SPECIES RICHNESS AND DIVERSITY REVEAL THAT HUMAN-MODIFIED ENVIRONMENTS ARE NOT WASTELANDS

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ABSTRACT

Urbanization is often associated with the loss of habitats for many species but the pattern of invertebrate abundance in increasingly human-dominated urban areas is less well documented particularly for the expanding urban Africa. This study investigated the composition and community structure of spiders in relation to human activities at the foot of the Uluguru Mountains in Morogoro city, Tanzania. Three different sampling methods: pitfall trapping, sweep netting and active searching were used to collect spiders in the study area and to allow comparison between structurally different habitat sites. Spider abundance differed significantly between habitat types and was influenced by the sampling methods used. Family diversity and richness showed no significant differences across the sites. The spider species consisted of primarily three functional groups: ground wanderers, web builders and plant wanderers, and showed no within-group differences in abundance between sites. Similarity index between the study sites revealed a considerable overlap in the spider families present. No correlation between habitat variables: tree shade, herbaceous cover and ground cover and spider functional groups were found, suggesting that habitat alteration has minimal effect on the abundance of these invertebrate taxa. Further, cluster analysis at the family level revealed that spiders formed clusters on the basis of their hunting strategies, suggesting the avoidance of competition among spider guilds. This study provides insight into the importance of human-dominated areas on invertebrate biodiversity and serves as a basis for future work.

Keywords: community structure, functional groups, spider composition and diversity, urban environment

INTRODUCTION

Although biodiversity research has increased worldwide over the last few decades, studies covering Afro-tropical invertebrate taxa have so far remained insufficient. Several reasons have been cited for this including disproportionately low interest among scientists in certain groups of animals (Humpries *et al.* 1995). Additionally, the extended timeframe often needed for invertebrate sampling (Gollan *et al.* 2010), limited invertebrate taxonomic expertise due to a lack of training (Noss 1996) and a consequent decline in amateur and professional taxonomists (Anonymous 2000; Hopkins and Freckleton2002) have also been mentioned. This is particularly the case for spiders, for which limited taxonomic expertise has increasingly hampered spider biodiversity research (Derraik *et al.* 2002). For example, South Africa has only a handful of practicing spider taxonomists (Dippenaar-Schoeman 2010) while the total number in Africa is currently unknown but presumed to be low. Furthermore, while spiders are important in the healthy functioning of many ecosystems due to their predatory roles on insect pests (Wise 1993; Entling *et al.*2007; Finch *et al.*2008; Cardoso *et al.* 2010), they are often ignored in conservation endeavors across many parts of Africa (Dippenaar-Schoeman and van den Berg 2010). As a result, many spider habitats continue to be threatened by human activities, both in rural and urban areas (Marc *et al.* 1999). Potentially, this habitat loss risks the extinction of species even before their taxonomic description. Understanding how urbanized areas support habitats for the disturbance-sensitive taxa such as spiders may provide insights into future conservation planning for the increasingly expanding urban cities, and also helps us to understand the natural history of these relatively understudied areas. This paper unravels spider repertoire in an expanding human-dominated area to build a basis for future work.

Studies investigating effects of humans on spider biodiversity in human-dominated landscapes are still strongly geographically biased towards developed countries (e.g. Fraser and Frankie 1986; Shochat *et al.* 2004; Magura *et al.* 2010; Varet *et al.* 2011; Moorhead and Philpott 2013; Kaltsas *et al.* 2014). There is very limited understanding of these processes in metropolitan areas of Afro-tropical regions (Cumming and Wesolowska 2004) where the effect of urbanization on biodiversity is increasingly evident (e.g. Rija *et al.* 2014). In Tanzania, very few spider studies exist and most were undertaken in protected areas, particularly in Mkomazi (e.g. Russell-Smith 2002; Haddad and Russell-Smith 2009) and Udzungwa Mountains National Parks (e.g. Sørensen *et al.* 2002; Sørensen 2004). Studies of biodiversity in urban areas are particularly important because they provide an understanding of the effects of human activities (McKinney 2008; Rija *et al.* 2014) and thus can greatly improve the conservation of species in areas where people live and work (Miller and Hobbs 2001; Rija 2010).

The lack of information on spiders potentially contributed to a general under-appreciation of the importance of these species, and their misrepresentation in Tanzania's conservation agenda. The aim of this study was to understand the composition, structure and diversity of the spider fauna in areas influenced by human activities at the foot of the Uluguru Mountains, one of the biodiversity hotspot areas in Tanzania. The objectives were to: (i) describe and compare spider community composition, abundance and distribution between the study sites, (ii) describe family diversity, richness and evenness of the spiders in respect to habitat characteristics, (iii) describe spider functional groups, community structure and similarity between habitats in the study area, and (iv) discuss these results in light of improving invertebrate research and conservation in Tanzania and across the region.

MATERIALS AND METHODS

Study area and sites

The study area is located at Sokoine University of Agriculture (SUA)in Morogoro municipality (37° 39'E, 6° 51'S) at the northern foot of the Uluguru

Mountains, Tanzania. The vegetation is dominated by stands of both fruit and non-fruit trees planted for various purposes including research, teaching and shelter (Rija *et al.* 2013). The original vegetation was miombo woodland, however due to human activities only a few patches of natural vegetation remain near the lower slopes of the Uluguru Mountains (Rija *et al.* 2013). This study was conducted in three sites used as experimental study fields of SUA. The sites are Botanical garden (B), Bushed-grassland (Bg) and Horticulture garden (H). Each study site measures at least 2 hectares in size. The Botanical garden is characterized by planted trees such as *Ficus* spp., *Senna* spp., *Milicia* spp., *Albizia* spp., *Khaya* spp. and *Azadirachta indica.* The Bushed-grassland site forms part of the grazing area for domestic herbivores managed by the Department of Animal Science and Production at SUA. The prominent grass species include star grass (*Cynodondactylon)* and herbaceous forage legumes such as *Trichanthera gigantean.* This site is also occupied by some planted non-indigenous trees (e.g. *Senna* spp., *Khaya* spp.) as well as native trees species such as *Makhamia* spp. The site is frequently used for grazing cows, goats and horses. This study was conducted during rainy season when the livestock are excluded to allow grasses to grow to a harvestable size for hay making. The Horticulture garden site comprises a stand of various fruit trees such as *Mangifera indica, Citrus* spp. and *Persea americana* planted and managed for horticultural field experiments. The garden is exposed to farm practices, including irrigation, fertilization, pruning and weeding, as well as pesticide application.

DATA COLLECTION

Sampling of spiders

Spiders were sampled for fourteen days between March and April, 2011 using a combination of three sampling methods: pitfall trapping, sweep netting, and active searching. Multiple approaches were used in order to facilitate collection of the maximum number of species available in the study area (Hore and Uniyal 2008). Pitfall traps consisted of cylindrical plastic bottles measuring 10 cm in diameter opening and 16 cm in depth. A total of 80 pitfall traps was used, with at least 25 pitfall traps at each sampling site. The traps were placed randomly at least 10 m apart, covering at least 10% of the study area, and were inserted into the ground quarter-filled with water and detergent to prevent escape of trapped individuals. Trapped spiders were collected each day and preserved in small glass bottles filled with 70% ethanol (Warui *et al.* 2005). Furthermore, 35 cm diameter sweep nets were used to collect grass and herbal layer spiders at the three sites. Sweep netting involved three researchers, each disturbing grass with sticks (at least 1.5 m long) followed by ten sweeps upon pacing and allowing at least twenty paces between sweeps after three minutes of resting. For each successful sweep, the collection was emptied into a 10-litre plastic bucket half-filled with water to prevent spiders from escaping. Sweeping was conducted for a total of 27 sweeping hours at each site. After the sweeping, all specimens were sorted and stored in glass bottles with 70% ethanol for identification in the laboratory. Additionally, active searching was conducted at all sites following standard procedure (Hore and Uniyal 2008).At each site, search for spiders in standing vegetation and dry grass on the ground was done for two hours at a time for a total of24 searching hours.

Sampling of habitat parameters

To gain knowledge of the influence of habitat attributes on spider abundance and diversity, tree shade, herbaceous cover and ground litter cover across the three study sites were measured (Costello *et al.* 1998). Habitat variables were sampled in 50 cm x 50 cm plots located at1 m intervals along each of two 100 m transects(McDonald 2007) laid at each site, and percentage grass and herb (herbaceous) and ground litter cover estimated independently by two researchers. Ground litter included all dead organic material lying on the ground, but excluded standing dead vegetation within the sampled plot. Shading was estimated as the percentage of canopy cover observed over each sampling plot.

Spider identification and analysis

The collection was sorted into groups according to habitat and sampling method and transferred into 70% ethanol. All adult and juvenile specimens were identified, mostly to family level and to genus or species level where possible. Spiders were identified using morphological characteristics such as somatic features, epigynes, number and patterns of eye arrangement and colour patterns, using identification keys for Afro-tropical spiders (Dippenaar-Schoeman and Jocque´ 1997; Jocque´ 2006) as well as using colour plated spider identification guide books (Holm and Dippenaar-Schoeman 2010; Dippenar-Schoeman and Van den Berg 2010). Spider identification was carried out by the first and second authors. Voucher specimens are being housed in the Zoology laboratory at Sokoine University of Agriculture.

Differences in spider abundance (the total number of spiders collected per site) between sites and between sampling methods were analysed using Kruskal-Wallis tests. One-way ANOVA with Sidak post-hoc multiple comparison test was used to test for differences in habitat characteristics (tree shade, herbaceous cover and ground litter cover) between the study sites after conforming to normality and homogeneity variance assumptions (Kolmogorov-Smirnov test $p >$ 0.05).Abundance of spiders in different functional diversity groups (web builders, ground wanderers and plant wanderers) between study sites was also compared using Kruskal-Wallis tests. To understand the relationship between habitat characteristics and spider functional group, Pearsoncorrelation tests was used for this analysis.To explore spider family diversity and richness across the study sites we used program PRIMER v6 (Clarke and Warwick 2001; Clarke and Gorley 2006) to calculate Shannon diversity and Simpson’s indices. Chao 1 estimator was used to obtain family richness. Furthermore, spider community structure in the study area was examined using cluster analysis. A dendrogram was plotted for different spider families and functional groups based on a Bray-Curtis similarity matrix of grouped variables on pooled data. This was performed after square-root transformation of the data to down weight high abundance genera and families (Clarke and Warwick 2001). A similarity profile permutation test was also performed to determine if there was statistically significant evidence for genuine clustering on a pooled sample (Clarke and Gorley 2006). Similarity in spiders (species and families) between any three sites was examined using Sørensen’s Quotient of Similarity (Maguran2004) using equation 1:

SQ = 2P/i + j;…………………………………………………………………………………….(1)

Where i and j are the number of species or families collected at each site and P is the total number of spiders from three sites.

Further, a multiple-site similarity measure (Diserud and Ødegaard 2007) was used to examine species and family similarity across the three sites. The measure is expressed as per equation 2:

(3/2)[(ab +ac + bc –abc)/a + b + c)]…………………………………................................ (2)

where a, b, and c are the species/families found in sites A, B and C, whereas ab is the species/families shared between sites A and B etc., and abc is the species/families found in all three sites.

RESULTS

Composition, abundance and distribution of spiders

The study recorded948 individual specimens represented by 24 Families in 34 genera (Table 1). Overall, spider abundance was not statistically different between sites (Kruskal Wallis χ^2 = 1.01; df = 2; p = 0.79). *Steatoda capensis* was the most abundant species at Horticulture garden (n = 170) as well as the most dominant across the study area (Simpson index = 0.71). Several species, including *Nephila* spp., *Thelechoris longipes,* Hepactira spp., and *Synema imitator* were among the least abundant (n = 1) each occurring at only one site. Species dominance was not statistically different between sites (Kruskal Wallis χ^2 = 0.929; df = 2; median dominance = 0.74, p = 0.819). Seven species (15.9%) were singletons collected at Horticulture (3 species), Bushed-grassland (3 species), and Botanical garden (1 species). Five (11.4%) were doubletons collected from the Botanical garden (1 species), Horticulture (2 species) and Bushed-grassland (2 species). Moreover, there was no significant difference in the median number of spiders collected using each of the sampling methods (Kruskal Wallis χ^2 = 2.409; median = 2.0, df = 2; p = 0.492). Active searching was relatively effective in collecting a large number of spider families (n = 22) from all study sites followed by pitfall trapping (n = 14) and sweep netting (n = 9).At the family level, Salticidae was the numerically most abundant family while Dipluridae and Scytodidae were least represented (Table 1). Furthermore, seven families (Theridiidae, Salticidae, Prodidomidae, Oxyopidae, Pisauridae, Thomisidae and Corinnidae) were present at all three sites while five families (Theraphosidae, Phyxelidae, Dipluridae, Sparassidae and Scytodidae) were found at one site only (Table 1).

Table 1: Spider families and their respective abundances, per sampling method in the three sites of the study area: B= Botanical garden, Bg = Bushed-grassland, H = Horticultural garden. The sampling methods: P = pitfall trap, A = active searching, S = sweep netting.

Study site and collection method										
Spider family	**BP**	**BA**	**BS**	**BgP**	**BgA**	**BgS**	**HP**	**HA**	**HS**	**Total per family**
Theridiidae	29	13		50	7		170			269
Prodidomidae	38			28			14			80
Salticidae	42	15	54	90	8	14	45	3	1	272
Gnaphosidae				3	1		2			6
Araneidae					2	1	2	1		6
Clubionidae			2					2		4
Oxyopidae	34	4	11	17	27	2	1	1	2	99
Pisauridae	8			29			6	18		60
Thomisidae		4	1	1	20	3	1	2	1	33
Miturgidae			1	1	2					4
Philodromidae	18			13						31
Lycosidae	1	1	1	1	14			7	4	29
Caponiidae				5				6		11
Pholcidae				1				2		3
Corinnidae		1		1	2			9		13
Theraphosidae								2		2
Phyxelidae								5		5
Palpimanidae		2						1		3
Zodaridae		7						1		8
Tetragnathidae		1	1		1					3
Nephilidae			1		2					3
Dipluridae		1								1
Sparassidae		2								2
Scytodidae					1					1
Spider subtotals	170	51	72	239	87	20	241	60	8	
Total number of spiders			**948**							

Spider diversity, richness and evenness in respect to habitat characteristics

Tree shade was significantly (F = 86.2; df = 2; p = 0.001) different between three habitats. Post-hoc tests showed significantly (mean = 16.43, SE 4.56; p = 0.001)higher mean percentage shade atBushed-grasslandthan Botanical garden and high percentage shade at Bushed-grassland than Horticulture garden (mean = 14.97, SE 3.96; p = 0.001). Herbaceous cover was significantly (F = 51.39; df = 2; p = 0.001) higher at Botanic garden than the other sites. Mean ground litter cover was significantly higher at Horticulture garden than the other sites (F = 47.07; df = 2; p = 0.001) and lowest at Bushed-grassland. Shannon diversity index for spider families was highest (H’ = 1.740) at Bushed-grassland habitat followed by the Botanical garden (H’ = 1.526) and lowest at Horticulture garden (H’ = 1.305). No significant (F = 0.169; df = 2; p = 0.915) difference in family diversity was observed between the sites. Furthermore, family richness was highest at the Bushed-grassland (J’ = 2.157) followed by Horticulture garden (J’ = 1.742) and lowest at Botanic garden (J’ = 1.548). On the other hand, family evenness was higher at the Bushed-grassland (d = 0.803), followed by Botanic garden (d = 0.712) and low at Horticulture garden (d = 0.664).

However, neither family richness nor evenness was statistically ([richness: F= 0.184; df = 2; p = 0.905]; [evenness: F = 0.266; df = 2; p = 0.849]) different across the study sites. Furthermore, there was no significant ($p > 0.05$) correlation between family diversity and tree shading or between family diversity and herbaceous cover. Also, there was no significant ($p > 0.05$) relationship between richness or evenness and these habitat variables. Pitfall traps were most efficient in collecting a high diversity (H' = 2.23) of spiders at theBushed-grasslandsite while active searching was most effective (H' = 2.44) at Horticulture garden and Botanical garden (H' = 2.47).

Functional diversity of spiders, community structure and similarity between sites

The collection consisted of three main functional groups based on habitat use: web builders, ground wanderers and plant wanderers. Ground wanderers included flat-bellied ground spiders (Gnaphosidae), wolf spiders (Lycosidae), spitting spiders (Scytodidae), ant-eating spiders (Zodariidae), palp-footed spiders (Palpimanidae), pale ground spiders (Prodidomidae), ant-like sac spiders (Corinnidae), orange lungless spiders (Caponiidae) and baboon spiders (Theraphosidae). This group contributed least to the total number of individual specimens (16.4%, n = 157). Plant wanderers were the most abundant group (n = 509) constituting 53.02% of the total collection. The plant wanderers included jumping spiders (Salticidae), nursery web spiders (Pisauridae), small huntsman spiders (Philodromidae), sac spiders (Miturgidae), grass lynx spiders (Oxyopidae), crab spiders (Thomisidae), grass huntsman spiders (Sparassidae) and shortlegged sac spiders (Clubionidae). Web builders comprised seven families including Araneidae, Theridiidae, Nephilidae, Phyxelidae, Dipluridae, Pholcidae and Tetragnathidae. Overall, spider abundances were not significantly (F = 0.779, df = 2, p = 0.472) different between the functional groups. Analysis of within-group variation between the sampling sites showed no difference in group abundance for the web builders (Kruskal Wallis χ^2 = 1.244; df = 2; p = 0.742), ground wanderers (F = 0.310, df = 2, p = 0.818) or plant wanderers (F = 0.454, df = 2, p = 716).Furthermore, the family level analysis revealed six main spider clusters. There was statistically significant (Pi = 48.23%; p = 0.1%) clustering between the different spider families on the far left of the dendrogram and between families on the far right (Pi = 20.26%; p = 0.1%(Figure 1). These groups were composed of species employing various hunting strategies. The similarity profile test showed distinct internal structuring (Pi = 2.59, p = 0.1%) among some groups of spiders. Comparisons between any two sites and across the study area (Table 2) show high species and family overlap.

Table 2. Similarity indices (Sorensen index and Diserud-Ødegaard multiple-site similarity index: asterisked) for species and families between habitats/sites showing high overlap between two sites, and across the sampled area.

Study sites	Similarity index		
Species level similarity	Botanic garden	Bushed-grassland	Horticultural garden
Botanic garden		0.545	0.545
Bushed grassland			
Horticultural garden		0.590	
Across sites*			**0.643**
Family level similarity			
Botanic garden		0.647	0.647
Bushed grassland			
Horticultural garden		0.705	
Across sites*			**0.764**

DISCUSSION

To the knowledge of the authors, this is the first study to inventory spider communities in human-dominated areas in Tanzania and is among the few spider studies undertaken in the country to date. As there are no species lists available for most areas in Tanzania, it is difficult to ascertain what proportion of the species richness this study recorded relative to the species total at a country level. Consequently, the study employed different sampling methods to account for the deficiencies of any one method and to provide as much information as possible from the study area. There was no difference in local abundances of spiders between sites. Despite some differences in the local habitat variables measured, it is likely that spider abundance could have been influenced by the local human activities conducted such as grazing animals and pruning in the study sites. This finding is consistent to observations by Warui *et al.* (2005) who documented that spider communities in Kenyan savanna biome was highly influenced by the grazing animals. Some genera were more abundant at the horticultural garden site due perhaps to some other habitat characteristics that may have contributed to their foraging and reproductive success. Supporting this argument, Samu *et al.* (1999) found that spider abundance and diversity were positively and variably correlated with environmental diversity such as microclimate, disturbance and habitat in agricultural ecosystems. Furthermore, the horticultural garden site supported the highest number of jumping spiders (Salticidae) and had more decaying litter and various habitat patches, including grasses and shrubs, than the other study sites. Such variables have been observed to influence local abundances and spider diversity (Rija *et al.* 2012; Hore and Uniyal 2008; Moretti *et al.* 2002). The number of specimens collected was influenced by the method employed, active searching overall providing the highest number of spiders. Similar results have been documented elsewhere whereby active searching was more effective than other collecting methods (Haddad and Russel-Smith 2009; Hore and Uniyal 2008). The distribution of spiders was random, with some families or genera only being collected once or twice at particular sites. These families may not necessarily be rare but rather, may consist of cryptic species or species that have a patchy distribution, and thus may have not been adequately sampled. On the other hand, the botanical garden site is separated from the bushed-grassland site by a road while the horticultural site is relatively isolated as it is approximately 0.5 km away from the other sites. With many human activities taking place between the sites, it may not be possible for spiders to disperse from one site to the other(Hore and Uniyal 2008). These physical barriers could explain why five species/genera were observed only at the horticultural site. Elsewhere, habitat connectivity and aerial dispersal ability have been observed as influencing the ability of spiders to move between habitat patches (Bonte *et al.* 2004).

Interestingly, richness and diversity of the spiders were high compared to the published values from other areas in Tanzania. More than half of the spider families collected in the larger Mkomazi National Park (Haddad and Russel-Smith 2009; 54 in Mkomazi compared to 34 families in this study) were also found in the SUA study fields. Although some spider families were over-represented at the Horticultural site (e.g. Salticidae), family richness and diversity were higher overall at the Bushed-grassland than at other sites. This may be due to the heterogeneous nature of this habitat characterized by grasslands, bushes and a mix of natural and exotic trees, which likely provides numerous microhabitats that support more spider families relative to the other sites. Habitat structure and complexity have been observed to correlate strongly with spider biodiversity (McDonald 2007; Hore and Uniyal 2008). On the other hand, the dominance of one family at the horticultural site may suggest that the area provides limited resources that may not favour colonization by other species. Salticidae is a common family recorded in many other studies across Africa, and inhabits various habitat ranging from montane forests to lowland savanna areas and is found in natural and human-dominated landscapes (Haddad and Russel-Smith 2009; Sørensen 2004; this study).

Spiders grouped into three main functional guilds with most of the taxa exhibiting a plant-wandering mode of life. This was not surprising given the complex vegetation structure of the study area that appears to support more foliage dwelling spider assemblages (Churchill and Ludwig 2004). The web-building communities were least represented in the study area, probably because of disturbances of human activities occurring in the study areas such as cattle grazing, mowing, and gardening. These disturbances reduce habitat suitability for the highly disturbance-sensitive orb weavers *Araneae* (Tsai *et al.* 2006) as they remove patch structures on which spiders attach their webs. This has been shown in Kenyan savanna biome, where Warui *et al.* (2005) reported negative influence of grazing wildlife on the abundance of web-building spiders. This suggests that human activities in urban landscapes can have far-reaching effects on the community assemblages of spiders, including the survival of some species. Cluster analysis revealed another interesting pattern whereby several different genera/families clustered together (Figure1). The clusters consisted of a large diversity of functional groups, each comprising web builders, plant wanderers and ground wanderers in a unique assemblage; and with individual species having various feeding and hunting strategies. Such diversity within assemblages is perhaps necessary to avoiding competition between relatively similar species, especially in species-rich communities such as spiders.

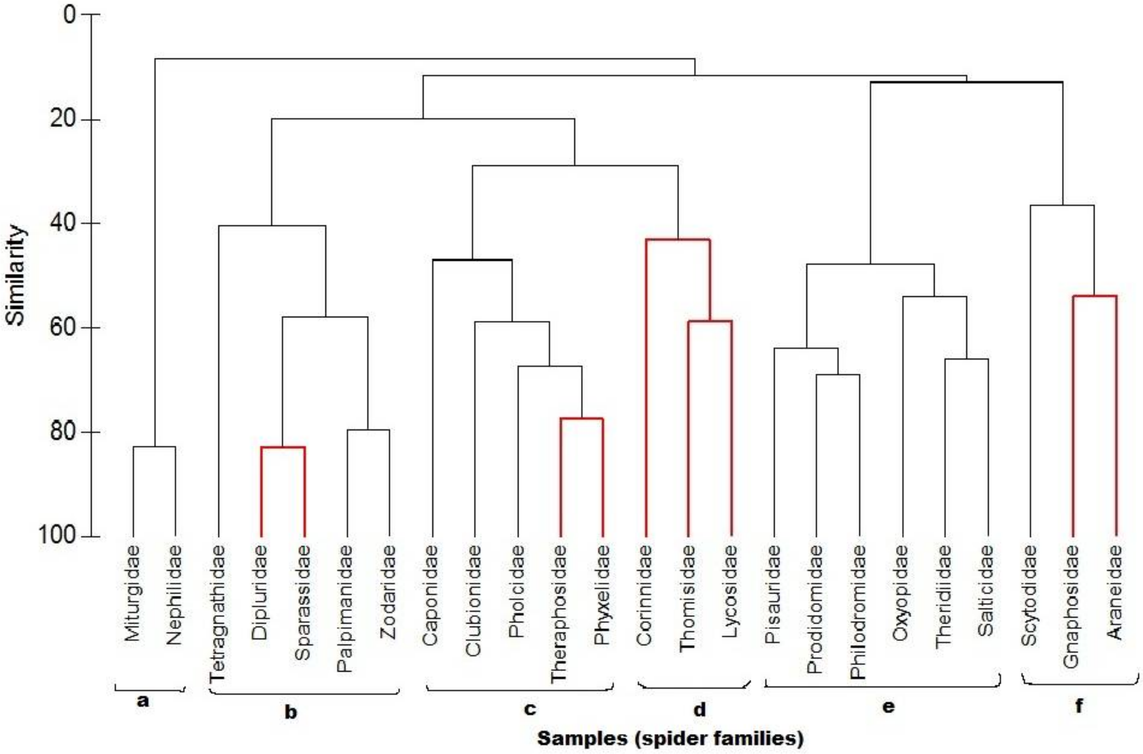

Figure 1. Dendrogram for the spider families collected in the study area based on Bray-Curtis similarity on the pooled data indicating six natural groupings (a-f) of spider families. The groups (a-f) indicate co-occurrence of spiders of different modes of feeding and habitat use in the study area.

CONCLUSION AND RECOMMENDATIONS

This work has demonstrated the importance of the study area for the spider communities. While revealing the natural history of this area, we also highlight the urgent need for further research on this subject. Taxonomic expertise has been a persistent challenge that needs to be addressed not only in Tanzania, but also across Africa and worldwide. As most urban and rural areas continue to develop, we envisage potential increasing loss of the spider habitats. As this study shows, human activities conducted in the study area may already have affected local richness and diversity of some web-building spiders. It is still not clear how potential decline in spider population may cascade on higher trophic level taxa such as birds which feed on spiders, and how this may in turn affect insect pests eaten by the spiders in the urban ecosystems. Future studies investigating how spider densities change across development gradients would increase our understanding of this predatory taxon and may help inform appropriate biodiversity conservation measures in urban ecosystems.

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