Monitoring entomofauna associated with cabbage, *Brassica oleracea* L. var *capitata* in eastern DRCongo

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ABSTRACT. Cabbage is an important component of agriculture in the eastern Democratic Republic of Congo (DRC) for its various food uses. It is important to identify pests that affect its production, which is still insufficient to meet the increasing consumer needs. Furthermore, insect data for tropical agroecosystems, particularly those of DRC are limited, making insect diversity poorly understood. The objective of this study is to assess the diversity and abundance of entomofauna related to cabbage in five different cabbage growing sites: Minova, Sake, Kibumba, Rutshuru and Lac Vert. This was achieved by trapping insects with the sweep net and yellow pantraps during 2021 and 2022. A total of 1109 insects from 9 orders and 48 families were collected. The most abundant pest families were Ciccadellidae (8%), Coreidae (7%), Chysomelidae (5%) and Pentatomidae (4%). The main families of beneficial insects (natural enemies and pollinators) identified were Syrphidae (7%), Carabidae (4%), Coccinellidae (3%) and Apidae (3%). Insect communities found in different locations were similar and diversified. Considering functions played by these different functional groups as ecological indicators, it is important to preserve entomological biodiversity. This is achieved through the rational selection of pest management methods to optimize ecosystem services provided by beneficial insects.

Keywords: cabbage, insects, natural enemies, pests, pollinators

INTRODUCTION

Cabbage, *Brassica oleracea* Linnaeus var *capitata* (Brassicales: Brassicaceae), is a widely used vegetable grown in the eastern Democratic Republic of Congo (DRC). Consumed in both raw and cooked form, cabbage contains several vitamins and other essential nutrients. It is also an important source of income

for many producers (Macharia et al., 2005). Cabbage is preferred for its relatively short growth cycle and year-round production. However, the quantities produced remain insufficient to meet the growing number of consumers. In 2020, annual cabbage production in DRC was estimated at 20,554 tonnes (FAO, 2020).

The Cabbage crops are seriously affected by attacks of many pests including aphids (Hemiptera: Aphididae) and caterpillars such as *Plutella xylostella* Linnaeus, 1758 (Lepidoptera: Plutellidae), *Hellula undalis* Fabricius, 1781 (Lepidoptera: Crambidae) and others from the genus *Spodoptera* Guenée, 1852 (Lepidoptera: Noctuidae) (Ngom et al., 2020). Aphids are harmful pests for cabbage as they suck sap useful for plant growth and transmit both toxins and viruses (Fidelis et al., 2018; Sarwar, 2020). Some aphids such as *Brevicoryne brassicae* Linnaeus, 1758 attack a specific host range (Brassicaceae) while others such as *Myzus persicae* Sulzer, 1776 attack hundreds of plant species from different families (Nalam et al., 2019). Other hemipterans belonging to the Aleyrodidae and Pentatomidae families, also polyphagous, can cause significant damage to common cabbage (Capinera, 2020). The diamondback moth *P. xylostella*, without adequate protection, can cause losses up to 90% or more (Macharia et al., 2005; Mondedji et al., 2014). It is present in almost all regions of the world and attacks mainly Brassicaceae plants to which it is attracted by glucosinolates, sulphur compounds characteristic of this family (Arvanikatis, 2013). To control pests, farmers from DRC usually use chemicals. Unfortunately, these products are toxic to humans, animals and the environment (Kumar et al., 2019). In addition, chemicals cause resistance in pests and lead to the death of non-target organisms such as pollinators and natural enemies (Tsaboula et al., 2016). The reported effects on beneficial insects can be direct (physiological and behavioural disorders) or indirect (destruction of oviposition and mating sites) with serious consequences for their survival and the ecosystem services they provide (Desneux et al., 2007).

The insect class is the largest group of multi-cellular organisms in the world, with a diversity of species providing many ecosystem services. The most well-known services are pollination, natural pest regulation and decomposition of organic matter (Losey & Vaughan, 2006). Quantitative and economic assessments of these services enable a better understanding of the contribution of functional groups. Gallai et al. (2009) estimated for example that the service provided by pollinators worldwide is worth 153 billion euros, representing 9.5% of the value of global food production. In this context, hoverflies (Diptera: Syrphidae) provide both pollination and biological control. Adults pollinate plants by visiting flowers on which they feed on nectar and pollen, while their larvae feed mainly on small insect pests such as aphids, thrips and caterpillars (Dunn et al., 2020). Hymenopteran parasitoids also contribute to the natural regulation of pests. For example, aphid parasitoids belonging to the Braconidae and Aphilinidae families have been shown to be effective as they mainly attack target pests. Many species of insects decompose plant and animal waste, thus recycling nutrients. Beetles, termites, ants and springtails contribute to the improvement of soil structure and fertility (Chagnon et al., 2001; Deprince, 2003).

Many farmers in the DRC are unaware of the benefits of maintaining entomological diversity and the roles that beneficials play in agroecosystems. Scientifically, very little research exists on the inventory of entomological diversity in vegetable crops. In the case of cabbage, no study has been found on the assessment of abundance, diversity, or functional groups of insects in DRC. In such a context, it is difficult to adopt sustainable pest management models without first knowing pests and natural enemies present in the environment. The purpose of this study is to assess the diversity and abundance of insect pests and beneficial insects associated with cabbage crops in the eastern DRC. In addition, the presence of different insect groups is assessed according to the geographical differences of the sampling sites.

MATERIAL AND METHODS

Study sites. The research was carried out in eastern DRC in 5 locations: Sake, Kibumba, Rutshuru, Lac Vert (North-Kivu province) and Minova (South-Kivu province) (Fig. 1). These areas have a humid tropical climate and/or a relatively temperate climate, particularly in Kibumba. The coordinates

collected indicate altitudes ranging from 1100m to 2200m. Table 1 provides latitude, longitude, and climate information of the study areas. The existing soils are Ferralsols and especially Andosols of volcanic origin. These materials are porous and rich in amorphous minerals (Ngongo et al., 2009). Local growing seasons refer to alternating dry and rainy periods. Sampling was carried out during the 2021 short rainy season (March to August) and during the 2022 long rainy season (September to February).

Collection and identification of insects. For each location, ten elementary plots of 10m² respectively selected from cabbage farms of at least 500m² were monitored (Yarou et al., 2018). Plots were selected at a minimum distance of three metres from field edges, in order to limit the border effect (Lozano et al., 2013). Each plot was used as an experimental unit and was trapped by two methods to collect as many insects as possible from different groups. Three samplings were carried out per site per cropping season following the cabbage growth. They were mainly carried out using yellow pan traps and the sweep net as proposed by Campbell & Hanula (2007) and Ghani & Maalik (2020) respectively. For the first method, yellow pan traps (diameter 27cm, height 10cm) were placed in the elementary plots with one trap per plot. Traps were placed in the morning and removed in the evening. They were adjusted to real crop height to favour insect capture (O'Connor et al., 2019). They contained an aqueous solution not exceeding the dipstick, adding a few drops of dishwashing liquid to reduce the surface tension of the water and increase the retention of trapped insects. The solution was renewed for each monitoring day. The trapped insects were collected with a sieve, a brush and soft tweezers to preserve their condition (Chmelíková & Wolfrum, 2019; Mignon et al., 2003). For the second trapping method, each elementary plot (10m²) was swept with a net (Fig. 2) for an average of fifteen minutes. This method is mainly used to catch flying insects. The collection consisted of moving through the field mowing any insects flying over the cabbage plants. In order to trap as many insects as possible, the surface vegetation was also mowed with rapid lateral movements (Yarou et al., 2018).

All insects collected (net & yellow trap) were kept in plastic bottles containing a 70% ethanol solution and then brought to the laboratory for identification. Insects were identified up to the family taxonomic level using the keys of Delvare & Aberlenc (1989), and Mignon et al. (2016). The main functional groups considered in the identification were pests, predators, parasitoids, pollinators, mixed (i.e. those grouping both genera and/or species of beneficial and phytophagous insects) and neutrals (i.e. insects with various functions without direct agronomic impact or not yet defined). Due to the high abundance of apterous aphids (Hemiptera: Aphididae) on cabbage leaves, direct observations on plants in the elementary plots were used to express infestation levels (Lopes et al., 2012). The evaluation scale was designed referring to Banks (1954), Fening et al. (2014) and Lopes et al., (2012) models. It is presented as follows: **0.** Absence of aphids; **1.** The presence of one aphid to a few individuals (<20 aphids); **2.** A few isolated colonies (20 to 50 aphids); **3.** Several isolated colonies (50 to 200 aphids); **4.** Strong presence in diffuse colonies (200 to 500 aphids); **5.** Very dense aphids (> 500) infesting several parts simultaneously.

Table 1. Geographical coordinates and Climate information of the study areas.

Sites	Geographical coordinates/Altitude	Climate information
Minova	01°42'42.7" S, 29°00'47.6" E; 1489 m	Highland agricultural area with a tropical climate bordering Kivu Lake
Rutshuru	01°08'47.8" S, 29°25'32,9" E; 1113 m	Mid-altitude zone with a humid tropical climate
Kibumba	01°30'42.1" S, 29°19'49.9" E; 2028 m	High altitude region with a relatively temperate climate, bordering the Virunga National Park.
Sake	01°33'56.6" S, 29°03'11.0" E; 1495 m	Humid tropical zone located to the west of Goma city.
Lac vert	01°33'53.2" S, 29°09'16.4" E; 1543 m	Peri-urban site in Goma city with a humid tropical climate and volcanic soil.
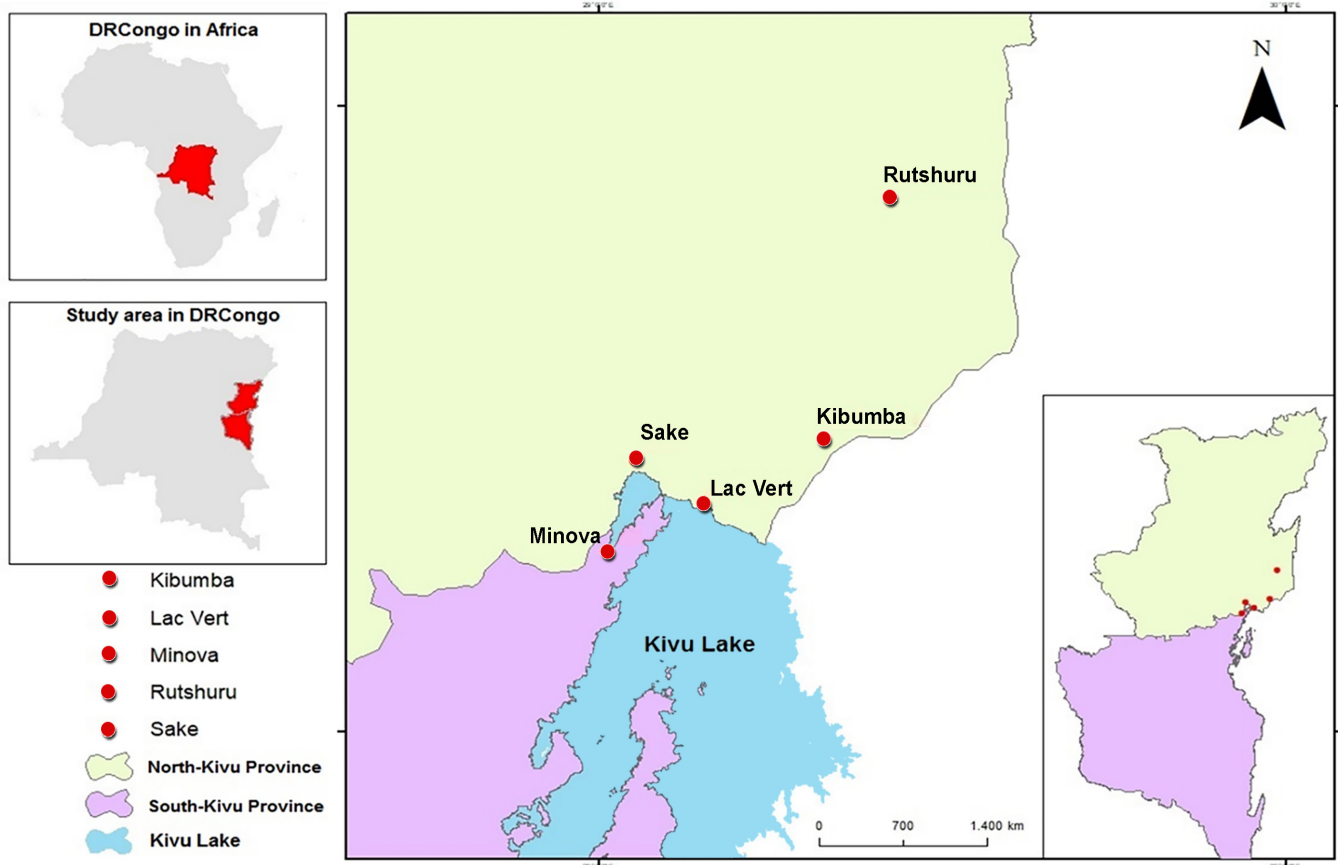
Figure 1. Location of cabbage entomofauna collection sites in eastern DRC.
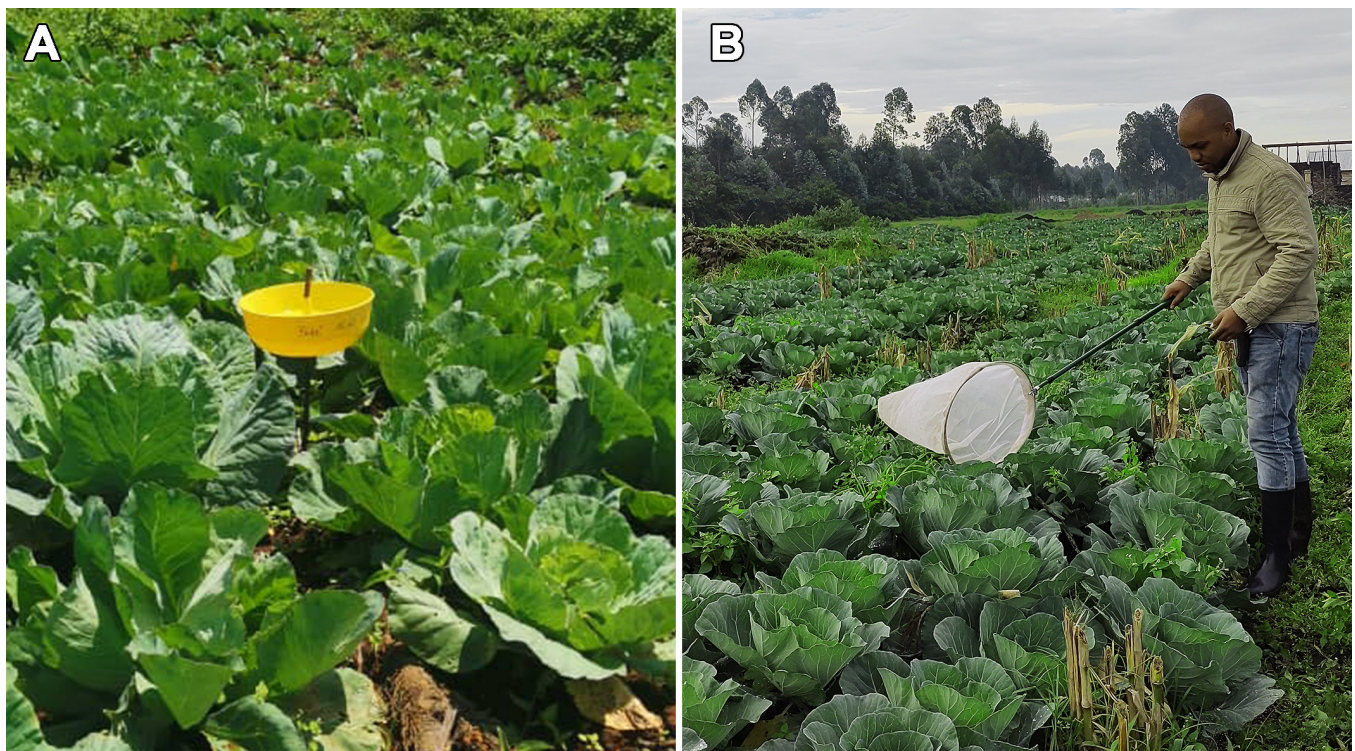
Figure 2. Methods used for collecting the cabbage entomofauna. **A.** Yellow pan trap; **B.** Sweep net.

Data analysis. The relative abundance (**F**) was calculated using the formula **F (%) = *ni/N**100**, where ***ni*** is the number of individuals in a family and **N** is the total number of individuals excluding Aphididae because of their high abundance. To assess the diversity of family taxa, the Shannon Index was calculated as follows:

$$H' = -\sum_{i=1}^{S} pi.log_2(pi)$$

where *pi* = *ni/N*; ni is the abundance of family i and N is the total abundance. The Pielou equitability (E) associated with the Shannon index was calculated as follows: **E = *H'*/*H'max*** with ***H'max* = log$_2$ (*S*)**; *H'max* is the maximum Shannon diversity and S represents the total number of families. The E value varies from 0 (dominance of one family) to 1 (equitable distribution of individuals across families) (Buckland et al., 2005).

To study the effect of sampling location on insect family diversity, we performed multivariate statistics, using two techniques: Principal Coordinate Analysis (PCoA) and Redundancy analysis (RDA). To determine whether families of insect composition of insect communities differed between different sites, a PCoA was developed using packages «*Vegan*» (Oksanen et al., 2015), «*ape*» (Legendre & Gallagher, 2001) and «*ggplot2*» (Wilkinson, 2011). PCoA is a nonlinear method to explore and visualize similarities or dissimilarities of data and its advantage is that it may be used with all types of variables. PCoA analyses generate ordination diagrams that allow us to compare how closely the different sites are related to each other in terms of insect family composition (Chahouki, 2011; Paliy & Shankar, 2016). RDA was carried out to determine the effect of environmental variables (elevation, latitude, longitude) on insect family richness and abundance using the packages «*ggvegan*» and «*ggord*». RDA is a method to extract and summarize the variation in a set of response variables that can be explained by a set of explanatory variables (Bellamy et al., 2018; Dyola et al., 2022). An Analysis of variance (ANOVA) was computed to test the overall significance (*p*-value < 0.05) of environmental variables. All tests were based on Bray-Curtis distance and performed in R software v.4.1.3.

RESULTS

Abundance and diversity of insect orders. A total of 1109 insects were collected during 2021 and 2022 in the five sampling locations: Minova (282 insects), Sake (239 insects), Kibumba (187 insects), Rutshuru (226 insects) and Lac Vert (175 insects). These insects are distributed in 9 orders, namely Hemiptera (30%), Coleoptera (21%), Diptera (19%), Orthoptera (10%), Hymenoptera (10%), Lepidoptera (8%), Thysanoptera (1%), Neuroptera (1%) and Odonata (<1%). Even without considering the Aphididae, Hemiptera represent the most numerous order with nearly a third of the total number of insects and are most important in Minova, Sake and Rutshuru. Coleoptera, second in total abundance (21%), are most present in Kibumba, while Diptera, with almost one-fifth of the total number of individuals, have the highest abundance in Lac Vert (Fig. 3A).

Abundance and diversity of insect families. Referring to Table 2, 48 insect families were identified, excluding the Aphididae which is the most abundant family (Fig. 3B). With respectively 12 and 11 families, Hemiptera and Coleoptera orders rank first and second with the highest number of identified families. Except for the Aphididae, the most abundant families in the Hemiptera order are the Cicadellidae, Coreidae and Pentatomidae, while among Coleopterans, Chrysomelidae and Carabidae are the most abundant. Hymenoptera was represented by seven families with a predominance of Apidae and Formicidae. Dipterans (6 families) are largely represented by Syrphidae and Sepsidae. Lepidopterans include 5 families among which Plutellidae and Noctuidae are the most numerous. The Tetrigidae and Tettigoniidae have the highest abundance of the 4 families found in the Orthoptera order. Lastly, the single families representing the Thysanoptera, Neuroptera and Odonata orders are respectively Thripidae, Chrysopidae and Coenagrionidae.
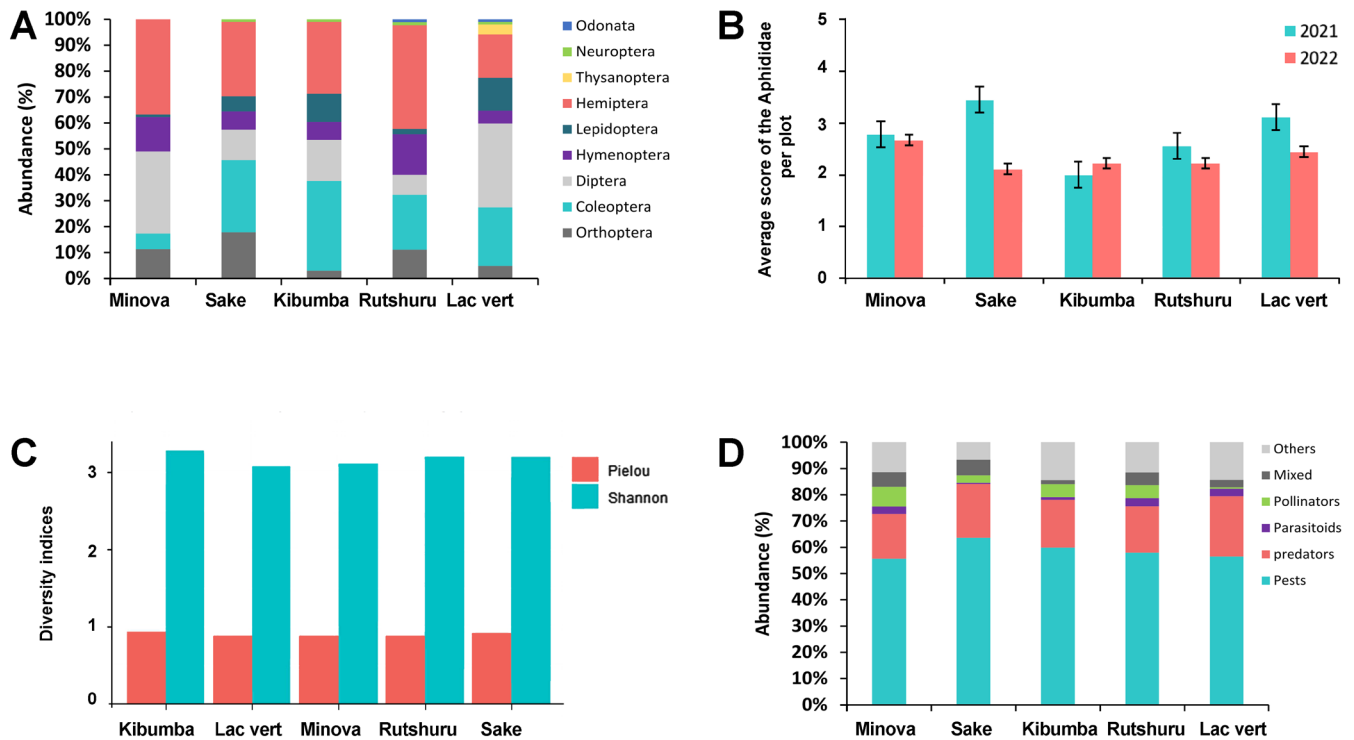
Figure 3. The relative abundance and diversity indices of entomofauna associated with Cabbage in the studied areas. **A.** Relative abundance of insect orders per site. **B.** Aphids (Hemiptera: Aphididae) abundance per site per year; **C.** Shannon Index diversity and Pielou Equitability within sampled sites; **D.** Relative abundance of functional insect groups per site.

Distribution of entomofauna according to site characteristics. The Shannon indices for different sites do not show large differences, with Kibumba having the highest index (3.25) followed by Sake (3.18); Rutshuru (3.14); Minova (3.09) and Lac Vert (3.03). All values are close to 3, meaning that all sites have high species diversity and are inhabited by nearly the same number of insect families. The Pielou equitability values are basically the same and tend to 1. Therefore, insect communities between different localities are similarly distributed with respect to the pattern of abundance and rarity within families (Fig. 3C).

The PCoA results show similarities between the insect communities found in the different sampled sites (Fig. 4). The lowest dispersion of insect families is observed in Kibumba. The redundancy analysis (RDA) shows in Figure 5 a correlation between environmental factors and the distribution of insect families. The full RDA model is statistically significant (*p = 0.001*). Latitude, i.e. the distance of a sampling position from the equator, is the variable that significantly influences (*p = 0.001*) the distribution of insect families in the study sites.

Distribution of entomofauna in functional groups. Overall, phytophagous are the most widespread insects across the cabbage crops in the survey sites. They cover more than half of the samples at each site. The 23 families (excluding Aphididae) grouping the phytophagous insects together represent 58% of the samples, including Cicadellidae (8%), Coreidae (7%) and Chrysomelidae (5%) (Table 2). Although less numerous than the pests, predators are in second place both in the number of families found (9) and in relative abundance (19%) (Fig. 3D). Syrphidae (7%), Carabidae (4%) and Coccinelidae (3%) are the most abundant. Pollinators (Apidea, Andrenidae and Megachilidae) account for 5% while parasitoids (Braconidae and Ichneumonidae) account for 2%. Mixed families and neutrals represent 5% and 11% respectively.

Table 2. Abundance and diversity of insect families per site.

|	Minova		Sake		Kibumba		Rutshuru		Lac vert		Total	
	N	F (%)	N	F (%)	N	F (%)	N	F (%)	N	F (%)	N	F (%)
ORTHOPTERA	**32**	**11**	**42**	**18**	**6**	**3**	**23**	**10**	**8**	**5**	**111**	**10**
Acrididae *	4	1	6	3	0	0	13	6	1	1	24	2
Gryllidae *	6	2	15	6	0	0	0	0	0	0	21	2
Tetrigidae *	13	5	16	7	3	2	1	0	4	2	37	3
Tettigoniidae *+	9	3	5	2	3	2	9	4	3	2	29	3
COLEOPTERA	**18**	**6**	**68**	**28**	**66**	**35**	**44**	**19**	**40**	**23**	**236**	**21**
Chrysomelidae *	5	2	8	3	18	10	7	3	21	12	59	5
Coccinellidae +	1	0	18	8	1	1	11	5	5	3	36	3
Cryptophagidae ±	3	1	5	2	0	0	3	1	1	1	12	1
Dryophthoridae *	0	0	1	0	6	3	1	0	0	0	8	1
Scarabaeidae *	1	0	17	7	13	7	2	1	1	1	34	3
Geotrupidae ±	0	0	0	0	3	2	0	0	2	1	5	0
Lampyridae *+	5	2	2	1	0	0	0	0	1	1	8	1
Malachiidae *+	2	1	7	3	0	0	2	1	1	1	12	1
Staphylinidae +	0	0	0	0	8	4	1	0	2	1	11	1
Oedemeridae ±	0	0	0	0	5	3	4	2	1	1	10	1
Carabidae +	1	0	10	4	12	6	13	6	5	3	41	4
DIPTERA	**88**	**31**	**28**	**12**	**29**	**16**	**16**	**7**	**57**	**33**	**218**	**19**
Diopsidae *	15	5	4	2	4	2	2	1	0	0	25	2
Tipulidae *	14	5	2	1	3	2	4	2	14	8	37	3
Rhinophoridae ±	2	1	0	0	4	2	0	0	4	2	10	1
Sepsidae ±	18	6	7	3	5	3	3	1	8	5	41	4
Syrphidae +	34	12	14	6	5	3	5	2	25	14	83	7
Rhagionidae ±	5	2	1	0	8	4	2	1	6	3	22	2
HYMENOPTERA	**38**	**13**	**16**	**7**	**13**	**7**	**31**	**14**	**8**	**5**	**106**	**10**
Andrenidae Ω	11	4	1	0	1	1	7	3	0	0	20	2
Apidae Ω	10	4	5	2	8	4	4	2	1	1	28	3
Braconidae σ	0	0	1	0	0	0	1	0	2	1	4	0
Formicidae ±	4	1	3	1	2	1	12	5	2	1	23	2
Megachilidae Ω	0	0	1	0	0	0	0	0	0	0	1	0
Sphecidae +	3	1	0	0	0	0	1	0	0	0	4	0
Vespidae +	2	1	5	2	0	0	0	0	0	0	7	1
Ichneumonidae σ	8	3	0	0	2	1	6	3	3	2	19	2
LEPIDOPTERA	**3**	**1**	**14**	**6**	**20**	**11**	**27**	**12**	**23**	**13**	**87**	**8**
Crambidae *	0	0	5	2	5	3	0	0	0	0	10	1
Noctuidae *	0	0	8	3	4	2	2	1	4	2	18	2
Papilionidae *	0	0	0	0	0	0	7	3	3	2	10	1
Pieridae *	0	0	0	0	3	2	2	1	9	5	14	1
Plutellidae *	3	1	1	0	8	4	16	7	7	4	35	3
HEMIPTERA	**101**	**36**	**69**	**29**	**52**	**28**	**81**	**36**	**29**	**17**	**332**	**30**
Acanthosomatidae*	0	0	3	1	8	4	0	0	0	0	11	1
Cicadellidae *	12	4	17	7	14	7	38	17	11	6	92	8
Reduviidae +	6	2	0	0	7	4	5	2	0	0	18	2
Cydnidae *	3	1	0	0	3	2	0	0	0	0	6	0
Cercopidae *	0	0	6	3	1	1	1	0	0	0	8	1
Coreidae *	39	14	19	8	6	3	9	4	1	1	74	7
Delphacidae *	17	6	11	5	0	0	2	1	0	0	30	3
Dictyopharidae *	5	2	0	0	0	0	5	2	7	4	17	1
Membracidae ±	0	0	0	0	0	0	2	1	1	1	3	0
Miridae *	8	3	1	0	7	4	15	7	0	0	31	3
Pentatomidae *	11	4	12	5	6	3	4	2	9	5	42	4
THYSANOPTERA	**1**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**7**	**4**	**8**	**1**
Thripidae *	1	0	0	0	0	0	0	0	7	4	8	1
NEUROPTERA	**1**	**0**	**2**	**1**	**1**	**1**	**2**	**1**	**1**	**1**	**7**	**1**
Chrysopidae +	1	0	2	1	1	1	2	1	1	1	7	1
ODONATA	**0**	**0**	**0**	**0**	**0**	**0**	**2**	**1**	**2**	**1**	**4**	**0**
Coenagrionidae +	0	0	0	0	0	0	2	1	2	1	4	0
TOTAL	**282**	**100**	**239**	**100**	**187**	**100**	**226**	**100**	**175**	**100**	**1109**	**100**

N. number, **F.** frequency, ***** Pests, **+** Predators, **σ** Parasitoid, **Ω** Pollinators, ***+** mixed, **±** Neutral insects.
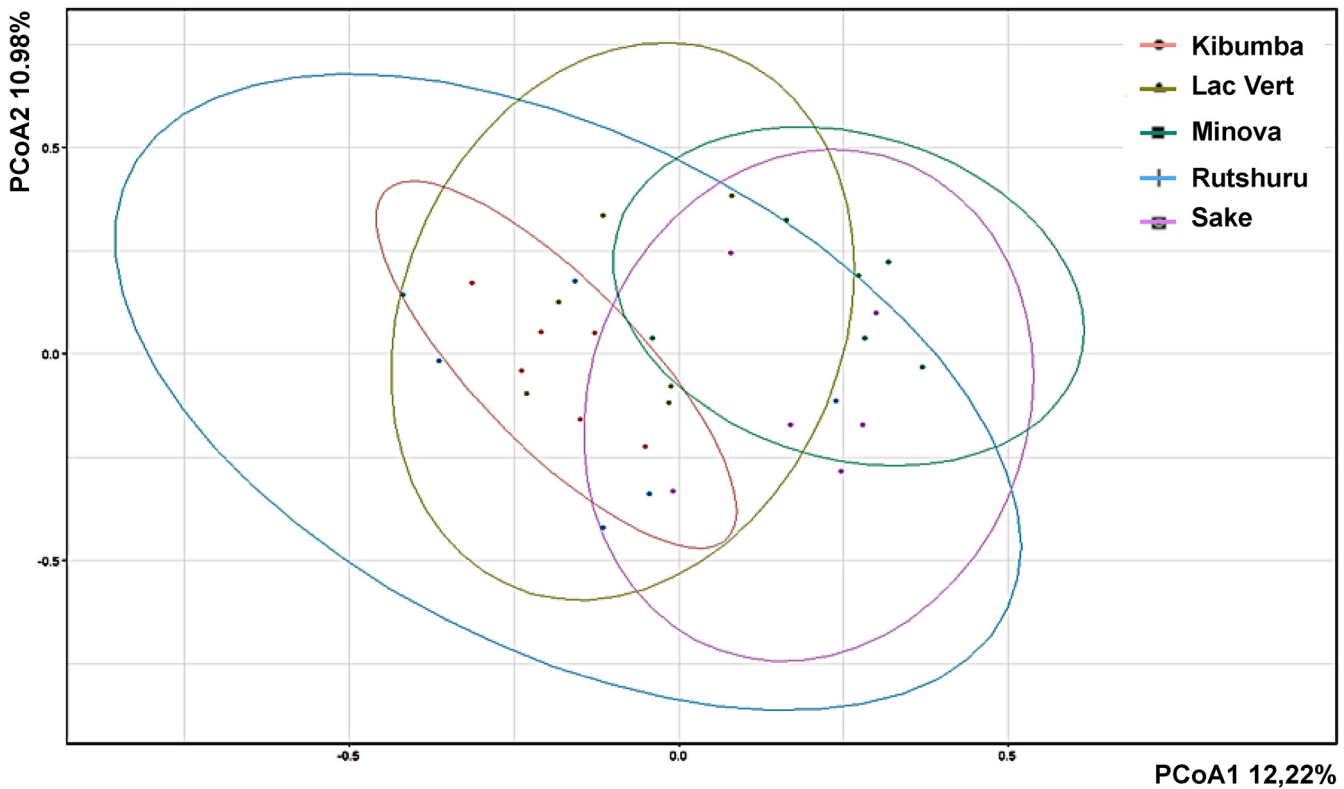
Figure 4. Principal Coordinate Analysis (PCoA) showing the community structure of insect families in five different habitats. Points in the PCoA plot represent insect samples each colored and shaped according to the sampling site.
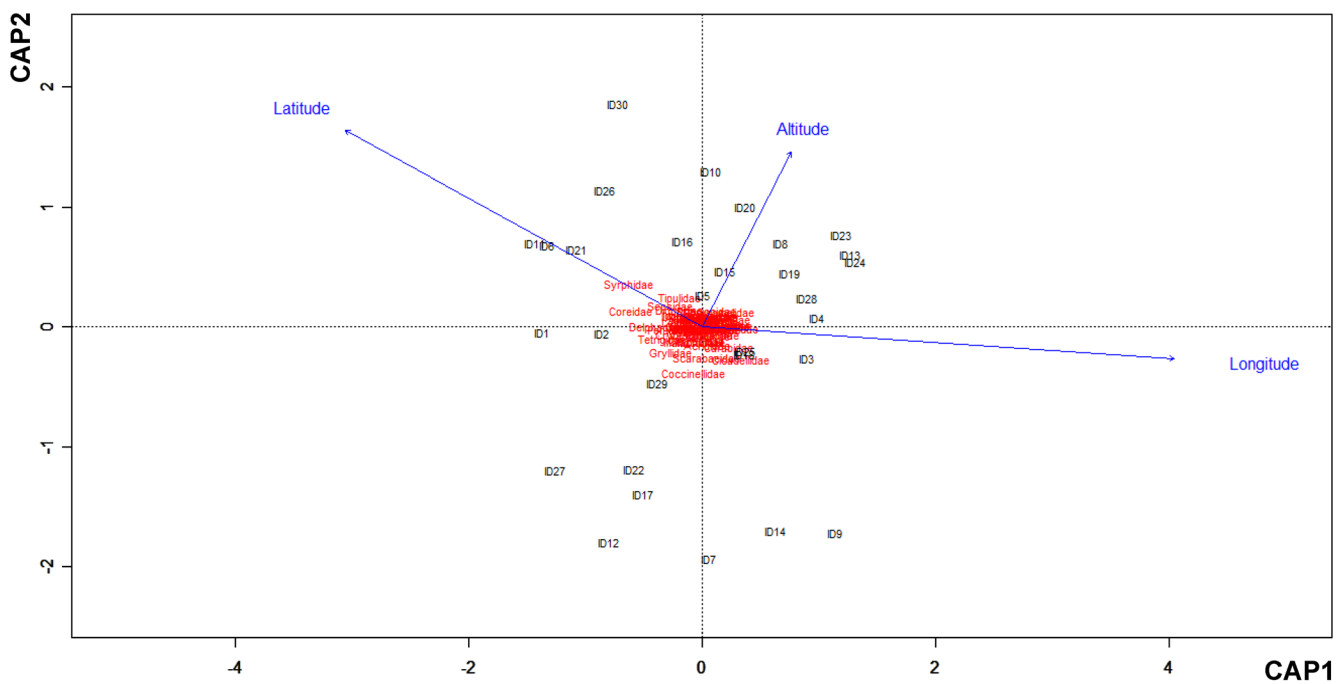
Figure 5. Redundancy Analysis (RDA) - biplot showing the correlation between cabbage insect families and the environmental variables. Red names represent insect families. Blue arrows correspond to the intensity of the environmental variables.

DISCUSSION

Findings indicate a dominance of Hemipteran insects. Hemipterans, with their many biting and sucking insects, are among the most damaging pests in vegetable crops. Similar studies (Tendeng et al., 2017; Vayssières et al., 2001) carried out in tropical regions have shown the high presence of hemipterans in vegetable crops. Regarding the found insect families, our results support those of Bayendi et al. (2018) in Gabon, based on an inventory of entomofauna on different vegetable crops (amaranth, tomato, cabbage, and sorrel). On cabbage as on other crops, they found Aphididae to be the most abundant pests. Aphididae are destructive pests because they suck sap from plants and transmit viral diseases. Chrysomelidae were the first and most abundant family of Coleoptera. Known for their small holes drilled through the leaf blade, the damage caused by Chrysomelidae increases with their abundance (Capinera, 2020). The results of the two diversity parameters (Shanon Index and Pielou Equitability) are similar to those of agricultural ecosystems. On the PCoA, similarities in insect families between the sampled sites are probably due to similar agricultural practices that can influence entomological diversity, such as monoculture and the use of the same chemical inputs.

Regarding the identified functional groups, phytophagous insects are clearly the most abundant because they are primary consumers of plant resources. Phytophagous insects are therefore the first biotic factor causing yield losses in agriculture (Prabaningrum & Moekasan, 2020). We find our results close to Cai et al. (2010) findings on cabbage cultivation in subtropical China. For them, neutral insects were more abundant but once again, phytophagous insects ranked second and were more numerous (27.24%) than predators and parasitoids combined (10.63%). Within collected insects, Hemiptera dominates because most of the insects (leafhoppers, bugs, …) are polyphagous and rapidly reproduce when resources are available. Concerning Aphididae, *B. brassicae* was found in all sites and rarely *M. persicae*. *Brevicoryne brassicae* mainly feeds on Brassicaceae particularly cabbage as found by Byamungu et al. (2019) in South-Kivu (DRC) while *M. persicae* has hundreds of hosts in different plant families (Nalam et al., 2019). The high presence of *B. brassicae* would be justified because apart from the Kibumba site where another Brassicaceae (Cauliflower) is grown, in all other sites, cabbage is the only host on which *B. brassicae* can feed. Leafhoppers (Hemiptera: Cicadellidae), which are also abundant, are considered important crop pests as they include disease vectors (Sarwar, 2020). Although limited in number, Lepidoptera included many damaging insects found on crops, especially, *P. xylostella* (Plutellidae), *H. undalis* (Crambidae), *Spodoptera* sp. (Noctuidae). Lepidoptera are most found in their larval stage (caterpillars) on crops, where they cause considerable economic losses. Caterpillars are highly destructive, particularly in the last larval stage (Wagner, 2013). Many studies highlighted the damage of these pests on cabbage in tropical environments (Labou et al., 2017; Macharia et al., 2005; Mpumi et al., 2020). Aphids and other sucking insects attract predators, especially gravid hoverflies that seek oviposition sites and food sources for their larvae (Colley & Luna, 2000). This would explain the high presence of Syrphidae during the sampling. Concerning ladybirds, one of the major groups of natural enemies listed, both adults and larvae are predators of aphids, whiteflies, and other small phytophagous insects. This is advantageous in biological control as it is not common for fully metamorphosing insects to have the same feeding regime at different developmental stages (Kundoo & Khan, 2017). Findings by Fidelis et al. (2018) confirm the predatory status of the found taxa in tropical regions. They noticed that the main predators (Coccinellidae, Syrphidae and Anhidoletes sp (Diptera: Cecidomyiidae)) settled where aphid colonies were located, and predators were found to be the main cause of aphid mortality. Pollinators were less numerous possibly because cabbage crops are harvested before they flower, and during our research there were no flowering plants in the sampling locations. The same observation applies to parasitoids. Recent studies showed that open flowering plants favor establishment of parasitoids, wasps and bees by providing them nectar (Harrison et al., 2019; Herrera et al., 2022).

This research aimed to assess the entomofauna related to cabbage under the growing conditions of eastern DRC. Aphids and caterpillars were among the main pests found as they caused severe losses on cabbage. Besides plant pests, pollinators, predators and parasitoids were identified. These insects

provide important ecosystem services (pollination, biological control) that it is wise to preserve through a good selection of control methods. Good cultural practices also have a positive influence on beneficial insects. In agroecosystems, this involves, for example, introducing uncultivated vegetation, aromatics or flowering plants in order to supply beneficials with shelter, oviposition sites, alternative prey and food resources. This research provided a general overview of the cabbage entomofauna in the investigated areas and proves to be a necessary basis for future investigations on insect dynamics in the DRC. For further studies, we suggest conducting isolated trials away from other crops to reduce interactions between plant species and to monitor all plant development stages to optimize temporal observations.

AUTHOR'S CONTRIBUTION

The authors confirm their contribution to the paper as follows: P. Niyibizi Gakuru, F. Francis and F. Muhashy Habiyaremye: Designed methodology; P. Niyibizi Gakuru: collected data and wrote the initial draft of the manuscript; F. Francis, G. Noël, and F. Muhashy Habiyaremye: Reviewed and edited the manuscript; P. Niyibizi Gakuru: Proofreading. All authors read and approved the final version of the manuscript.

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AVAILABILITY OF DATA AND MATERIAL

The specimens listed in this study are deposited in the Faculty of Agricultural Sciences and Environment (Department of Crop Sciences), University of Goma, DRCongo and are available from the curator, upon request.

ETHICS APPROVAL AND CONSENT TO PARTICIPATE

This study only included plants and arthropod material, and all required ethical guidelines for the treatment and use of animals were strictly adhered to in accordance with international, national, and institutional regulations. No human participants were involved in any studies conducted by the authors for this article.

CONSENT FOR PUBLICATION

Not applicable.

CONFLICT OF INTERESTS

The authors declare that there is no conflict of interest regarding the publication of this paper.

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رصد فون حشرات مرتبط با کلم، *Brassica oleracea* L. var *capitata* در شرق کنگو

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چکیـده: به دلیل کاربری غذایی متنوع، کلم بخش مهمی از کشاورزی در جمهوری دموکراتیک کنگوی شرقی را به خود اختصاص داده است. شناسایی آفات موثر بر تولید این محصول که مقدار آن هنوز هم برای برآورده کردن نیازهای رو به افزایش مصرف‌کنندگان کافی نیست، اهمیت زیادی دارد. علاوه بر این، اطلاعات مربوط به حشرات در اکوسیستم‌های گرمسیری، به خصوص در کشور کنگو بسیار محدود است و امکان شناخت مناسب از تنوع زیستی آنها را سلب می‌کند. هدف این مطالعه ارزیابی تنوع و فراوانی حشرات مرتبط با کلم در پنج منطقه کشت عمده شامل Minova، Sake، Kibumba، Rutshuru و Lac Vert بود. این بخش از فعالیت با استفاده از تله تشتکی زردرنگ و تورجارو طی سال‌های ۲۰۲۱ و ۲۰۲۲ انجام شد. مجموعاً ۱۱۰۹ نمونه حشرات از ۹ رده و ۴۸ خانواده جمع‌آوری شد. خانواده‌های آفات بسیار فراوان شامل Ciccadellidae (۸٪)، Coreidae (۷٪)، Chysomelidae (۵٪) و Pentatomidae (۴٪) بودند. اصلی‌ترین خانواده‌های حشرات مفید (دشمنان طبیعی و گرده‌افشان‌ها) شناسایی شده شامل Syrphidae (۷٪)، Carabidae (۴٪)، Coccinellidae (۳٪) و Apidae (۳٪) بودند. جوامع حشرات در مکان‌های مختلف مشابه و متنوع بودند. با توجه به نقش عملکردی این گروه‌ها به عنوان نشانگرهای اکولوژیک، حفظ تنوع زیستی حشرات از اهمیت بالایی برخوردار است. این هدف از طریق انتخاب منطقی روش‌های مدیریت آفات برای بهینه‌سازی خدمات اکولوژیک ارایه شده توسط حشرات مفید به دست می‌آید.

واژگـان کلیدی: کلم، حشرات، دشمنان طبیعی، آفات، گرده‌افشان‌ها