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Impact of waste from the municipal slaughterhouse in Nkongsamba on plant diversity (Littoral-Cameroon)

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ABSTRACT

Waste management in Cameroonian cities remains a major concern. This study aims to assess the impact of untreated waste from the municipal slaughterhouse in Nkongsamba (Barehock) on vegetation. To achieve this objective, a floristic inventory of the different study sites (upstream, near the slaughterhouse, downstream) was carried out based on surface surveys combined with itinerant surveys. Twenty-five square plots of 100 m² were spread out on each site, following the four cardinal points. Indeed, the inventories generated a floristic list of 105 species from 79 genera and 41 families. The greatest species richness was recorded at the downstream site, with 81 species from 70 genera belonging to 35 families, compared to the other sites. These results reveal a dominance of ruderal taxa and pollution bio-indicators, such as *Commelina benghalensis*, *Achyranthes aspera, Sida acuta, Tithoniadi versifolia, Echinocloa pyramidalis, Echinocloa cruis-parvonis, Brillantaisia owariensis, and Eleusine indica*, reflecting ecological disturbance of the plant environment. In addition, faeces could be recycled by using as compost, thereby promoting urban and peri-urban agriculture in Cameroonian cities threatened by food insecurity.

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INTRODUCTION

The urban population in Africa, which accounted for 40% of the total population in 1960, is expected to rise to over 60% by 2050 (Ongonkoa and Song, 2019; Tsama *et al.*, 2025). This rapid urbanisation, coupled with a population explosion, is leading to high demand in cities and the production of all kinds of waste, with harmful consequences for aesthetics and the environment. Indeed, waste production is mainly due to human activities, whether domestic, agricultural, industrial or commercial (Ouattara *et al.*, 2022; N'gouran *et al.*, 2023; Tsama *et al.*, 2025). The treatment of liquid and solid waste such as sewage sludge, household waste, industrial waste and effluents before they are released into the environment is a major challenge for most African countries (Reounodji, 2016; N'gouran *et al.*, 2023). This challenge is more acute in developing countries, which not only suffer from a lack of capital, but are also faced with uncontrolled urbanisation and industrialisation (Reounodji, 2016). In Africa, the situation regarding wastewater disposal and treatment is dire; most of the wastewater disposal networks connected to mechanised treatment plants set up in the aftermath of independence are now non-functional, and raw wastewater is discharged into low-lying areas (Kengne *et al.*, 2009; Kone *et al.*, 2010). However, numerous studies highlight the negative consequences of poor sanitation, in terms of health, the environment and the economy. Chevalier (2002) mentions that hundreds of millions of people worldwide suffer from schistosomiasis, cholera, typhoid fever, worms responsible for various health disorders, and other infectious diseases. Indeed, waterborne diseases are the main public health problem in developing countries.

In Cameroon, most wastewater and waste from urban areas and industrial facilities is currently discharged into the natural environment without prior treatment (Kone *et al.*, 2019).

In fact, almost all wastewater treatment plants have been out of service, overloaded or abandoned for more than a decade (Mbog, 2013). As a result, all industrial facilities such as breweries, sugar refineries, and food processing plants, tanneries and slaughterhouses discharge large quantities of organic waste into watercourses without prior treatment (Kengne *et al.*, 2008). Among agro-industrial effluents, slaughterhouse waste and waste dumped on open land have been among the most damaging to the environment (Ojekunle and Lateef, 2017; Kone *et al.*, 2019). The development of slaughterhouses in developing countries rarely takes into account environmental and human hygiene needs. As a result, critical public health and environmental concerns are associated with large-scale animal slaughter (Ayoade and Olayioye, 2016); lack of access to safe drinking water (Ayoade and Olayioye, 2016); poor environmental hygiene; the purchase of animals for slaughter by individuals who may conceal defects to avoid financial losses; and non-compliance with and enforcement of laws concerning animal welfare and meat safety (Omotosho *et al.*, 2016). There are also no adequate sewage or waste disposal systems (Timothy, 2020). This leads to environmental hazards and health risks for residents living near slaughterhouses. In addition, slaughterhouse waste is usually dumped into waterways or the drains of neighbouring buildings, polluting water resources and causing odour pollution (Timothy, 2020). In some cases, this waste is piled up behind the slaughterhouse, creating fertile ground for disease vectors such as mosquitoes, rodents and other insects. Previous studies have shown that unmanaged waste can lead to water, air and soil pollution, as well as risks to public health (FAO, 2013; Leila, 2015). However, few studies to date have focused on the impact of wastewater on the flora of disposal sites. According to Savoy (2005), the biodiversity of urban cities has been recognised as an important future issue for climate change mitigation. Furthermore, the conservation of this biological diversity could improve human health in cities around the world. Unfortunately, more than 50% of known plant and animal species are believed to be negatively affected by human activities in urban areas (Mckinney and Lockwood, 1999; UN, 2012; Tsana *et al.* 2025). It is in this context that the present study aims to assess the impact of waste from the municipal slaughterhouse in Nkongsamba on the surrounding vegetation in the village of Barehock. More specifically, this study will analyse the diversity of flora in order to assess its influence on the diversity of the residual flora in the area.

MATERIALS AND METHODS

Study site

The study was conducted in the municipality of Baré-Bakem, specifically in the village of Baréhock, where the municipal slaughterhouse is located. The municipality of Baré-Bakem is located in the Moungo Division, Littoral Region of Cameroon. It covers an area of 200 km² divided into two cantons (Bareko and Bakem) with 21 villages, including Baréhock. The population of the municipality of Baré is estimated at 16,485 inhabitants, or approximately 82.42 inhabitants per km². This municipality is bordered to the north by Mélong, to the south by Nkongsamba II, to the east by the Nkam River, and to the west by Nkongsamba II and Nkongsamba I. The town of Baré is located approximately 120 km from Douala (regional capital) and approximately 10 km from Nkongsamba (capital of the Moungo Division). This area is characterised by an equatorial climate with two distinct seasons: a rainy season from March to October and a dry season from November to February. The soil is volcanic and black in colour in places and is used for peri-urban agriculture, with 40% devoted to food and vegetable production. The soils are generally rugged, consisting of hills, plateaus, lowlands and valleys.

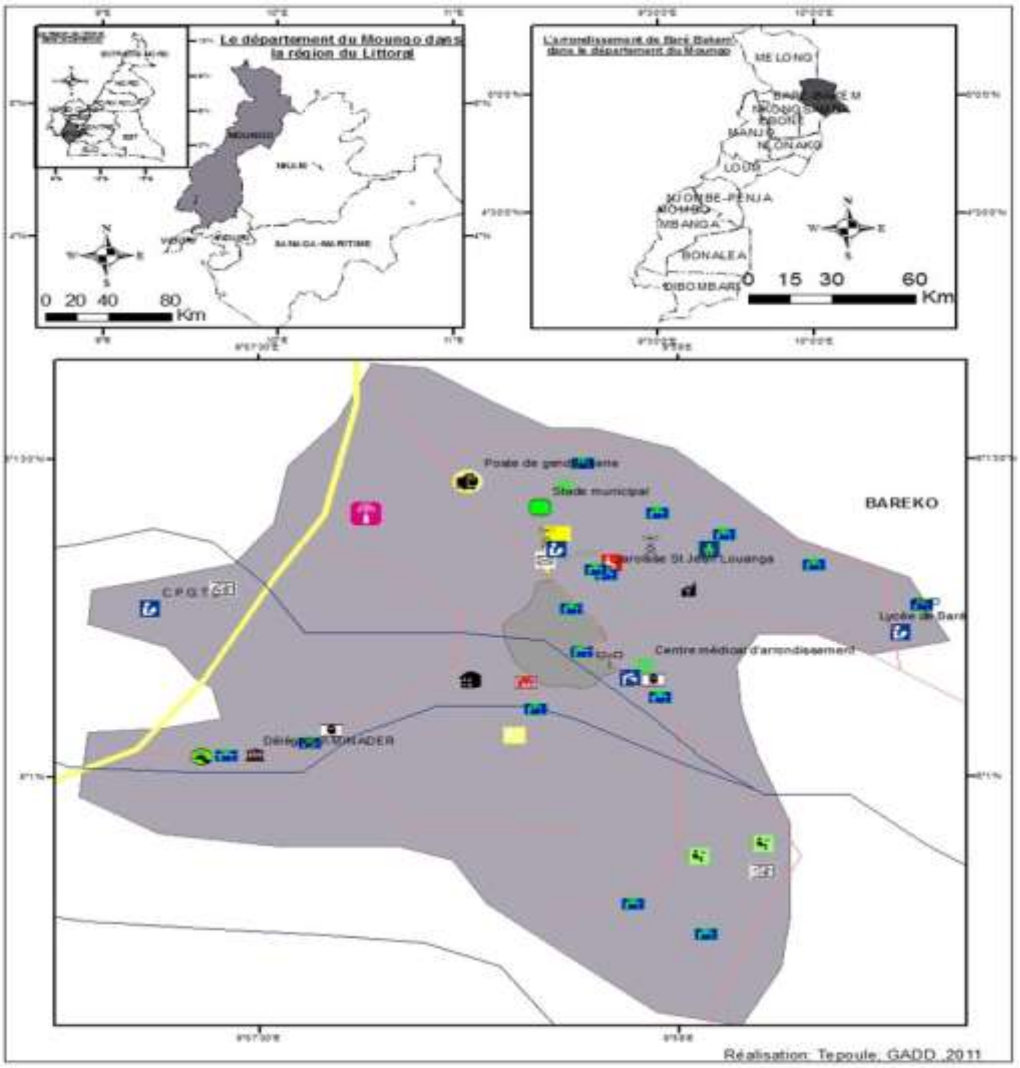


Fig. 1. Location of study area (PCD, 2021)

Data collection

To better assess the impact of slaughterhouse discharges on flora, transects were carried out upstream, downstream of the slaughterhouse and in the discharge area. The floristic inventory at each site was carried out using surface surveys combined with itinerant surveys (N'gouran *et al.*, 2023; Tsama *et al.*, 2025). A total of 25 square plots (10 m x 10 m) were laid out, including 9 upstream, 4 in the discharge area and 12 downstream. Each plot was subdivided into 25 sub-plots measuring 2 m x 2 m; Five sub-plots were selected at random without replacement to record the number of times each species appeared on the sub-plots (2 m x 2 m) (Fig. 2). In each Phytodiversity plots of 4 m², the surface inventory consisted of collecting all species. The itinerant survey consisted of walking through the 100 m² plots to complete the list of plant species inventoried at the various study sites (N'gouran *et al.*, 2023; Tsama *et al.*, 2025). This choice allowed us to compare the plant diversity of the three sites and note the presence of taxa. Species identification was done directly in the field by the assistance of a plant botanist who had knowledge in identifying plant species of the area using common identification criteria such as leaf type and arrangement, trunk and morphology. Unidentified plant species were harvested, labelled and pressed, then preserved in 70° alcohol and taken to be compared with those of the National herbarium in Yaounde, Cameroon for further identification.

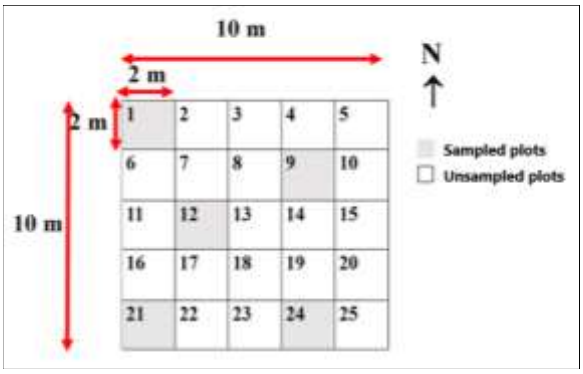


Fig. 2. Sampling device for the plots (N'gouran *et al.,* 2023).

Data processing and analysis

With regard to the analysis of floristic data, the number of species and families of all plant species encountered during inventories at the study sites were determined. Floristic richness was counted at the various sites sampled. It corresponds to the total number of species recorded at the sites, without taking into account their frequency or relative abundance. Species richness was determined by tallying all species inventoried (Yap *et al.*, 2016). Specific diversity of the area was described using the following indices: These are the relative frequency of species (Fr), the Shannon diversity index (H') and the Piélou equitability index (E).

Relative frequency

Relative frequency indicates the preferences of an environment for a given taxon. It consists of counting the number of times taxon i appears in the plots (Dajoz, 2000). The ratio is expressed as a percentage of the number of plots where the taxon is present over the total number of plots (Hyslop, 1980). It was obtained from the following equation:

$Fr = ni/n \times 100$; Fr being the relative frequency, ni the number of surveys in which species i is present, and n the total number of surveys. Depending on the value of Fr, three groups of taxa can be distinguished: dominant taxa with Fr > 50%, secondary taxa with 25% < Fr ≤ 50%, and finally rare taxa with Fr ≤ 25%.

Shannon diversity index

Shannon and Wiener diversity index, which measures the uncertainty as regards an individual taken at random belonging to a species in the sample unit. This index is well suited to comparative studies of populations because it is relatively independent of sample size. It increases with an increase in diversity and is calculated by using the formula: $H' = -\sum (ni/N) \, Log2 \, (ni/N)$, where ni is the number of species i and N the total number of species (Shannon and Wiener, 1949).

Piélou's equitability index

The evenness index is used to study the regularity of taxon distribution and to compare the diversity of two areas with different numbers of taxa. It was developed to account for the relative abundance of each taxon. Equity varies from 0 to 1 and reflects the quality of organisation of a population (Piélou, 1969). It tends towards 1 when all taxa tend to have the same abundance and towards 0 when one taxon, more resistant to environmental conditions than the others, predominates (Seou *et al.*, 2022). Pielou's equitability index, which makes it possible to measure the distribution of individuals within species, determining specific richness (Adamou, 2010). It is calculated by using the formula: Eq= H'/Hmax=H'/lnN, where Eq is Pielou's index, H= Shannon diversity index, N= total of species (Pielou, 1975).

RESULTS

Taxonomic richness of plant species

The floristic inventory at the three sites identified 105 species divided into 79 genera and 41 families. The greatest species richness was recorded at the downstream site, with 81 species from 70 genera belonging to 35 families, followed by the upstream site, with 61 species from 50 genera divided into 30 families, and finally the site near the slaughterhouse, with 47 species divided into 42 genera and 27 families. The most represented families with more than 3 species are Poaceae (12 species), Malvaceae (11 species), Asteraceae (10 species), Fabaceae (9 species), Euphorbiaceae (6 species), Acanthaceae (3 species), Amaranthaceae (3 species), Cyperaceae (3 species) and Urticaceae (3 species) (Table 1). The other families, representing 78.04% of the total number of families recorded, have 3 species. These are: Apiaceae, Araceae, Arecaceae, Commelinaceae, Convolvulaceae, Curcubitaceae, Dioscoriacaceae, Rubiaceae, Balsaminaceae, Costaceae, Marantaceae and Melastomataceae.

Table 1. List of the most represented families (at least 3 species), ranked in descending order across the entire flora studied

Families	Species
Poaceae	*Arundinaria alpina* K.Schum
	Arundinaria madagascariensis
	Brachiara sp1
	Brachiara sp2
	Brachiara sp3
	Echinochloa crus-pavonis
	Echinochloa pyramidalis
	Eleusine indica
	Panicum laxum
	Panicum sp2
	Pennisetum purpureum
	Zea mays
Malvaceae	*Abelmoschus esculentus*
	Cola nitida
	Hibiscus asper
	Hibiscus rosa-sinensis
	Hibiscus sp2
	Malvabiscus arboreus
	Sida acuta
	Sida rhombifolia L
	Theobroma cacao
	Triumfetta pentadra
	Triumfetta sp2
Asteraceae	*Ageratum conyzoides*
	Ageratum houstonianum
	Aspilia africana
	Bidens pilosa
	Chromolaena odorata
	Emilia coccinea
	Erigeron floribundus
	Tithonia diversifolia
	Vernonia amygdalina
	Vernonia sp2
Fabaceae	*Albizia adianthifolia*
	Albizia ferruginea
	Albizia zygia
	Desmodium adscendens
	Desmodium sp2
	Desmodium hirtum
	Mimosa invisa
	Mimosa pudica
	Phaseolus vulgaris
Euphorbiaceae	*Alchornea cordifolia*
	Bridelia micrantha
	Euphorbia hirta
	Macaranga assas
	Macaranga monodora Müll.Arg
	Manihot esculenta
Acanthaceae	*Brillantaisia owariensis* P. Beauv
	Eremomastax speciosa
	Sanchezia sp
Amaranthaceae	*Achyranthes aspera* L
	Amaranthus hibridus
	Amaranthus spinosus
Cyperaceae	*Cyperus iria*
	Cyperus ligularis
	Cyperus rotundus
Urticaceae	*Laportea aestuans* (L.) Chew
	Musanga cercropioides
	Myrianthus arboreus

Furthermore, these results revealed that 30 species, or 28.57% of the total number of species inventoried, are common to all three sites. These include *Brillantaisia owariensis* P. Beauv, *Achyranthes aspera* L, *Eryngium foetidum, Ageratum conyzoides, Cassia mimosoides* Linn, *Tithonia diversifolia, Commelina benghalensis, Costus afer, Cyperus rotundus, Macaranga assas, Sida acuta, Ludwigia abyssinica, Piper umbellatum,* and *Solanum torvum.*

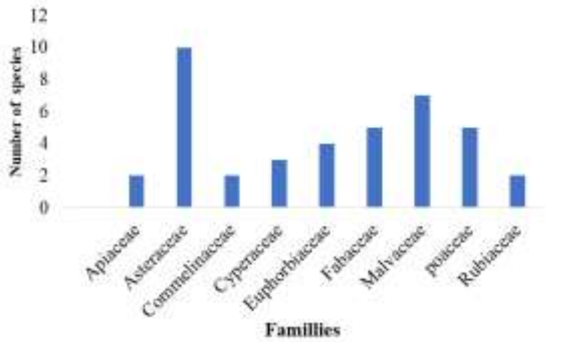


Fig. 3. Distribution of the most represented families (at least 3 species) upstream of the slaughterhouse

Distribution of species and families upstream of the slaughterhouse

Upstream of the slaughterhouse, 61 species from 50 genera divided into 30 families were identified (Fig. 3). The characteristic families in this area are Asteraceae, Malvaceae, Fabaceae, Poaceae, Euphorbiaceae and Cyperaceae, with at least three species each. The other families (25), representing 83.33% of the total families recorded at the site, have fewer than 3 species. These are: Apiaceae, Commelinaceae, Rubiaceae, Acanthaceae, Amaranthaceae, Curcubitaceae, Convolvulaceae, Costaceae and Dioscoriaceae.

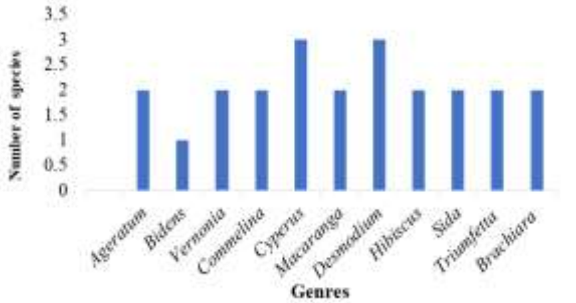


Fig. 4. Distribution of the diversity of genera encountered upstream of the slaughterhouse

Generic diversity of genera

Analysis of the various inventories in this area shows that two genera (representing 3.14% of the total number of genera) have more than two species for all individuals recorded at the site (Fig. 4). These are the genera *Cyperus* and *Desmodium*. Eight genera, or 15.38% of the genera recorded in the area, have two species. These are the genera *Ageratum, Commelina, Dioscorea, Macaranga, Hibiscus, Vernonia, Mimosa*, and *Brachiara*. The other genera (98.42%) have only one species, including the genera *Chromolaena, Mimosa, Echninochloa, Eleusine, Eremomastax, Eryngium, Dracaena, Dioscorea, Brillantaisia, Panicum, Solanum, Ludwigia Raphia, Asplenium, Aspilia and Alchornea*.

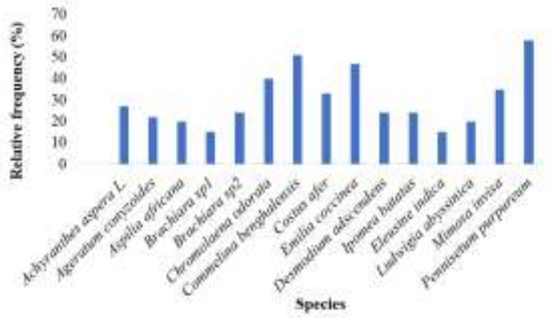


Fig. 5. Distribution of the relative frequency of species identified upstream of the slaughterhouse

Relative frequency by species

Fig. 5 shows the frequency of species recorded upstream of the slaughterhouse. Of the 61 species, three species, or 1.23% of the total, have a relative frequency of between 40 and 60%. These are *Pennisetum purpureum, Commelina benghalensis, Emilia coccinea* and *Chromolaena odorata*. Seven species, or 11.47%, have a relative frequency between 20 and 40%. These are *Achyranthes aspera* L., *Mimosa invisa, Costus afer, Desmodium ascendens, Ipomea batatas, Brachiara* sp2, and *Ageratum conyzoides*. The remaining species (87.3%) have a low relative frequency (< 20%). These *include Coffea arabica, Colocasia esculenta, Cyperus ligularis, Cyperus rodontus, Echinochloa crus-pavonis, Dioscorea alata, Eryngium foetidum, Emilia coccinea, Hibiscus asper, Erigeron floribundus, Sida rhombifolia* L, *Sida acuta, Pteridium aquilinum, Psychotria pedoncularis, Psidium guajava, Piper umbellatum, Panicum laxum, Mimosa invisa, Macaranga monodora* Müll. Arg, *Macaranga assas* and *Ludwigia abyssinica*.

Distribution of species and families at the slaughterhouse

At the site near to the slaughterhouse (discharge area), 47 species divided into 42 genera and 27 families were identified (Fig. 6). The characteristic families of this site are represented by Poaceae, Asteraceae, and Euphorbiaceae, with at least three species. The other families, representing 88.88% of the families present, have fewer than three species. These are Acanthaceae, Amaranthaceae, Fabaceae, Araceae, Cyperaceae and Moraceae.

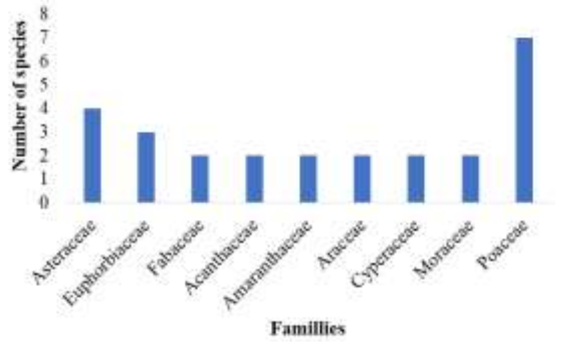


Fig. 6. Distribution of the most represented families (at least 3 species) at the slaughterhouse

Generic diversity of genera around the slaughterhouse

Analysis of the various surveys shows that two genera (representing 4.87% of the total number of genera) have a relative abundance of 2% for all individuals recorded at the site (Fig. 7). These are the genera *Cyperus* and *Ficus*. The other genera (95.13%) have a relatively low relative abundance (<1.5%), including the genera *Chromolaena, Mimosa, Echninochloa, Eleusine, Eremomastax, Eryngium, Dracaena, Dioscorea, Brachiara, Brillantaisia* and *Ludwigia*.

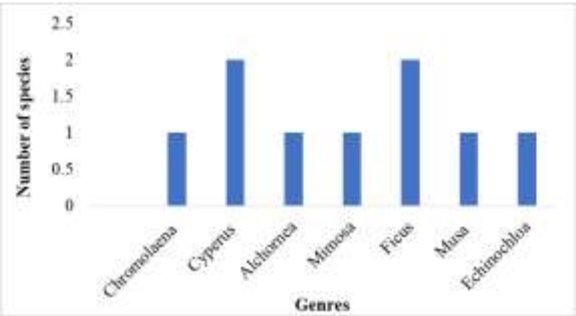


Fig. 7. Distribution of the diversity of genera encountered at the slaughterhouse

Distribution of relative frequency by species

The relative frequency of species provides an overview of the spatial distribution of species. Of the 47 species, one species (*Commelina benghalensis*), representing 2.12% of the total number of species, has a relative frequency of 60% (Fig. 8). Eight species, or 10.63%, have a relative frequency between 30 and 50%. These are *Achyranthes aspera, Sida acuta, Tithonia diversifolia, Ipomea batatas, Costus afer, Musa paradisiaca, Eleusine indica* and *Brachiara* sp1. The other species (83.1%) have a low relative frequency (less than 20%).

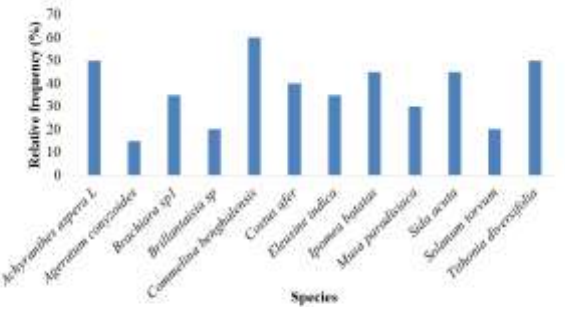
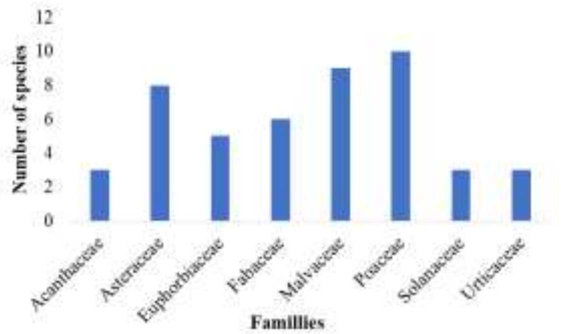


Fig. 8. Distribution of the relative frequency of species identified at the slaughterhouse

These include *Chromolaena odorata, Coffea arabica, Colocasia esculenta, Cyperus ligularis, Cyperus rodontus, Echinochloa crus-pavonis, Dioscorea alata, Eryngium foetidum, Ludwigia* sp, *Megaphrynium macrostachium* and *Pennisetum purpureum.*

Distribution of species and families at the site downstream of the slaughterhouse

The surveys include a total of 81 species distributed across 70 genera and 35 families. Among these families, 14 have at least 3 species. Fig. 9 shows the distribution of the most represented families according to species. The families characteristic of this area are represented by Poaceae, Asteraceae, Euphorbiaceae, Fabaceae, Malvaceae, Solanaceae, and Urticaceae, with at least three species each. The other families (26), representing 74.28% of the total families recorded on the site, have fewer than three species. These are the Phyllantaceae, Aspleniaceae, Acanthaceae, Caricaceae, Araceae, Solanaceae, Malvaceae, Costaceae, Melastomataceae and Dioscoriaceae.



Figy. 9. Distribution of the most represented families (at least 3 species) at the downstream of the slaughterhouse

Generic diversity of genera downstream from the slaughterhouse

Analysis of the various surveys shows that two genera (representing 2.87% of the total number of genera) have more than two species for all individuals recorded at the site (Fig. 10). These are the genera *Hibiscus* and *Brachiaria*. Eleven genera, or 15.71% of the genera recorded in the area, have at least two species. These are the genera *Ageratum, Ipomea, Cyperus, Dioscorea, Macaranga, Albizia, Desmodium, Mimosa, Panicum, Solanum* and *Ludwigia*. The other genera (98.42%) have only one species, including the genera *Chromolaena, Mimosa, Echninochloa, Eleusine, Eremomastax, Eryngium, Dracaena, Dioscorea, Brachiara, Brillantaisia, Ludwigia, Raphia, Asplenium* and *Aspilia*.

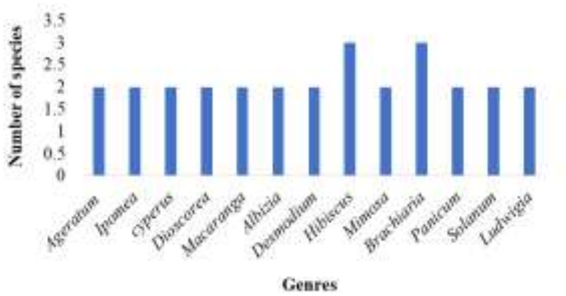


Fig. 10. Distribution of the diversity of genera encountered at the downstream of the slaughterhouse

Distribution of relative frequency of species in the downstream of the slaughterhouse

Fig. 11 shows the relative frequency of species recorded downstream of the slaughterhouse. Of the 81 species, one species (*Commelina benghalensis*), representing 1.23% of the total number of species, has a relative frequency of 60%. Four species, or 4.94%, have a relative frequency of between 30% and 40%. These are *Achyranthes aspera, Ageratum conyzoides, Pennisetum purpureum* and *Ipomea batatas*. The other species (94%) have a low relative frequency (<30%). These include *Chromolaena odorata, Coffea arabica, Colocasia esculenta, Cyperus ligularis, Cyperus rodontus, Echinochloa crus-pavonis, Dioscoreaalata, Eryngiumfoetidum, Ludwigia* sp, *Megaphrynium macrostachium, Sida acuta, Tithonia diversifolia, Ipomea batatas, Costus afer, Musa paradisiaca, Eleusine indica and Brachiara* sp1. *Brillantaisia owariensis* and *Pennisetum purpureum.*

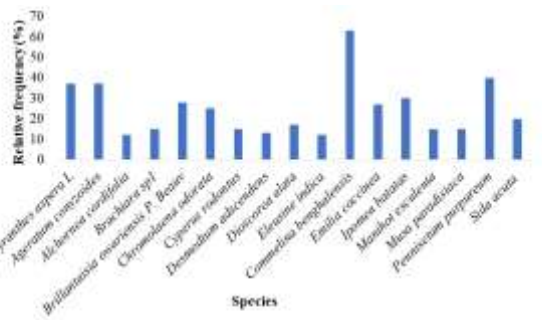


Fig. 11. Distribution of the relative frequency of species identified at the downstream of the slaughterhouse

Quantitative diversity of flora and vegetation structure

Table 2 shows the Shannon (H') and Piélou diversity index values for the three study sites. The results show that the Shannon diversity index values range from 1.7 to 1.84. As for the Piélou evenness index for the three sites, the values show an evenness of the plant community with values ranging from 0.90 to 0.94.

Table 2. Shannon diversity and Piélou evenness indices

	Shannon diversity	Piélou's equitability
Upstream	1,7	0,9
Discharge area	1,8	0,9
Downstream	1,84	0,94

DISCUSSION

The floristic inventory at the various sites identified 105 species divided into 79 genera and 41 families. The greatest species richness was recorded downstream from the slaughterhouse, with 81 species, and the lowest around the slaughterhouse (41 species recorded). The low species richness observed at the slaughterhouse would indicate an alteration of the environment caused by soil and water contamination from slaughterhouse waste. This result is consistent with those of Fonkou (1996 and 2006), who showed that highly polluted swamps contain few macrophyte species compared to those that are less polluted. N'Gouran *et al.* (2023) found that certain species cannot tolerate high organic content; an increase in nutrients and certain toxic substances would lead to the disappearance of sensitive species.

The slaughterhouse site is characterised by obligate hydrophytes species such as *Eleusine indica* and facultative hydrophytes that grow on dry land (*Pennisetum purpureum, Echinochloa pyramidalis, Alchornea cordifolia*) and plants with high organic matter absorption capacities (*Thithonia diversifolia, Brillantaisia* sp). These are also species characteristic of riverbanks. Tita *et al.* (2008) showed that *Thithonia diversifolia, Pennisetum pupureum*, and *Chromaelaena odorata* were abundant in fragments of the Nkoup River in Foumbot. Furthermore, the most represented families with more than three species are Poaceae (12 species), Malvaceae (11 species), Asteraceae (10 species), Fabaceae (9 species), Euphorbiaceae (6 species), Acanthaceae (3 species), Amaranthaceae (3 species), Cyperaceae (3 species) and Urticaceae (3 species). Similar studies reveal that the dominance of Poaceae can be explained by the fact that species in this family are able to cope with harsh environmental conditions (Melon *et al.* 2015; Kaou *et al.*, 2017). This predominance of the Poaceae and Asteraceae families provides information on the type of vegetation characteristic of African savannahs or areas heavily disturbed by human activities (Mahamane *et al.*, 2009; Wouokoue *et al.*, 2017ab; Ngyete *et al.,* 2020). The predominance of these families could be explained by their high tillering potential, their ability to regrow after grazing, cultivation, and bush fires when environmental conditions become favourable again (Wouokoue *et al.*, 2020ab). They are also resistant to climatic hazards and cryptogamic diseases (Kouadja *et al.*, 2021). These results are similar to those of Akossoua and Kouassi (2010) in Abidjan, Côte d'Ivoire, Masharabu (2010) in Burundi, and Ngyete *et al.* (2020) in Cameroon. According to these authors, the strong presence of species from the Gramineae family can be explained by the fact that savannahs are ecosystems dominated by grasses. In addition, Poaceae have high ploughing potential and a high regrowth rate after grazing, if environmental conditions are favourable. The abundance of Asteraceae and Poaceae can be attributed to their high ecological tolerance and significant seed dispersal capacity (Ramirez, 2007). Thanks to their wide ecological range, Poaceae and Asteraceae species are present in a wide variety of habitats. Indeed, the large number of ruderal species present at the various sites could be explained by the anthropised nature of the environments. These annual and perennial ruderal formations are pioneer and post-pioneer herbaceous vegetation associated with disturbed and reworked areas. These annual and perennial ruderal formations are pioneer and post-pioneer herbaceous vegetation associated with areas disturbed and reshaped by human activities such as agriculture and grazing (Maire *et al.*, 2020; N'gouran *et al.*, 2023; Tsama *et al.*, 2025).

According to Saulais (2011), urban flora consists mainly of ruderal species. Ruderal species are characterised by their short life cycle and high dispersal capacity (Kowarik, 2011). For Bullock *et al.* (2018), species dispersal is strongly influenced, directly or indirectly, by human activities. These activities can therefore alter the taxonomic composition of spontaneous plant communities, including dispersal mechanisms (Omar *et al.*, 2018; Vergnes *et al.*, 2017). The dominant presence of ruderal plants such as *Commelina bengalensis, Sida acuta* and *Tithonia diversifolia* in the discharge area, and their relatively high abundance, indicates selective resilience in polluted environments, as highlighted by Essia (2019) and Kamdem *et al.* (2023). These species are bioaccumulators and establish themselves in soils saturated with organic matter. These results corroborate the work of Ogun *et al.* (2023) and Jimoh *et al.* (2022), who observed a dominance of chemically stress-tolerant species in environments contaminated by agro-industrial discharges. Zébazé *et al.* (2006) mentioned that the ecological pressure created by waste leads to the decline of sensitive species and a simplification of the floristic composition. These results are also consistent with those of Bakare-Abidola (2025), who observed plant structures dominated by tolerant species in areas of untreated waste accumulation.

Analysis of diversity indices confirms this alteration: Shannon's index is slightly lower near the slaughterhouse (H' = 1.8) compared to downstream (H' = 1.84); these low values of Shannon's diversity index would indicate low floristic diversity (Seou *et al.*, 2022). These values remain very low compared to those found in other formations. These include Gommandje *et al.* (2011) in the low-altitude forests of southern Cameroon in Ngovayang, which show values between (3.90 and 4.12 bits), and Ngueguim *et al.* (2010) in the Mangombe forest plantation (2.74 bits). These authors concluded that this high value reflects a high diversity and good recovery of floristic diversity, undoubtedly due to favourable environmental conditions. The Pielou's Equitability values found in our work tend towards 1, indicating that the species in these sites have the same abundance. These values are higher than those of Nguegium *et al.* (2010) in the Mangombe forest plantation (0.27 and 0.69) and are comparable to those of Tiokeng *et al.*, (2015) in the Lebialem highlands (western Cameroon) (0.52 and 0.96). These authors assert that the high Piélou Equitability value indicates a good distribution of individuals within the population. The values found in our study fall within the range considered optimal (0.6 to 0.8) by Odum (1976); they reflect a good distribution of individuals within species; ecosystems that have reached maturity and are not subject to disruptive constraints have an optimal evenness between 0.6 and 0.8. We can say that the stands at our sites show stability, balance and good recovery of the diversity of these plant formations, undoubtedly due to favourable environmental conditions.

CONCLUSION

Our study on the impact of waste from the municipal slaughterhouse in Nkongsamba on the surrounding vegetation revealed significant pollution of natural resources in the Barehock area. The most common families, with more than three species, are Poaceae, Malvaceae, Asteraceae, Fabaceae, Euphorbiacea and Acanthaceae. These different sites are characterised by the predominance of ruderal and/or cultivated species, which could be explained by the anthropised nature of the different sites. Floristic analysis revealed a reduction in species richness and a dominance of ruderal species around the slaughterhouse, indicating an alteration in the ecological structure of local plant communities.

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