



Molecular Identification of *Neoechinorhynchus iraqensis* (*Acanthocephala*: *Neoechinorhynchidae*) from *Planiliza abu* in Darbandikhan Lake

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Authors' contributions

This work was carried out in collaboration between both authors. Both authors read and approved the final manuscript.

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ABSTRACT

A total of 100 fishes belonged to *Planiliza abu* (Heckel, 1843) were taken from Darbandikhan Lake in Sulaimani Province, Kurdistan Region, Iraq from December 2023 to February 2024. The fish were checked for parasitic acanthocephalan. The research showed that *Neoechinorhynchus iraqensis* existed. In this study, 18S rDNA and DNA sequencing were used to identify *N. iraqensis*. The findings of the molecular analysis show that 533 bp was the PCR product of *N. iraqensis* and

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observed the smallest genetic distance with *Neoechinorhynchus* sp. GL-2015 (KU363972.1) and *Neoechinorhynchus* sp. XL-2014 (KM507363.1) was (0.025), and the highest genetic distance was recorded with *Tenuisentis niloticus* (MZ727194.1) was (0.194). Neighbor - Joining trees inferred for 18S rDNA showed that *N. iraqensis* as a separate clade in the trees, demonstrating that this species originated in Iraq. This finding indicates that the species is the same species that was morphologically identified and described for the first time in Iraq.

Keywords: *Neoechinorhynchus iraqensis*; *Planiliza abu*; 18S rDNA; Darbandikhan Lake; DNA sequencing.

1. INTRODUCTION

There are several different types of parasites that belong to the main groups, such as trematoda, cestoda, acanthocephala, and monogenea, infest fish [1]. According to earlier research, the fish culture sector in Iraq was having a significant effect and beneficial impact on the parasite populations of freshwater fish [2]. The significance of fish parasites is closely related to the significance of the fish they may infect. Consequently, the previous knowledge of fish's breeders, parasites, and their effects is crucial from an economic perspective [3].

Acanthocephala, often known as thorny-headed worms, have an ever-present proboscis that is equipped with hooks and spines. It frequently attaches to the intestine of the final host and is an obligatory endoparasite [4]. The basic life cycle and developmental stages are the same for all acanthocephalans. For the development of the larva, all require an arthropod as an intermediate host, and all use vertebrates as their only host [5].

Regarding the genus *Neoechinorhynchus* 11 species have been recorded in freshwater fish in Iraq [6]. Amin et al [7] Described for the first time *N. iraqensis* in intestine of the mugilid fish

Planiliza abu (as *Liza abu*) from Euphrates River in Al-Anbar Province, Iraq.

The family Mugilidae is distributed widely. Its major species are found in temperate and tropical coastal waters. Some species survive all or part of their lifespan in lakes, rivers, and coastal lagoons [8]. Only 80 of the 304 species that were available in this family were valid [9].

There isn't any extensive research on the molecular of *N. iraqensis* in the Iraq and Kurdistan region. The objective of this research is to use DNA sequencing by Polymerase chain reaction (PCR) to identify *N. iraqensis* in Darbandikhan Lake.

2. MATERIALS AND METHODS

2.1 Sample Collection

A total of 100 fish belonging to mugilid species (*Planilizaabu*) (Fig.1) were collected from the Darbandikhan Lake in Sulaimani, Kurdistan region, Iraq. It is confined to latitudes 35° 06' 58"-35° 21' 07" N and longitudes 45° 40' 59"-45° 44' 42" E, 65 kilometers southeast of the city of Sulaimani (Fig. 2).



Fig. 1. *Palaniliza abu*

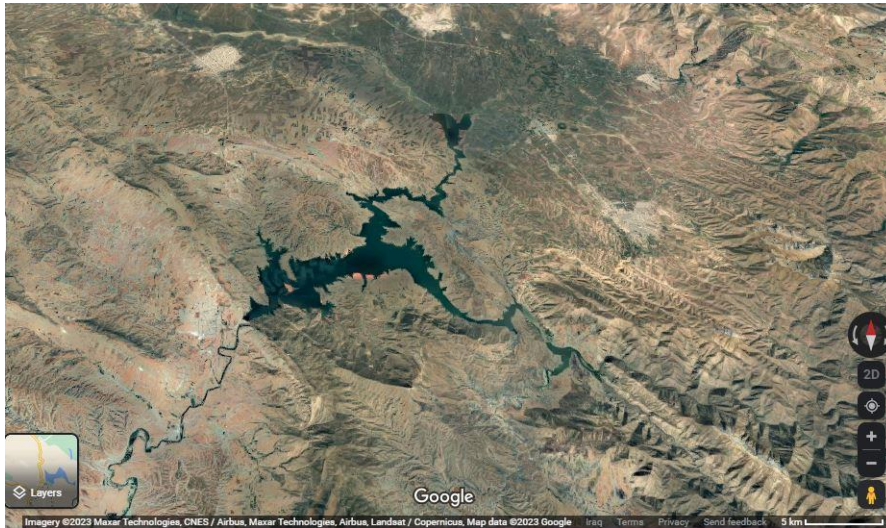


Fig. 2. Map of Darbandikhan Lake

Gill nets or cast nets were used for collecting fish, from December 2023 to February 2024. Shortly after being caught, newly obtained fish were checked in the lab for parasites. Fish names are based on Froese and Pauly [10]. The recovered acanthocephalans had been first cleaned in saline solution, then chilled in chilly water for 12 hours, and finally preserved in seventy percent ethanol [11].

2.2 DNA Extraction

The AddPrep Genomic DNA Extraction Kit (ADD BIO INC. Korea) was used to extract DNA from *N. iraqensis* samples according to the instructions provided by the manufacturer. One percent agarose gel was used to determine the DNA purity, and the DNA concentration was determined using a Nanodrop spectrophotometer. In preparation for use, DNA Samples had been stored at -20 °C.

2.2.1 Primer sequence and PCR conditions

The primers were used to amplify the nuclear ribosomal DNA's 18S rDNA region, (forward: 5'-: CGGGGGGAGTATGGTTGC-3') and (reverse: 5'TGATCCTTCTGCAGGTTACCTAC-3'). The thermo cycling conditions were as follows: an initial denaturation at 94 °C for 8 min, followed by 35 cycles for 30 s at 94 °C, for 30 s at 56 °C for annealing, an extension for 30 s at 72 °C, a final extension for 10 min, and then storage at 4 °C.

The genomic DNA had been diluted into a volume of 25 µl for the PCR reaction, and it also contained 2 µl of each primer, 12.5 µl of Master

Mix 10 X buffer containing MgCl₂, 3 l of dNTPs (10 mM), 0.9 l of 1 U of Taq DNA polymerase (Biotoools, Spain), 7 µl of the genomic DNA, and 3.5µl of distilled water.

Using the same primer as above, the sequencing processes were carried out using a Genetic Analyzer 3500, Applied Bio Systems (USA), in accordance with the instructions provided by the manufacturer. The 18S rDNA sequences were obtained, and using Mega X's default ClustalW [12], they were matched with sequences from other similarly associated species.

3. RESULTS

During the current study period, *Planiliza abu* was surveyed for parasitic acanthocephalans. One acanthocephalan, a species of the genus *Neoechinorhynchus*, was found during the survey. A brief description of this parasite is given below.

Neoechinorhynchus iraqensis Amin, Al-Sady, Mhaisen and Bassat, 2001

Host: *Planiliza abu* (Heckel, 1843).
Prevalence of infection: 7 %.
Mean intensity: 2.4 worm/ fish.
Site infection: Intestine.
Locality: Darbandikhan Lake

In this present research, the DNA sequences of *Neoechinorhynchus iraqensis* have been compared to the sequences of other acanthocephalans and closely associated species that belong to the same genus obtained from GenBank (Table 1).

The 18S rDNA fragment was 533 bp after editing by using the BioEdit program 7.2 (Fig 3). The genetic distance estimated between *acanthocephalan* species used for phylogenetic analysis varied from 0.025 to 0.194 (Table 2). The nucleotide composition was as follows: 24.95% T, 28.57% C, 25.67% A, and 20.79% G are shown in (Table 3).

As a result, Fig 4 shows the Neighbor Joining tree. The 18S rDNA dataset's phylogenetic tree reveals that *N. iraqensis* in the separation position in this tree.

4. DISCUSSION

There have not been any studies on molecular identification for *Neoechinorhynchus iraqensis* to classify it; it was only characterized morphologically by Amin et al [7,13] and Ali [14]. This study investigated *N. iraqensis*, which was identified for the first time by molecular technique and compared to the same genus and other acanthocephalan species recorded in the Genbank.

The eleven species of *Neoechinorhynchus* reported according to GBIF [15] so far in freshwater fish in Iraq are: *N. australis* (Van Cleave, 1931), *N. chilkaensis*, (Podder, 1937), *N. cristatus* (Lynch, 1936), *N. dimorphospinus* (Amin and Sey, 1996), *N. iraqensis* (Amin, Al-Sady, Mhaisen & Bassat, 2001), *N. macronucleatus* (Machado Filho, 1954), *N. rutili* (Müller, 1780 re described by Hamann in Stiles and Hassall, 1905), *N. zabensis* (Amin, Abdullah & Mhaisen, 2003), *N. tigrisensis* (Al-Ayash, Gustinelli, Al-Nasiri & Caffara, 2021), *N. planilizai* (Al-Ayash, Gustinelli, Al-Nasiri & Caffara, 2021) and *N. Barbi* (Al-Ayash, Gustinelli, Al-Nasiri & Caffara, 2021).

In the present study, the low value of genetic distance recorded between *N. iraqensis*, *Neoechinorhynchus* sp. GL-2015 (KU363972.1) and *Neoechinorhynchus* sp. XL-2014 (KM507363.1) was 0.025 and the high value of genetic distance was recorded between *N. iraqensis* and *Tenuisentis niloticus* (MZ727194.1) was 0.194. Phylogenetic study revealed that *N. iraqensis* takes a separate location within the

Table 1. Acanthocephala, host and accession numbers used for phylogenetic analysis based on the 18S rDNA region

Acanthocephala	Host	GenBank accession no.
<i>Neoechinorhynchus</i> sp. GL-2015	<i>Capoeta aculeata</i>	KU363972.1
<i>Neoechinorhynchus saginata</i>	Na	AY830150.1
<i>Neoechinorhynchus pseudemydis</i>	Na	U41400.1
<i>Neoechinorhynchus crassus</i>	<i>Capoeta aculeata</i>	KU363974.1
<i>Neoechinorhynchus qinghaiensis</i>	Na	MW144440.1
<i>Neoechinorhynchus cylindratus</i>	<i>Micropterus salmoides</i>	MF974925.1
<i>Neoechinorhynchus buttnerae</i>	Na	MW590330.1
<i>Neoechinorhynchus buttnerae</i>	Na	MK249749.1
<i>Neoechinorhynchus</i> sp. XL-2014	BH-liaoning	KM507363.1
<i>Neoechinorhynchus crassus</i>	Na	AF001842.1
<i>Neoechinorhynchus</i> sp. JDC-2005	Na	DQ181946.1
<i>Neoechinorhynchus personatus</i>	<i>Mugil cephalus</i>	MT020795.1
<i>Neoechinorhynchus personatus</i>	<i>Mugil cephalus</i>	MT020793.1
<i>Neoechinorhynchus pseudemydis</i>	<i>Capoeta aculeata</i>	KU363973.1
<i>Neoechinorhynchus agilis</i>	<i>Mugil cephalus</i>	MN705824.1
<i>Neoechinorhynchus simansularis</i>	Na	KF156877.1
<i>Neoechinorhynchus</i> sp. JYW-2010	<i>Siganus fuscescens</i>	HM545898.1
<i>Neoechinorhynchus aldrichettae</i>	<i>Aldrichetta forsteri</i>	OM103595.1
<i>Neoechinorhynchus salmonis</i>	Na	KF156878.1
<i>Neoechinorhynchus tumidus</i>	Na	KF156876.1
<i>Neoechinorhynchus beringianus</i>	Na	KF156875.1
<i>Neoechinorhynchus</i> sp. AC3	<i>Heteropneustes fossilis</i>	MF784256.1
<i>Tenuisentis niloticus</i>	<i>Lates niloticus</i>	MZ727194.1

❖ Na= Not Available

Table 2. Genetic distance between *Neoechinorhynchus iraqensis* and other genus of *Neoechinorhynchus* and *Acanthocephalan* species

Acanthocephalan species	Genetic distance
<i>Neoechinorhynchus iraqensis</i>	
<i>Neoechinorhynchus</i> sp. GL-2015	0.025
<i>Neoechinorhynchus saginata</i>	0.059
<i>Neoechinorhynchus pseudemydis</i>	0.054
<i>Neoechinorhynchus crassus</i>	0.057
<i>Neoechinorhynchus qinghaiensis</i>	0.054
<i>Neoechinorhynchus cylindratus</i>	0.050
<i>Neoechinorhynchus buttnerae</i>	0.045
<i>Neoechinorhynchus buttnerae</i>	0.047
<i>Neoechinorhynchus</i> sp. XL-2014	0.025
<i>Neoechinorhynchus crassus</i>	0.057
<i>Neoechinorhynchus</i> sp. JDC-2005	0.071
<i>Neoechinorhynchus personatus</i>	0.086
<i>Neoechinorhynchus personatus</i>	0.086
<i>Neoechinorhynchus pseudemydis</i>	0.053
<i>Neoechinorhynchus agilis</i>	0.089
<i>Neoechinorhynchus simansularis</i>	0.057
<i>Neoechinorhynchus</i> sp. JYW-2010	0.091
<i>Neoechinorhynchus aldrichettae</i>	0.093
<i>Neoechinorhynchus salmonis</i>	0.065
<i>Neoechinorhynchus tumidus</i>	0.061
<i>Neoechinorhynchus beringianus</i>	0.064
<i>Neoechinorhynchus</i> sp. AC3	0.095
<i>Tenuisentis niloticus</i>	0.194

Table 3. Nucleotide composition for *Neoechinorhynchus iraqensis* and other acanthocephalan species recorded in Genbank

Acanthocephalan species	T	C	A	G
<i>Neoechinorhynchus iraqensis</i>	24.954	28.571	25.678	20.795
<i>Neoechinorhynchus</i> sp. GL-2015	25.836	20.057	27.252	26.856
<i>Neoechinorhynchus saginata</i>	25.845	19.542	27.908	26.705
<i>Neoechinorhynchus pseudemydis</i>	26.441	19.379	27.627	26.554
<i>Neoechinorhynchus crassus</i>	26.509	20.069	26.740	26.682
<i>Neoechinorhynchus qinghaiensis</i>	25.899	19.927	27.300	26.874
<i>Neoechinorhynchus cylindratus</i>	25.916	19.987	26.849	27.249
<i>Neoechinorhynchus buttnerae</i>	26.442	20.052	27.065	26.442
<i>Neoechinorhynchus buttnerae</i>	25.888	19.853	27.580	26.678
<i>Neoechinorhynchus</i> sp. XL-2014	25.730	20.000	27.303	26.966
<i>Neoechinorhynchus crassus</i>	25.622	20.474	26.778	27.126
<i>Neoechinorhynchus</i> sp. JDC-2005	25.634	20.828	26.569	26.969
<i>Neoechinorhynchus personatus</i>	26.615	19.844	26.848	26.693
<i>Neoechinorhynchus personatus</i>	26.714	20.016	26.556	26.714
<i>Neoechinorhynchus pseudemydis</i>	26.507	20.364	26.962	26.166
<i>Neoechinorhynchus agilis</i>	26.416	19.976	26.237	27.370
<i>Neoechinorhynchus simansularis</i>	26.452	19.140	26.667	27.742
<i>Neoechinorhynchus</i> sp. JYW-2010	26.545	19.613	26.814	27.028
<i>Neoechinorhynchus aldrichettae</i>	27.314	19.364	26.405	26.917
<i>Neoechinorhynchus salmonis</i>	26.372	19.268	26.480	27.879
<i>Neoechinorhynchus tumidus</i>	25.781	19.531	26.674	28.013
<i>Neoechinorhynchus beringianus</i>	26.316	19.261	26.316	28.108
<i>Neoechinorhynchus</i> sp. AC3	25.952	19.940	27.555	26.553
<i>Tenuisentis niloticus</i>	26.811	20.289	26.268	26.630
Average	26.238	20.019	26.924	26.820

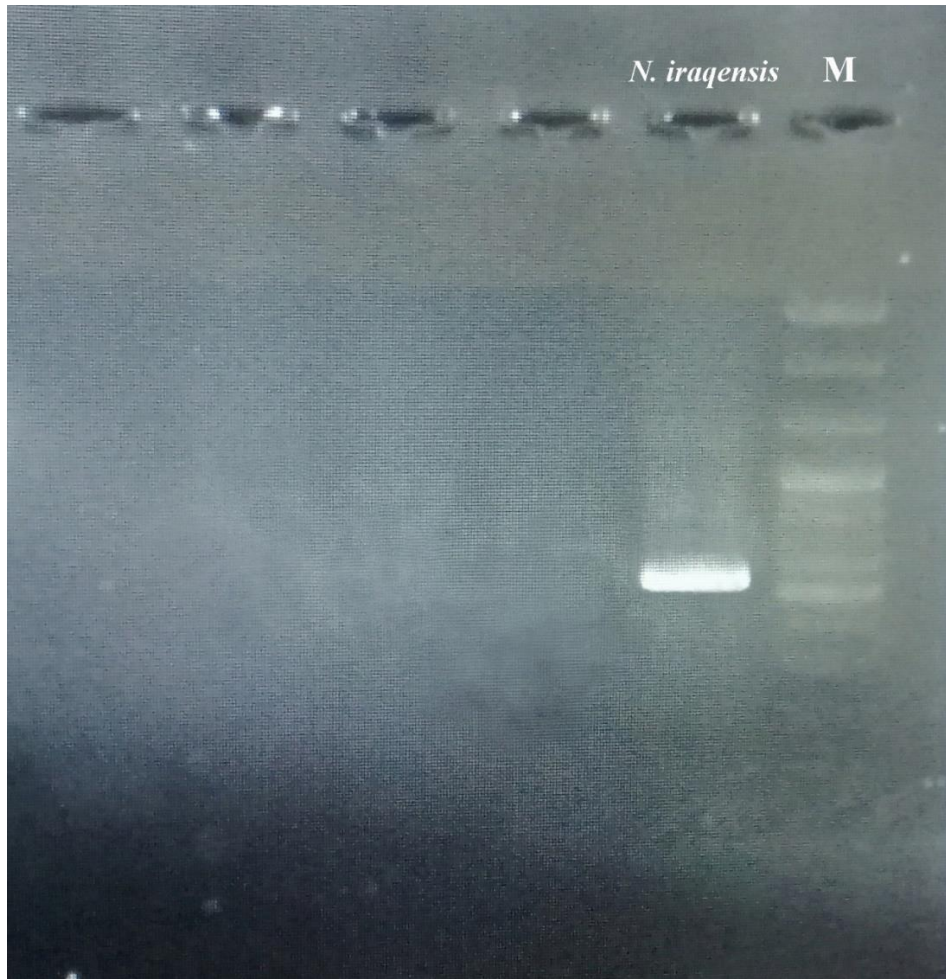


Fig. 3. PCR product for *Neoechinorhynchus iraqensis* from *Planiliza abu* fish. M: DNA ladder. The size of band = 533 bp

trees, denoting that this species originated in Iraq because it was originally discovered and described by [7]. *Neoechinorhynchus* is a genus that contains a wide variety of species, as already noted in several studies [16,17] and [18]. According to a phylogenetic tree study, *N. zabensis* is in a separate position from other species [14]. Phylogenetic study showed that *N. johnii* has a distinct location in the trees, most likely indicating that this species originated in Asia [19]. Nuclear DNA sequences of the 18S rDNA gene and mitochondrial DNA sequences of COX1 of *N. poonchensis* sp. n. have been amplified and matched with other sequences on GenBank.

N. poonchensis sp. n. was shown to be nested in a separate position based on ML and BI method calculated for 18S rDNA and cox1 [20]. For the 18S rRNA gene, the estimated genetic difference between the *Neoechinorhynchus* species varied from 0 to 2.5%. [21]. The genetic identification of

the species *N. personatus* and *N. yamagutii* in gray mullets fish that are caught in the Atlantic and Pacific Oceans was reported by Sarabeev et al [22]. The intra specific differences ranged from 0.01 to 0.02%, while the genetic divergence between *N. schmidtii* and *N. emyditoides* was 4%. The pairwise variations ranging from 9.5 to 33% were found among these two species and four other congeners that are parasitic in fresh and brackish water fishes: *Neoechinorhynchus golvani*, *Neoechinorhynchus roseum*, *Neoechinorhynchus saginatus* and *Neoechinorhynchus* sp. [23]. Using a partial 18S rDNA dataset, the relatively large genetic differences among *N. ponticus* n. sp. and other *Neoechinorhynchus* species confirm its status of independence. *Neoechinorhynchus personatus* and *Neoechinorhynchus ponticus* n. sp. share an ancestry with *Neoechinorhynchus* species that are gathered from saltwater fish [24].

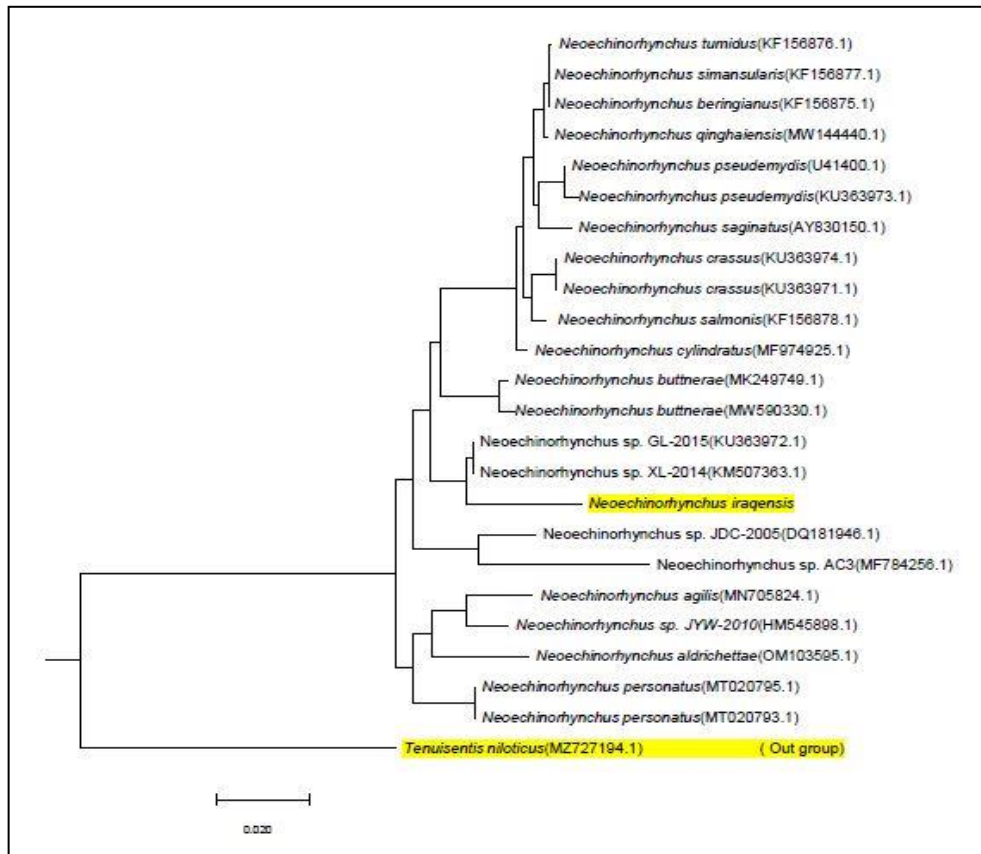


Fig. 4. The phylogenetic tree of *Neoechinorhynchus iraqensis* obtained for the present research and the other genus of *Neoechinorhynchus* were received from GenBank based on the partial 18S rDNA gene. This phylogenetic tree has been created dependent on the neighbor joining tree. *Tenuisentis niloticus* out group

5. CONCLUSION

The findings of this study demonstrate the importance of identifying *N. iraqensis* using molecular techniques. For a study of the upper-level phylogeny, 18S rDNA was well preserved and appropriate. The results of this research show that *N. iraqensis* occupied an independent position within the trees; this result confirms that the species is the same type that was initially found and identified morphologically, showing that Iraq was the location where this species first appeared.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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