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Diversity and distribution patterns of aquatic insects in fish farm ponds in South Côte d'Ivoire

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Abstract

A study was conducted in five fish farm ponds in Southern Ivory Coast from December 2007 to November 2008. Overall, 79 taxa belonging to 35 families and 8 orders of aquatic insects were identified. Hemiptera and Coleoptera dominated qualitatively aquatic insect community. Taxa richness is higher in Banco and lower in Layo. Three taxa of Coleoptera (*Pseudobagous* sp., *Bagous* sp., *Macroplea* sp.), one taxa of Hemiptera (*Valleriola* sp.) and one taxa of Megaloptera (Corydalidae) have been recorded from Côte d'Ivoire for the first time. The Self-Organizing Map (SOM) was used to analyze patterns of insect assemblages. Samples were classified into three clusters. Samples from Azaguié, Anyama I and Anyama II were mainly gathered in cluster I while clusters II and III were respectively characterized primarily by samples from Banco and Layo. Salinity and conductivity were the most dominant variables governing aquatic insect distribution. This study allowed to know the community structure of aquatic insects and the distribution of samples based on environmental parameters and taxa assemblages.

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Introduction

Natural or man-made ecosystems, such as ponds provide a wide variety of resources that have a social and economic value (Chase and Ryberg, 2004; Hanson *et al*., 2005; Ruggiero *et al*., 2008). Ponds are small, man-made or natural shallow water bodies which permanently or temporarily hold water (De Meester *et al*., 2008). They can be used as reservoirs during water-stressed periods (Apinda-Legnouo, 2007), water supply, floodwater retention, recreation and education, management and research (Oertli *et al*., 2005) or breeding fish. Ponds have been recognized as important habitats for the maintenance of biodiversity (Oertli *et al*., 2005). They often constitute biodiversity "hotspots" within landscape (Williams *et al*., 2004; Karaus *et al*., 2005). Despite this important function, ecologist and environmental managers devoted a few attentions to these waterbodies (Scheffer *et al*., 2006). Their interest to these ecosystems has increased over the past decade, with an increasing focus on species diversity (Apinda-Legnouo,2007).

When ponds are artificially created for human activities, into the bargain services they offer, they have an added value to sustain macroinvertabrates, in particular aquatic insects (Ruggiero *et al*., 2008, Apinda-Legnouo, 2007; Oertli *et al.,* 2005; Yapo *et al*., 2007, 2012, 2013). Insects are mostly the diverse group of organisms in freshwater ecosystems. They play an important role in aquatic ecosystem function (Dumbar *et al*., 2010). They are involved in nutrient recycling and form an important component of natural food web (Kouamelan *et al*., 2000; Dietoa *et al*., 2007; Konan *et al*., 2008; Diomandé *et al*., 2009 a). They were also used as bioindicators for water quality (Bonada *et al*., 2005; Kasangaki *et al*., 2007; Varandas and Cortes, 2010).

In Côte d'Ivoire, many studies have been carried out on the ecological aspects of aquatic insects. But, most of these studies have been conducted in running water bodies (Déjoux *et al*., 1981; EDia *et al*., 2007, 2010; Diomandé *et al*., 2009). In stagnant habitats such as ponds, there are few studies that have investigated aquatic biodiversity (Yapo *et al*., 2007, 2012, 2013; Bony *et al*., 2008). Likewise, only few studies regarding aquatic insects in ponds were investigated in our country (Yapo *et al*., 2007, 2012, 2013). In the aforementioned context, this study is focused on artificial ponds dug in five fish farms situated in southern Côte d'Ivoire. The objective of this article is to present the distribution patterns of the aquatic insect in a network (Ruggiero *et al*., 2008, Céréghino *et al*., 2008) of ponds with a special focus on the community structure and the composition of the taxonomic assemblages.

Material and methods

Study sites

This study was undertaken in Southern Ivory Coast. Five fish farms were selected for this study according to the nature of water (fresh and brackish water) and the source water ponds (man-made lake, brook and river). These farms are Aquaculture Experiment Station of Layo, fish farms of Banco, Anyama I, Anyama II and Azaguié (Fig. 1). In each fish farm, three ponds were selected for this study. All ponds chosen were shallow (depth< 2 m). The main water supplies were different between the five sites. In Anyama I and Azaguié sites, ponds were fed respectively by a man-made lake and brook. Ponds in Banco were fed by Banco River while in Aquaculture Experimental Station of Layo and fish farm Anyama II, they were fed by groundwater. Ponds in Aquaculture Experimental Station of Layo were fed by brackish water with salinity ranging from 0 to 10 mg/l during the year (Legendre *et al*., 1987). At the others sites, ponds were supplied with fresh water. The pond area is ranging from 280 to 800 m^2. The characteristics of each study site are summarized in Table1. Banco site is located in National Park of Banco which contained primary forest. In Azaguié, Anyama I and Anyama II, ecosystems were constituted by agricultural landscape and at Layo site immediate environment was characterized by habitations.

Table 1. Characteristics of the study sites.

Characters	Sites				
	Banco	**Layo**	**Azaguié**	**Anyama I**	**Anyama II**
Geographical positions	05°23'N 04°03'W	05°19'N 04°18'W	05°39'N 04°05'W	05°33'N 04°03'W	05°34'N 04°02'W
Pond area (m²)	400-800	400-800	280-300	300-400	300-400
Predominant substratum	Mud	Sand	Sand	Gravel/sand/clay	Mud/sand
Adjacent land use	Housing Primary forest	Housing Cultivated lagoon	cultivated deteriorate forest	cultivated deteriorate forest	cultivated deteriorate forest

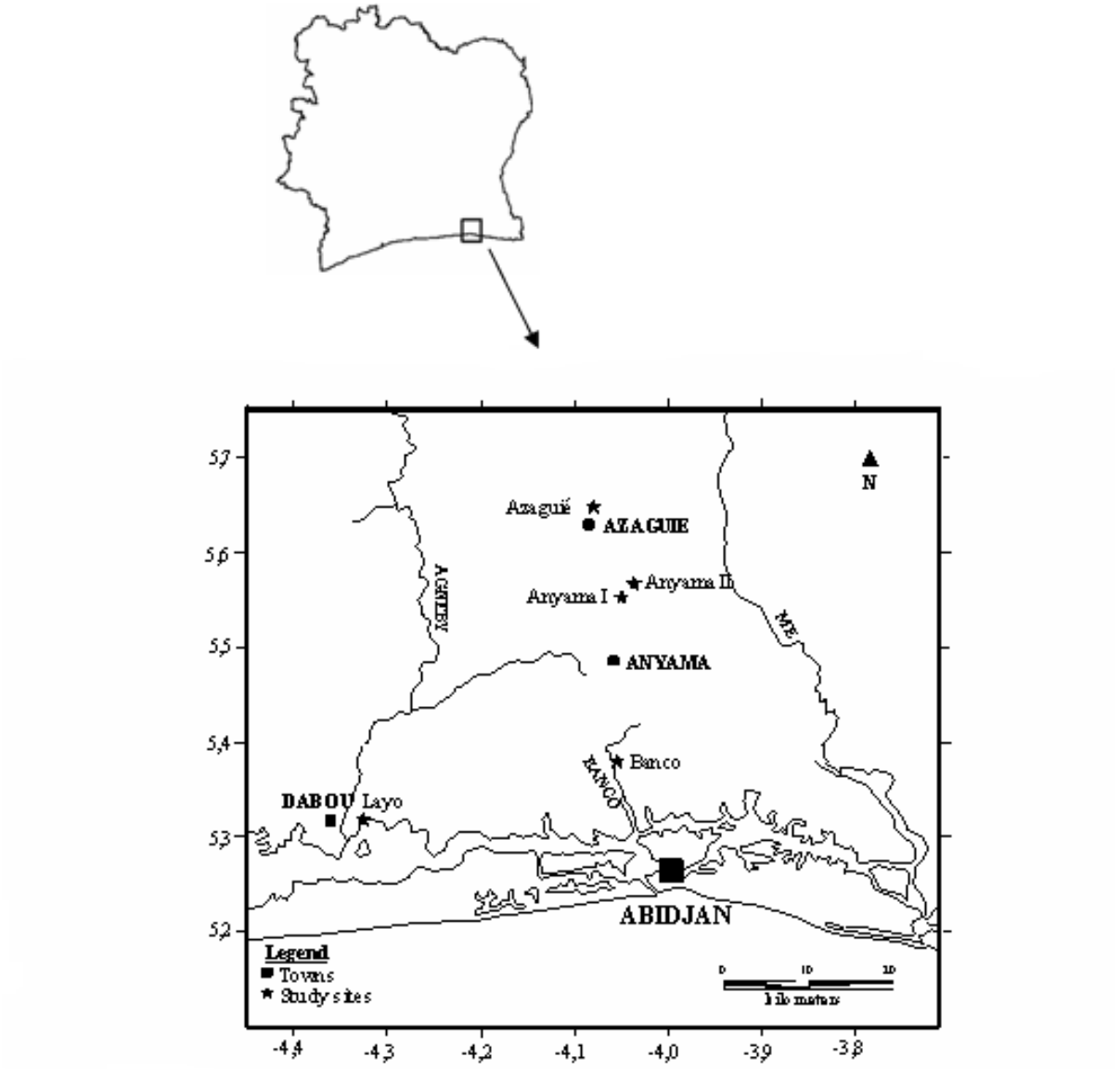


Fig.1. Location of the study sites.

Aquatic insect and environmental variables collection

In each pond, samples were collected monthly from December 2007 to November 2008. Water column and sediment were sampled using respectively a 350µm mesh hand net and a grab (area = 0.12 m^2). Each habitat was collected in six replicates. The water column and sediment samples collected were respectively sieved through 300 µm and 1 mm aperture size sieve. The materials retained were preserved *in situ* in 10% formalin. In the laboratory, specimens were sorted and identified to the lowest possible taxonomic level by means of the keys in (Déjoux *et al*., 1981; Tachet *et al*., 2003; de Moor *et al*.,2003 a; de Moor *et al*.,2003 b). At each sampling period, environmental variables such as transparency, temperature, pH, dissolved oxygen, salinity and conductivity were measured. Water temperature and pH were measured with a WTW pH 330 pH meter. Dissolved oxygen concentration was measured with a WTW DIGI 330 oxygen meter. Water salinity and conductivity were measured using a WTW-LF 340 conductivity meter and water transparency was determined using a 20-cm-diameter Secchi disk.

Data analysis

A species occurrence data set was arranged as a matrix of 180 rows (i.e. samples in the fifteen ponds on twelve sampling periods) and 79 columns (i.e. taxa). Species occurrence was used to avoid biases due to both patchiness in aquatic insect spatial distribution and temporal dynamics of abundance (Williams and Felmate, 1992). Each of the 180 samples of the data set can be considered as a vector of 79 dimensions. The species occurrence data set was patterned by training the Self-Organizing Map (SOM). The architecture of the SOM consisted of two layers of neurons (or nodes) i) the input layer that was composed of 79 neurons connected to each vector of the data set and ii) the two-dimensional output layer that was composed of 56 neurons (i.e. a rectangular grid with 8 by 7 neurons laid out on a hexagonal lattice). We chose a 56 neuron grid because this configuration presented minimum values of both quantization and topographic errors. The SOM algorithm calculates the connection intensities (i.e. vector weights) between input and output layers using an unsupervised competitive learning procedure (Kohonen, 2001), which iteratively classifies samples in each node according to their similarity in species composition. The SOM preserves the neighbourhood so samples with close species occurrences are grouped together on the map, whereas samples with very different species occurrences are far from each other. The connection intensity of the SOM corresponds to the probability of occurrence of a species in a group of samples, and can be displayed on the map as shades of grey: the darker the colour, the higher the probability (e.g., black means a species occurred in >90% of the samples) (Lek *et al*. 2000). For more details concerning the SOM algorithm and its applications, we refer the readers to (Kohonen, 2001; Giraudel and Lek, 2001; and Park *et al*. 2003). The analysis was carried out using the SOM toolbox (version 2) for Matlab® developed by the Laboratory of Information and Computer Science at the Helsinki University of Technology (http://www.cis.hut.fi/projects/somtoolbox/). We also employed a discriminant function analysis (DFA) to identify the variables most able to discriminate between the clusters defined by the SOM on the basis of biological attributes (Johnson, 1992; Wunderlin *et al*., 2001). To do this, the normalized weighting factor of each environmental variable was calculated to determine their contribution in sample clustering. An environmental descriptor was regarded as most able to discriminate between the clusters when its weighting factor, in absolute value, was at least 0.7. We assessed the accuracy of the DFA by applying a 'leave-one-out' cross-validation test (Efron, 1983). This test consists of removing one observation from the original matrix followed by DFA on the remaining observations to predict the group membership of the omitted observation. This operation was repeated for all of the observations of the data matrix. These analyses were conducted using the R package (Ihaka and Gentleman, 1996).

Results

A summary of some physical and chemical conditions of the study sites is given in Table 2. The mean value of water salinity was 1.53 mg/l in Layo site. Conductivity value was highest in Layo (3038 µS/cm) and Lowest in Banco (35.85 µS/cm). Dissolved oxygen was lowest in Banco (4.19 mg/l) and highest in Anyama I (6.33 mg/l). The highest value of temperature (28.97°C) was in Azaguié while the lowest value (27.20°C) was recorded in Banco. The maximum transparency level (30.15 cm) was recorded in Banco while the lowest (21.66 cm) was recorded in Layo. The pH value (7.09) was maximal in Anyama I and minimal in Banco (6.76). A total of 79 taxa belonging to 35 families and 8 orders were collected in the present study (Table 3). The richest groups were Hemiptera (21 taxa) and Coleoptera (21 taxa), followed by Diptera (15 taxa), Odonata (11 taxa), Ephemeroptera (5 taxa) and Trichoptera (4 taxa). Other represented groups were less diverse: Megaloptera and Lepidoptera (each with only one taxon). Among the 79 species, 21 taxa (*Hydrochara* sp., *Canthydrus xanthinus*., *Diplonychus* sp., *Eurymetra* sp., *Limnogonus chopardi*, *Micronecta* sp., Notonectidae, *Anisops sardea*, *Anisops* sp., *Mesovelia* sp., *Ranatra parvipes*, *Polypedilum* sp., *Nilodorum fractilobus*, ,*Tanypus fuscus*, *Chironomus imicola*, *Cloeon bellum, Cloeon gambiae, Cloeon smaeleni*, *Pseudagrion wellani*, *Pseudagrion* sp.and *Brachythemis* sp.) were collected from all sites (Table 3). Taxa richness was higher in Banco (52). It was followed by Azaguié (48), Anyama II (47), Anyama I (46) and Layo (44).

Table 2. Summary of environmental variables of the study sites.

Parameters		Sites				
		Banco	**Layo**	**Azaguié**	**Anyama I**	**Anyama II**
Transparency (cm)	Min.	21.30	10	11	12	16
	Mean	30.15	21.66	22.05	21.99	23.05
	Max.	42	33.50	51	33.30	37
Temperature (°C)	Min.	25.9	25.9	27	27.5	21.10
	Mean	27.20	28.37	28.97	28.8	28.81
	Max.	28.20	30.10	30.50	30.6	30.30
Dissolved oxygen (mg/l)	Min.	2.20	3.20	4	5.60	5.2
	Mean	4.19	5.55	5.72	6.33	6.17
	Max.	6.10	8.7	6.6	7.1	6.9
pH	Min.	6.5	6.7	6.7	6.8	6.5
	Mean	6.76	6.93	6.91	7.09	7.04
	Max.	7.1	7.1	7.2	7.3	7.3
Salinity (mg/l)	Min.	0	0.1	0	0	0
	Mean	0	1.53	0	0	0
	Max.	0	4.90	0	0	0
Conductivity (µS/cm)	Min.	30.10	331	25.4	48.3	22.`10
	Mean	35.85	3038	38.05	71.22	49.15
	Max.	41	8610	44.30	123.40	93.3

Table 3. Taxa composition of insects at the study sites. Bc= Banco; Ly= Layo; Az= Azaguié; AnI= Anyama I; AnII= Anyama II; 1= presence; 0=absence; in bold= Taxon which is reported for the first time in Ivory Coast; *= taxa which were common to all sites.

Orders	Families	Taxa	Sites				
			Bc	Ly	Az	An I	An II
Coleoptera	Hydrophilidae	*Amphiops* sp.	1	1	1	0	1
		*Hydrochara rickseckeri**	1	1	1	1	1
	Dytiscidae	*Hydrobius* sp.	0	1	0	0	0
		Canthydrus minutus.	0	1	0	0	0
		*Canthydrus xanthinus**	1	1	1	1	1
		Cybister tripunctatus	0	1	1	0	0
		Hydrocanthus micans	0	1	0	0	0
		Hydrocoptus simplex	0	1	0	0	0
		Laccophilus vermiculosus	0	0	1	0	1
		Yola tuberculata	0	1	0	0	0
		Hyphydrus sp.	1	0	0	0	0
		Limnius sp.	1	1	0	1	1
		Esolus sp.	1	0	0	1	0
	Elmidae	*Potamodytes* sp.	0	0	1	0	1
		Potamophilus sp.	0	1	0	0	0
	Curculionidae	***Pseudobagous* sp.**	1	1	1	0	1
		***Bagous* sp.**	1	1	0	1	0
	Gyrinidae	*Orectogyrus* sp.	0	0	0	1	1
		Aulonogyrus sp.	0	0	0	0	1
	Chrysomelidae	***Macroplea* sp.**	1	0	0	0	0
	Spercheidae	*Sperchus ceriyisi*	0	0	1	0	0
Hemiptera	Belostomatidae	*Appasus* sp.	1	1	1	0	1
	Gerridae	*Dyplonichus* sp.*	1	1	1	1	1
		Eurymetra sp.*	1	1	1	1	1
		*Limnogonus chopardi**	1	1	1	1	1
	Corixidae	*Naboandelus* sp.	0	1	1	1	1
		Micronecta sp.*	1	1	1	1	1
		Sigara sp.	0	0	1	0	0
	Notonectidae	*Stenocorisea protrusa*	1	1	1	0	1
		Notonectidae*	1	1	1	1	1
		*Anisops sardea**	1	1	1	1	1
		Anisops sp.*	1	1	1	1	1
	Naucoridae	*Enithares* sp.	1	1	0	1	1
		Naucoris sp.	1	1	0	0	0
		Macrocoris flavicollis	1	0	0	1	0
	Pleidae	*Plea pullula*	1	1	1	0	0
	Veliidae	*Rhagovelia reitteri*	1	0	1	1	0
	Mesoveliidae	*Mesovelia* sp.*	1	1	1	1	1
	Hydrometridae	*Hydrometra ambulator*	0	0	0	1	0
	Nepidae	*Laccotrephes ater*	0	0	0	1	1
		*Ranatra parvipes**	1	1	1	1	1
	Leptopodidae	***Valleriola* sp.**	0	0	0	1	0
	Chironomidae	*Tanypus fuscus**	1	1	1	1	1
		*Nilodorum fractilobus**	1	1	1	1	1
		Nilodorum brevipalpis	1	0	1	1	1
		Polypedilum sp.*	1	1	1	1	1
		*Chironomus imicola**	1	1	1	1	1

Orders	Families	Taxa	Sites				
			Bc	Ly	Az	An I	An II
Diptera		*Stictochironomus* sp.	1	0	1	1	1
		Clinotanypus claripennis	1	0	1	1	1
		Ablabesmyia dusoleili	1	0	0	0	1
		Cryptochironomus sp.	1	0	1	0	0
		Cricotopus kisantuensis	0	0	0	0	1
		Stenochironomus sp.	1	0	0	1	0
	Tabanidae	*Tabanus* sp.	1	0	0	0	1
	Chaoboridae	*Chaoborus anomalus*	1	0	1	1	1
	Ceratopogonidae	*Ceratopogon* sp.	0	1	1	1	1
	Culicidae	*Culex fatigans*	1	1	1	1	0
Ephemeroptera		*Cloeon bellum**	1	1	1	1	1
	Baetidae	*Cloeon gambiae**	1	1	1	1	1
		*Cloeon smaeleni**	1	1	1	1	1
	Polymitarcyidae	*Povilla adusta*	1	0	1	1	1
	Caenidae	*Caenis* sp.	0	0	1	1	1
Trichoptera	**Polycentropodidae**	*Dipseudopsis capensis*	1	0	0	0	1
	Hydropsychidae	*Protomacronema* sp.	1	0	0	0	0
	Hydroptilidae	*Hydroptila* sp.	1	0	0	0	0
	Ecnomidae	*Ecnomus* sp.	0	0	0	1	0
Odonata		Coenagrionidae	0	0	1	0	1
	Coenagrionidae	*Ceriagrion* sp.	1	1	1	1	0
		*Pseudagrion wellani**	1	1	1	1	1
		Pseudagrion sp.*	1	1	1	1	1
		Ischnura sp.	0	1	1	0	0
		Libellula sp.	1	0	1	1	1
		Orthetrum sp.	0	0	1	1	0
	Libellulidae	*Crocothemis* sp.	0	1	0	0	0
		Brachythemis sp.*	1	1	1	1	1
		Pantala flavescens	0	0	1	0	0
	Gomphidae	*Ictinogomphus* sp.	0	0	0	1	0
Lepidoptera	**Pyralidae**	Pyralidae	1	1	0	0	1
Mgaloptera	**Corydalidae**	**Corydalidae**	1	0	0	0	0
Total=8	**35**	**79**	**52**	**44**	**48**	**46**	**47**

After training the SOM, the hierarchical cluster analysis classified the samples into three clusters (Fig. 2). The aquatic insect assemblage pattern in the SOM map is presented by Fig. 3. The upper areas of the SOM (cluster I) gathered mainly samples of Azaguié, Anyama I and Anyama II sites (94.73%). Cluster II located on the left bottom of the map hosted in majority samples of Banco site (87.23%). The right top area of the SOM (cluster III) included predominantly samples of Layo site (84.21%) where high values of salinity and conductivity were recorded. Azaguié, Anyama I and Anyama II were characterized by agricultural landscape and Banco site was characterized by low values of physicochemical parameters and by presence of primary forest.

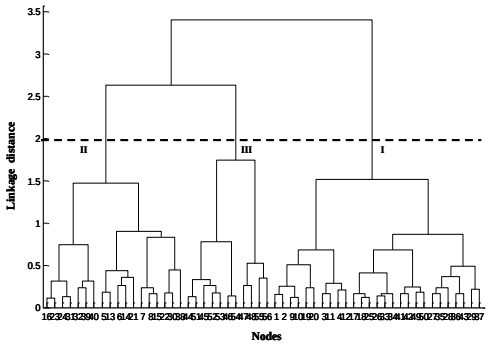


Fig. 2. Hierarchical clustering of the SOM (Self-organizing map) nodes with a Euclidean. The number ranging from 1 to 56 correspond to those assigned on each node of the SOM; the number I, II, and III correspond to the clusters selected.

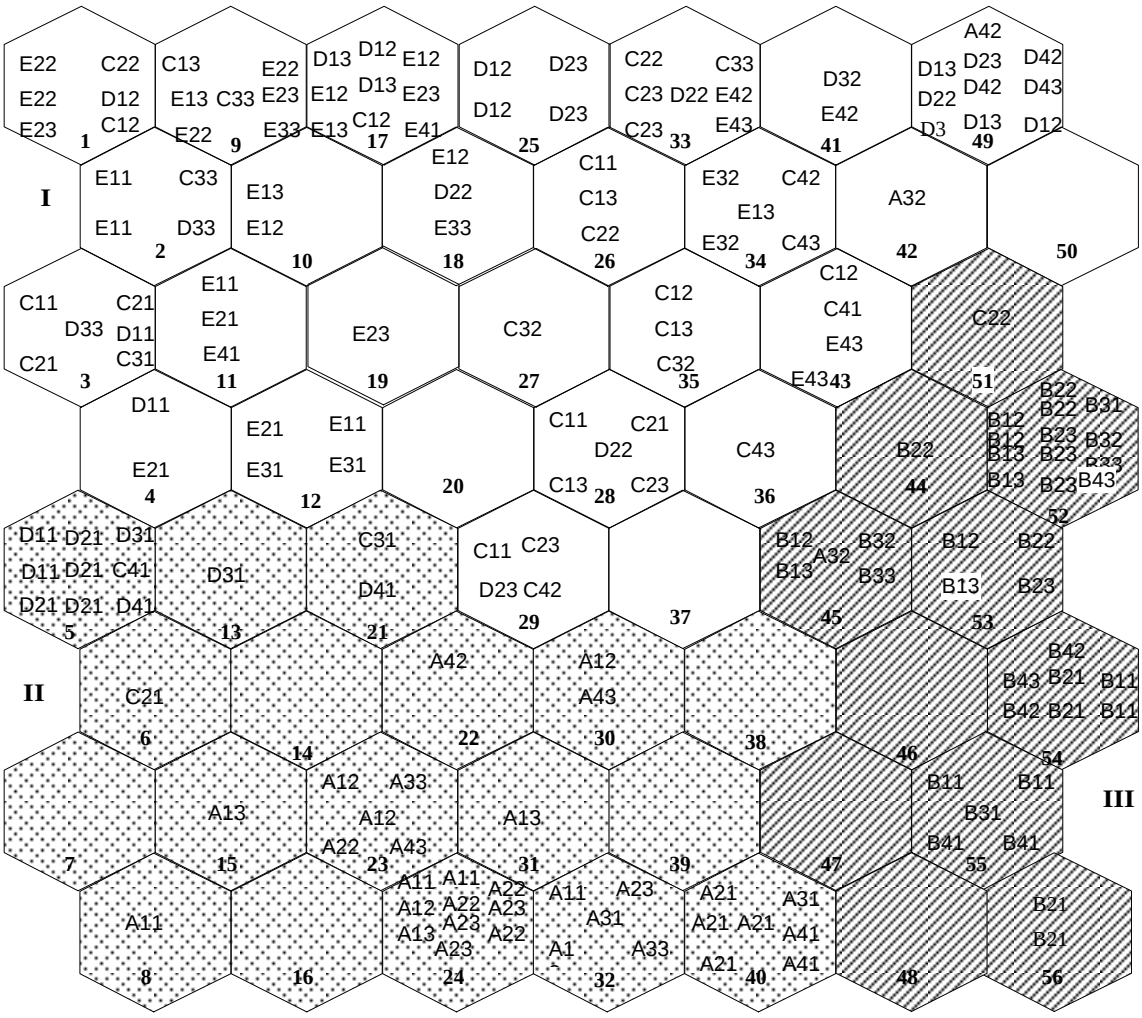
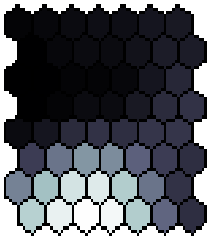


Fig. 3. Self-organizing map (SOM) for aquatic insect pattern reported from the ponds. Roman number represent different clusters. The letters (A, B, C, D, E) represent respectively Banco, Layo, Azaguié, Anyama I and Anyama II sites. Arabic number ranging from 1 to 56 correspond to those assigned on each node of the SOM. The first arabic numbers ranging from 1 to 4 in front of each letter correspond to the season and the second ranging from 1 to 3 correspond to the number of pond in each site.

Clusters	**Taxa**
Cluster I	*Amphiops* sp., *Hydrochara rickseckeri*, *Canthydrus xanthinus*., *Sperchus ceriyisi*, *Laccophilus vermiculosus*, *Orectogyrus* sp., ***Aulonogyrus* sp.**, *Potamodytes* sp., *Limnius* sp., *Pseudobagous* sp., *Esolus* sp., *Appasus* sp., *Diplonychus* sp., *Eurymetra* sp., *Limnogonus chopardi*, *Naboandelus* sp., *Micronecta* sp., *Stenocorisea protrusa*, *Sigara* sp., Notonectidae, *Anisops sardea*, *Anisops* sp., *Enithares* sp., *Plea pullula*, *Macrocoris flavicolis*, *Mesovelia* sp., *Ranatra parvipes*, ***Laccotrephes ater***, *Ablabesmyia dusoleili*, *Nilodorum fractilobus*, *Nilodorum brevipalpis*, *Chironomus imicola* , *Tanypus fuscus*, *Clinotanypus claripennis* ,*Polypedilum* sp., *Cryptochironomus* sp., ***Cricotopus kisantuensis***, *Stictochironomus* sp., *Ceratopogon* sp., *Culex fatigans*, *Chaoborus anomalus*, *Tabanus* sp., *Ceriagrion* sp., *Pseudagrion wellani*, *Pseudagrion* sp., *Ischnura* sp., *Orthetrum* sp., *Libellula* sp., *Brachythemis* sp., Coenagrionidae, *Ictinogomphus* sp., ***Pantala flavescens***, *Caenis* sp., *Cloeon bellum*, *Cloeon smaeleni*, *Cloeon gambiae*, *Povilla adusta*, *Ecnomus* sp., *Dipseudopsis capensis*, Pyralidae.



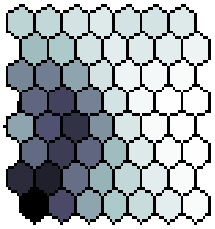
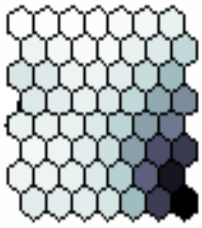
Clusters	Taxa
Cluster II 	*Amphiops* sp., *Hydrochara rickseckeri, Canthydrus xanthinus., Cybister tripunctatus*, *Pseudobagous* sp., *Bagous* sp., *Sperchus ceriyisi, Laccophilus vermiculosus*, ***Hyphydrus* sp.**, *Macroplea* sp., *Esolus* sp., *Orectogyrus* sp., *Limnius* sp., *Appasus* sp., *Diplonychus* sp., *Eurymetra* sp., *Limnogonus chopardi, Micronecta* sp., ***Valleriola* sp.**, *Stenocorisea protrusa*, Notonectidae, *Anisops sardea, Anisops* sp., *Enithares* sp., *Naucoris* sp., *Naboandelus* sp., *Macrocoris flavicollis, Plea pullula, Sigara* sp., *Mesovelia* sp., *Rhagovelia reitteri, Ranatra parvipes*, ***Hydrometra ambulator***., *Ablabesmyia dusoleili, Nilodorum fractilobus, Nilodorum brevipalpis,Tanypus fuscus, Clinotanypus claripennis, Chironomus imicola*, *Polypedilum* sp., *Cryptochironomus* sp. *Stenochironomus* sp., *Stictochironomus* sp., *Ceratopogon* sp., *Culex fatigans*, *Chaoborus anomalus*, Tabanidae, *Ceriagrion* sp., *Pseudagrion wellani, Pseudagrion* sp., *Orthetrum* sp., *Libellula* sp., *Brachythemis* sp., *Ictinogomphus* sp., *Cloeon bellum, Cloeon smaeleni, Cloeon gambiae, Povilla adusta, Enomus* sp., ***Protomacronema* sp.**, *Dipseudopsis capensis*, ***Hydroptila* sp.**, Pyralidae, Corydalidae.
Cluster III 	*Amphiops* sp., *Hydrochara rickseckeri,* ***Hydrobius* sp.**, ***Canthydrus minutus***, *Canthydrus xanthinus, Cybister tripunctatus,* ***Yola tuberculata***, ***Hydrocanthus micans***, ***Hydrocoptus simplex***, *Limnius* sp., *Pseudobagous* sp., *Bagous* sp., *Macroplea* sp., ***Potamophilus* sp.**, *Appasus* sp., *Diplonychus* sp., *Eurymetra* sp., *Limnogonus chopardi, Naboandelus* sp., *Micronecta* sp., *Stenocorisea protrusa*, Notonectidae, *Anisops sardea, Anisops* sp., *Enithares* sp., *Naucoris* sp., *Plea pullula, Mesovelia sp., Ranatra parvipes, Nilodorum fractilobus, Tanypus fuscus, Clinotanypus claripennis, Chironomus imicola, Polypedilum* sp., *Cryptochironomus* sp., *Stictochironomus* sp., *Chaoborus anomalus, Ceratopogon* sp., Culex fatigans, Ceriagrion sp., Pseudagrion wellani, Pseudagrion sp., Ischnura sp., ***Crocothemis* sp.**, *Brachythemis* sp., *Cloeon bellum*, *Cloeon smaeleni, Cloeon gambiae, Dipseudopsis capensis*, Pyralidae

Fig. 4. Distribution patterns of insect) in each cluster defined by the hierarchical clustering applied on the SOM units. Characteristic taxa were in bold. Dark represents high probability of occurrence, and light indicates lower probability.

The distribution of taxa was visualized on the trained SOM (Fig. 4). Most taxa occurred in cluster II (65 taxa) which was followed by cluster I (60) and cluster III (50 taxa). Cluster I was characterized by the presence of *Pantala flavescens*, *Aulonogyrus* sp., *Laccotrephes ater* and *Cricotopus kisantuensis*. Cluster II was distinguished from the others by presence of *Hyphydrus* sp., *Hydroptila* sp., *Protomacronema* sp., *Hydrometra ambulator, Vallerloria* sp. and Corydalidae. Some taxa contributed to discriminate cluster III (*Canthydrus minutus, Hydrobius* sp., *Yola tuberculata*, *Hydrocanthus micans*, *Hydrocoptus simplex*, *Potamophilus* sp. and *Crocothemis* sp.) (Fig. 4). The result of discriminant function analysis (DFA) allowed a distinction between the clusters defined by the SOM on the basis of biological attributes (Fig. 5). Factorial F1 and F2 axis which explained respectively 26.65% and 25.34% of information were used for ordination. The different groups were clearly discriminated. Groups I and II which were negatively correlated to F1 axis were dissociated to group III. Along F2 axis, group I and II were opposite. They were respectively located at the positive and negative sides of this axis. The test of Monte-Carlo (1000 permutation) proved that the groups were correctly predicted ($p < 0.05$). The contribution of the environmental variables is shown in Table 4. Salinity and conductivity discriminated essentially the various groups. Confusion matrix established by Jacknife technique indicated that 90.55% of samples were correctly occurred in different clusters (Table 5).

Cluster I, II and III had respectively prediction rate of 94.7%; 87.23% and 84.21%.

Table 4. Contribution of environmental parameters according to the two first axis of DFA.Contribution of parameters which discriminated are thick.

Parameters	Axis 1	Axis 2
Transparency	-0.2112	-0.3925
Temperature	0.0002	0.5371
Salinity	0.7110	-0.0929
Conductivity	0.7615	-0.0978
Oxygen	0.0405	0.6194
pH	-0.0036	0.4813
Vegetation	0.2795	-0.4985
Mud	-0.5901	-0.4714
Gravel	-0.2961	0.4555
Sand	0.6716	0.3290
Clay	-0.2946	-0.0891

Table 5. Result of the classification of the DFA by applying a 'leave-one-out' cross-validation test. Number of samples correctly classified are thick.

Clusters	Number of samples	Number of samples predict			
		I	II	III	Percentage of prediction
I	95	**90**	5	0	94.74
II	47	6	**41**	0	87.23
III	38	5	1	**32**	84.21
Total	180	101	47	32	90.55

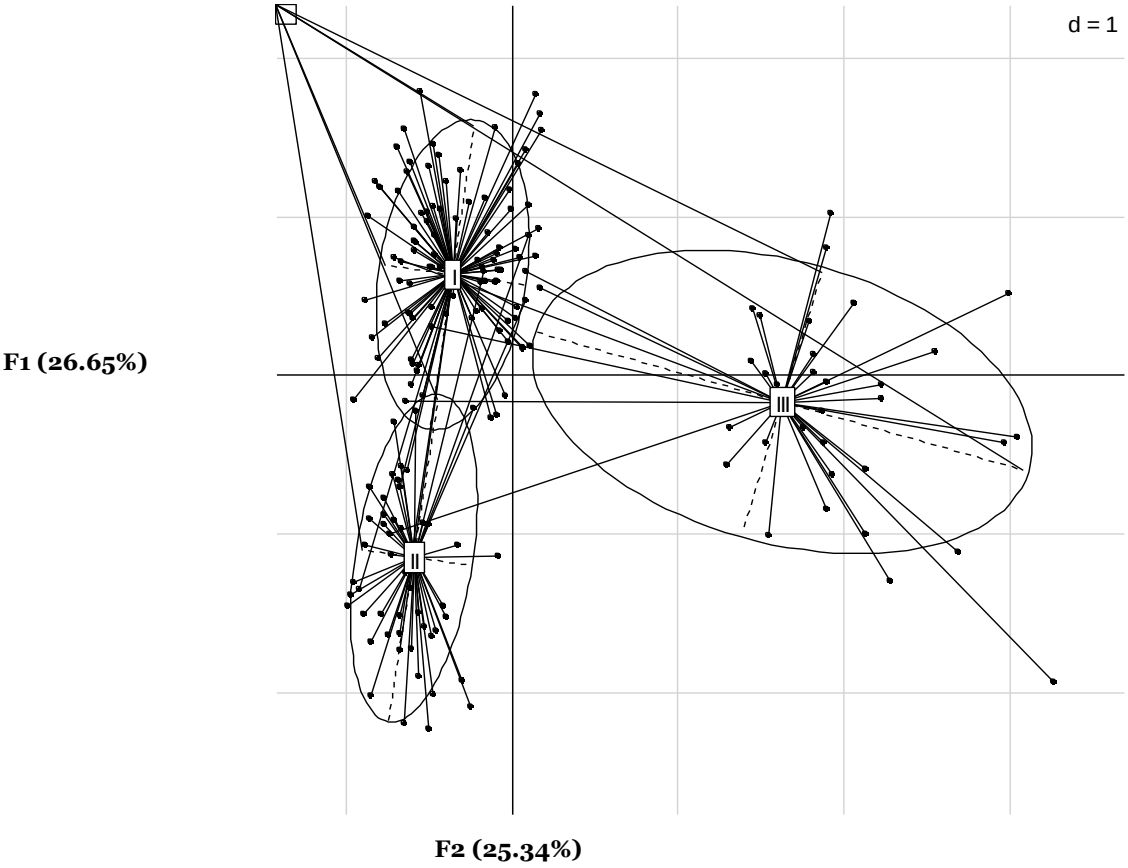


Fig. 5. Discriminant function analysis (DFA) of the group on the trained SOM. Roman numeral (I-III) correspond of the barycenter of each group.

Discussion

The results indicate that 79 taxa of aquatic insect were identified in this study. Among these taxa, five (*Pseudobagous* sp., *Bagous* sp., *Macroplea* sp., *Valleriola* sp. and Corydalidae) are reported for the first time from Côte d'Ivoire. The others taxa were previously recorded (Déjoux *et al*., 1981, Edia *et al*., 2007, 2010). Hemipterans and Coleopterans were mostly the diverse groups. This showed that these orders are the predominant in artificial ponds in Côte d'Ivoire as it was shown in ponds in Italy by Della Bella *et al*. (2005) and in South Africa by Apinda-Legnouo (2007). Céréghino *et al*. (2008) emphasized that particularly, farm ponds contributed strongly to the taxonomic richness of Hemiptera and Coleoptera. In this study, insect assemblages were patterned through an adaptive learning algorithm, the self-organizing map (SOM). Association of Azaguié, Anyama I and Anyama II sites in cluster I may be due to the fact that these sites appertained to the same area. This association suggested a small-scale autocorrelation of assemblages (Céréghino *et al*., 2008). Banco recorded the greatest number of taxa (52). It followed by Azaguié (48), Anyama II (47), Anyama I (46 taxa) and Layo (44 taxa). The difference in richness taxonomic would be also related to the environmental conditions of the sites. Indeed, Banco site is located in National Park of Banco (primary forest). This site is least disturbed indicating relatively better environmental quality. Even so ponds within this site were abandoned. Both characteristics could contribute to host higher number of taxa. Abandoned farm ponds tented to host higher number of taxa as it was shown by Céréghino *et al*. (2008) in some agricultural landscape farm ponds in south-western France. The other sites were located in agricultural landscape. They therefore were disturbed by anthropogenic activities. This situation justifying the decreasing richness observed in these study sites. Conductivity and salinity were the most strongly distinguished among the aquatic insect assemblages. These two parameters were higher in Layo where ponds were fed by brackish water. The decreasing of taxa number in this site may be due to influence of these factors. Reduction of taxa richness and change in the structure of macroinvertebrates by salinity and conductivity was shown by Quintana *et al*. (2006) and Boix *et al*. (2007).

Twenty-one taxa were common to all sites, this seems indicating that those taxa would be ecologically less demanding. The different clusters differ from each other by presence of certain taxa. The taxa richness hosted by fish farm ponds were also related to their ecological patterns.

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