

FIRST TAXONOMICAL ANALYSES OF PIKE POPULATIONS (ESOCIDAE, *ESOX*) IN FRIULI VENEZIA GIULIA (NORTHEAST ITALY)

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ABSTRACT

*Recent studies have addressed to the taxonomical characterization of Italian pike as a new species named *Esox cisalpinus*, which differs from the European *Esox lucius*. A taxonomical study of the pike features in the Friuli Venezia Giulia region (Northeast Italy) is here presented, since previous studies did not consider this area which could represent an overlapping zone for the two species. Main meristic characters were investigated, and genetic analyses were carried out using molecular markers. Our results confirm the genetic separation from the *E. lucius*, while among meristic characters only the number of lateral-line scales differs between the species. *E. cisalpinus* was observed in most of the investigated sites, except for an isolated lentic habitat where *E. lucius* was found. As *E. cisalpinus* is likely autochthonous in Friuli Venezia Giulia as in other Italian regions, we highlight the requirement of further analyses in order to clarify if hybridization can occur and to plan appropriate management safeguards for native populations.*

Key words: *Esox cisalpinus*, *Esox lucius*, taxonomy, COI, Cytb

PRIME INDAGINI TASSONOMICHE A CARICO DELLE POPOLAZIONI DI LUCCIO (ESOCIDAE, *ESOX*) IN FRIULI VENEZIA GIULIA (NORDEST ITALIA)

SINTESI

*Studi recenti hanno permesso la caratterizzazione tassonomica del luccio in Italia identificando una nuova specie, chiamata *Esox cisalpinus*, la quale differisce dalla specie europea *Esox lucius*. In questo lavoro viene presentato uno studio tassonomico sulle caratteristiche del luccio, effettuato nella regione Friuli Venezia Giulia (Nordest Italia) poiché i precedenti studi non hanno considerato quest'area, la quale può rappresentare una potenziale zona di sovrapposizione per le due specie. Sono stati indagati i principali caratteri meristici e sono state condotte analisi genetiche utilizzando marcatori molecolari. I risultati confermano la separazione a livello genetico da *E. lucius*, mentre per quanto attiene i caratteri meristici soltanto il numero di scaglie della linea laterale differisce tra le due specie. *E. cisalpinus* è stato rinvenuto nella maggior parte dei siti monitorati, ad eccezione di un habitat lentic isolato, in cui è stata registrata la presenza di *E. lucius*, probabilmente dovuta a immissioni per scopi alieutici. Poiché *E. cisalpinus* è verosimilmente autoctono in Friuli Venezia Giulia come in altre regioni italiane, si evidenzia il bisogno di ulteriori analisi volte allo scopo di verificare la possibilità di ibridazione tra le due specie, e la pianificazione di appropriate azioni di gestione volte alla salvaguardia delle popolazioni native.*

Parole chiave: *Esox cisalpinus*, *Esox lucius*, tassonomia, COI, Cytb

INTRODUCTION

The northern pike (*Esox lucius* Linnaeus, 1758) is widespread in the temperate and cold temperate belts, occurring in Europe, North America and Asia, north of 40° N and south of the Arctic Circle (Jacobsen *et al.*, 2005; Lucentini *et al.*, 2006, 2010a). Furthermore, the northern pike natural distribution area has been considerably expanded because of introductions conducted in Spain, Madagascar, Uganda, Morocco, Portugal, Tunisia, Ethiopia and Azores (Welcomme, 1988). In fact, this is the most widespread Esocidae species in the world and is naturally present in Europe, occupying a wide range of different lotic and lentic habitats (Lucentini *et al.*, 2014).

Despite the great geographical variability distribution, Nilsson *et al.* (2008) consider all pike populations as a part of the same species, even though molecular analyses carried out by Nicod *et al.* (2004) highlighted some distinctive characters in the populations of the Lake Maggiore and Lake Trasimeno (Italy), allowing the hypothesis of an isolation of the Italian populations. In Italy, pike is native to the Po river basin, Tuscany and Lazio regions (Zerunian, 2004), where it was classified as *E. lucius* until a few years ago. However, Bianco and Delmastro (2011) have recently assigned Italian populations to a new species named *Esox cisalpinus*, on the basis of phenotypic analyses, in agreement with genetic investigations conducted by Lucentini *et al.* (2011), which describe the distinct Italian species named *Esox flaviae*. These two species nomenclatures probably refer to the same organism (Skog *et al.*, 2014), because their description are very similar for the main characters, such as color pattern and number of scales on the lateral line (Bianco, 2014a, 2014b). For priority rule and used hereafter in the manuscript, *E. cisalpinus* is the reference name and *E. flaviae* represents a junior synonym, as the vernacular name is cisalpine pike (Bianco, 2014a) or southern pike (Skog *et al.*, 2014). Following findings of these recent works, pike's taxonomical identification is gaining increasing scientific attention, particularly in Italy and in the Mediterranean area, even though it was already essential because of the pike ecological role. In fact, it is the main native predator in its habitat and acts as an active control factor in the balancing of different populations within the fish communities (Craig, 2008). However, in the past pike was often treated as a harmful species for freshwater environments due to its dietary requirements (Paradisi, 2005) and it was subjected to intensive recreational fishing pressure. More recently, the concept of this Esocid, as a voracious predator, has been reconsidered from an ecological perspective and its presence has become of great worth, even though the interest for pike as a fishery resource remains high (Gandolfi *et al.*, 1991). Nevertheless, the decline of pike populations is well documented in Europe (Lorenzoni *et al.*, 2002; Westin & Limburg, 2002; Jacobsen *et al.*,

2005; Lucentini *et al.*, 2006, 2009), especially in the main Mediterranean countries, such as Italy, where declining population trends have led to some recovery projects both for conservation and for fishing purposes. Unfortunately, the lack of knowledge about proper taxonomical identification caused allochthonous introductions in the last decades, because the species was often stocked with fry of unknown origin or from Northern Europe (Lucentini *et al.*, 2006, 2011, 2014). Anthropogenic alterations represent another cause of decline for *Esox* populations, especially when changes involve the elimination of aquatic vegetation (Casselman & Lewis, 1996; Craig, 2008), which is one of the most important factors for survival of this species (Raaij, 1988; Grimm, 1989; Bry, 1996; Grimm & Klinge, 1996).

Friuli Venezia Giulia is a region in the northeastern Italy, where pike lives primarily in the alluvial spring watercourses and drainage channels of the lowland hydrographic network, with generally large and well-structured populations (Stoch *et al.*, 1992; Pizzul *et al.*, 2006). Except for two specimens from the Isonzo Basin, examined by Bianco and Delmastro (2011), Friuli Venezia Giulia was not included in recent studies regarding pike taxonomical identification. Therefore, a clarification about the systematics of Esocidae populations was deemed necessary, especially considering the geographical position of this region, bordering Austria and Slovenia. In addition, increasing informations are needed and result fundamental for the managing activities and for the biodiversity safeguard of this area.

Consequently, phenotypical and genetic analyses were carried out, using information provided by Bianco and Delmastro (2011) and by Lucentini *et al.* (2011) as a starting point. Our main goal was to check for the presence of southern pike *E. cisalpinus* and/or the northern species *E. lucius* in freshwater habitats of Friuli Venezia Giulia.

MATERIALS AND METHODS

Ethical statement

The treatments of the specimens and procedures applied in this survey are consistent with National regulations and indications of the Ethic Committee of the University of Trieste. Further approvals from the Ethics Committee were not necessary given the nature of the data collected, such as the collection of morphometric measurements, pictures of individuals, or the cut of a small portion of the dorsal fin. Samples for DNA analysis were collected with non-invasive techniques and once collected the samples, animals were released at the same sampling site.

Sample collection

Fish were captured at 6 sampling sites included in four river basins (Fig. 1), representative for the habitat

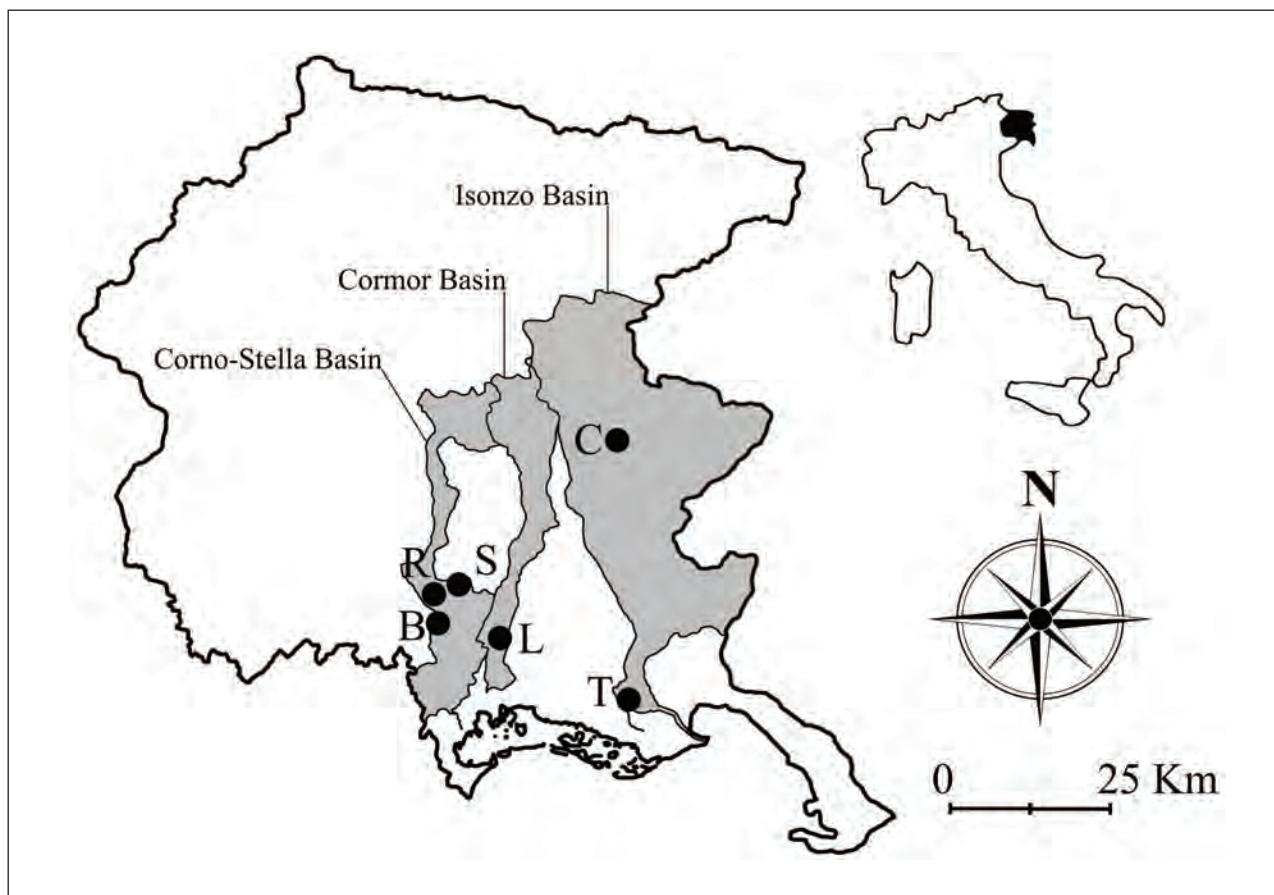


Fig. 1: Geographic position of sampling sites located in the Friuli Venezia Giulia Region (UTM coordinates) and relative basins: B – Roggia Barbariga (33T 346674 E; 5082594 N); R – Roggia Ribosa (33T 347336 E; 5086680 N); S – Springs of the Stella River (33T 350299 E; 5087525 N); L – Roggia Levada (33T 356793 E; 5079430 N); C – Campeglio Fish Ponds (33T 375966 E; 5069040 N); T – Tiel ditch (33T 374615 E; 5109142 N).

Sl. 1: Geografski položaj vzorčevalnih lokalitet na območju Furlanije Julijske krajine (UTM koordinate) in v vzorčevalnih vodnih telesih: B – Roggia Barbariga (33T 346674 E; 5082594 N); R – Roggia Ribosa (33T 347336 E; 5086680 N); S – izviri reke Stella (33T 350299 E; 5087525 N); L – Roggia Levada (33T 356793 E; 5079430 N); C – ribniki Campeglio (33T 375966 E; 5069040 N); T – lokaliteta Tiel (33T 374615 E; 5109142 N).

of the investigated species. In detail, the sampling sites Roggia Barbariga (site B), Roggia Ribosa (site R) and Springs of the Stella River (site S) belong to the Corno-Stella basin, Roggia Levada (site L) is included in the Cormor basin and Tiel ditch (site T) is an independent watercourse belonging to a little isolated alluvial spring basin (A.A.V.V., 2010), formerly included in the Isonzo basin by Mosetti (1983). Finally, Campeglio Fish ponds (site C) is considered as separate from the other basins, because they are hydrologically isolated even though these ponds are placed within the Isonzo basin area.

Overall, 51 specimens were collected, partially by electrofishing (pulsed direct current; 0.7-7 A; 150-380 V), partially with fishing rods by local fishermen.

Standard length (SL) and weight (W) were recorded for each captured specimen (length was expressed in centimeters; weight was expressed in grams). Mean,

median, minimum and maximum values and CV [%] were calculated for each basin except for the specimen sampled in the Tiel ditch, because only one fish was captured. Data are reported in Table 1.

Pictures of each captured fish were taken, in order to have information about the color pattern, and a small portion of the dorsal fin was cut for genetic analyses and stored in 96% ethanol until DNA extraction. Once sampled, fish were released at the same site to minimize consequences for vitality and to avoid possible mixing among populations constituted by the two different *Esox* species.

Phenotypic analysis

The following meristic characters were recorded for each captured specimen: number of lateral-line scales

Tab. 1: Mean, median, minimum, maximum and [%] values Coefficient of Variation calculated for each biometric parameter relative to the different monitored basins. Corno-Stella basin= sites B, R and S; Cormor basin=site L; Campeglio Fish Ponds= site C; Tiel basin= site T.

Tab. 1: Srednja, mediana, minimalna, maksimalna vrednost ter delež [%] vrednosti koeficienta variacije. Vrednosti so podane za vsak biometrični parameter v vzorčevanih vodnih telesih. Legenda: bazen Corno-Stella = lokalitete B, R in S; bazen Cormor = lokaliteta L; ribniki Campeglio = lokaliteta C; bazen Tiel = lokaliteta T.

Basin	N		Weight (g)	SL (cm)
Corno-Stella	35	Mean	120.74	22.05
		Median	58.00	19.50
		Min	4.00	5.98
		Max	950.00	43.31
		CV %	151.01	39.69
Cormor	12	Mean	223.83	28.47
		Median	151.50	27.05
		Min	62.00	17.25
		Max	861.00	41.33
		CV %	104.70	28.27
Campeglio Fish Ponds	3	Mean	172.67	27.83
		Median	173.00	26.50
		Min	135.00	21.67
		Max	210.00	27.90
		CV %	21.72	13.55
Tiel	1	Mean	688.00	47.00
		Median	-	-
		Min	-	-
		Max	-	-
		CV %	-	-

(LL), number of undivided dorsal fin rays (UDFR), number of divided dorsal fin rays (DDFR), number of undivided anal fin rays (UAFR), number of divided anal fin rays (DAFR), and number of submandibular pores (PM). Mean, median, minimum and maximum and CV

[%] values were reported for all considered parameters (Tabs. 1 and 3) and for each group of specimens collected in the different basins (Corno-Stella, Cormor and Campeglio Lakes), except for the specimen sampled in the Tiel ditch, because only one fish was captured.

Genetic analysis

Subsets of at least four specimens collected in each site investigated in this study were randomly selected. Genomic DNA (gDNA) was extracted from each fin by using the E.Z.N.A.® Mollusc DNA Kit (Omega Biotek) following the manufacturer's instructions and its quality was assessed through the Nanodrop 2000 (Thermo Scientific).

Two fragments from the mitochondrial genes Cytochrome Oxidase Subunit I (COI) and Cytochrome b (Cytb) were selected to perform genetic analysis. In addition, we tested two nuclear AFLP-derived markers called "band 9" and "band 24" (Lucentini *et al.*, 2011). Table 2 reports the complete collection of primers used in this study. Standard PCR reactions were accomplished for all the systems tested by following the thermal profile: 94°C for 2'30", 35 cycles at 95°C for 30", 57°C for 30" and 72°C for 45" with a final extension step at 72°C for 5', and by using Go Taq (R) G2 DNA polymerase (Promega).

Phylogenetic analysis

PCR products were sequenced by an external service (IGA, Udine, Italy) and sequences were aligned and analyzed through MEGA 6 software (Tamura *et al.*, 2013). One sample from Roggia Levada (site L, Corno-Stella basin), indicated as L2 in Figure 2, was excluded from the COI analysis since the sequence was of poor quality. First, the most suitable model was tested by using the internal tool of MEGA 6, and then the Maximum Likelihood statistic method with 1000 bootstrap replica was selected. For both the COI and Cytb markers the best model resulted to be the Hasegawa-Kishino-Yano model (Hasegawa *et al.*, 1985) plus Gamma distribution, which has been settled to a number of 5 discrete Gamma categories. All the branches that were not supported at the default cutoff value of bootstrap confidence level ≥ 50 were condensed together. The sequences reported in Table 2 by Lucentini *et al.* (2011) were used as a reference dataset.

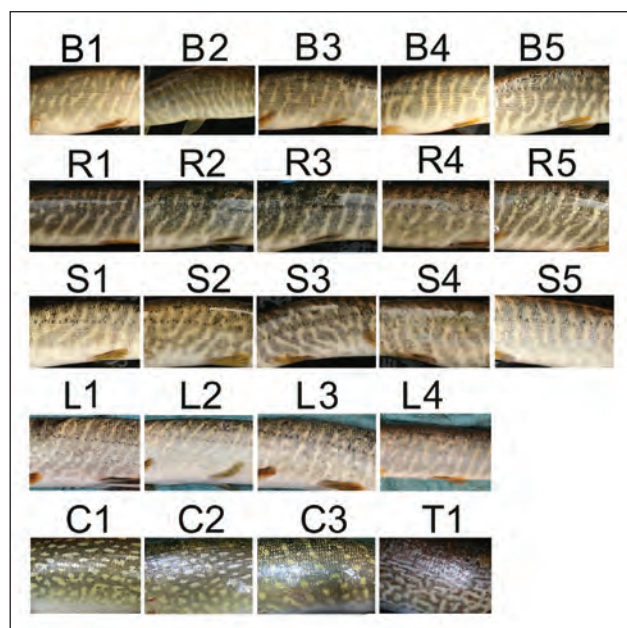
RESULTS

Phenotypic analysis

Color pattern of the 51 captured pikes belonged to four types of those described by Lucentini *et al.* (2010b): diagonal bars, vertical bars, stellate spots and round spots were taken into account (Fig. 2). The diagonal bar pat-

Tab. 2: Sets of primers used in this study (Lucentini et al., 2011).**Tab. 2: Nizi začetnih oligonukleotidov uporabljenih v raziskavi (Lucentini et al., 2011).**

Primer ID	5'-3' sequence
F-COI-EI	GTGGCAATCACACGCTG
R-COI-EI	CGGGTGTCCGAAGAATC
cytbF	TCGGACTCTACAAAACCAA
cytbR	GTTCAACGGGTATTCCTCCA
9FW	CAGTTGTAAGGCCCAAGGAAG
9RV	GGAAATACGTTGTGGAAGTGC
24extFW	GATCTCTGGACCATTTGGAC
24extRV	TGGCTACATGCGACATCAG

**Fig. 2: Colored patterns collection from adult pikes analyzed in this study. B, R, S, L, C and T represent different sampling sites: B – Roggia Barbariga; R – Roggia Ribosa; S – Springs of the Stella River; L – Roggia Levada; C – Fish Ponds of Campeglio; T – Tiel ditch.**

Sl. 2: Zbirka barvnih vzorcev odraslih ščuk, ki smo jih analizirali v pričujoči raziskavi. B, R, S, L, C in T so različne vzorčevalne lokalitete: B – Roggia Barbariga; R – Roggia Ribosa; S – izviri reke Stelle; L – Roggia Levada; C – ribniki Campeglio; T – lokaliteta Tiel.

tern was the most frequent (88% of collected specimens) and it was observed in all fish captured in the Cormor basin (site/samples L) and in the Corno-Stella basin (sites/samples B, R, S). Round spot pattern was found only in the samples collected from the Campeglio Lakes (site/samples C) and it was observed for each fish; the only specimen analyzed from the Tiel ditch (site/sample T) was stellate spotted. In agreement with color pattern reported by Bianco and Delmastro (2011), Lucentini et al. (2011) and Bianco (2014a, 2014b), two groups were identified: the first showing the southern pike color patterns (sites/samples B, R, S, and T) and the second showing the northern pike color pattern (site C) (Fig. 2).

Concerning the meristic characters (Tab. 3), the number of lateral-line scales (LL) ranged from 95 to 107 in the first group, and from 109 to 115 in the second group. Regarding other meristic characters (number of undivided dorsal fin rays: UDFR; number of divided dorsal fin rays: DDFR; number of undivided anal fin rays: UAFR; number of divided anal fin rays: DAFR; and number of submandibular pores: PM), observed ranges always seem to overlap.

Analysis of the two AFLP-derived markers

The molecular analyses were conducted by using two AFLP-derived markers, hereafter named “band 9” and “band 24” (Lucentini et al., 2011). However, only “band 24” was amplified from our samples, and the resulting PCR amplicon has been sequenced, confirming the presence of the reported C/G polymorphism (C in round spotted color-pattern specimens and G in the other color-pattern phenotypes).

Phylogenetic analysis

Fragments of Cytochrome Oxidase I (COI) and Cytochrome b (Cytb) mitochondrial genes were sequenced to assign our samples to one of the two species of pike, accordingly to Lucentini et al. (2011).

Phylogenetic trees for COI (Fig. 3) and Cytb (Fig. 4) were obtained by applying the Hasegawa-Kishino-Yano model (Hasegawa et al., 1985) plus Gamma distribution. In both trees, two groups, corresponding to the *E. cisalpinus* and *E. lucius* clades, were well defined and separated from the other *Esox* spp.

The three specimens, characterized by the round-spotted colored pattern (namely, C1, C2, and C3), clustered within the *E. lucius* clade, whereas the stellate spot pattern specimen (T1) and all the other pikes characterized by vertical and diagonal bars grouped within *E. cisalpinus* clade.

DISCUSSION

Recent studies pointed out the existence of two pike lineages, the first one corresponding to the northern pike

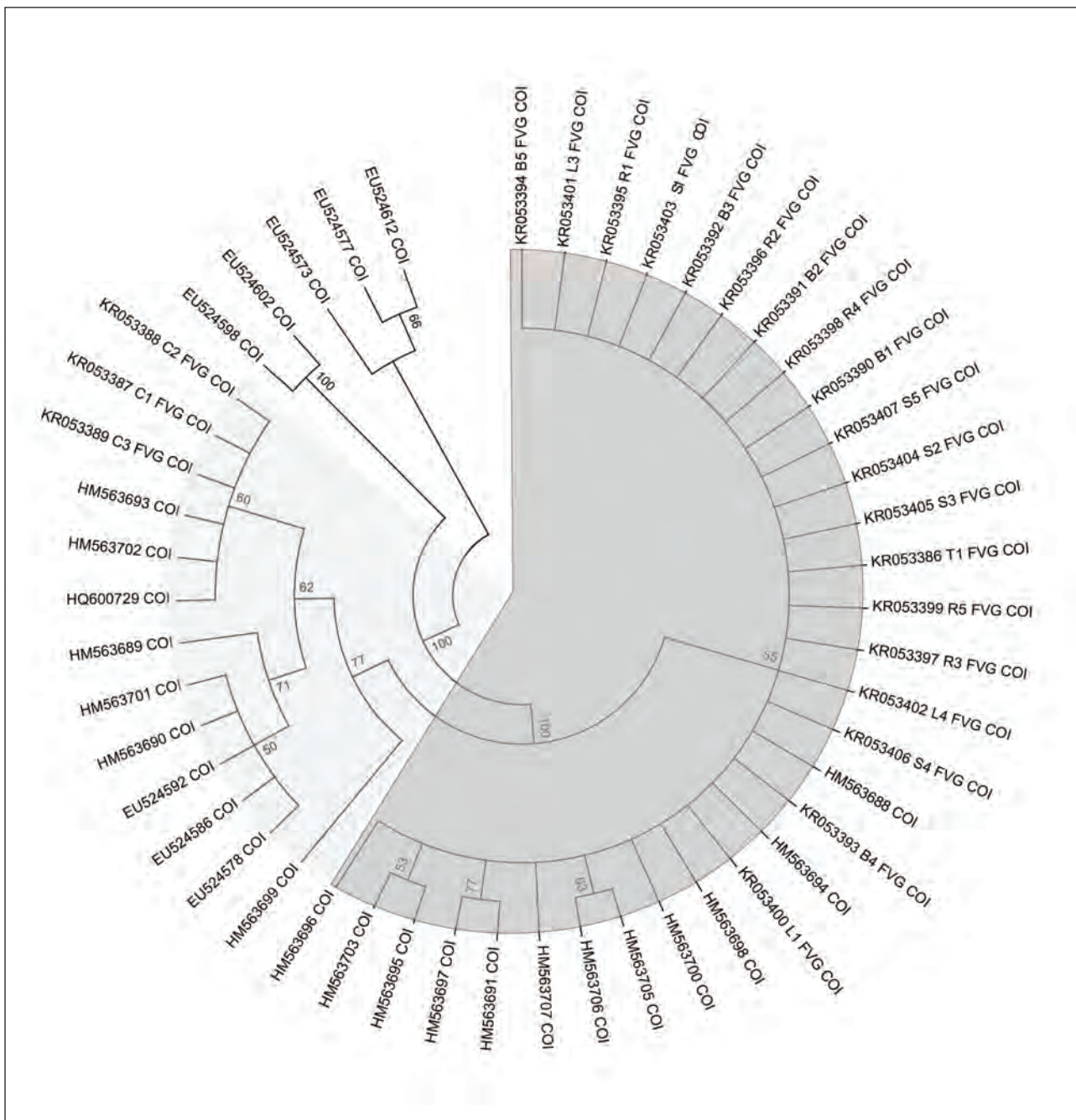


Fig. 3: Bootstrap consensus of the COI gene tree. All the branches that were not supported at the default cutoff value of bootstrap confidence level ≥ 50 were condensed together. Light grey groups the *Esox lucius* clade, whereas dark grey clusters *E. cisalpinus* specimens. Specimens are listed with their GenBank IDs and, for pikes sampled in this study, by the site names as in Fig. 1. Outgroups of the two clades are: *Esox niger* (EU524612), *Esox americanus americanus* (EU524577), *Esox americanus vermiculatus* (EU524573), *Esox masquinongy* (EU524602), and *Esox masquinongy* (EU524598).

Sl. 3: Filogenetsko drevo na osnovi gena za COI. Statistične podpore drevesa so določene z neparametričnim testom ponovnega vzorčenja. Vse razvejitve pod mejo zaupanja ≥ 50 so bile združene. S svetlo sivo barvo so označene skupine iz klada navadne ščuke *Esox lucius*, s temno sivo pa primerki vrste *E. cisalpinus*. Primerki so razvrščeni skupaj z njihovimi GenBank IDs in pri ščukah, vzorčenih v tej študiji na podlagi lokalitet tako kot na sliki 1. Izdanki obeh kladov so: *Esox niger* (EU524612), *Esox americanus americanus* (EU524577), *Esox americanus vermiculatus* (EU524573), *Esox masquinongy* (EU524602) in *Esox masquinongy* (EU524598).

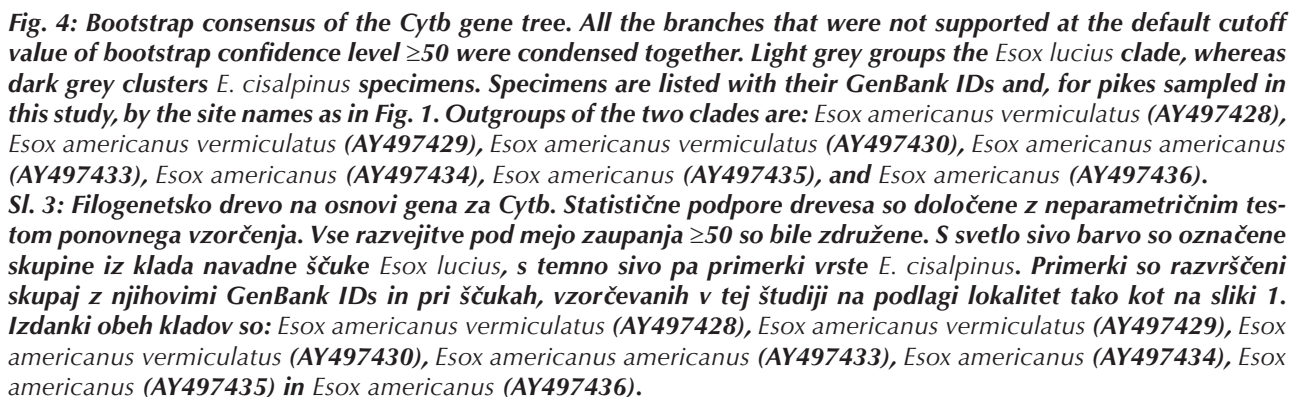
Tab. 3: Mean, median, minimum, maximum, and [%] Coefficient of Variation calculated for each meristic parameter relative to the different monitored basins. Corno-Stella basin= sites B, R and S; Cormor basin=site L; Campeglio Fish Ponds= site C; Tiel basin= site T.

Tab. 3: Srednja, mediana, minimalna, maksimalna vrednost in delež [%] vrednosti koeficienta variacije, izračunane za vsak biometrični parameter v preiskanih vodnih telesih. Legenda: bazen Corno-Stella = lokalitete B, R in S; bazen Cormor = lokaliteta L; ribniki Campeglio = lokaliteta C; bazen Tiel = lokaliteta T.

Basin	N		LL	UDFR	DDFR	UAFR	DAFR	PM
Corno-Stella	35	Mean	99.17	5.06	13.37	3.97	12.46	4.03
		Median	99.00	5.00	13.00	4.00	13.00	4.00
		Min	95.00	5.00	11.00	3.00	11.00	4.00
		Max	107.00	6.00	15.00	4.00	14.00	5.00
		CV %	2.58	4.66	7.71	4.26	7.63	4.20
Cormor	12	Mean	99.92	5.00	13.75	4.00	12.75	4.08
		Median	99.50	5.00	13.50	4.00	13.00	4.00
		Min	95.00	5.00	11.00	4.00	10.00	4.00
		Max	106.00	5.00	15.00	4.00	13.00	5.00
		CV %	3.00	0.00	9.37	0.00	6.79	7.07
Campeglio Fish Ponds	3	Mean	112.33	5.00	14.33	4.00	13.00	4.33
		Median	113.00	5.00	13.00	4.00	13.00	4.00
		Min	109.00	5.00	13.00	4.00	13.00	4.00
		Max	115.00	5.00	17.00	4.00	13.00	5.00
		CV %	2.72	0.00	16.11	0.00	0.00	13.32
Tiel	1	Mean	105.00	5.00	13.00	4.00	13.00	5.00
		Median	-	-	-	-	-	-
		Min	-	-	-	-	-	-
		Max	-	-	-	-	-	-
		CV %	-	-	-	-	-	-

(*E. lucius*), widely distributed in the Palearctic region, and the second lineage of southern pike, naturally occurring in Italy (Bianco & Delmastro, 2011; Lucentini et al., 2011; Bianco, 2014a; Lucentini et al., 2014). Based on the use of meristic characters, and mtDNA (COI and Cytb gene fragments) genetic traits, this study supports the proposal of a newly described endemic species, southern pike *E. cisalpinus* here reported in Friuli Venezia Giulia (FVG) region, as well.

Following the observation of meristic characters and color patterns, two groups have been identified in the samples: the first group comprises pikes collected in the Corno-Stella basin, Tiel basin (in the context of the Isonzo basin) and Cormor basin, and it shows a lower number of lateral line scales (95-107) and color patterns with diagonal bars, vertical bars and stellate spots. These characters correspond to those of the typically Italian species *E. cisalpinus*. These features are



reported by Bianco and Delmastro (2011), who analyzed specimens collected in the Po basin, Central Italy and two specimens from Friuli Venezia Giulia, and by Lucentini *et al.* (2011), Lucentini *et al.* (2014), who analyzed populations from Northern Italy (Po basin) and Central Italy (Tevere basin) and compared them with populations of *E. lucius* collected in continental Europe (the Netherlands, Switzerland, Czech Republic, Hungary and Sweden). Specimens belonging to the second group, including only individuals collected in the Campeglio Lakes, show a higher number of lateral line scales (109-115) and round spotted color patterns, which are typical characters of the northern pike *E. lucius* (Bianco & Delmastro, 2011; Bianco, 2014a). These are public lakes, managed by the local Authority for recreational fishing.

In agreement with these results, molecular analyses confirmed the discrimination between *E. lucius* and *E. cisalpinus* species with 3 out of 4 molecular markers proposed by Lucentini *et al.* (2011): COI sequence, Cyt b sequence, and band 24.

In conclusion, most of the analyzed specimens are recognized as *E. cisalpinus*, while *E. lucius* was only found in the Campeglio lakes, where sport fishing is usually practiced, and where introductions of allochtho-

nous specimens could be probably conducted by some private fishermen without the permission of the regional management agency.

Therefore, appropriate management practices are urgently needed for the safeguard of native populations and for preserving their distribution within the local habitats. In addition, repopulations could be carried out if necessary, but only with severely genetically controlled material.

Due to these reasons, further analyses are planned over a wider number of sampling sites, covering the whole pike distribution area. Moreover, it is of great interest to extend this analysis to the nearby Austrian and Slovenian populations, not investigated by the authors cited above, which share waters with some populations from Friuli Venezia Giulia.

ACKNOWLEDGMENTS

We would like to thank the Fishing Management Agency of Friuli Venezia Giulia (Ente Tutela Pesca – ETP in its Italian acronym) which provided personnel for the sampling operations. Many thanks to Valdo Barbiani, Stefano Gigante and Davide Lesa, who provided additional data and samples.

PRVA TAKSONOMSKA ANALIZA POPULACIJ ŠČUKE (ESOCIDAE, *ESOX*) V FURLANIJ JULIJSKI KRAJINI (SEVEROVZHODNA ITALIJA)

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POVZETEK

Recentne raziskave taksonomske opredelitve ščuk v Italiji so obelodanile prisotnost nove vrste ščuke, opisane kot *Esox cisalpinus*, ki se loči od vrste *Esox lucius*. V prispevku avtorji poročajo o taksonomski raziskavi ščuk na območju Furlanije Julijske krajine (severovzhod Italije), kjer se je izkazalo, da se prekrivata areala dveh vrst. Avtorji so raziskali glavne meristične značilnosti, poleg njih pa so opravili še genetsko analizo na podlagi molekularnih markerjev. Dobljeni rezultati potrjujejo genetsko razmejitev med vrstama, medtem ko se na merističnem nivoju razlikujeta le na podlagi števila lusk v pobočnici. Vrsta *E. cisalpinus* je bila ugotovljena na veliki večini raziskanih lokalitet z izjemo le enega izoliranega lentičnega habitata, kjer je bila najdena le navadna ščuka *E. lucius*, ki so jo verjetno naselili ribiči. Glede na dejstvo, da je vrsta *E. cisalpinus* avtohtona v Furlaniji Julijski krajini in v drugih italijanskih pokrajinah, so potrebne nadaljnje analize z namenom ugotavljanja potencialnega križanja med vrstama in pripravo akcijskega načrta za ohranjanje naravnih populacij.

Ključne besede: *Esox cisalpinus*, *Esox lucius*, taksonomija, COI, Cytb

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