.38 (0.09)</td>
<td>200 (100)</td>
</tr>
<tr>
<td>Namuki River</td>
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<td></td>
</tr>
<tr>
<td>July 2009</td>
<td>7.86 (0.43)</td>
<td>0.05 (0.02)</td>
<td>3500 (200)</td>
</tr>
<tr>
<td>April 2009</td>
<td>5.29 (0.19)</td>
<td>0.19 (0.04)</td>
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</tr>
<tr>
<td>June 2009</td>
<td>4.80 (0.09)</td>
<td>2.83 (0.50)</td>
<td>600 (0)</td>
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<td>10.66 (4.01)</td>
<td>1.35 (1.84)</td>
<td>3300 (100)</td>
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<tr>
<td>April 2009</td>
<td>11.93 (8.53)</td>
<td>2.30 (0.23)</td>
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</tr>
<tr>
<td>June 2009</td>
<td>3.62 (3.44)</td>
<td>2.50 (1.36)</td>
<td>1500 (700)</td>
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<tr>
<td>July 2008</td>
<td>5.28 (1.29)</td>
<td>0.25 (0.10)</td>
<td>2700 (200)</td>
</tr>
<tr>
<td>April 2009</td>
<td>2.51 (0.68)</td>
<td>2.97 (0.05)</td>
<td>1300 (100)</td>
</tr>
<tr>
<td>June 2009</td>
<td>14.1 (2.46)</td>
<td>3.33 (1.32)</td>
<td>2200 (100)</td>
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</table>

### Table 2. F-ratio, degrees of freedom (d.f.) and P-value of environmental factors of predictor variables for the multiple-regression analysis modelling the concentrations of total coliform and *Escherichia coli* bacteria in Serengeti rivers from 2008 to 2009

<table>
<thead>
<tr>
<th>Parameter</th>
<th>F</th>
<th>d.f.</th>
<th>P</th>
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<tr>
<td>Total coliform</td>
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<td></td>
<td></td>
</tr>
<tr>
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<tr>
<td>Salinity</td>
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<td>0.15</td>
</tr>
<tr>
<td>Season</td>
<td>14.6</td>
<td>1</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>River</td>
<td>4.29</td>
<td>4</td>
<td>0.003</td>
</tr>
<tr>
<td><em>E. coli</em></td>
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<td></td>
<td></td>
</tr>
<tr>
<td>Rainfall</td>
<td>17.2</td>
<td>1</td>
<td>&lt;0.001</td>
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<tr>
<td>Salinity</td>
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<td>1</td>
<td>0.68</td>
</tr>
<tr>
<td>NH₃</td>
<td>13.1</td>
<td>1</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>DO</td>
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<td>0.43</td>
</tr>
<tr>
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<td>3.31</td>
<td>1</td>
<td>0.07</td>
</tr>
<tr>
<td>River</td>
<td>10.2</td>
<td>4</td>
<td>&lt;0.001</td>
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</table>
bacteria are a biproduct of the success of ungulates in the Serengeti ecosystem, and consequently, the substantial animal waste generated. However, the rapid decay of faecal bacteria in the Seronera River suggests that the downstream transport of bacteria in surface waters may not be as significant. Considering that these rivers eventually flow into the economically, recreationally and culturally important Lake Victoria, this is important. The development of border regions near protected areas continues to constrain the distribution and movement of wildlife, which may have additional consequences for the contamination of surface waters by animal waste.

Faecal bacteria in Serengeti rivers tended to be less concentrated than those in farm ponds and lagoons that are commonly used for the confinement of large quantities of animal waste. Petkov et al. (2006) found that annual average E. coli concentration in fresh pig slurry ranged from 933 to 131 825 cfu per g of slurry, whereas Otabbong et al. (2007) found E. coli concentrations in a pig lagoon near St Petersburg to have concentrations as high as 10^7 cfu per 100 mL. Even though farm lagoons prevent waste and runoff from entering nearby surface-water systems, possibly improving biochemical oxygen demand in local aquatic environments (Robbins 1978), they are often a source of bacteria (Jones and Matthews 1975).

The importance of faecal bacteria to water quality in semiarid environments

The present study highlighted one of the first examples of the influence of wildlife on surface-water faecal pollution in sub-Saharan Africa. It also provided some indication of the substantial spatial and seasonal variability in the abundance of faecal bacteria in surface waters of protected areas and identified the effects of rainfall and physiochemical water quality on the concentrations of faecal bacteria. Coliform and E. coli bacteria are important indicator organisms used to evaluate the potability of surface water, indicating the presence of faecal contamination and the possible contamination by pathogenic organisms (Meehan and Platts 1978; Bohn and Buckhouse 1985). However, we have a poor understanding of the natural fluctuations in the abundance of faecal bacteria in surface waters within protected areas (Collins and Rutherford 2004; McDonald et al. 2008), especially in semiarid environments where competition for water strains existing water sources. Previous studies have demonstrated the rarity of high levels of faecal contamination in protected areas at higher latitudes, with only 11–21% of samples in western Oregon testing positive for E. coli (van Ess and Harding 1997), and 100% of samples having a TC lower than 100 mpn cfu per 100 mL in northern Utah (Colthorp and Darling 1975). In East Africa, few rivers are protected from anthropogenic sources of contamination and the influence of seasonally abundant wildlife on the quality of surface water is unknown. Large populations of wildlife that occupy seasonally distinct regions can heavily influence the amount of animal waste deposited in a watershed and the potential for bacterial contamination.

Seasonal grazing patterns are common among wildlife in protected regions (Biggs et al. 2003), and managers should anticipate how such behaviour affects surface-water quality in rivers that cross into unprotected regions, especially where such fluctuations in the concentration of faecal bacteria can pose a substantial threat to downstream communities, especially when they are dependent on surface waters for consumption (White et al. 1972). The observed concentrations of TC and E. coli generally exceeded those previously reported in surface waters of protected ecosystems (McDonald et al. 2008) and spring-fed rivers outside of the Serengeti (Strauch and Almedom 2011), although they were comparable to concentrations in the regions with heavy livestock grazing (Shah et al. 2007). The high concentrations of E. coli are a concern for communities that border the national park, because animals are important vectors of pathogens, including Giardia, Cryptosporidium and Campylobacter (Atwill 1996; Curtis et al. 2000; Collins and Rutherford 2004). For potable water supply, the World Health Organisation (WHO) prohibits the detection of E. coli in any 100-mL sample (WHO 2008). Despite this, the WHO commonly recognises that natural surface waters are heavily affected by faecal pollution and bacterial standards for irrigation water in various countries are 1000 cfu per 100 mL (WHO 1973). This standard was exceeded in most samples in the present study, suggesting that wildlife pose a significant threat to surface-water quality for subsistence-farming communities. Further research is needed to understand the fate of faecal bacteria in these surface waters, the short- and long-term variability in the abundance of faecal bacteria, and the consequences of changing social-ecological parameters, such as rainfall, migrating wildlife or development, on the quality of surface water. Population growth in rural communities will continue to degrade savanna environments, altering the hydrology of watersheds and further straining surface-water resources outside of protected regions. By quantifying these natural fluctuations in bacteria, stakeholders can begin to develop management strategies for addressing water quality-related issues.

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References


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