

## STUDY OF THE ISOTOPIC ECOLOGICAL NICHE OF THE COMMON COOT *FULICA ATRA* (LAC TONGA, NORTH- EASTERN ALGERIA)

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**Abstract.** This study aims to determine patterns of isotope discrimination between diet and blood and feathers in the common coot (*Fulica atra*) in Lake Tonga, North-eastern Algeria, the first time in Algeria on the aquatic avifauna. For this purpose, we investigate the trophic position of the species looking for the seasonal variations in the diet. The stable isotope analysis of nitrogen and carbon was carried out to provide a comprehensive evaluation of the feeding ecology. After plotting the isotopic composition of all potential food sources in the mixing plot, consumed by the coot, whether it is on feathers or blood, the results revealed that the main source of the coot diet in all seasons is *Najas pectinata*, followed by *Gambusia affinis*. Whereas, for *Nymphaea alba* a stable contribution was recorded during both seasons (breeding and reproduction). The food selection of a species is predetermined by its ability to exploit its trophic space, on one hand, and specific nutritional requirements are also essential to various biological functions of the species concerned.

**Keywords:** waterbirds, diet, stable isotopes, wetland, feeding ecology

### Introduction

Algerian wetlands are home to a wide variety of waterbirds. Among the species composing the family Rallidae, the common coot (*Fulica atra*) is a cosmopolitan species adaptable to different environmental conditions (Nouri et al., 2022). In North Africa, the coot is the most abundant species among the Rallidae (Etchecopar et al., 1964; Baaziz and Samraoui, 2008; Metna, 2013). It winters on the permanent waters of north-eastern Algeria and the Sahara (Ledant et al., 1981; Isenmann et Moali, 2000; Houhamedi, 2002; Bourriach, 2010; Meddour, 2012). It is partly a sedentary species and partly a migratory aquatic bird (Harrison, 1982). Its ecology is well documented in Europe (Blüms, 1973; Fjeldsa, 1977; Horsfall, 1981; Allouche et Tamisier, 1984; Asensio et al., 1986; Salathé, 1986; Salathé and Boy, 1987; Draulans et Vanherck, 1987; Pelsy-Mozimann, 1999; Guillemain and Fritz, 2002).

The common coot is rarely observed in other regions of the world, where other species of the same genus, such as the American coot and the crested coot, can be observed. In Algeria, common coot covers the whole north and nests in large marshes and on lakes (El Kala, Macta, Boughzoul, Réghaia, lakes of hill reservoirs in Kabylie, as well as some oases like El Goléa (Metna et al., 2013). According to Cramp and Perrins (1993), the species has an omnivorous diet in which plants are generally predominant. According to Pratte (2003), the diet of the coot' primarily comprises

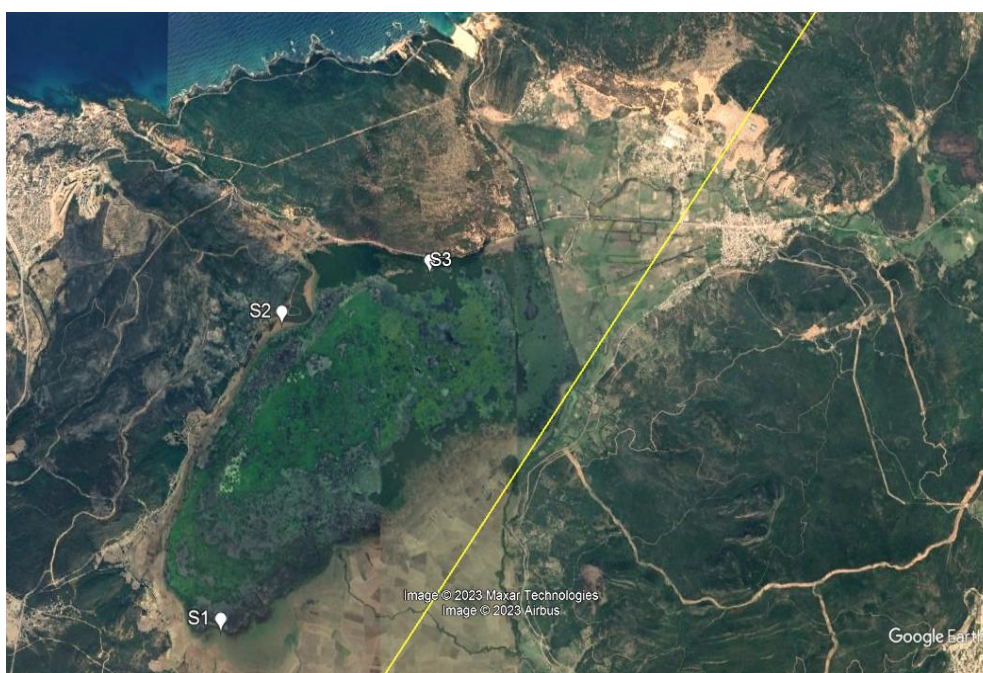
aquatic plants. The study of its trophic ecology has always been carried out traditionally, either by the desiccation of the crop and gizzard or the droppings. Thus, the use of stable isotopes is unknown. The latter has often led to reconsidering the trophic role of specific sources of organic matter in the various levels of a food web (Fry, 2006, 2013).

In trophic ecology, natural heavy carbon and nitrogen isotope tracing is used to determine the fate of organic matter sources from their origins to their transfers to the various levels of a food web. Currently, there is considerable interest in using stable isotope methods to study diet and migration patterns in birds (Marco-Méndez et al., 2015). This study, carried out for the first time in Algeria on the aquatic avifauna of the integral reserve of Lake Tonga, aims to study the food relations between the coot and its various preys belonging to several ecological compartments. The objective is to highlight the functioning of this ecosystem and the animal-vegetation relationships by studying the diet of the coot using stable isotope analysis.

## Materials and methods

### Study area

Our study was conducted at Lac Tonga (36° 52'N, 8° 31'E): A freshwater shallow lake of 2400 ha with a Ramsar Site status of international importance and integral reserve within the El Kala National Park. Located in the extreme northeast of Algeria, it is a freshwater marsh with an area of 2,600 ha and an average depth of 120 cm (*Fig. 1*). It is connected to the sea, the channel of the Messida (Lazli et al., 2011 a, b; Gherib and Lazli, 2017; Gherib, 2018; Mecif et al., 2020). Lake Tonga is characterized by a significant heterogeneity of plant formations that constitute nesting sites for many water birds while providing them with a rich and varied food source (Kadid, 1990; Guerfi et al., 2018) (*Photo 1*).



**Figure 1.** Representation of the Lac Tonga wetland (Google earth)



*Photo 1. Site lac Tonga (copyright Nouri, 2018)*

## **Methodology**

### *Assessment of trophic resource availability at the study site*

The study was conducted in 2017/2018 and spanned wintering (from February to March 2018) and breeding (from April to July 2018) seasons. The choice of sampling sites was made after studying the region and, following a prospection of the banks of the lac, 3 stations were selected according to the criteria of accessibility of the sites, their distance, their geographical position, the nature of the terrain (sandy, rocky, marshy) and the presence of plants. These are: (S1) center of the lac 36° 22'N, 8° 37'E, (S2) Maizila 36° 86'N, 8° 73'E, (S3) Chalet 36° 34'N, 8° 81'E. The evaluation of the availability of trophic resources (plants and aquatic invertebrates) potentially exploited by the common coot was carried out following an inventory of the plant species available at the site, on the one hand, and of the aquatic invertebrates collected by a dip net, on the other hand.

We used a surber (250 µm empty mesh) and a butterfly net to collect the different habitats. The sampler placed on the bottom was pushed in different directions with traction of 50 cm. the surface prayers and pebbles were cleaned and turned over to pull out the fixed species as well as those attached to the substrates. The various sampled habitats were the aquatic and the banks plants, the station funds (muddy and sandy), the immersed and the bordering rocks, the cracks on the banks soils and the clods on the lake banks.

The choice of the surface of the station is 150 m long; 5 m in depth on sandy or rocky soil; 1–2 m in depth on muddy soil and based on the number of microhabitats per station and their importance, the number of sampling varies from 8 to 12 per station in order to collect the main part of macroinvertebrates present in the lake.

The samples taken from the different micro-habitats are transferred to sieves in order to eliminate mud, stones, twigs, and limit the risk of deterioration. After each sampling, the content was put in numbered plastic bags and boxes containing alcohol. The

captured potential preys were identified ( $n = 1250$  individuals) in the laboratory using a binocular magnifying glass and an identification guide (Tachet, 2010).

The coot were found freshly dead or accidentally caught by fishermen catching the birds in the fishing nets. Captured coot individuals were weighed using a digital scale and measured with a caliper. For each specimen processed, we collected the following data: body size (mm), wing length (mm), total weight WW (g) and beak size (mm). Blood and feathers were collected from 20 individuals (10 overwintering and 10 post-breeding). Blood was centrifuged and stored at  $-20^{\circ}\text{C}$  until isotopic analysis at the Oceanology laboratory (University of Liege).

### Isotopic analysis

Feather samples ( $n = 20$ ) and prey ( $n = \text{XXX}$  per potential prey,  $n = Y$  prey) ( $x$  and  $Y$ : number and replica of prey) were dried at  $60^{\circ}\text{C}$  (48h), powdered, weighed with a microbalance and placed in tin cups. They were then precisely weighed (*ca* 2.5-3 mg) in  $5 \times 8$  tin cups with *ca* 3 mg of tungsten trioxide, and analyzed with an elemental analyzer (vario MICRO Cube, Elementar, Hanau, Germany) coupled to a continuous-flow isotope-ratio mass spectrometer (IsoPrime100, Elementar UK, Cheadle, United Kingdom). Stable isotope ratios of carbon and nitrogen expressed in  $\delta$  notation ( $\delta^{13}\text{C}$ ,  $\delta^{15}\text{N}$  and  $\delta^{34}\text{S}$  respectively) and in ‰ relative to international references (Vienna Pee Dee Belemnite for  $\delta^{13}\text{C}$ ,  $\text{N}_2$  in atmospheric air for  $\delta^{15}\text{N}$ ) according to Equation 1.

$$\delta X_{\text{sample}} = \left[ \frac{(X/x)_{\text{sample}}}{(X/x)_{\text{standard}}} - 1 \right] \times 1000 \quad (\text{Eq.1})$$

where  $X$  is the heavy isotope ( $^{13}\text{C}$ ,  $^{15}\text{N}$ , or  $^{34}\text{S}$ ) and  $x$  is the lighter isotope ( $^{12}\text{C}$ ,  $^{14}\text{N}$ , or  $^{32}\text{S}$ ) and  $(X/x)_{\text{sample}}$  and  $(X/x)_{\text{standard}}$  are the ratios of both stable isotopes in the sample and the standard, respectively.

Certified reference materials from the International Atomic Energy Agency (IAEA, Vienna, Austria), IAEA N-2 (ammonium sulphate;  $\delta^{15}\text{N} = 20.3 \pm 0.2\text{‰}$ ) and IAEA C-6 (sucrose;  $\delta^{13}\text{C} = -10.8 \pm 0.5\text{‰}$ ) were used as primary standards. Glycine (Sigma-Aldrich, Overijse, Belgium;  $\delta^{13}\text{C} = -47.5 \pm 0.4\text{‰}$ ;  $\delta^{15}\text{N} = 2.25 \pm 0.4$  (means  $\pm$  SD) was used as a secondary standard.

### Data analysis

Comparisons of multiple parameters (seasons, animal source and plant source) were tested by ANOVA (General Linear Model). The relationship between beak length, beak weight, animal and plant sources was carried out by Pearson correlation analysis. The results were expressed as means  $\pm$  standard deviation (mean  $\pm$  SD). The data analyses were performed using the statistical software (Minitab 18, version 1.1.0).

The stable isotope mixing model in R with Simmr (Stable Isotope Analysis in R) (Parnell et al., 2013) was run to estimate potential food sources for coot under R software (R Development Core Team, 2009).

The sources used were selected from those highlighted as dominant in the coot diet, based on gut content (Johnsgard, 2012). After plotting the isotopic composition of these potential food sources against that of the consumer in the mixing plot, the three plant species and two animals that constructed the best mixing polygon were selected for running the mixing models applied to both the feather and blood samples. The plant



species were *Myriophyllum spicatum*, *Nymphaea alba*, *Najas pectinata*, and for animals, we selected the two most consumed species: *Culex pipiens*, and *Gambusia affinis*. Trophic enrichment factors (TEFs; i.e., the net differences between consumer delta values and diet delta values) were deduced to potential sources to build a mixing polygon (Phillips et al., 2014). According to Nico et al. (2007), we have used a TEF of  $2.3 \pm 0.3\%$  for  $\delta^{13}\text{C}$  and  $2.8 \pm 0.8\%$  for  $\delta^{15}\text{N}$ . The iteration number was set at  $10^6$  and burn-in size at  $10^5$ . The model results are presented either as the full distribution of the posterior probability density function or as modes with min - max interval of the distribution.

## Results

### Morphometric parameters of individuals

Coot showed an average of  $747.15 \pm 139.5$  g body mass and a length of  $42.45$  (SD  $\pm 4.14$ ) cm ( $n = 20$ ) (Table 1). There were no significant differences between the two seasons (ANOVA (General Linear Model)  $T = -1.07$ ,  $P = 0.301$ ) for any of measured biometric parameters.

**Table 1.** Morphological parameters of individual coots (*Fulica atra*) sampled in Lake Tonga during the study period

	Weight	Length	Left wing length	Right wing length	Beak	Neck	Leg
Wintering	$714 \pm 132.62$	$43 \pm 2.62$	$31.75 \pm 1.3$	$31.85 \pm 1.72$	$3.7 \pm 0.26$	$3.7 \pm 0.26$	$16.25 \pm 0.49$
Reproduction	$780.3 \pm 145.9$	$41.9 \pm 5.35$	$30.45 \pm 1.07$	$30.65 \pm 1.16$	$3.81 \pm 0.48$	$3.81 \pm 0.48$	$16.02 \pm 0.26$
Total	$747.15 \pm 135$	$42.45 \pm 4.14$	$31.1 \pm 1.33$	$32.25 \pm 1.55$	$3.75 \pm 0.38$	$3.75 \pm 0.38$	$16.13 \pm 0.4$

### Inventory of resources in Lac Tonga

The inventory of plant species recorded showed a significant floristic diversity. 13 plant species were identified, of which the most abundant was *Myriophyllum spicatum*, followed by *Nymphaea alba*, *Najas pectinata*, *Potamogeton nodosus*, *Scirpus lacustris*, *Typha angustifolia*, *Iris pseudacorus*, *Cynodon dactylon*, *Ranunculus ophioglossum* and *Phragmites australis* (Table 2). These species are present during the entire study period. The inventory of fauna with the dip net allowed to count 20 species of invertebrates and vertebrate belonging to 6 classes, 13 orders and 20 families. Among these species, the most abundant were two insects *Culex pipiens*, *Naucoris cimicoides*, respectively, the mollusk *Planorbis corneus*, and the fish *Gambusia affinis* (Table 2).

### Isotopic compositions

#### Stable isotope ratios of potential resources

The stable isotope compositions of potential food sources ranged from  $-31.68$  to  $-7.4\%$  for the  $\delta^{13}\text{C}$  values and from  $-5.6$  to  $9.58\%$  for the  $\delta^{15}\text{N}$  values (Table 2). Most plant resources had very negative  $\delta^{13}\text{C}$  values (range  $-24$  to  $-28.8\%$ ), except *Najas* and *Potamogeton* (range  $-15$  to  $-16\%$ ) and the Poaceae *Cynodon* ( $-7.4\%$ ). Plant resource  $\delta^{15}\text{N}$  values were spread all along the total  $\delta^{15}\text{N}$  range.

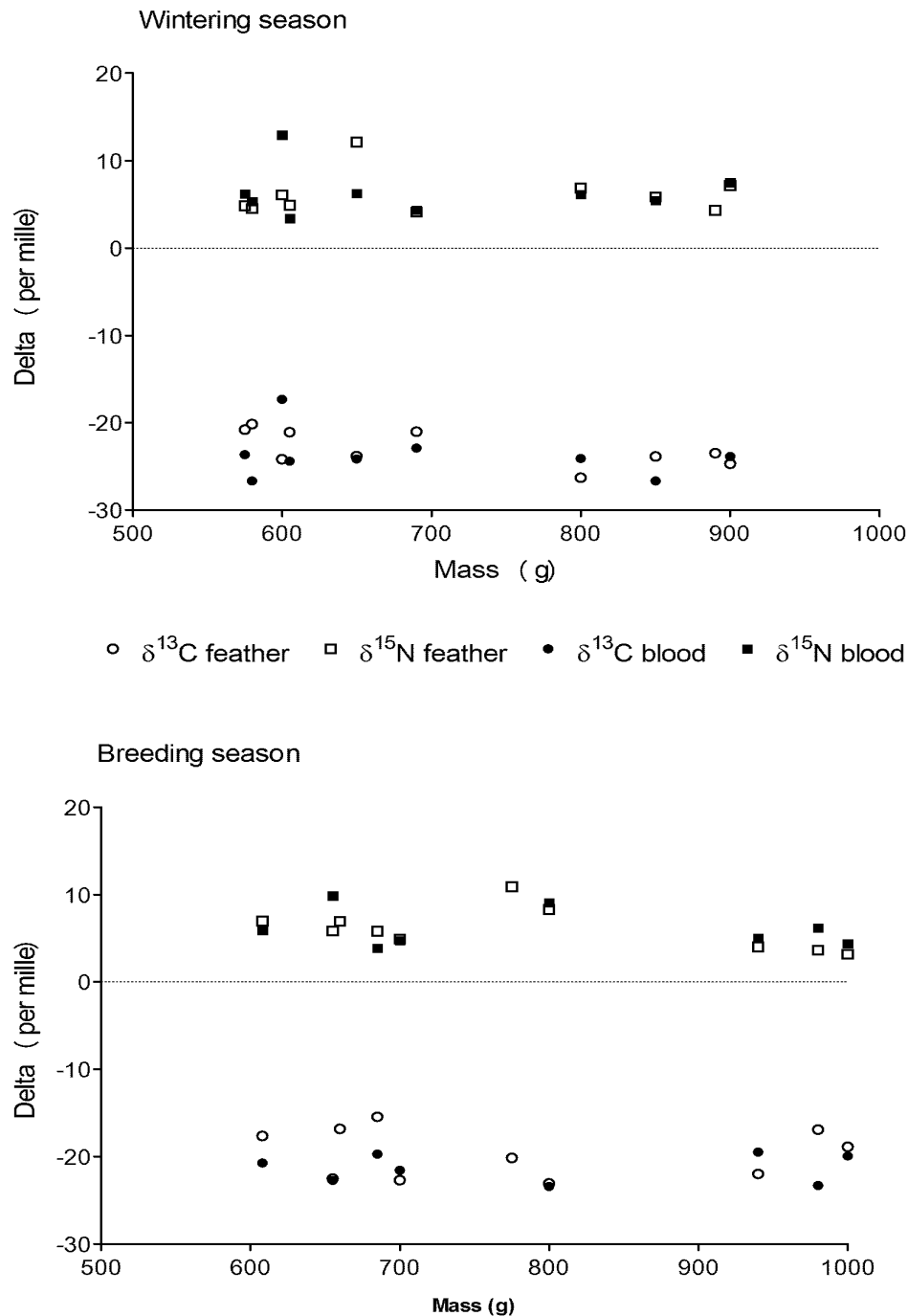
Animal  $\delta^{13}\text{C}$  values ranged from  $-31.68$  to  $-19.9\%$  and their  $\delta^{15}\text{N}$  values from  $-0.1$  to  $8.3\%$ .

**Table 2.** Plant resources identified at the study site

Classes	Orders	Families	Species	$\delta^{13}\text{C}$	$\delta^{15}\text{N}$
Magnoliopsida	Nymphaeales	Nymphaeaceae	<i>Nymphaea alba</i>	-28.49 ± 0.09	4.31 ± 0.18
	Haloragales	Haloragaceae	<i>Myriophyllum spicatum</i>	-27.91 ± 0.19	2.58 ± 0.25
	Ranunculales	Ranunculaceae	<i>Ranunculus aquatilis</i>	-27.78 ± 0.79	1.27 ± 4.28
<i>Ranunculus ophioglossifolius</i>			-24.78 ± 0.8	3.20 ± 0.12	
Asteroids	Lamiales	Plantaginaceae	<i>Callitriche cophocarpa</i>	-27.84 ± 1.18	-5.65 ± 1.40
Commelinids	Poales	Cyperaceae	<i>Scirpus lacustris</i>	-28.72 ± 0.18	3.35 ± 1.75
Liliopsida	Tyophales	Typhaceae	<i>Typha angustifolia</i>	-28.06 ± 0.18	9.14 ± 0.74
	Najadales	Potamogetonaceae	<i>Potamogeton trichoides</i>	-27.41 ± 0.06	2.44 ± 1.98
	Liliales	Iridaceae	<i>Iris pseudacorus</i>	-27.90 ± 0.79	2.70 ± 0.4
	Cyperales	Poaceae	<i>Phragmites australis</i>	-28.53 ± 1.09	9.58 ± 0.86
	Najadales	Hydrilloideae	<i>Najas pectinata</i>	-15.73 ± 0.02	3.98 ± 0.03
Monocotylédones	Alismatales	Potamogetonaceae	<i>Potamogeton nodosus</i>	-15.97 ± 0.12	4.64 ± 1.1
Commelinidés	Poales	Poaceae	<i>Cynodon dactylon</i>	-7.40 ± 0.01	7.26 ± 0.33
Insecta	Odonata	Lestidae	<i>Lestes sponsa</i>	-31.68 ± 0.62	1.81 ± 0.12
	Coleoptera	Dytiscidae	<i>Dytiscus marginalis</i>	-28.40 ± 0.39	7.01 ± 0.21
			<i>Hydaticus transversalis</i>	-27.22 ± 0.27	-0.11 ± 0.06
			<i>Copelatus chevrolati</i>	-22.84 ± 1.18	4.39 ± 0.88
	Hemiptera	Haliplidae	<i>Haliplus ruficollis</i>	-24.34 ± 0.11	4.58 ± 0.07
		Notonectidae	<i>Notonecta glauca</i>	-19.83 ± 0.29	6.63 ± 1.02
		Nepidae	<i>Nepa rubra</i>	-22.61 ± 1.36	4.76 ± 2.75
		Corixidae	<i>Corixa punctate</i>	-25.15 ± 4.35	2.35 ± 0.02
		Naucoridae	<i>Naucoris cimicoides</i>	-32.06 ± 0.57	8.32 ± 1.13
	Ephemeroptera	Ephemeroptera	<i>Caenis pseudorivulorum</i>	-22.84 ± 1.14	4.39 ± 1.20
		Baetidae	<i>Cloëon dipterum</i>	-24.34 ± 0.15	4.58 ± 0.89
	Diptera	Chironomidae	<i>Chironomus plumosus</i>	-19.83 ± 0.37	6.63 ± 0.24
		Culicidae	<i>Culex pipiens</i>	-30.97 ± 1.19	7.57 ± 0.08
Clitellata	Hirudinida	Hirudinidae	<i>Hirudo medicinalis</i>	-22.61 ± 1.20	4.76 ± 0.11
Actinopterygii	Cyprinodontiformes	Poeciliidae	<i>Gambusia affinis</i>	-25.11 ± 0.30	7.22 ± 1.06
	Hygrophila	Planorbidae	<i>Planorbarius corneus</i>	-31.21 ± 0.38	4.67 ± 0.59
Gastropoda	Pulmonata	Lymnaeidae	<i>Lymnaea stagnalis</i>	-23.55 ± 2.58	6.22 ± 0.34
	Decapoda	Crangonidae	<i>Crangon crangon</i>	-19.19 ± 0.16	3.36 ± 1.10
Malacostraca	Isopoda	Asellidae	<i>Asellus aquaticus</i>	-25.11 ± 4.35	3.16 ± 0.21
Arachnide	Trombidiformes	Hydrachnellae	<i>Hydrachnidia</i>	-28.40 ± 0.14	7.01 ± 0.98

Values of  $\delta^{15}\text{N}$  measured on common coot feathers ranged from 5‰ (SD ± 1.99) in specimens collected in wintering to 6‰ (SD ± 2.54) in breeding specimens. In contrast, blood measurements reveal values from 6‰ (SD ± 2.42) in overwintering to 7‰ (SD ± 2.40). Furthermore, the ANOVA test (GLM) showed no significant difference in  $\delta^{15}\text{N}$  between the two seasons for feathers ( $F = 1.13$ ,  $p > 0.05$ ), for blood ( $F = 0.67$ ;  $p > 0.05$ ) and between the two compartments ( $F = 1.30$ ;  $p > 0.05$ ). Values of  $\delta^{13}\text{C}$  measured from blood collected from wintering coots ranged from -23.21‰ (SD ± 2.62) to -21.48‰ (SD ± 1.82) of the individuals sampled in the breeding season. However, values from -21.65‰ (SD ± 2.81) in wintering to -18.46‰ (SD ± 1.82) in the breeding period, measured on feathers, are recorded (Table 3). The ANOVA-test (GLM) showed a significant difference in  $\delta^{13}\text{C}$  measured from feathers between the two seasons ( $F = 6.62$ ;  $p < 0.05$ ). The significant difference in the  $\delta^{13}\text{C}$  of feathers and blood ( $F = 5.87$ ;  $p < 0.05$ ). The ANOVA-test (GLM) applied on coot blood measured in wintering period shows a very highly significant difference between  $\delta^{13}\text{C}$  and  $\delta^{15}\text{N}$

( $F = 808.9$ ,  $p < 0.001$ ), with a highly significant correlation ( $r = 0.888$ ;  $P = 0.008$ ). Furthermore, the breeding period results show a very highly significant difference between  $\delta^{13}\text{C}$  and  $\delta^{15}\text{N}$  ( $F = 626.59$ ,  $p < 0.001$ ). The GLM-test results applied to feathers collected in wintering indicate a very highly significant difference between  $\delta^{13}\text{C}$ ;  $\delta^{15}\text{N}$  ( $F = 987.23$   $p < 0.001$ ). The latter indicates also a very highly significant difference during the breeding season ( $F = 356.71$ ,  $p < 0.001$ ). *Figure 2* illustrates the stable isotopes ratios of coot feather and blood measured in relation to body mass during wintering and breeding season.



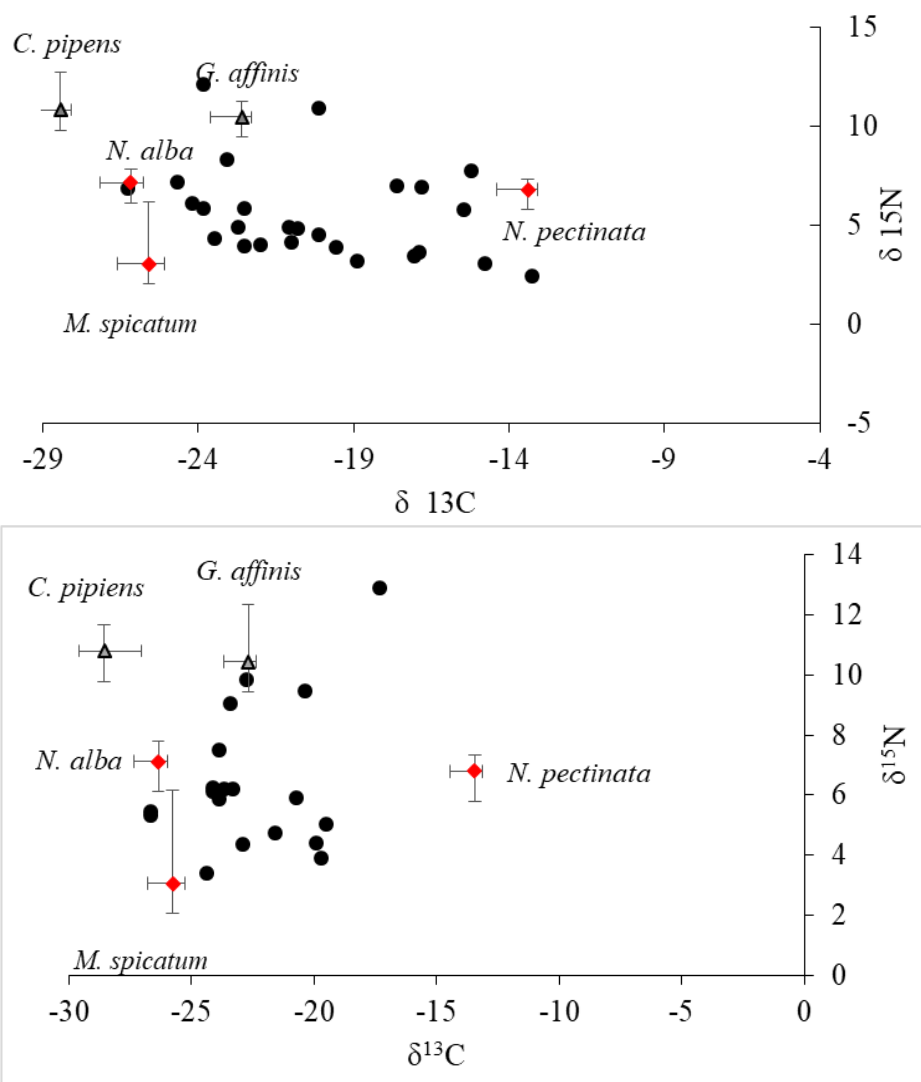
**Figure 2.** Stable isotopes ratios of coot feather and blood measured in relation to body mass during wintering (upper) and breeding season (lower), respectively

**Table 3.** Mean values  $\pm$  standard deviation of nitrogen and carbon isotope ratios of feathers and blood of common coots sampled during wintering and breeding season

		$\delta^{13}\text{C}$	$\delta^{15}\text{N}$
<b>Feathers</b>	Wintering	$-21.65 \pm 2.81$	$5.04 \pm 1.99$
	Breeding	$-18.46 \pm 3.62$	$6.02 \pm 2.54$
<b>Blood</b>	Wintering	$-23.21 \pm 2.62$	$6.08 \pm 2.42$
	Breeding	$-21.48 \pm 1.82$	$7.01 \pm 2.40$

### Mixing models

After plotting the isotopic composition of all potential food sources that of the consumer in the mixing plot. The five species that allowed to build the best mixing polygon were chosen for running mixing models. The plant species were *Myriophyllum spicatum*, *Nymphaea alba*, *Najas pectinata*, and for animals, we have two most consumed species: *Culex pipiens* and *Gambusia affinis* (Fig. 3).

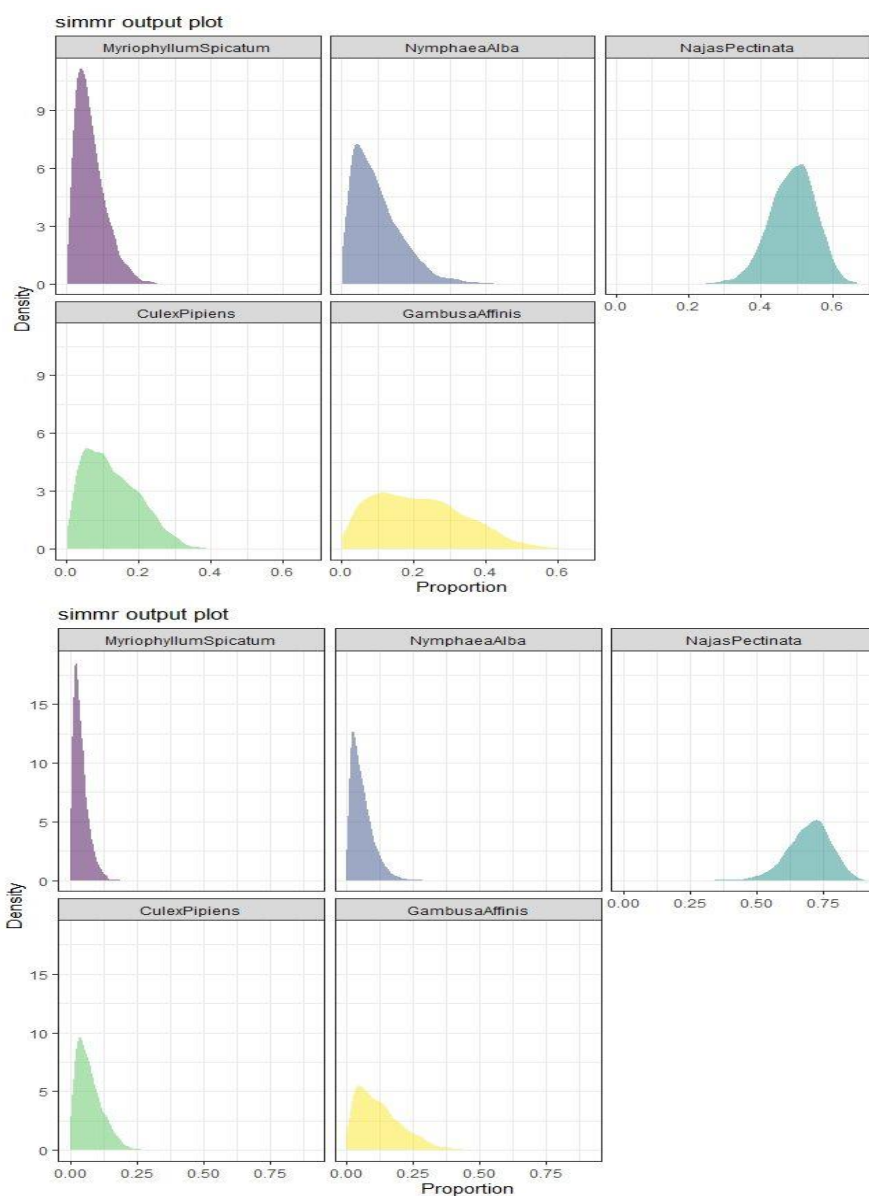


**Figure 3.** Mixing polygon generated from isotopic data of common coots feathers (upper) and blood (lower) and selected potential food sources, accounting for trophic enrichment factors

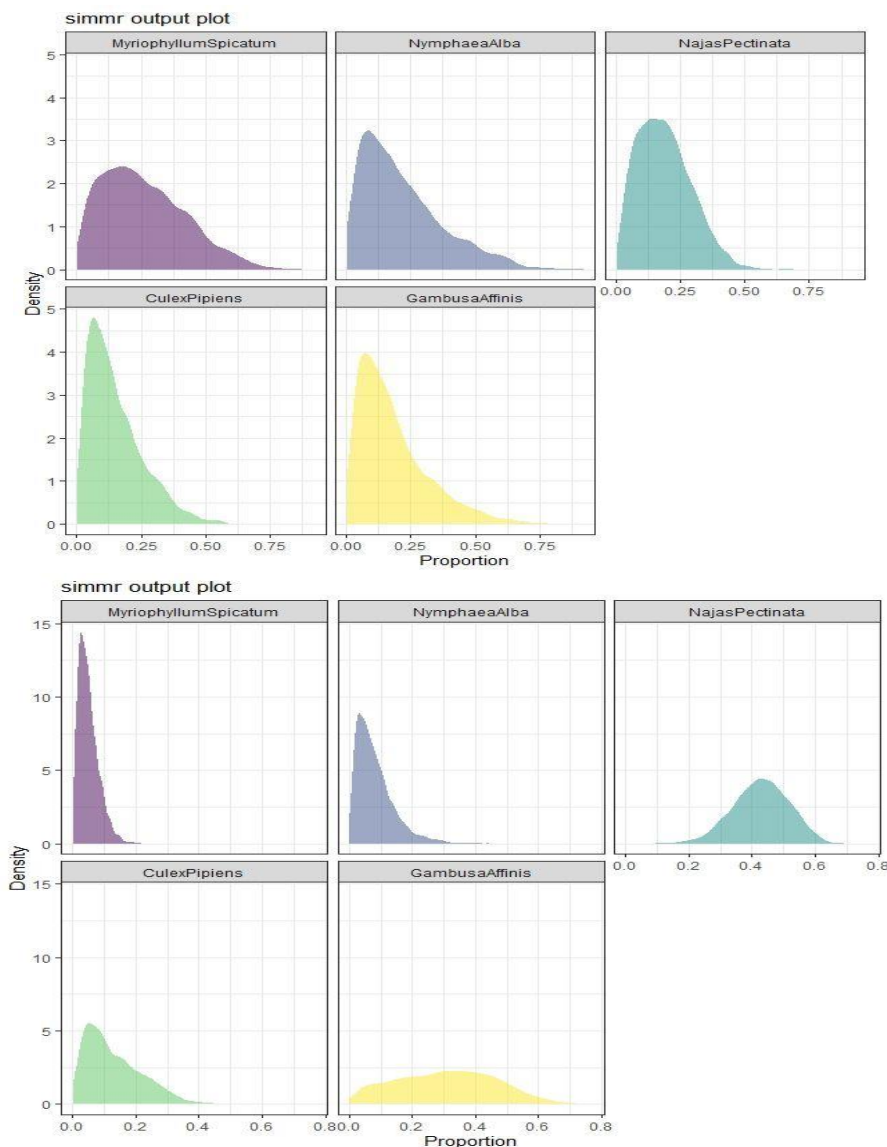


The simmr model on feather specimens reveals that the main dietary source to the coot diet in all seasons is *Najas pectinata*, with a major contribution during the breeding season (mode: 70% [min: 53- max: 85]), and minor one in wintering (mode: 50% [min: 28- max: 60]), followed by *Gambusia affinis* which was maximal in wintering (mode: 46% [min: 35- max: 58]) and minimal in breeding (mode: 30% [min: 16- max: 40%]) (Fig. 4).

On the other hand, the findings on blood specimens indicate that the main supplier to the coot diet remain *Najas pectinata* for all seasons, with a greatest contribution in wintering (mode: 73% [min: 41- max: 84]) and lowest one in breeding (mode: 30% [min: 18- max: 41]), followed by *Gambusia affinis* which a maximum value in breeding (mode: 62% [min: 50- max: 76]) and minimum one in wintering (mode: 30% [min: 16- max: 40%]). The contribution of *Culex pipiens* is important in wintering during both seasons (mode: 20% [min: 10- max: 20]) (Fig. 5).



**Figure 4.** Proportions of each food source in the diet of coot based on feather samples collected in A (upper) = wintering, B (lower) = breeding seasons. The simmr output is presented as the full distribution of the posterior probability density function



**Figure 5.** Proportions of each food source in the diet of coot based on blood samples collected in A (upper) = wintering, B (lower) = breeding seasons. The simmr output is presented as the full distribution of the posterior probability density function

## Discussion

Our study aims to investigate the diet of a widespread Rallid species in the north-east of Algeria, the coot (*Fulica atra*), by the stable isotope process, showing how seasonal changes could affect the whole trophic systems. The use of stable isotopes for tracking migration and dispersal of animals, including coot (*Fulica atra*), is a rapidly growing area of research. (Natsumeda et al., 2014). Food webs have multiple and complex connections. In order the major food web interactions and the trophic position of the important players within it. However, this can be a daunting task when relying solely on more traditional methods such as direct observation and gut analysis, suggesting that other approaches must also be taken (Hong et al., 2019).

The variation in  $\delta^{13}\text{C}$  values is useful for detecting the different sources of carbon in the consumers diet (Haramis et al., 2001; Hobson et al., 2003; Sponheimer et al., 2003a,

b). The  $\delta^{13}\text{C}$  and  $\delta^{15}\text{N}$  values measured from potential food sources collected in the Lake Tonga indicating a generally constant food chain system over this period. On the other hand, plasma  $\delta^{13}\text{C}$  values reflected a little seasonal change in diet of coots during the study period, with plasma  $\delta^{15}\text{N}$  values suggesting a slight trophic level increase. (Natsumeda et al., 2014; Karmiris et al., 2010).

These patterns are in agreement with food section since stable isotopes provide an integral metric of assimilated food; therefore, a delay is expected between what is observed in the stomach and what is assimilated (Stuart et al., 1996; Bada et al., 2020).

Significant differences in  $\delta^{13}\text{C}$  values within coot occurred from their feeding on different food sources ( $\delta^{13}\text{C}$ ), otherwise of  $\delta^{15}\text{N}$  at different trophic positions (Wersal et al., 2005; Johnsgard, 2012).

The  $\delta^{13}\text{C}$  differed significantly between seasons, the coot generally increase their selection of food resources to offset the physiological costs imposed by egg production (Cruz-Rivera and Hay, 2001). Such differences in  $\delta^{15}\text{N}$  values may be a response to both the availability of different resources and variations in metabolism as well as the needs of the species during its annual life cycle. Showed the highest  $\delta^{15}\text{N}$  values at breeding and the lowest at over wintering is explained That oocyte production and vitellogenesis influence diet being both a protein- and energy-intensive process and dependent on previously accumulated body reserves (Kennish, 1997; Healy et al., 2018; Hamesadeghi et al., 2019).

The investigations revealed that the coot's diet is exclusively based on plants. In the other the coot has an omnivorous diet where plants are generally predominant (Metna et al., 2015, 2013; Bouriache et al., 2010; Meddour, 2012). Tamisier and Dehorter (1999) found that plants are the most dominant diet, followed by seeds and algae, which constitute the coot's main diet. Whereas the proportion of animal prey is almost irrelevant and specific. Its occurrence is attributed to the decrease in the plant cover caused by its dryness during this period, requiring coots to consume alternative species to keep their dietary balance. After plotting the isotopic composition of all potential food sources that of the consumer in the mixing plot estimated the probability distributions of different sources' contributions, (Caut et al., 2008 a, b; Auerswald et al., 2010; Phillips et al., 2014). The simmr model on feather specimens reveals that the main dietary source to the coot diet in all seasons is *Najas pectinata*, with a major contribution during the breeding season (mode: 70% [min: 53- max: 85]), and minor one in wintering (mode: 50% [min: 28- max: 60]), followed by *Gambusia affinis* which was maximal in wintering (mode: 46% [min: 35- max: 58]) and minimal in breeding (mode: 30% [min: 16- max: 40]). On the other hand, the findings on blood specimens indicate that the main supplier to the coot diet remain *Najas pectinata* for all seasons, with a greatest contribution in wintering (mode: 73% [min: 41- max: 84]) and lowest one in breeding (mode: 30% [min: 18- max: 41]), followed by *Gambusia affinis* with a maximum value in breeding (mode: 62% [min: 50- max: 76]) and minimum one in wintering (mode: 30% [min: 16- max: 40]). The contribution of *Culex pipiens* is important in wintering during both seasons (mode: 20% [min: 10- max: 20]). The food choices of a species are predetermined by its ability to exploit its trophic space, on the one hand, and specific nutritional requirements essential to various biological functions of the species concerned, on the other. They thus confirm using different sources linked to local differences in distribution/community composition.

This confirms the supposition of Cramp and Perrins (1993), where proportions vary among seasons. In fact, the decrease in vegetation density in summer improves

the visibility of other species as well as many animals considered as potential prey for the coot. According to Bernard (2001). This species consumes insects and small fish during the breeding season). Indeed, fish seems to be a regular component of the coot's diet. At Lac des Puys in the Pays-de-Dôme (France), a coot was observed eating a dead fish (cyprinid). In fact, the fish represented 2.3% of the animal prey residues found in the stomach contents of coots in Britain (Cramp and Perrins, 1993).

This study agrees with that Karmiris et al. (2010), who determined the diet composition of coot in Greece, found a high percentage of invertebrates matter (31.2%). Furthermore, the coot was omnivorous with an importance intake of animal prey in their diet composition. (Guillemain and Fritz, 2002).

the selection of diets and wintering habitats by coot is the ultimate outcome of the combined influence of several factors other than food availability, such as predation and hunting pressure, protection from adverse weather conditions, human disturbance, morphological and physiological intra - and inter - specific differences (Guillemain et al., 2002a, 2002b; Paillisson et al., 2002; Durant et al., 2004).

Diet and wintering habitat selectivity by coots is eventually the result of several interrelated factors beyond food availability, including predation and hunting intensity, weather avoidance, human disturbances, intra- and inter-specific morphological and physiological differences (Guillemain et al., 2002a, b; Paillisson et al., 2002; Durant et al., 2004).

The coot has a great ability to explore their spaces and can exhibit large overlap in prey selection when the food abundance is high (Nummi and Vaananen, 2001). While they show some divergence signs, once there is a decrease in resources (Guillemain et al., 2002c). Even though competition drives resource partitioning, our study was conducted in a period of likely abundant resources, creating a large available habitat in the study area.

## Conclusion

The use of stable isotopes in this study was based on two main principles. First, the isotopic composition of tissues reflects that of the food in a reliable way. On the other hand, tissues are renewed at different rhythms, they integrate these data on several time scales.

For this purpose, this work focuses, for the first time, on the trophic ecology of a Rallidae coot using the stable isotope process, in order to enlighten the management strategies specific to the site and the species by demonstrating how changes in the prey community present in the site can affect the total trophic systems.

The results of  $\delta^{13}\text{C}$  and  $\delta^{15}\text{N}$ , measured from feathers and blood collected from individuals in the Lake Tonga Wilderness Area were relatively consistent among sampling periods, determining a food chain that is relatively stable during the two seasons (nesting and reproduction).

Nevertheless, the simmr model on feather and blood specimens reveals that the main contributor to the diet of the coot in all survey periods is the plant *Najas pectinata* followed by the fish *Gambusia affinis* with proportions varying according to the season suggesting that coots are able to explore their spaces and may exhibit a great overlapping in the selection of their prey, recognizing that the fish is a regular component of the diet of the coot.

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