

## Article

# Response of Chironomids to Key Environmental Factors: Perspective for Biomonitoring

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**Simple Summary:** Benthic macroinvertebrates of inland waters are frequently used in biomonitoring. Sometime environmental data associated to species lists are not available; in this situation traits or functional adaptations of species to environment can be considered as a tool to translate the list of species into an index useful to evaluate the environmental quality of a water body.

**Abstract:** Chironomids are the species richest family among macroinvertebrates and are often used as indicators of ecological condition in inland waters. High taxonomic expertise is needed for identification and new species are still described even in the well-known West Palearctic region. Data were filed in a Microsoft Access relational database and analysed using the R environment. Our database comprises data on Chironomid species collected in rivers and lakes in Italy and some other European countries over a period of about 50 years, often associated with physical-chemical data, but in some cases only benthic macroinvertebrates are available with no associated environmental data. In this case, the possibility of estimating water quality with only species composition available is discussed. Traits summarizing the species response to environmental variables were evaluated, with emphasis on natural and man influenced factors: current velocity, water temperature, conductivity, dissolved oxygen, nutrients. Traits calculations was possible using the subset of database including both environmental data and Chironomid abundances. The relations between sites, species and traits were evaluated using correspondence analysis and other multivariate methods. The response of species showed an interaction among different factors, with the possibility to order species along a single environmental gradient, extending from cold running waters to warm standing waters, with few exceptions. The utility and limits of the use of ecological traits are discussed.

**Keywords:** Chironomidae; freshwaters; macroinvertebrates; ecological indicators

## 1. Introduction

The analysis of environmental factors responsible of macroinvertebrate assemblage structure has a long history. Chironomids inside macroinvertebrates are considered a hard to identify group [1], therefore studies concerning macroinvertebrates as bioindicators have been often limited to Ephemeroptera, Plecoptera, Trichoptera (EPT). Taxonomic problems were forwarded to justify this choice, but even though Chironomids are a hard to identify group is not a valid reason to disregard them. Chironomids include species living in almost all water bodies, sometimes present with a very large number of species, so their exclusion can lead to a serious misjudgement in formulating an assessment of the ecological status of waters.

A frequently overlooked problem in the development of a biotic index is the species identification accuracy. Especially in taxonomic hard groups, frequent mistakes in species identification were observed. It must be pointed out that different species within the same genus may show a different indicator value, therefore an index based only on genus identification can lead to misleading conclusions with respect to an index based on the identification of species [2].

It is well known that different Chironomid species colonize different river reaches and lake types, suggesting the existence of krenal, rhithral and potamal species in running waters, and littoral, sublittoral and profundal species in lakes [3]. This can be easily related to few environmental factors as substrate type, water temperature, conductivity, oxygen content, current velocity. This result was evident in running waters just one century ago, with *Orthocladiini* and *Tanytarsini* dominating the upper reaches of rivers and *Chironomini* the lower reaches. A similar separation of tribes was observed in lakes, leading to the separation of oligotrophic *Orthocladius/Tanytarsus* lakes, opposed to eutrophic *Chironomus* lakes [1].

Different environmental factors were considered as responsible of Chironomids distribution. There is a huge number of contributions to this topic; temperature, salinity and oxygen [4], habitat heterogeneity and water quality [5], water temperature [6], submerged plants, sediments organic matter, distance from the mouth of river, pH [7], oxygen [8, 9], depth in lakes [10, 11, 12] were considered key factors responsible of fauna composition.

On the contrary, the attempt to use Chironomid species as indicators of toxic chemicals [13] did not make much progress, being the same tolerant/intolerant species probably tolerant/intolerant to a set of many other different factors. In contrast, studies concerning the response of Chironomid species to habitat alteration were more fruitful [14].

The use of species identification in the assessment of water quality was criticized and refined considering biological and ecological traits [15, 16, 17, 18, 19, 20], suggesting that non-taxonomic aggregation of taxa as similar as possible in their species traits could aid in interpretation of information given by taxonomic list of species. For example, biological traits were preferred to taxonomic species lists in analysing the response of multiple stressors in central European lowland rivers [21]

The problem is that the possibility to translate a list of species into biological and ecological traits needs basic research to prepare this translation.

The aim of the present paper is to discuss the advantages and limitations of the use of ecological traits respect to taxonomic approach, testing a large database with multivariate data analysis. The discussion considers the situations where environmental data associated to species lists are lacking or scanty, so the traits calculation is proposed as a method overcoming the problem of missing environmental data.

## 2. Materials and Methods

### 2.1. Chironomid database

A large database including data on Chironomid species collected in rivers and lakes in Italy and in some other European countries over a period of about 50 years was considered. Physico-chemical data associated with Chironomid samples were available, but only for a subset of data.

Data were filed in a relational database in Microsoft Access© in different **Tables**; the description of these **Tables** is here summarized.

1 **Species:** this **Table** contains a list of the variables used, including both environmental variables (morphometric, physical, chemical) and species belonging to the Chironomidae family; the species were aggregated in species groups (morphotypes), each morphotype corresponding to a genus, a subgenus, a species group or single species [3]. The **Table** contains the species name, author, year of the original description, and

taxonomic status (senior synonym, junior synonym, new combination) as additional fields.

2 **Sites:** this **Table** contains a list of the sampling localities, and other additional fields as latitude, longitude, altitude, source distance (for running waters), depth (for lakes), habitat (krenal, kryal, rhithral, potamal, littoral, sublittoral, profundal, etc.).

3 **Conn:** this **Table** connects each environmental variable or species with the sampling station and a numerical value; for environmental variables is the value measured, for species is an index of abundance (see below); additional fields are sampling year, month, day, sampling tool, bibliographic source of information.

The samples here selected for data analysis included larvae collected with different tools, as Surber net, kick net, hand net, etc., and environmental variables measures (water temperature, conductivity, nutrients, etc.) associated to Chironomid samples, when available. The species abundance value was the number of specimens identified per unit effort, that is the number of specimens identified in the full sample, carrying out the analysis in a reasonable time, at least 15 minutes, at a stereomicroscope LEICA MZ12.5 (<https://archive.epa.gov/water/archive/web/html/ch07b.html>). A crosstab query was then created with sites and other variables describing the sampling site as rows, and environmental variables or species as columns.

The crosstab query created produced a matrix with 9127 sampling sites, including lentic and lotic waters, sampled in different years and months, in Italy above all, but including also data from Algeria [22] and other countries in Europe [14]. The same query included **160** columns, that is a row label, a sequence number, **6** factors, **11** environmental variables and **143** Chironomid taxa. The **11** environmental variables included were: sampling year, sampling month, altitude in m, source distance in km, O<sub>2</sub> content in mg l<sup>-1</sup>, conductivity in µS cm<sup>-1</sup>, pH, total phosphorous in µg l<sup>-1</sup>, N-NO<sub>3</sub> in mg l<sup>-1</sup>, N-NH<sub>4</sub> in µg l<sup>-1</sup>, water temperature in °C. The **4** factors were habitat, river basin, water body, sampling station (**Table S1**).

The taxa included in the analysis were the morphotypes or species groups described in [3] (Rossaro et al., 2022); in the next part of the present work these taxa will be named “species” for simplicity, even if they are often taxa larger than species (genus, group of species).

The sites where less than 5 species were present and species present in less than 50 sites were excluded, leaving a matrix with **91** species in **2258** sites aggregated in 10 different habitats: glacial stream (k=kryal), springs (s=krenal), streams (r=rhithral), lowland rivers (p=potamal), alpine lakes (ALA), lowland large lakes (LL), small lakes (LS), volcanic lakes (V), Mediterranean lakes (ME) and brackish waters (B). These 10 habitats were further divided into 102 waterbodies. The delimitation of these habitats is described in other publications [3, 23, 24, 25].

## 2.2. Data analysis

The crosstab query generated a matrix with n sites as rows and p species + s environmental variables as columns (**nM<sub>p+s</sub>**), which was input in an R script (**Table S1**).

The **M** matrix was separated into an **nL<sub>p</sub>** matrix of species and in a **nR<sub>s</sub>** matrix of environmental variables. Each environmental variable was used to calculate: 1- a correlation matrix between each species and the environmental variables **pC<sub>s</sub>**; 2- a weighted mean of each environmental variable for each species, i.e. means of each environmental variable weighted according to species abundances, which can be considered the optimum for each species; 3- a weighted standard deviation, which can be considered a measure of species tolerance. The weighted mean of each species with each environmental variable generated a trait matrix **pU<sub>s</sub>** with p species as rows and s environmental variables as columns [3, 26]. The presence of missing data in **nR<sub>s</sub>** matrix forced to calculate matrices **pC<sub>s</sub>** and **pU<sub>s</sub>** matrices using only the available data.

The **nL<sub>p</sub>** matrix, including the reduced n (=2258) sites and p (=91) species, and the **pU<sub>s</sub>** matrix, including the same species and s (=11) traits, were analysed with a correspondence

analysis (unconstrained ordination) [27, 28]. The  $nL_p$  values were  $\log(x+1)$  transformed before calculation. As a second step, a canonical constrained ordination was carried out using the transpose of  $nL_p$ , that is  $pL'_n$ , and  $pU_s$  as input matrices. As a last step the  $nL_p$  matrix was post multiplied by the  $pU_s$  matrix, submitted an unconstrained ordination and compared with the previous results. The large number of missing data in the  $nR_s$  matrix hindered to carry out a canonical constrained ordination between the  $nL_p$  and  $nR_s$  matrices.

The **sites x species** matrix  $nL_p$  was post-multiplied by **species x traits**  $pU_s$  matrix to obtain a **site x traits** matrix ( $nL_pU_s$ ), i.e., a matrix with sites as rows and species traits as columns. This  $nL_pU_s$  matrix was also submitted to correspondence analysis.

A discriminant analysis was carried out to test the goodness of classification in different habitats using the Chironomid taxa assemblages: both the  $nL_p$  and the  $nL_pU_s$  matrices were submitted to multiple discriminant analysis, using the habitats as grouping factor.

At last a cluster analysis of site x species matrix was carried out using complete linkage clustering method [28] to detect clusters of species.

3. Results

Measures of the 11 environmental variables were available for a reduced number of sites (Table 1), so the correlations, weighted means and standard deviations of each environmental variable with each species were calculated using sites where both species and environmental data values were available (see Methods); when less than 4 records were available for the couple environmental variable-species, correlations were not calculated and mean values and standard deviations of the environmental variable calculated over all the other species were assigned to these species.

**Table 1.** Number of sites available for each environmental variable: altit=altitude, dist=source distance, year, month, temp=water temperature, cond=conductivity, pH, O<sub>2</sub>=dissolved oxygen, TP=total phosphorous, N-NO<sub>3</sub> =nitrate nitrogen, N-NH<sub>4</sub>=ammonium nitrogen.

Altit	dist	Year	month	temp	pH	cond	O <sub>2</sub>	N-NO <sub>3</sub>	TP	N-NH <sub>4</sub>
9127	7546	9127	9045	5951	4797	4823	5335	3530	2854	2045

Highly significant correlations ( $p<0.01$ ) between species abundance and environmental variables were observed for a reduced number of species (Table 2, Table S2).

**Table 2.** Highly significant correlations (\* = p<0.01) between species and environmental variables, + = positive correlations, - =negative correlations. Detailed results in Table S2.

	alt	dist	y	m	T	pH	cond	O <sub>2</sub>	N-NO <sub>3</sub>	TP	N-NH <sub>4</sub>
<i>Ablabesmyia</i>	+	*	-	*	+	*	+	*	-	*	-
<i>Brillia</i>	-	-	-	+	-	-	*	-	+	-	-
<i>C.anthracinus</i>	+	*	-	+	+	-	+	*	-	-	-
<i>C.bicinctus</i>	-	-	+	-	-	*	+	+	+	-	-
<i>C.fuscus</i>	+	*	-	+	-	-	*	+	-	-	*
<i>C.plumosus</i>	+	*	-	*	-	*	-	+	*	+	-
<i>C.thummi</i>	+	-	+	+	-	+	*	-	+	+	-
<i>C.tremulus</i>	-	-	-	-	-	-	+	+	-	-	-
<i>C.trifascia</i>	-	+	-	-	-	+	+	+	+	-	-
<i>Chaetocladius</i>	+	*	-	*	+	-	*	+	-	+	-
<i>Cladopelma</i>	+	-	*	+	+	*	+	-	+	-	-
<i>Cladotanytarsus</i>	+	*	-	*	-	-	+	*	+	-	-
<i>Conchapelopia</i>	+	-	-	*	+	-	*	+	*	-	*
<i>Corynoneura</i>	+	*	-	+	+	*	-	*	-	*	*
<i>Cryptochironomus</i>	+	*	-	*	-	*	+	*	-	*	*
<i>D.aberrata</i>	+	+	+	+	-	-	+	+	+	-	-
<i>D.cinerella</i>	-	+	+	-	+	+	-	-	-	-	-
<i>D.dampfi</i>	+	-	+	+	-	+	-	+	-	-	-
<i>D.latitarsis</i>	+	*	-	*	+	*	-	*	+	-	-
<i>D.tonsa</i>	+	*	-	+	+	-	*	-	*	+	*
<i>D.zernyi</i>	+	*	-	+	*	+	-	*	+	*	-
<i>Demicryptochironomus</i>	-	-	-	*	+	-	-	+	-	+	+
<i>Diamesa</i>	+	*	-	+	*	+	-	*	+	-	-
<i>Dicrotendipes</i>	+	*	-	*	+	-	*	-	+	*	*
<i>E.claripennis</i>	+	*	-	*	+	-	-	*	-	-	-
<i>E.devonica</i>	-	+	+	*	+	+	+	-	+	+	-
<i>E.minor</i>	+	*	-	+	*	+	-	*	-	*	-
<i>Endochironomus</i>	+	*	-	*	-	+	-	+	-	-	*
<i>Eudactylocladius</i>	+	+	*	+	*	-	-	+	-	-	-
<i>Eukiefferiella</i>	+	+	+	-	+	+	-	-	+	-	-
<i>Euorthocladius</i>	+	*	-	*	+	*	-	+	-	-	*
<i>Glyptotendipes</i>	+	-	+	+	+	-	+	*	-	-	-
<i>Harnischia</i>	+	*	-	*	+	*	+	*	-	-	*
<i>Heleniella</i>	+	*	-	+	*	+	-	*	+	-	-
<i>Heterotrissocladius</i>	+	*	-	+	*	+	*	-	*	+	*
<i>Holotanypus</i>	+	-	*	-	-	-	*	+	*	-	*
<i>I.sylvestris</i>	-	-	-	*	-	-	+	-	+	-	-
<i>M.atrofasciata</i>	+	*	-	*	+	*	-	*	-	*	*
<i>M.notescens</i>	+	+	+	-	+	+	+	-	+	+	+
<i>M.radialis</i>	+	+	-	-	-	+	-	*	+	*	-
<i>Macropelopia</i>	+	*	+	+	*	+	-	*	+	-	-
<i>Mesorthocladius</i>	+	*	-	+	*	+	-	*	-	-	-
<i>Microchironomus</i>	-	+	-	-	-	+	-	+	*	-	*
<i>Microtendipes</i>	+	-	-	*	-	-	+	*	-	-	-
<i>Nanocladius</i>	-	-	+	+	+	-	*	+	-	-	-
<i>O.decoratus</i>	+	-	*	+	*	-	-	+	+	+	-
<i>O.oblidens</i>	+	-	-	*	-	-	*	-	+	-	*
<i>Orthocladius</i>	-	-	+	*	-	*	+	+	-	-	-
<i>P.austriacus</i>	+	-	+	+	-	+	-	+	-	-	+
<i>P.laetum</i>	+	-	+	+	-	+	+	+	+	-	-
<i>P.limbatellus</i>	+	-	*	-	*	-	*	+	*	-	-
<i>P.nubeculosum</i>	+	-	*	-	*	-	+	*	-	-	*

<i>P.rufiventris</i>	-	-	+	*	-	+	+	-	-	+	+	+
<i>P.skirwithensis</i>	-	+	+	-	-	-	+	-	-	-	-	-
<i>P.sordens</i>	-	+	-	-	-	-	+	+	-	-	-	+
<i>P.sordidellus</i>	+	-	+	+	+	-	+	-	+	-	*	-
<i>Pagastiella</i>	+	-	*	+	-	-	+	+	*	+	-	-
<i>Parachironomus</i>	-	-	-	*	-	-	+	+	+	+	-	-
<i>Paracladius</i>	+	-	+	+	+	-	+	-	+	-	-	+
<i>Paracladopelma</i>	+	*	-	*	+	*	-	+	-	+	+	*
<i>Paracricotopus</i>	-	-	+	+	-	+	-	+	-	-	+	+
<i>Parakiefferiella</i>	-	+	+	+	-	+	+	-	+	*	+	-
<i>Paralauterborniella</i>	+	*	-	*	+	*	-	*	+	*	+	-
<i>Parametriocnemus</i>	+	*	-	+	+	+	-	*	-	*	-	-
<i>Paratanytarsus</i>	+	*	-	*	-	-	-	+	-	+	*	-
<i>Paratendipes</i>	-	*	-	*	-	*	-	+	*	-	+	*
<i>Paratrissocladius</i>	+	+	+	+	-	+	-	+	-	+	-	-
<i>Parorthocladius</i>	+	*	-	+	*	+	-	*	-	*	+	-
<i>Phaenopsectra</i>	+	*	-	+	+	-	-	+	-	+	*	-
<i>Potthastia</i>	-	-	+	*	-	+	+	-	-	-	-	-
<i>Prodiamesa</i>	+	+	+	*	+	+	-	*	+	*	-	-
<i>Pseudochironomus</i>	+	-	*	-	-	-	-	+	-	+	*	-
<i>Pseudodiamesa</i>	+	*	+	+	*	+	-	*	-	*	-	-
<i>Psilocricotopus</i>	-	-	+	+	+	+	+	+	+	-	-	-
<i>Rheocricotopus</i>	-	-	+	+	-	+	+	-	-	-	+	+
<i>Rheopelopia</i>	+	+	*	+	+	-	*	+	-	-	+	-
<i>Rheotanytarsus</i>	+	-	+	+	+	-	+	-	+	-	+	-
<i>Stempellina</i>	+	*	-	*	+	+	-	+	+	+	*	+
<i>Sympotthastia</i>	+	-	+	*	-	-	+	-	-	-	-	-
<i>Synorthocladius</i>	+	*	-	+	*	-	-	-	-	-	-	-
<i>Tegarius</i>	+	*	-	*	+	+	-	-	-	+	*	-
<i>Tanytus</i>	-	+	-	+	+	+	+	+	-	-	-	+
<i>Tanytarsus</i>	+	*	-	*	+	*	-	*	+	*	-	*
<i>Thienemannimyia</i>	+	*	-	+	+	+	-	+	-	+	-	-
<i>Tripodura</i>	+	*	-	*	+	*	+	+	+	+	-	-
<i>Trissopelepis</i>	+	+	-	*	-	-	-	-	-	-	-	-
<i>Tvetenia</i>	+	+	+	*	-	+	+	-	-	-	-	-
<i>Uresipedium</i>	+	-	-	-	-	-	+	+	+	-	-	-
<i>Virgatanytarsus</i>	+	-	+	+	+	+	+	+	-	-	-	-
<i>Xenochironomus</i>	+	-	*	-	*	-	-	+	*	-	-	-
<i>Zavrelimyia</i>	+	*	-	+	*	+	-	*	-	+	-	-

The weighted means, considered the optimum values for all species [27], were used to create a **species x traits** matrix  $pU_s$  with p species as rows and s environmental variables as columns (**Table 3**). Weighted standard deviation as a measure of species tolerance and the number of observations available are in **Table S3**.

**Table 3.** Matrix of traits: weighted mean of each environmental variable for each species. Standard deviations and number of sites used in Table S3.

Traits	altit	dist	year	month	temp	pH	cond	O <sub>2</sub>	N-NO <sub>3</sub>	TP	N-NH <sub>4</sub>
<i>Ablabesmyia</i>	516	41	1999	6	18	7	273	7	1	69	239
<i>Brillia</i>	522	19	1988	6	17	7	328	5	2	207	973
<i>C.anthracinus</i>	319	55	1981	6	17	8	239	8	1	53	119
<i>C.bicinctus</i>	220	109	1993	6	21	7	775	5	3	212	885
<i>C.fuscus</i>	809	28	1992	6	16	7	415	4	2	34	502
<i>C.plumosus</i>	212	95	1981	6	20	7	349	6	1	127	469
<i>C.thummi</i>	223	122	1993	6	22	7	669	4	2	335	920
<i>C.tremulus</i>	354	94	1990	6	20	7	455	4	1	143	372
<i>C.trifascia</i>	269	65	1996	6	21	7	569	3	3	141	560
<i>Chaetocladius</i>	1872	4	1996	8	8	6	75	7	1	80	241
<i>Cladopelma</i>	284	40	1983	7	19	7	281	7	1	98	410
<i>Cladotanytarsus</i>	361	24	1989	6	17	8	318	8	1	57	101
<i>Conchapelopia</i>	414	53	1987	6	18	7	632	5	2	99	696
<i>Corynoneura</i>	1229	33	1995	7	15	7	180	6	0	26	84
<i>Cryptochironomus</i>	269	54	1982	6	18	7	281	8	1	67	218
<i>D.aberrata</i>	1329	15	1985	6	12	7	279	4	2	246	457
<i>D.cinerella</i>	1272	35	1998	6	11	7	218	4	1	178	626
<i>D.dampfi</i>	1384	7	1990	6	11	7	147	8	1	114	428
<i>D.latitarsis</i>	2089	4	1999	8	7	6	108	8	1	61	90
<i>D.tonsa</i>	1051	22	1991	6	15	7	253	5	2	124	509
<i>D.zernyi</i>	1917	6	1996	8	8	6	127	7	0	53	153
<i>Demicryptochironomus</i>	217	62	1977	7	20	7	314	8	1	116	298
<i>Diamesa</i>	1735	6	1992	8	8	6	158	6	0	50	118
<i>Dicrotendipes</i>	254	74	1987	6	20	7	513	6	1	72	278
<i>E.claripennis</i>	830	33	1994	6	17	7	433	5	1	101	606
<i>E.devonica</i>	305	79	1998	6	21	7	441	4	2	154	505
<i>E.minor</i>	1433	15	1993	7	11	7	219	5	1	76	486
<i>Endochironomus</i>	215	90	1981	7	19	8	352	4	1	64	165
<i>Eudactylocladius</i>	1144	39	1995	7	15	7	248	6	1	100	596
<i>Eukiefferiella</i>	511	81	2000	6	19	7	352	3	1	190	509
<i>Euorthocladius</i>	702	59	1994	6	18	7	394	4	1	218	467
<i>Glyptotendipes</i>	164	176	1985	7	21	7	264	4	1	86	297
<i>Harnischia</i>	205	155	1991	6	21	8	535	5	1	73	397
<i>Heleniella</i>	1978	6	1998	8	8	6	62	7	0	29	59
<i>Heterotrissocladius</i>	1604	14	1995	7	11	7	69	7	0	13	28
<i>Holotanypus</i>	367	48	1985	6	17	7	300	8	1	67	216
<i>I.sylvestris</i>	280	118	1990	6	22	7	649	4	1	126	543
<i>M.atrofasciata</i>	807	35	1994	6	17	7	382	4	1	105	559
<i>M.notescens</i>	651	45	1989	6	19	7	600	2	4	180	1107
<i>M.radialis</i>	743	62	1996	7	16	7	187	8	1	81	414
<i>Macropelopia</i>	1081	32	1998	7	13	7	180	7	1	61	219
<i>Mesorthocladius</i>	1354	16	1994	6	13	7	224	5	1	64	381
<i>Microchironomus</i>	233	64	1988	6	16	8	296	7	1	38	49
<i>Microtendipes</i>	341	48	1990	6	20	7	459	6	2	80	409
<i>Nanocladius</i>	252	108	1990	7	24	7	497	4	1	267	616
<i>O.decoratus</i>	425	107	1997	5	21	7	528	5	2	242	886
<i>O.oblidens</i>	261	66	1987	5	19	7	422	6	1	87	186
<i>Orthocladius.sstr</i>	331	69	1994	5	20	7	560	4	2	199	663
<i>P.austriacus</i>	1899	3	2000	8	10	7	81	8	0	5	51
<i>P.laetum</i>	312	111	1990	6	23	7	681	4	3	283	974
<i>P.limbatellus</i>	497	29	1980	6	17	7	207	7	1	66	194
<i>P.nubeculosum</i>	302	72	1983	6	19	7	357	6	1	78	334
<i>P.rufiventris</i>	432	42	1996	6	20	7	678	4	2	176	778
<i>P.skirwithensis</i>	1193	20	1994	7	11	7	249	5	1	70	200

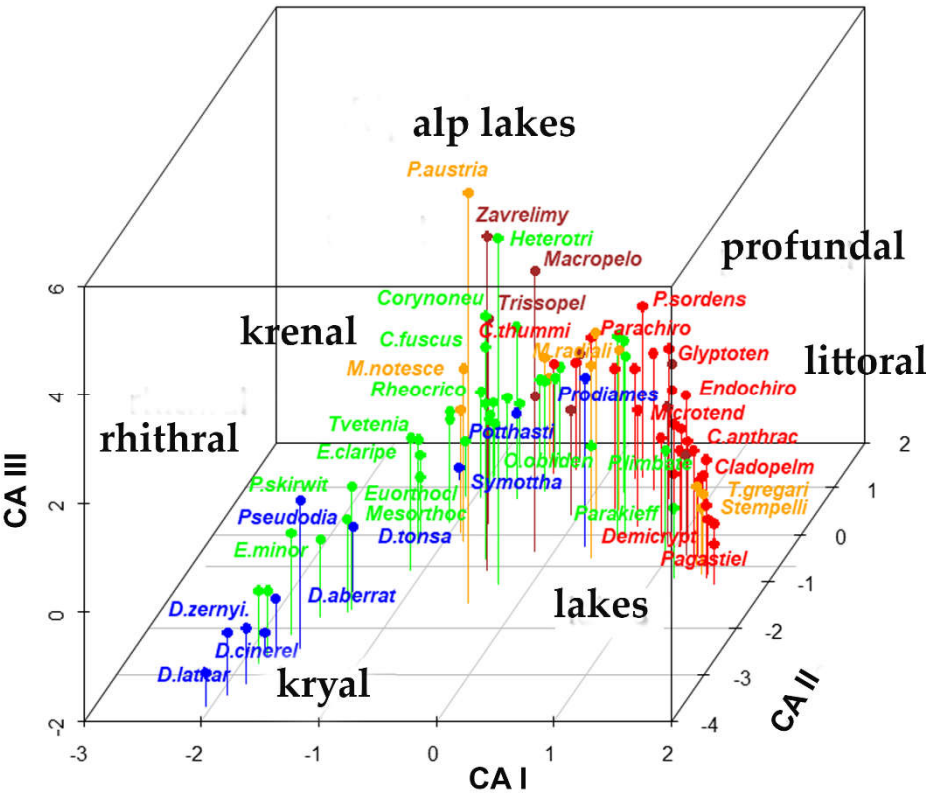


<i>P.sordens</i>	123	179	1990	6	22	7	596	2	1	116	718
<i>P.sordidellus</i>	693	35	2001	6	19	7	214	6	1	92	283
<i>Pagastiella</i>	294	50	1979	6	20	7	263	9	1	60	54
<i>Parachironomus</i>	136	143	1986	6	23	7	466	4	2	161	409
<i>Paracladius</i>	607	54	1992	6	17	7	291	6	1	105	772
<i>Paracladopelma</i>	530	54	1997	5	17	8	213	8	1	57	50
<i>Paracricotopus</i>	391	38	1996	6	19	7	506	5	1	225	1292
<i>Parakiefferiella</i>	426	36	1987	5	16	7	208	9	1	47	51
<i>Paralauterborniella</i>	378	48	1992	6	13	7	236	9	1	16	31
<i>Parametrioctenemus</i>	896	19	1994	6	15	7	360	5	1	73	382
<i>Paratanytarsus</i>	408	85	1988	6	21	7	427	5	2	60	391
<i>Paratendipes</i>	370	33	1979	6	16	8	308	7	1	45	102
<i>Paratrissocladius</i>	535	17	1996	6	16	7	623	7	1	75	428
<i>Parorthocladius</i>	1806	4	1997	8	10	6	187	6	0	55	122
<i>Phaenopsectra</i>	335	69	1995	6	21	7	450	6	1	127	812
<i>Potthastia</i>	211	107	1996	5	22	7	349	4	2	140	448
<i>Prodiamesa</i>	557	53	1990	6	16	7	263	7	1	92	389
<i>Pseudochironomus</i>	290	36	1981	6	20	7	273	8	1	55	123
<i>Pseudodiamesa</i>	1733	16	1993	7	9	7	109	5	0	28	135
<i>Psilocricotopus</i>	237	90	1994	7	22	7	503	4	2	265	457
<i>Rheocricotopus</i>	501	46	1992	6	18	7	698	4	3	225	1300
<i>Rheopelopia</i>	226	249	1993	6	18	7	395	5	3	201	573
<i>Rheotanytarsus</i>	225	152	1992	6	20	7	452	4	2	456	393
<i>Stempellina</i>	322	51	1984	6	16	7	215	9	1	55	52
<i>Sympotthastia</i>	246	88	2003	4	21	7	365	4	1	122	94
<i>Synorthocladius</i>	313	81	1996	6	21	7	444	4	1	188	764
<i>Tegarius</i>	339	50	1981	6	17	7	228	8	1	42	74
<i>Tanytus.sstr</i>	170	133	1990	7	24	7	763	4	2	283	1448
<i>Tanytarsus</i>	573	65	1996	6	19	7	480	6	2	67	320
<i>Thienemannimyia</i>	599	55	2002	6	17	7	492	6	1	16	38
<i>Tripodura</i>	214	156	1995	7	23	7	853	5	1	202	459
<i>Trissopelopia</i>	680	38	1992	7	16	7	438	3	0	22	428
<i>Tvetenia</i>	668	38	1995	6	18	7	429	5	2	93	387
<i>Uresipedium</i>	249	129	1990	7	22	7	998	5	4	191	909
<i>Virgatanytarsus</i>	375	49	1995	7	22	7	951	3	5	114	1417
<i>Xenochironomus</i>	224	56	1976	6	20	7	387	7	1	59	174
<i>Zavrelimyia</i>	1480	11	1997	7	12	7	176	7	0	29	41

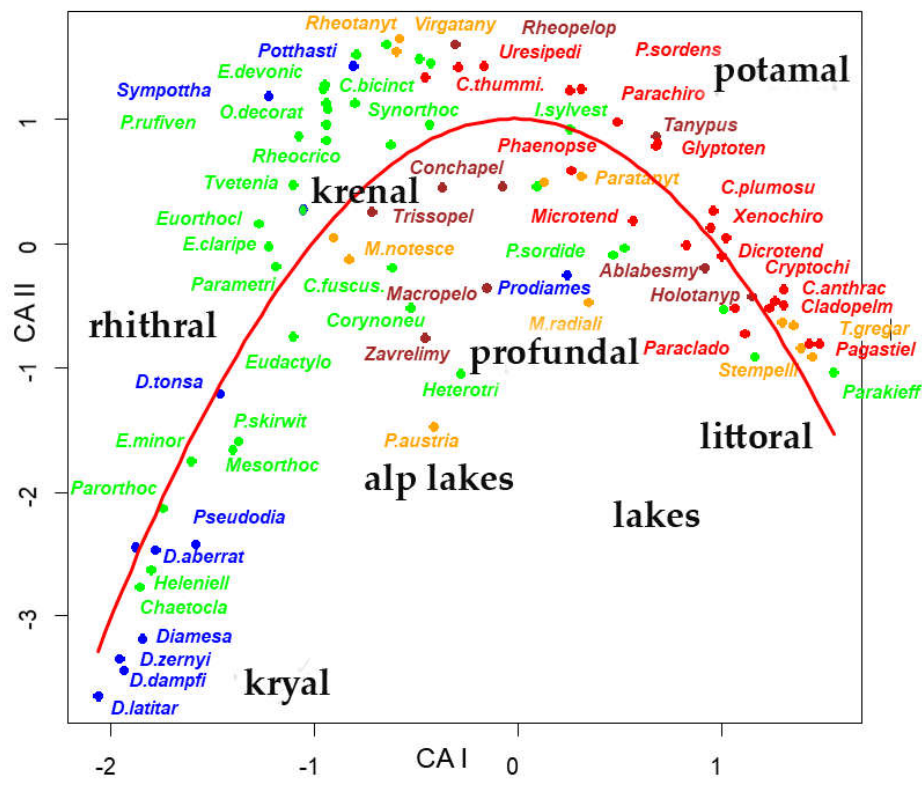
The **sites x species** matrix „L<sub>P</sub>“ was submitted to a correspondence analysis; three major gradients (**Figs. 1, 2, Figs. S1, S2, Table 4**) were evidenced, the former accounting for 7.6 % of total variance, the second 5.1 %, the third 3.8 % of the total variance, with eigenvalues equal to 0.71, 0.48, 0.35 respectively; the species and sites ordered in the plane of the two axes showed the typical horseshow or arch effect [28]. The first gradient separated running waters from standing waters, the second separated upstream stations from downstream stations in running waters, with the following sequence (**Figs. 1, 2, Figs. S1, S2**): 1- frigo-stenothermal species living in kryal were plotted in the bottom left of the graph; 2- rhithral species living in streams were plotted above the former; 3- eurithermal species, living in potamal, were plotted at the apex of the arch, extending from the top to the right part of the plot; 4- species living preferably in lentic waters, were plotted on the right part of the graph; 5- species living in springs were plotted in the central part of the area. A further separation was of species from small alpine lakes as *Paratanytarsus austriacus*, *Heterotrissocladius*, *Corynoneura* and *Zavrelimyia* plotted in the centre of the area, species characterizing profundal zone of lowland large lakes as *Micropsectra radialis*, *Paracladopelma* also plotted closer to the centre of the area at right of alpine lakes species, small prealpine and volcanic lakes were grouped on the right of the plot. This separation was



still better emphasized in a 3D plot (Fig. 1, Fig. S1), where kryal, rhithral, krenal, potamal and lentic species was evident.



**Figure 1.** plot of the species scores in the first 3 axes resulting from CA carried out from sites x species ( $nL_p$ ) matrix (the full set of species names is in Fig. S1).



**Figure 2.** plot of the species scores in the first 2 axes resulting from CA carried out from sites x species ( $nL_p$ ) matrix and the fitted second degree polynomial (the full set of species names is in Fig. S2).

**Table 4.** Correspondence analysis (CA) results of sites x species matrix; eigenvalues, proportion of variance explained, factor loadings of species. Results of other multivariate analysis in Tables S4, S5, S6.

	Eigenvalue	CA1	CA2	CA3	
	Proportion Explained	0.715	0.480	0.353	
		7.6 %	5.1 %	3.8 %	
species	CA1	CA2	CA3	CA4	CA5
<i>Ablabesmyia</i>	0.919	-0.194	0.514	-0.087	0.548
<i>Brillia</i>	-1.057	0.277	0.025	0.692	-2.146
<i>C.anthracinus</i>	1.237	-0.522	-0.010	0.028	0.863
<i>C.bicinctus</i>	-0.431	1.451	-0.135	-0.312	0.055
<i>C.fuscus</i>	-0.616	-0.201	1.636	0.596	-1.708
<i>C.plumosus</i>	0.949	0.129	-0.162	-0.940	0.818
<i>C.thummi</i>	-0.291	1.422	-0.023	-0.720	0.161
<i>C.tremulus</i>	-0.434	0.957	0.032	-0.587	-0.194
<i>C.trifascia</i>	-0.796	1.521	-0.882	0.865	1.516
<i>Chaetocladius</i>	-1.857	-2.763	-0.646	-1.242	-0.403
<i>Cladopelma</i>	1.309	-0.493	-0.477	-0.072	0.295
<i>Cladotanytarsus</i>	1.358	-0.655	-0.696	0.586	-0.098
<i>Conchapelopia</i>	-0.074	0.459	-0.097	0.514	-1.571
<i>Corynoneura</i>	-0.529	-0.524	2.502	0.065	0.669
<i>Cryptochironomus</i>	1.263	-0.465	-0.630	0.280	0.059
<i>D.aberrata</i>	-1.781	-2.463	-1.056	-1.494	-0.697
<i>D.cinerella</i>	-1.878	-2.447	-1.693	-1.271	2.449
<i>D.dampfi</i>	-1.940	-3.429	-0.850	-1.640	-0.151
<i>D.latitarsis</i>	-2.065	-3.645	-1.417	-2.169	0.678
<i>D.tonsa</i>	-1.465	-1.214	-0.817	-0.296	-0.145
<i>D.zernyi</i>	-1.959	-3.345	-0.939	-1.806	0.568
<i>Demicryptochironomus</i>	1.434	-0.812	-0.996	1.185	-0.417
<i>Diamesa</i>	-1.845	-3.178	-0.972	-2.015	0.141
<i>Dicrotendipes</i>	1.006	-0.101	-0.356	-0.262	-0.112
<i>E.claripennis</i>	-1.225	-0.020	-0.501	0.222	-0.099
<i>E.devonica</i>	-0.949	1.278	-1.057	1.190	2.353
<i>E.minor</i>	-1.603	-1.747	-0.569	-0.480	-0.716
<i>Endochironomus</i>	0.958	0.265	0.350	-2.380	0.031
<i>Eudactylocladius</i>	-1.104	-0.755	0.436	-0.058	0.438
<i>Eukiefferiella</i>	-1.079	0.865	-1.019	1.134	2.492
<i>Euorthocladius</i>	-1.274	0.159	-1.063	0.386	1.313
<i>Glyptotendipes</i>	0.676	0.780	0.775	-3.588	-0.147
<i>Harnischia</i>	0.688	0.808	-0.011	-1.820	0.997
<i>Heleniella</i>	-1.804	-2.633	-0.773	-1.272	0.180
<i>Heterotrissocladius</i>	-0.280	-1.046	4.377	1.436	1.791
<i>Holotanypus</i>	1.153	-0.430	-0.172	0.144	0.055
<i>I.sylvestris</i>	0.254	0.924	0.785	-2.154	0.230
<i>M.atrofasciata</i>	-0.905	0.051	0.245	0.412	-0.693
<i>M.notescens</i>	-0.829	-0.132	1.177	0.706	-4.154
<i>M.radialis</i>	0.347	-0.475	1.536	1.026	1.007
<i>Macropelopia</i>	-0.153	-0.352	3.178	1.196	-0.538
<i>Mesorthocladius</i>	-1.403	-1.659	-0.277	-0.325	-0.007
<i>Microchironomus</i>	1.306	-0.371	-0.285	-0.938	2.111
<i>Microtendipes</i>	0.567	0.188	0.125	-0.238	-0.445
<i>Nanocladius</i>	-0.484	1.488	-0.374	-0.262	0.037
<i>O.decoratus</i>	-0.942	1.133	-0.757	0.681	2.077
<i>O.oblidens</i>	0.094	0.460	-0.754	0.992	0.153
<i>Orthocladius</i>	-0.938	1.087	-0.805	0.841	1.154

<i>P.austriacus</i>	-0.416	-1.470	5.558	1.585	3.067
<i>P.laetum</i>	-0.455	1.332	0.003	-0.501	-0.761
<i>P.limbatellus</i>	1.007	-0.534	0.015	0.717	-0.108
<i>P.nubeculosum</i>	0.825	-0.007	-0.203	-0.619	-0.422
<i>P.rufiventris</i>	-0.942	0.961	-0.420	0.628	-0.254
<i>P.skirwithensis</i>	-1.373	-1.588	0.248	-0.165	-0.518
<i>P.sordens</i>	0.314	1.250	1.147	-4.057	-0.605
<i>P.sordidellus</i>	0.468	-0.087	1.744	0.222	1.588
<i>Pagastiella</i>	1.551	-1.038	-1.272	1.861	-0.875
<i>Parachironomus</i>	0.488	0.986	0.499	-2.691	0.481
<i>Paracladius</i>	0.525	-0.032	1.335	0.378	1.521
<i>Paracladopelma</i>	1.115	-0.726	0.669	1.077	1.159
<i>Paracricotopus</i>	-0.955	1.250	-0.629	1.008	0.242
<i>Parakiefferiella</i>	1.169	-0.910	-0.724	1.579	-0.538
<i>Paralauterborniella</i>	1.448	-0.908	-0.672	1.340	0.008
<i>Parametriocnemus</i>	-1.192	-0.185	-0.090	0.465	-1.188
<i>Paratanytarsus</i>	0.310	0.541	0.964	-1.438	0.061
<i>Paratendipes</i>	1.069	-0.517	-0.422	-0.069	-0.062
<i>Paratrisocladius</i>	-0.628	0.793	1.167	0.954	-4.519
<i>Parorthocladius</i>	-1.743	-2.135	-0.132	-0.590	0.310
<i>Phaenopsectra</i>	0.264	0.587	0.561	-0.492	-0.300
<i>Potthastia</i>	-0.808	1.435	-0.994	1.057	2.775
<i>Prodiamesa</i>	0.244	-0.253	1.121	0.684	-0.459
<i>Pseudochironomus</i>	1.482	-0.807	-1.096	0.999	-0.632
<i>Pseudodiamesa</i>	-1.583	-2.418	0.699	-0.648	-0.671
<i>Psilocricotopus</i>	-0.645	1.603	-0.508	0.297	0.286
<i>Rheocricotopus</i>	-0.943	0.828	-0.053	0.621	-1.605
<i>Rheopelopia</i>	-0.308	1.607	-0.017	-0.522	-0.639
<i>Rheotanytarsus</i>	-0.582	1.653	-0.516	0.271	0.875
<i>Stempellina</i>	1.393	-0.837	-0.799	1.436	-0.372
<i>Sympotthastia</i>	-1.227	1.186	-1.761	1.595	5.236
<i>Synorthocladius</i>	-0.800	1.135	-0.447	0.917	0.710
<i>Tanypus</i>	0.680	0.868	0.408	-2.783	0.910
<i>Tanytarsus</i>	0.132	0.499	1.312	-0.202	0.524
<i>Tegarius</i>	1.298	-0.639	-0.542	0.752	-0.063
<i>Thienemannimyia</i>	-0.375	0.449	0.184	1.309	0.383
<i>Tripodura</i>	0.253	1.230	0.003	-1.328	0.792
<i>Trissopelopia</i>	-0.715	0.249	1.784	1.108	-5.422
<i>Tvetenia</i>	-1.105	0.468	-0.284	0.878	0.223
<i>Uresipedilum</i>	-0.166	1.434	0.423	-1.454	-1.375
<i>Virgatanytarsus</i>	-0.595	1.541	-0.046	0.412	-2.829
<i>Xenochironomus</i>	1.025	0.052	-0.318	-0.857	-0.021
<i>Zavrelimyia</i>	-0.459	-0.756	4.151	1.508	0.321

A polynomial of second degree was fitted to species scores of the two first axes (**Fig. 2**), resulting in a multiple R-squared 0.6845, adjusted R-squared 0.6773, F-statistic: 95.47 with 2 and 88 degrees of freedom (D.F.), p-value 2.2e-16, residual standard error 0.7344 with 88 D.F. The species more distant from the parabolic curve are visible in **Fig. 2** and are also evident in **Fig. S2**, where all species names are plotted. Species from small Alpine lakes and from profundal areas of large lakes are the ones more deviating from parabolic curve.

The environmental variables were included as passive variables in the map and were converted into factors with 6 different levels; when missing data were present a level, plotted as void circles, grouped these data. The factors included were: habitat, station (**Fig. 3**), altitude, source distance (**Fig. 4**), temperature, conductivity (**Fig. 5**), oxygen, total phosphorous (**Fig. 6**), nitrate and ammonium nitrogen (**Fig. 7**).

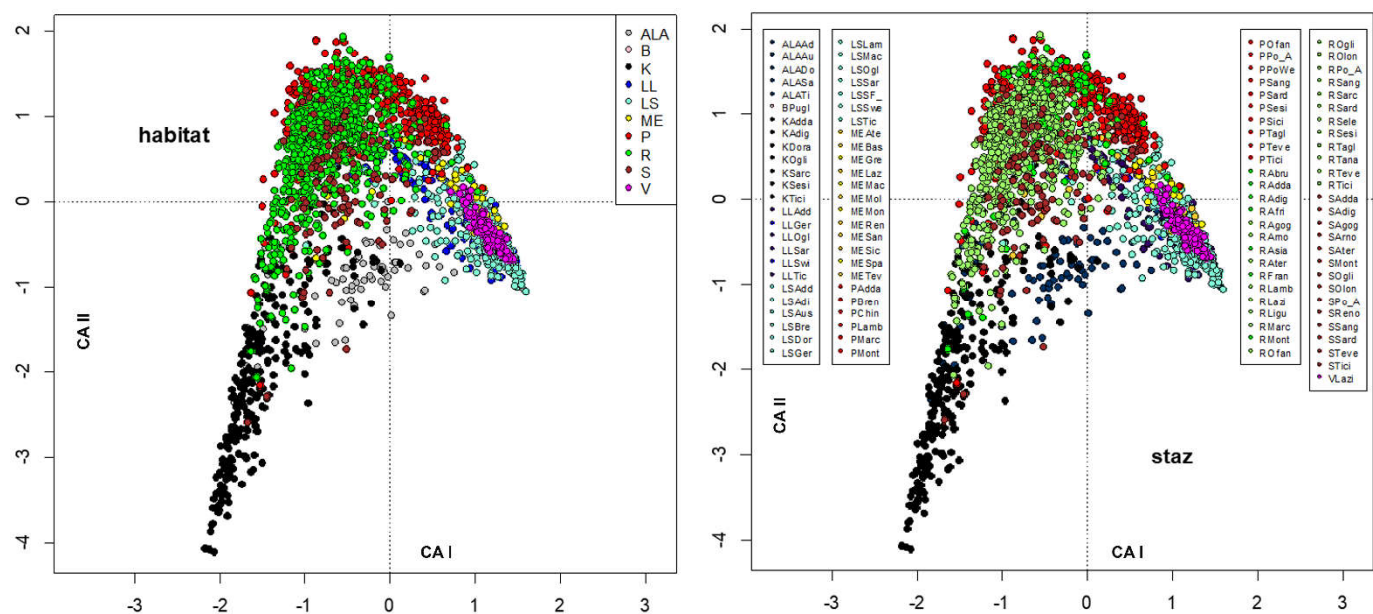


Figure 3. plot of sites scores in the first 2 axes resulting from CA of sites x species ( $nL_p$ ) matrix, by marking sites with different colours according to habitat (left) and to sampling station (right).

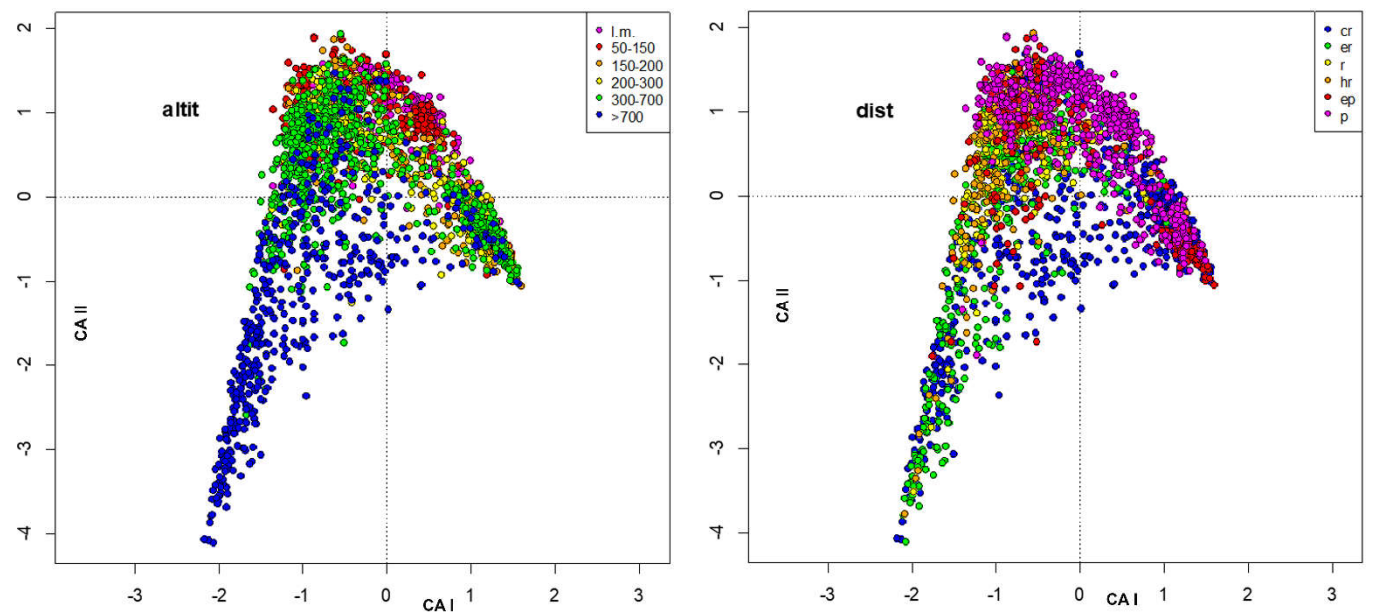
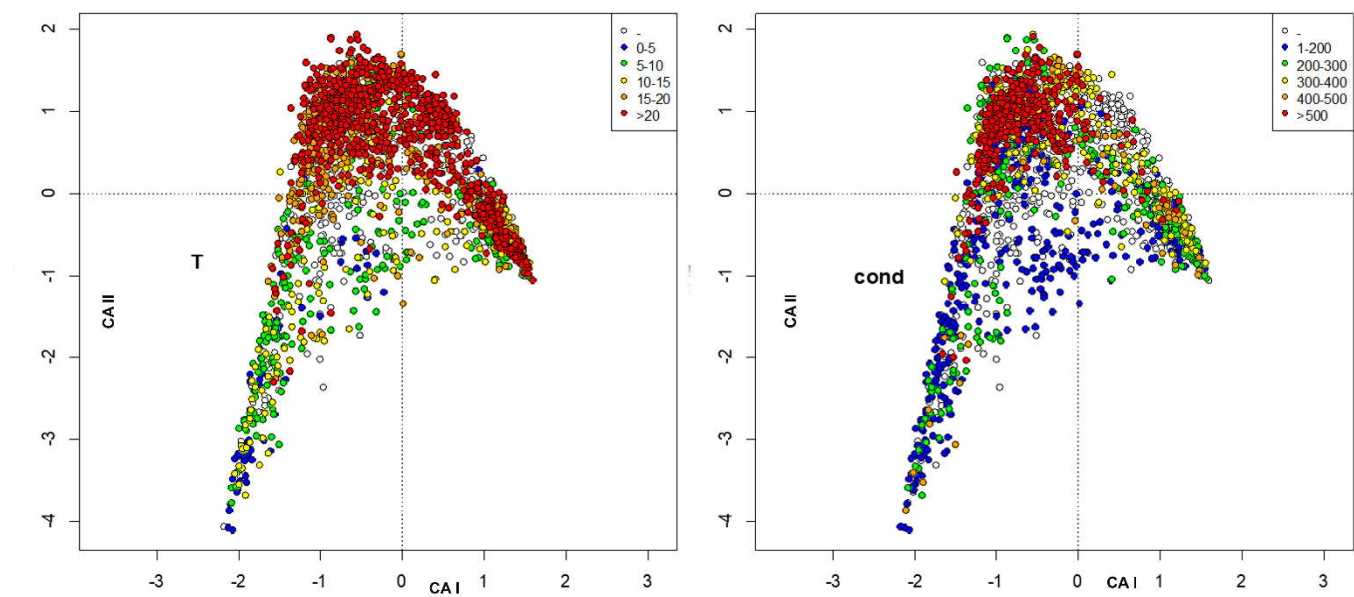
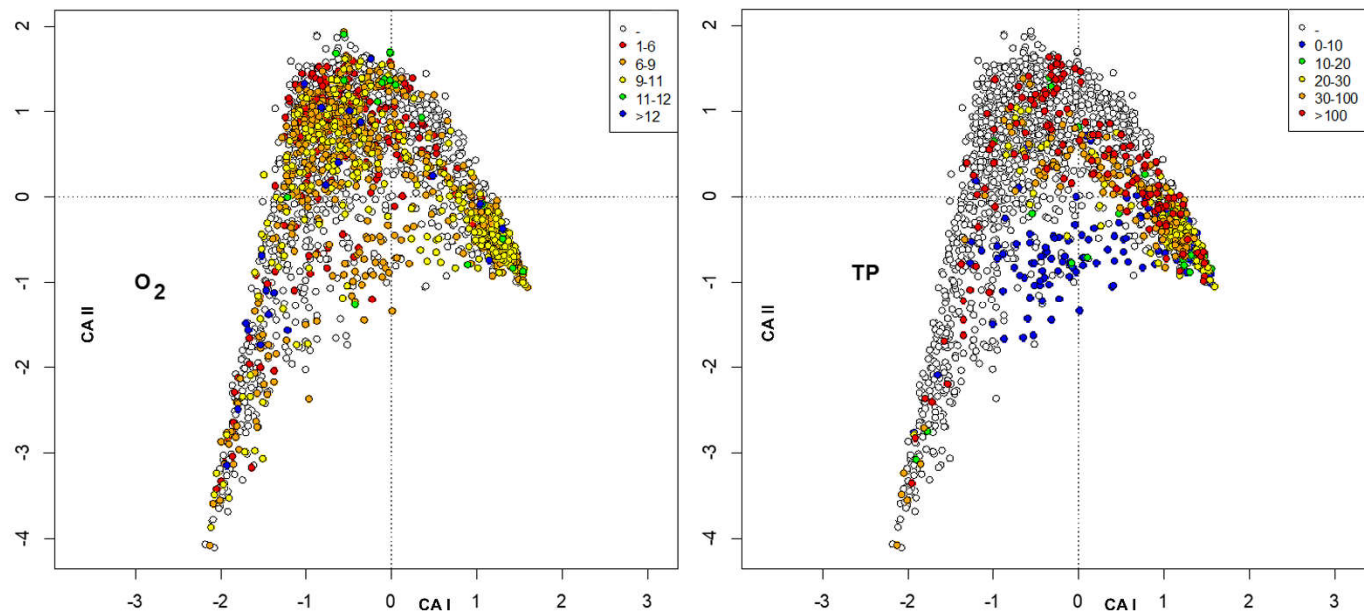


Figure 4. plot of sites scores in the first 2 axes resulting from CA of sites x species ( $nL_p$ ) matrix, by marking sites with different colours according to altitude (left) and to source distance (right); cr: crenal, er: epirhithral, r: rhithral, hp: hyporhithral, ep: epipotamal, p: potamal.

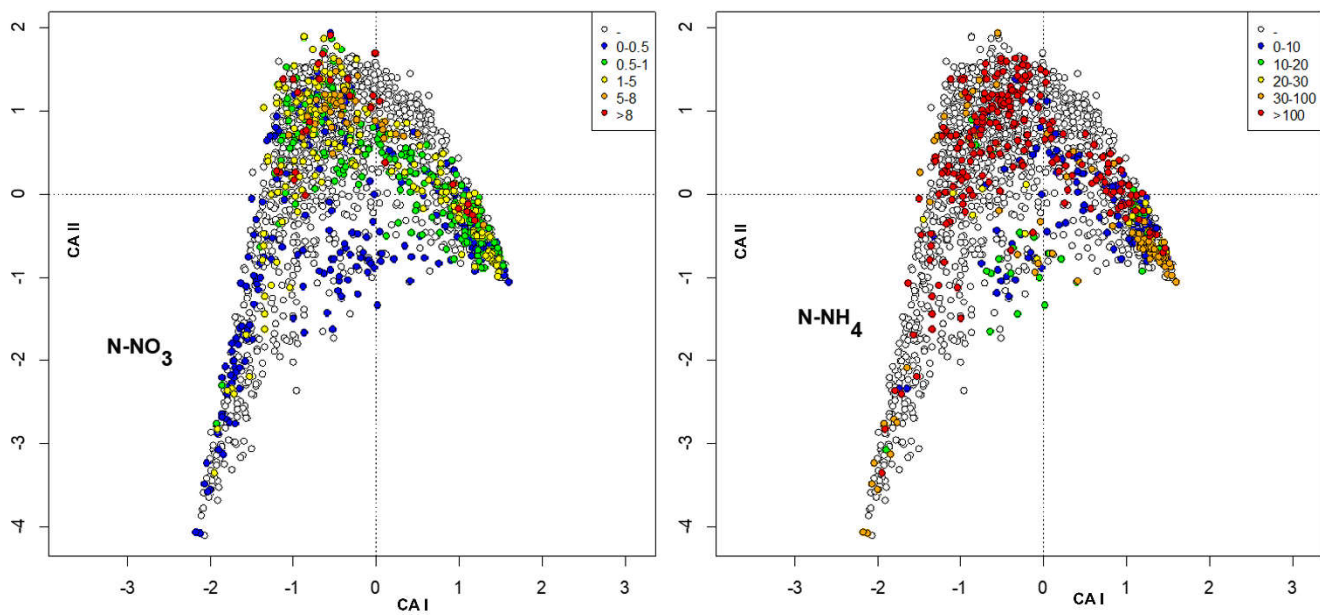




**Figure 5.** plot of sites scores in the first 2 axes resulting from CA of sites x species ( $nL_p$ ) matrix, by marking sites with different colours according to water temperature ( $^{\circ}\text{C}$ ) (left) and to water conductivity ( $\mu\text{S cm}^{-1}$ ) (right).



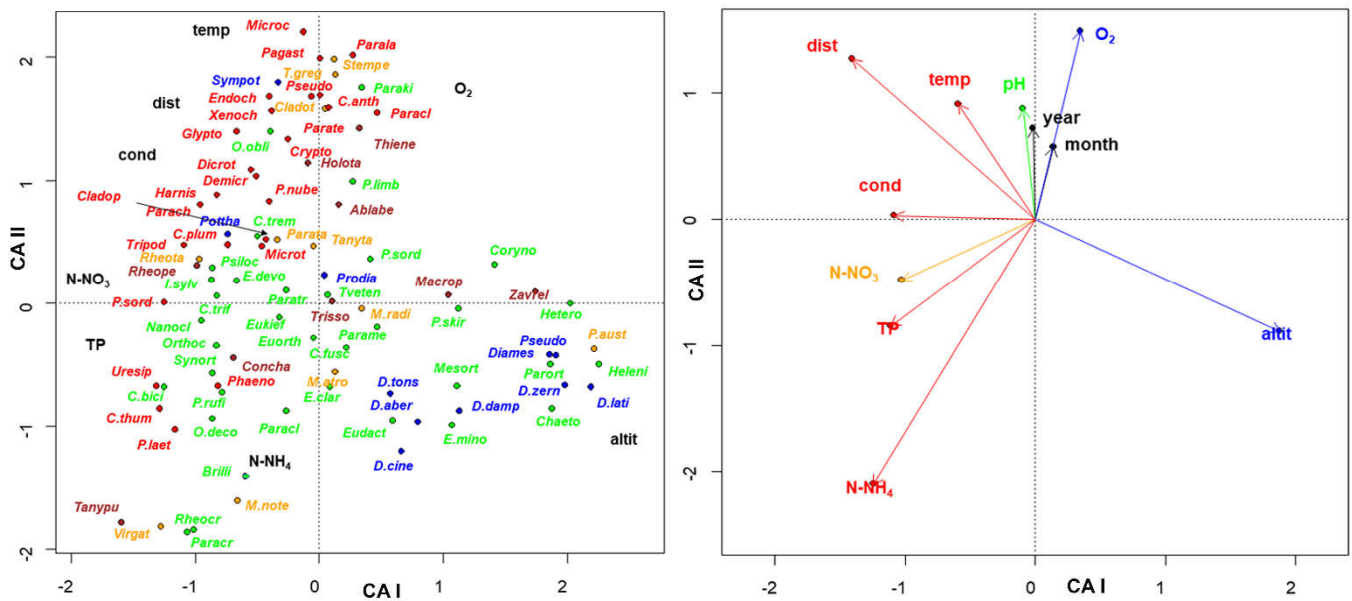
**Figure 6.** plot of sites scores in the first 2 axes resulting from CA of sites x species ( $nL_p$ ) matrix, by marking sites with different colours according to dissolved oxygen ( $\text{mg l}^{-1}$ ) (left) and total phosphorous (TP) ( $\mu\text{g P l}^{-1}$ ) (right).



**Figure 7.** plot of sites scores in the first 2 axes resulting from CA of sites x species ( $nL_p$ ) matrix, by marking sites with different colours according to  $N-NO_3$  ( $mg\ N\ l^{-1}$ ) (left) and to  $N-NH_4$  ( $\mu g\ N\ l^{-1}$ ) (right).

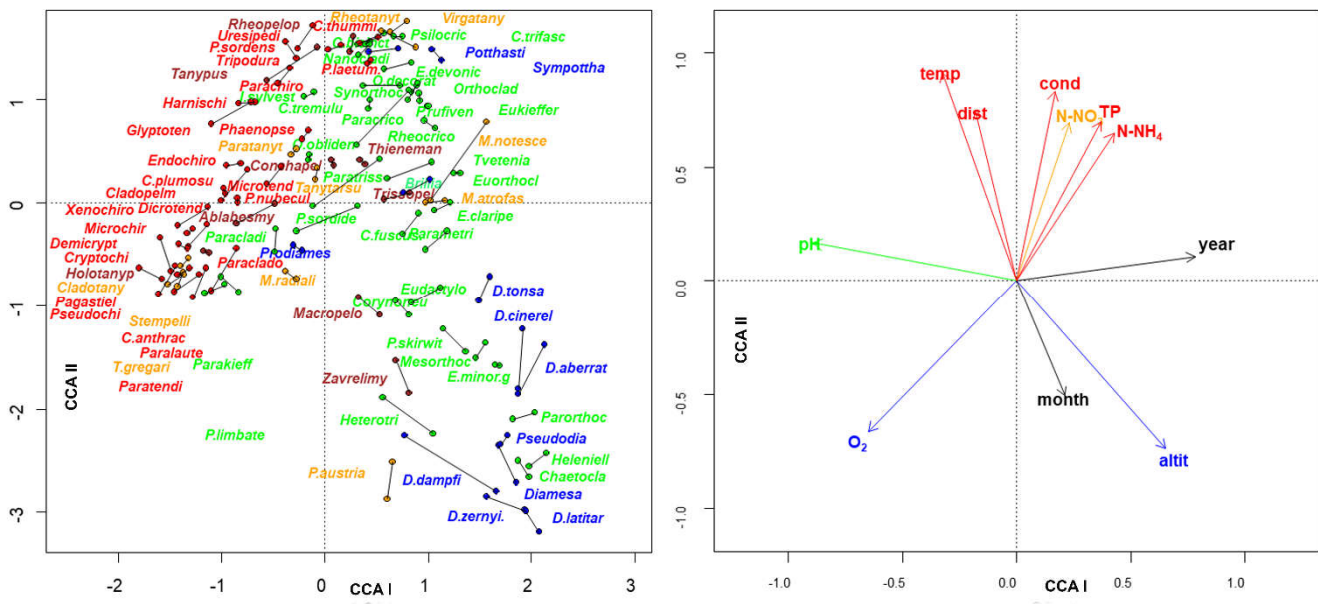
The **species x traits** matrix  $pU_s$  was also submitted to a correspondence analysis (**Fig. 8, Table S4**). The first 2 axes accounted for 70 and 21 % of the total variance, eigenvalues were 0.14 and 0.04 respectively. The first gradient separated species according to an up-stream-downstream gradient, with the extreme scores assigned to altitude, source distance and conductivity, the second gradient separated species according to a trophic gradient, with the extreme scores assigned to oxygen, and  $N-NH_4$ , with *Tanypus* and *Chironomus thummi* plotted in the bottom left area as other tolerant species, *Diamesa* species were plotted in the bottom right area. Species requiring high  $O_2$  content as *Paralauterborniella*, *Pagastiella*, *Stempellina* were plotted at the top of the graph.





**Figure 8.** plot of the species scores (left), and of the trait scores (right) in the first 2 axes resulting from CA carried out from species x traits ( $pU_s$ ) matrix.

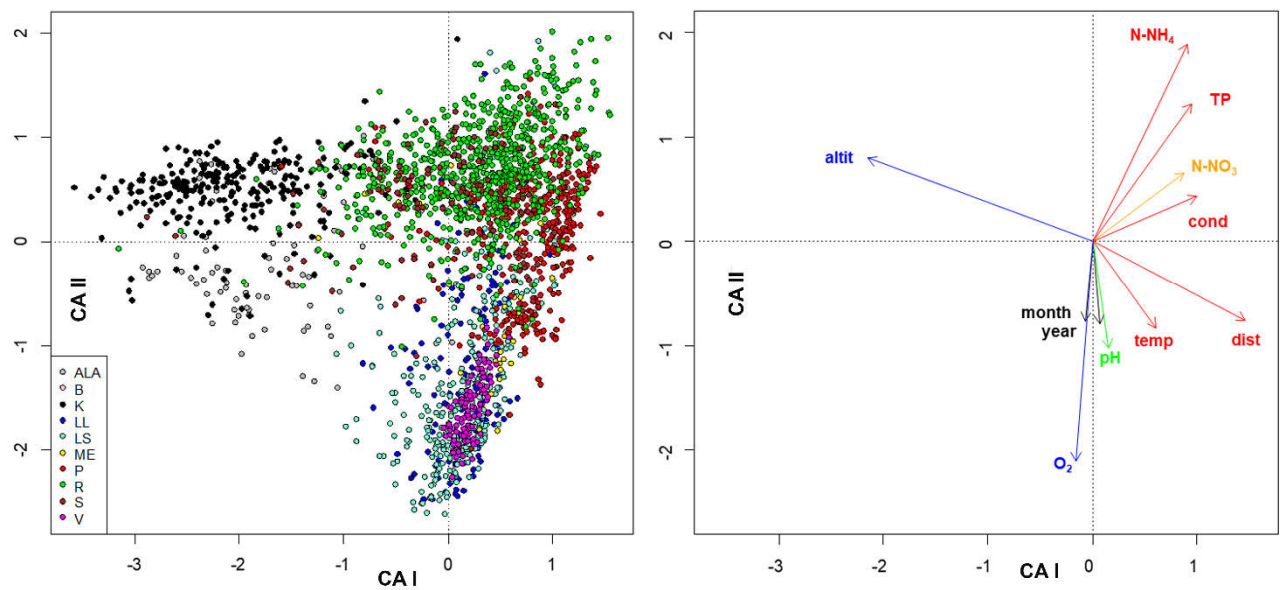
The **sites x species** matrix was transposed ( $pL'_n$ ) and a canonical constrained ordination (CCA) was carried out relating this matrix with the species x traits matrix  $pU_s$  ( $pL'_n \sim pU_s$ ) (Fig. 9, Fig. S3, Table S5). The first and second axis accounted for 7 % and 5 % of the total variance and eigenvalues 0.69, 0.46 respectively. The scores of each species calculated according to the left (sites) and right (traits) set were joined by a line in the figure. The species showing preferences for the cold sites at high altitude were plotted in the bottom right of the graphs, the ones present sites with high oxygen content in the bottom left, tolerant species as *Chironomus thummi*, *Cricotopus* (*Cricotopus*) *trifascia* and *Virgatanytarsus* present in high  $N-NO_3$ , TP,  $N-NH_4$  and low oxygen content waters were plotted in the top part of the graph, *Rheopelopia*, *Uresipedilum*, *Tanypus* from sites with high temperature and conductivity were mapped in the top left part. An arch/horseshoe effect was also visible here, with species preferring lentic waters plotted on the left, kryal and cold spring species on the bottom right and species characterizing potamon in the top right.



**Figure 9.** plot of the species scores (left) of the trait scores (right) in the first 2 axes resulting from CCA analysis carried out from  $pL'_n \sim pU_s$  matrices; the scores of the same species obtained with the first and second matrix are joined with a line (see Fig. S4 for the full set of species names).

A comparison between factor loadings of species in canonical constrained and unconstrained ordination showed a good agreement in the species ordination, except for a few species such as *Diamesa dampfi*, *Micropsectra notescens*, *Paratrissocladius*, *Paracricotopus*, *Psectrocladius sordidellus*, *Heterotrissocladius*, which showed different scores in the CA first axis (calculated from  $nL_p$  matrix) and in the CCA first axis (calculated from  $pL'_n \sim pU_s$  matrices) (Fig. S4, Table S5) and as a consequence were plotted at some distance from the regression line.

The **sites x species** matrix  $nL_p$  was post-multiplied by **species x traits**  $pU_s$  matrix to obtain a **site x traits** matrix ( $nL_p U_s$ ). This  $nL_p U_s$  was also submitted to correspondence analysis (Fig. 10, Table S6). In this case sites were rows and traits were columns. The first two axes accounted for 72 % and 24 % of total variance with eigenvalues 0.05, 0.02. The first axis reproduced an upstream downstream and a water temperature gradient, the second axis a water quality gradient (Fig. 10). This analysis does not allow to map species, because the species (columns of the first matrix and rows of the second) do not appear in the product matrix.



**Figure 10.** sites scores (left) traits scores (right) from the first 2 axes of the site x traits (nLpUs) matrix.

A discriminant analysis was carried out to test the goodness of classification of sites in different habitats when Chironomid taxa assemblages are used to discriminate among habitats (Table 5, Table S7). Both nLp and nLpUs matrices were submitted to multiple discriminant analysis, using habitat as grouping factor; the % of correct classifications was 46 % for the nLp matrix and 47 % for the nLpUs, emphasizing that the addition of the trait matrix does not improve the classification significantly, in any case the result is that Chironomid assemblages are good discriminators of the different habitats.

A cluster analysis of species confirmed that separation of species clusters is in agreement with different habitats (Fig. 11).

**Table 5.** Results of discriminant analysis: hits and misses in samples classification according to taxonomic and traits analysis. ALA: alpine lakes, B: brackish waters, K: kryal, LL: large lakes, LS: small lakes, ME: Mediterranean lakes, P: potamal, R: rhithral, S: krenal, V: volcanic lakes. Detailed results of Discriminant Analysis in Table S7.

		ALA	B	K	LL	LS	ME	P	R	S	V
nLp	hits	56	100	79	9	11	28	40	38	33	68
	misses	44	0	21	91	89	72	60	62	68	32
nLpUs	Hits	59	100	83	14	10	28	36	34	38	72
	misses	41	0	17	86	90	72	64	66	63	28

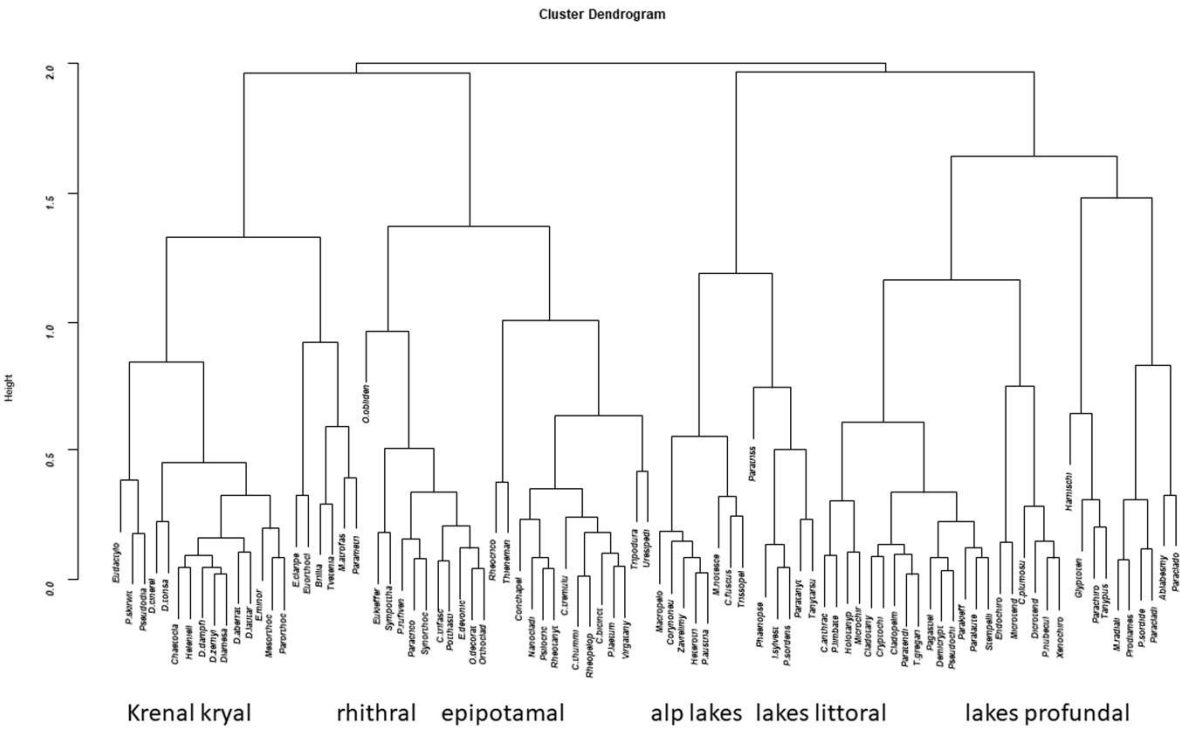


Figure 11. cluster analysis of species from sites x species (nLp) matrix.

4. Discussion

Chironomids species distribution in the environment is confirmed to be related to ecological conditions. Distribution of Chironomids linked to biogeographic factors were never observed within the western Palearctic area, except for the species linked to glacial areas [29], so biogeographic factors are not considered in the present discussion.

Chironomids have been frequently used as indicators of past climatic change [30], while it is impossible to establish the occurrence of alien species [31], even if it is expected. Some species like *Polypedilum nubifer* are probably invaders [32], but it is impossible to state if and when they reached the West Palaearctic region. It is well known that Chironomid distribution is related to ecological factors, such as water temperature [33,34], so an extension or reduction of the home range of a species is expected in relation to global warming [35].

Being the ecological niche known, it is possible to translate the information given by each species into information about habitat. From a mathematical point of view, the ecological niche can be expressed as a vector whose elements are the optimum values of the species for each factor, expressed as weighted mean, while the measure of niche extension can be expressed as a weighted standard deviation. [27]. The vectors can be aggregated to create a trait matrix  $pU_s$  with  $p$  species as rows and  $s$  traits as columns. This  $pU_s$  matrix was firstly proposed calculating aquatic beetle traits and a fuzzy coding analysis was suggested to allow the inclusion of diverse kinds of biological information [36]. Species abundances can be expressed as a matrix  $nL_p$  with  $n$  samples as rows and  $p$  species as columns. A matrix multiplication of the matrix  $nL_p$  by the  $pU_s$  matrix generate a  $nL_pU_s$  product matrix, with  $n$  sites as rows and  $s$  traits as columns; this approach was proposed for vegetation studies [37], it was used for invertebrates living in running waters [38] and extended to Chironomids [19, 20, 39]:

$$nM_s = nL_p * pU_s$$

This approach allows to translate the information given by a species list in ecological traits, allowing the construction of an index of environmental quality. Attempts to create the  $pU_s$  matrix for Chironomids and other benthic invertebrates were matter of many efforts [3, 39, 40, 41, 42], but the results were obviously dependent by the database used for calculations. In the present paper, we tried to develop a new trait matrix considering the largest database available from collections of larval samples from both lotic and lentic habitats. Indeed, traits of chironomids were often assigned without a well-founded support of information, this was underlined in estimating recovery of lakes after measures of restoration from acidification [43]. Significant differences were observed between traits developed for North American and European species [44] and between Scandinavian and Mediterranean species [45]. Lack of information may lead to apparently contradicting results. For example, the haemoglobin content, tube building ability, feeding habit, voltinism and body size of Chironomid larvae suggested that haemoglobin-rich species, with tube building capacity and short generation time be dominant in disturbed sites, the reverse should be in less disturbed sites. But this approach gave some unexpected results, such as the presence of: 1- haemoglobin-rich species also in less disturbed sites; 2- species with long generation time in disturbed sites [38], and/or 3- small body sized species in less disturbed habitats [20]. These apparently conflicting results were explained supposing that oxygen deficit was not the only factor determining disturbed conditions. It was supposed that not all haemoglobin-rich species are tolerant to low oxygen levels [8]. For example, species belonging to *Polypedilum* may be responsible of this conflicting result, because this haemoglobin-rich genus is often present in undisturbed sites, possibly due to the presence of small oxygen-poor microhabitats included in large oxygen-rich habitats. Chironomini genera (*Chironomus*, *Glyptotendipes*, *Polypedilum*, *Paratendipes*, *Microtendipes* etc.) are all haemoglobin-rich, but have very different response to pollution. The same is true for body size: the large *Chironomus* and *Procladius* often prevail in disturbed sites, while it is expected that the small body sized trait prevail in disturbed sites [46].

Another attractive approach is the so-called 4<sup>th</sup> corner solution problem [47, 48], where the sites  $\times$  species matrix  $nL_p$ , the species  $\times$  traits matrix  $pU_s$  and the sites  $\times$  environmental variables matrix  $nR_q$  are combined to produce a  $qD_s = qR' nL_p U_s$  matrix, which allows a comparison between an expected and an observed community [49]. In the present case, the  $nR_q$  matrix presents a lot of missing data, so this analysis was not performed. It is suggested to be cautious in using this matrix approach to evaluate the ecological status, because an incomplete information available about the ecology of single taxa can conduce to misleading results or false representations. This approach could be useful in the future when more accurate information will be available about different Chironomid species.

In the present study, as in many others [3, 40, 50], it is evident that Chironomid species respond to a limited number of factors, so they can be ordered according to few gradients. We preferred to start the analysis ordering taxa with an unconstrained ordination method [27], because environmental data supporting the description of sampled sites were incomplete. Moreover, it is well known that the presence-absence of a species is not bound to the point instantaneous water condition, but the result of an integration of factors over a relatively long time period, information that cannot be given by physico-chemical analysis.

Despite these limitations, the ordination of sites, based only on Chironomid species assemblages available in the present database, emphasized few major gradients responsible of the observed distributions: 1- a gradient separating lotic from lentic habitats, with species living in fast running waters separated from species living in standing waters; 2- a gradient emphasizing an upstream-downstream gradient in running waters, separating: a) intolerant species living at high altitudes, low water temperatures, high oxygen concentrations, low conductivity, from b) tolerant species living downstream, at higher temperatures, lower oxygen concentrations, higher conductivity and salinity; 3- a trophic gradient separating species living in oligotrophic nutrient-poor waters from species living in organic-rich or eutrophic waters. Each of these gradients does not necessarily coincide with the principal axes resulting from canonical ordination. In the present case, the first



axis separates lotic from lentic habitats, the second axis is explained as an oxygen-temperature gradient, and the ordering of sites resulted in the classic arch or horseshoe effect [27, 28]. This effect observed in the correspondence analysis [27] is generated by species data having unimodal distribution along a single gradient [28]; in the present case, it is a gradient from high altitude, cold, oxygen-rich, fast flowing running waters observed in glacial streams, toward lowland, warmer, oxygen-poor, slow flowing waters observed in lowland rivers, and continuing in still slow flowing, but cooling down and oxygen enriching waters, as observed in large lakes with increasing depth. Conductivity and nutrients are often included in this principal gradient, in several possible interactions. In relation to this principal gradient, each species can adjust with its own peculiarities, moving more or less far from this gradient. For example, species living in small-sized cold waters lakes at high altitude (*Zavrelimyia*, *Heterotrissocladius*, *Corynoneura*, *P. austriacus*) and species living at high depth in large lakes (*M. radialis*, *Paracladopelma*) appear displaced toward the centre of the plot (Fig. 2, Fig. S2).

Species cannot be clustered in well-defined groups, because only few species are restricted to well defined habitats, most species are opportunistic. For example, few species belonging to *Diamesa* are restricted to kryal (*Diamesa laticauda*), but most (*Diamesa tonsa*, *Diamesa zernyi*) colonize different types of cold waters, some Orthocladiinae genera (*Eukiefferiella*, *Rheocricotopus*, *Euorthocladius*, *Orthocladius*, *Cricotopus*) characterize rhithral streams with moderate or fast current, but can be collected also in slow flowing waters, many Tanytarsini are typical of oligotrophic lakes, but are also common in spring and streams, many Chironomini genera (e.g. *Dicrotendipes*, *Chironomus*) characterize eutrophic lakes, but many of them live also in potamal and in littoral of lakes associated to vegetation (*Endochironomus*, *Glyptotendipes*) or to sand banks (*Cryptochironomus*, *Harnischia*).

In conclusion, the key factors separating Chironomid species are confirmed to be substrate, current velocity, water temperature, dissolved oxygen, conductivity, nutrients, but these factors are differently related in various situations and anthropogenic stress can contribute in creating other more complex interactions [9].

The advantage of having a matrix of ecological traits available ( $\mathbf{pU}_s$ ) is the possibility to use only assemblage structure information to evaluate the ecological status of an ecosystem, without the support of environmental data, this is a necessity when sampling campaigns include only the monitoring of macrobenthos; in this case, be a trait matrix available, taxonomic information can be translated into water quality assessment.

## 5. Conclusions

It is often stated that functional traits analysis is better than taxonomic composition analysis [20]. Indeed, this statement stresses the obvious, because the use of functional traits requires to have a traits matrix available, and the development of a traits matrix implies to have a sound taxonomic knowledge, needed to create the traits matrix. It is more appropriate to state that when a trait matrix is available, a less thorough taxonomic knowledge is sufficient to evaluate the ecological status of a water body. In other words, a species groups list, instead of a more thorough species list, can be sufficient to analyse the system. The traits matrix approach has the advantage that a taxonomic species list can provide information comparable with the one given by a physical-chemical analysis, when a trait matrix is available. If both a traits matrix  $\mathbf{pU}_s$  and an environmental variables matrix  $\mathbf{nR}_q$  are available, you can go a further step, calculating an expected ecological status and comparing with an observed one [49] (Brown et al., 2014).

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**Supplementary Materials:** Fig. S1 plot of the species scores in the first 3 axes resulting from CA carried out from sites x species matrix. As Fig. 1, but with all species plotted; Fig. S2 plot of the species scores in the first 2 axes resulting from CA carried out from sites x species matrix and the fitted second degree polynomial. As Fig. 2, but with all species plotted; Fig. S3 plot of the species scores in the first 2 axes resulting from CCA analysis carried out from  $pL'n$  and  $pUs$  matrices; the scores of the same species obtained with the first and second matrix are joined with a line. As Fig. 9 (left), but with all species plotted; Fig. S4 plot of the species scores in the first axis resulting from CA analysis of  $nLp$  (abscissa) against species scores in the first axis resulting from CCA analysis of  $pL'n \sim pUs$  (ordinate) with the fitted regression line; Table S1 input data matrix; Table S2 correlations between species and environmental variables, p values and number of samples; Table S3 Matrix of traits: weighted standard deviation of each environmental variable for each species; Table S4 correspondence analysis (CA) results of species x traits matrix  $pUs$ ; Table S5 canonical constrained ordination (CCA) results between species x sites  $pL'n$  matrix and species x traits  $pUs$  matrix =  $pL'n \sim pUs$ ; Table S6 correspondence analysis (CA) results of sites x traits  $nLpUs$ , matrix = sites x species multiplied by species x traits; Table S7 discriminant analysis results using habitat as grouping factor of the first two CA scores, calculated from from  $nLp$  and  $nLpUs$  matrices

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