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**ISOLATION AND CHARACTERIZATION OF *FUSARIUM* SPP. FROM UNHATCHED
EGGS OF *CARETTA CARETTA* IN TUSCANY (ITALY)**

Samuele Risoli^{1,2}, Sabrina Sarrocco^{1*}, Giuliana Terracciano³, Luana Papetti⁴, Riccardo Baroncelli⁵,
Cristina Nali¹

¹Department of Agriculture, Food and Environment, University of Pisa, Via del Borghetto 80, 56124
Pisa (Italy)

²University School for Advanced Studies IUSS, Palazzo del Broletto, Piazza della Vittoria 15, 27100
Pavia (Italy)

³Istituto Zooprofilattico Sperimentale delle Regioni Lazio e Toscana, SS Dell' Abetone e del Brennero
4, 56123, Pisa (Italy)

⁴tartAmare, Centro Recupero Tartarughe Marine, via Bramante n. 83 Marina di Grosseto, Italy

⁵Department of Agricultural and Food Sciences (DISTAL), University of Bologna, Viale Giuseppe
Fanin 42, 40127 Bologna (Italy)

*Corresponding Author: sabrina.sarrocco@unipi.it

Keywords

STEF, biodiversity conservation, sea turtle, FSSC, phylogenetic analysis

23 **Abstract**

24 Sea Turtle Egg Fusariosis (STEF) is a worldwide emergent fungal disease affecting eggs and causing
25 embryos mortality in turtle's nests such as those of *Caretta caretta*. The disease is caused by a
26 complex of species belonging to *Fusarium* genus, particularly those included in the Fusarium Solani
27 Species Complex (FSSC). During the samplings carried out in summer 2020 along the Tuscany
28 coastlines (Italy), *C. caretta* eggs showed clinical signs resembling those caused by STEF. A total of
29 32 fungal isolates were obtained from lesioned eggs whose molecular characterization allowing
30 identifying as belonging to FSSC / *Neocosmospora* spp., *Fusarium oxysporum* Species Complex
31 (FOSC) / *F. oxysporum* and *Fusarium nodosum*, i.e., fungal genera and species including also well-
32 known plant pathogens. However, sampled isolates inoculated on several plant hosts did not result in
33 any pathogenic activity except for *F. nodosum* causing, when inoculated on wheat spikes, disease
34 symptoms.

35 While FSSC / *Neocosmospora* spp. and *F. oxysporum* have previously been associated to *C. caretta*
36 eggs displaying signs of STEF, this is the first time *F. nodosum* has been isolated from portions of
37 eggs showing evident signs of fungal infection. This work represents the first report of *Fusarium* spp.
38 isolated from *C. caretta* eggs showing lesions resembling those caused by STEF on Tuscan coast thus
39 posing a significant concern to loggerhead sea turtle conservation also in this region.

40

41

42 **Introduction**

43

44 In the recent years an increase of emerging infectious diseases caused by fungi and fungal-like species
45 has been registered in all ecosystems, thus contributing to a decline across a broad range of taxa with
46 a consequent biodiversity loss. As example, the emerging disease Ophidiomycosis, whose causal
47 agent is the fungus *Ophidiomyces ophidiicola*, causing local and systemic infection in affected snakes
48 (Di Nicola et al., 2022), represents a threaten to wild snake safeguard. The white-nose syndrome
49 (WNS), caused by the fungal pathogen *Pseudogymnoascus destructans*, caused widespread mortality
50 in many communities of hibernating bats and decimated some species (Langwig et al., 2016). The
51 discovery of the disease chytridiomycosis in amphibians, due to chytrid fungi belonging to the genus
52 *Batrachochytrium*, is considered as the link between emerging infections and global amphibian
53 declines (Fisher et al., 2020). Similarly, hatching failure in eggs linked to symptoms of fusariosis was
54 reported in the Amazon River turtles (*Podocnemis unifilis*), highlighting important implications for
55 turtle conservation worldwide (Carranco et al., 2022).

56 *Fusarium* (Hypocreales, Nectriaceae) genus includes approximately 300 species distributed in 23
57 monophyletic groups, referred to as species complexes (Summerell, 2019). These fungi cause a
58 variety of diseases in several plant species with important damages in terms of yield and quality (Dean
59 et al., 2012; Summerell, 2019) even if some species are now widely recognized as a major threat to
60 animal health and biodiversity conservation worldwide (Fisher et al., 2012, 2016; Sandoval-Denis
61 and Crous, 2018).

62 Sea Turtle Egg Fusariosis (STEF) has been marked as a worldwide emerging fungal disease,
63 associated with eggs and embryos mortality of loggerhead sea turtles (*Caretta caretta* L.) (Gleason
64 et al., 2020; Smyth et al., 2019). According to the International Union for Conservation of Nature
65 (IUCN; Ceriani et al., 2019), *C. caretta* is considered as a vulnerable species whose conservation
66 deserves continuous attention and efforts, to the point to be included under several international
67 conventions. STEF can cause significant mass mortality in the nests infected by a complex of species
68 mainly belonging to the Fusarium Solani Species Complex (FSSC; Sarmiento-Ramírez et al., 2010,
69 2014a). These fungi can infect and grow within *C. caretta* nests by, first, completely covering the egg
70 surface with a mycelial network, then destroying the shell by enzymes and organic acids that dissolve
71 organic substrates and calcium carbonate (Gleason et al., 2020; Phillott et al., 2006; Sarmiento-
72 Ramírez et al., 2010). Lesions, easily detectable by their colours on the colonized eggs, can turn into
73 necrotic portions and kill the surviving embryos. However, the aetiology and epidemiology of this
74 disease is still not completely known, while the biology and ecology of the causal agents need
75 additional investigation to reply as an example, to the question whether these pathogens are invasive
76 species or natural nest inhabitants able to cause disease under a changing environmental scenario
77 (Gleason et al., 2020; Smyth et al., 2019).

78 Despite STEF occurrence improved in the recent years at a global level (Gleason et al., 2020), in Italy
79 only few cases have been reported on *C. caretta* as in the case of Sicily (Gambino et al., 2019) and
80 Veneto (Pietroluongo et al., 2023), while any previous report in Tuscany is available. *C. caretta* is
81 the only sea turtle species nesting along the Tuscan coastline and the Tuscan archipelago, where nests
82 are becoming more numerous and widespread, as well as the number of affected nests, presumably

83 due to STEF. During the samplings carried out in summer 2020 in several localities along the Tuscan
84 coast (province of Grosseto, Italy), eggs showing signs resembling those caused by STEF were found.
85 In this work, we analysed, for the first time, eggs collected from natural nests of *C. caretta* along the
86 Tuscan coastline, that showed visual symptoms of putative *Fusarium* infection, with the aim to (i)
87 isolate *Fusarium* spp. present in unhatched eggs, (ii) morphologically and molecularly characterize
88 the isolates, (iii) reconstruct the phylogenetic relationships between our isolates and those already
89 known (animal and plant pathogens), and finally (iv) perform pathogenicity tests on plant model
90 species known to be susceptible to infections with previously isolated pathogenic fungi.

91

92 **Materials and Methods**

93

94 **Egg sampling, fungal isolation and morphological observation**

95 Nests located in three locations along the coast (Table 1) were manually excavated after the last
96 hatchling emergence according to ISPRA guidelines ([https://www.isprambiente.gov.it/it/attivita/CN-](https://www.isprambiente.gov.it/it/attivita/CN-LAB/aree/area-metrologia/prodotti/linee-guida)
97 [LAB/aree/area-metrologia/prodotti/linee-guida](https://www.isprambiente.gov.it/it/attivita/CN-LAB/aree/area-metrologia/prodotti/linee-guida)); only in the case of Rocchette location, the nest was
98 sampled also before hatchling. In order to be sure to work in sterile conditions, and avoid external
99 contaminations, single-use sterile gloves were used for all excavations and changed before contact
100 with different nests. Unhatched eggs were collected and transferred in individual sterile plastic bags
101 for successive examination. Lesioned eggs were characterized by unusual, coloured spots (reddish
102 and grayish) of the shell compared with healthy ones and/or covered with mycelium. The content of

all contaminated eggs appeared dense and yellow apart from egg # 20106837/5, whose content appeared abnormally red.

Egg sampling was authorized by the Italian Ministry of Environment and Energy Security (authorization n. 35848, released in date 05/18/2020), according to the Council Directive 92/43/EEC of 21 May 1992.

Egg portions were firstly plated on Sabouraud Dextrose Agar (SDA, Biolife Italiana S.r.l., Milan, Italy) in order to allow the development of associated fungi. After a first mass isolation of each developing colony, pure culture, for each isolate, were obtained by single hyphal tips or, when sporulating, by single-spore cultivations on Potato Dextrose Agar (PDA, Biolife Italiana S.r.l., Milan, Italy) added with streptomycin sulphate (SIGMA-Aldrich. Milan, Italy, 300 mg L⁻¹). Plates, incubated at 24 ± 2°C, were used for morphological and molecular identification. All isolates were stored at the fungal collection of the University of Pisa, Italy (Department of Agriculture, Food, and Environment) on PDA under mineral oil at 4°C.

Table 1. List of sampling locations and corresponding nest ID number, sampling period, geographic coordinates (GCS)

Nest site (ID)	Sampling period	GCS	Eggs n°
Rocchette (2080970)	before hatching	42°46'9.75" N 10°50'43.07" E	4
Rocchette (20106836)	after hatching	42°46'9.75" N 10°50'43.07" E	4
Rocca a mare (20106837)	after hatching	42°46'22.04" N 10°49'31.76" E	5
Riva del Sole (20106864)	after hatching	42°46'35.28" N 10°47'50.08" E	5

Morphological characterisation of colonies resembling those of *Fusarium* spp. was based on the taxonomic keys of Leslie and Summerell (2007), including colony colour and morphology on top and the reverse side of the plate, colony size and texture of the mycelium growth as well as, by

121 microscopic observation (under 200X and 400X magnification, Leica Dialux 22 equipped with a
122 Leica DFC450 C camera, Leica Application Suite X –LAS X), micro- and macro-conidia shape, size,
123 number of septa, conidiogenic cells and conidiomata (if present) such as sporodochia.

124

125 **Molecular identification**

126 Fungal gDNA was extracted from all pure cultures according to Chelex 100 (Chelex® 100 sodium
127 form, MERCK SERONO S.P.A., Rome, Italy) protocol (Baroncelli et al., 2015). To identify and
128 analyse the genetic variability within *Fusarium* isolates, a region including the Translation elongation
129 factor 1 alpha (Tef1- α) gene, a useful region for fungal taxonomic and phylogenetic studies
130 (Baroncelli et al., 2015), was amplified. PCR reaction (25 μ L) contained 2.0 μ L of gDNA (10 ng),
131 2.5 μ L of each primer (0.5 μ M), 5.5 μ L nuclease free H₂O and 12.5 μ L GoTaq® Green Master Mix
132 (Promega Italia S.r.l, Milan, Italy). Primers Tef1- α (EF1-728F 5'-CATCGAGAAGTTCGAGAAGG-
133 3' as forward and EF1-986R 5'-TACTTGAAGGAACCCTTACC-3' as reverse) were used (Carbone
134 et al., 1999). The amplification program consisted in: 2 min denaturation (95°C); 30 cycles of
135 amplification (1 min at 94°C for denaturation, 1 min at 55°C for the annealing and 1 min at 72°C for
136 the extension); and a final extension at 72°C for 5 min. All amplifications were performed in a Q-
137 Cycler 24 (HAIN, Lifescience, Nehren, Germany). PCR products were checked by 2.0% gel
138 electrophoresis run and purified using a QIAquick PCR Purification Kit (QIAGEN, Hilden,
139 Germany). PCR products were sequenced by the Bio Molecular Research Genomics (BMR
140 Genomics, Padova, Italy). For phylogenetic analyses, reference Tef1- α sequences from the

141 FUSARIOID-ID database (<https://www.fusarium.org>) and from the FUSARIUM-ID v.3.0 (Torres-
142 Crus et al., 2022) were retrieved and used to build a local BLAST database. Sequence produced in
143 this work as well as Tef1- α sequences from other studies (Zhang et al., 2006; Sidique et al., 2017;
144 García-Martín et al., 2021; Greeff-Laubscher and Jacobs, 2022) were analysed with the top-3 records
145 retrieved from the BLAST analyses. All the sequences were aligned using MAFFT v. 7.402 (Katoh
146 et al., 2002). FastTree v2.1.11 (Price et al., 2010) with default settings was used to perform the
147 phylogenetic tree. Finally, each sequence was deposited in NCBI (GenBank,
148 <https://www.ncbi.nlm.nih.gov/genbank/>) and an Accession number has been given.

149

150 **Pathogenicity tests**

151 In order to check the pathogenicity potential of *F. nodosum* - a species recently included within the
152 Fusarium Head Blight Species Complex being isolated from *Triticum aestivum* in Iran (Lombard et
153 al., 2019) and for the first time in Italy from *Triticum durum* associated with Fusarium head blight
154 (FHB) (Felici et al., 2021) - the isolate t2 (Table 2) was tested on *T. aestivum* cv. Apogee flowering
155 spikes, according to Vicente *et al.* (2020). In details, wheat seeds (surface sterilized with a NaClO
156 solution - 0.6% active chlorine - for 3 min under shaking, three time washed, 10 min each, with sterile
157 distilled water and stored in sterile distilled water at 4°C for 3 days before sowing) were sown in pots
158 until plants reached anthesis (5 weeks). Three biological replicates, each consisting of three plants,
159 were inoculated, by spraying, with an aqueous spore suspension of *F. nodosum* (10^5 spores mL⁻¹)
160 made from two week old colony grown on PDA, added with Tween 80 (0.01%). Plants were covered
161 with a white bag, previously moistened inside with water, then a black bag was placed above to favour

the infection process by the pathogen. Plants, whose spikes were inoculated with water + Tween 80 without spores, were used as negative control. After 24 h, bags were removed for plant aeration and after 1 h white bags were placed back for additional 24 h. After one week, for the following 7 days (14 dpi) plants were daily monitored for FHB symptoms in order to check the premature spike/spikelet bleaching compared to control ones.

With respect to isolates belonging to FSSC, including well known pathogens of Cucurbitaceae (Gomez et al., 2014), the isolate 3AF (Table 2) was used to inoculate *Cucumis melo* cv. Honeydew seedlings according to Gonzalez et al. (2020a, 2020b). In details, roots of melon seedlings at the 3-4 true-leaf stage, grown in pots, were immersed for 20 min in an aqueous spore suspension of the putative pathogen (10^5 spores mL⁻¹) and transplanted back in the pots. Plants whose roots were immersed for 20 min in uninoculated water were used as negative control. After one week, for the following 4 weeks, plants were daily monitored in order to check the typical symptoms of *F. solani* infection.

Finally, in order to verify if *F. oxysporum* belonged to a specific *forma specialis* or could be considered as saprotroph, artificial inoculations were performed on several model plants, according to Velarde-Felix et al. (2018). In details, tests were performed on *Capsicum annuum* (var. Cayenne and Viagra), *Cucumis melo* (var. Cantalupensis), *Cucurbita pepo* (var. Romanesco), *Eruca vesicaria* (subsp. *sativa*; var. Saetta), *Leucanthemum vulgare* (var. Bianca May Queen), *Mentha x piperita* (var. Rossa Glaciale), *Ocimum basilicum* (var. Red Rubin, Italiano and Fine Verde), *Phaseolus vulgaris* (var. Borlotto), *Pisum sativum* (var. Alderman), *Solanum lycopersicum* (var. San Marzano, Cerasiforme, Roma), *Solanum melongena* (var. Black Beauty) and *Vigna unguiculata* (var. Nano

183 Dolico), chosen because among the most frequent hosts for *F. oxysporum*. Three-four true-leaf stage
184 seedlings were inoculated by immersing, for 20 min in an aqueous spore suspension (10^5 spores
185 mL^{-1}) of the putative pathogen their roots then transplanted in plots. For this test *F. oxysporum* t7
186 (Table 2) was used, while plants whose roots were immersed for 20 min in uninoculated water were
187 used as negative control. After one week, for the following 3 weeks, plants were daily monitored in
188 order to check the typical wilt symptoms due to tracheomycosis.

189 All the pathogenicity tests have been performed, in triplicate, in a greenhouse with natural lighting
190 (at plant height, the average photon flux density during measurements was around $500 \mu\text{mol photons}$
191 $\text{m}^{-2} \text{s}^{-1}$) and an average temperature of 25°C .

192 In case of symptomatic plants, in order to re-isolate the putative pathogen, roots and/or stem portions,
193 as well as spikelets (for wheat) have been collected, surface sterilized for 1-3 min (depending on the
194 host plant) in a NaClO (1% active chlorine) in 50% ethanol, washed three times in sterile water and
195 plated on PDA added with streptomycin sulphate (SIGMA-Aldrich, Milan, Italy) at the concentration
196 of 300 mg L^{-1} . Plates were incubated at $24 \pm 2^\circ\text{C}$, under 12 h light/12 h darkness for two weeks to
197 allow the eventual fungal colony to be developed.

198

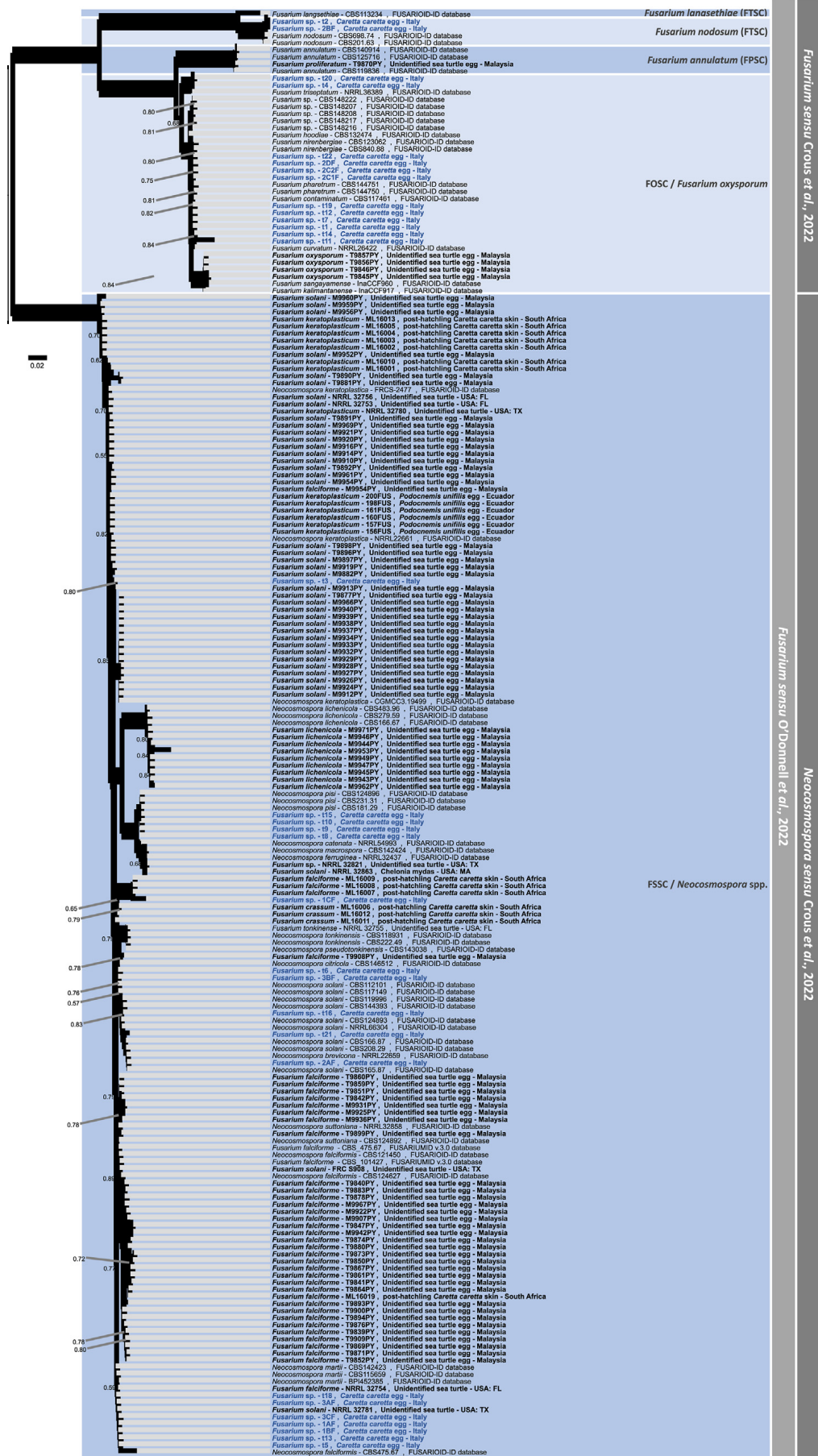
199 **Results**

200

201 **Fungal isolation, morphological observation and molecular identification**

202 After the isolation to pure culture of the fungal colonies developed from the eggs, a total of 32 isolates
203 (Table 2) were obtained and submitted, after single-spore cultures, to a first morphological

observation followed by a molecular identification and characterization. Morphological
 identification, by microscopic observation, allowed to preliminary assign all the isolates to the
Fusarium genus, according to size and shape of conidia, conidiogenic cells and conidiophores
 structures. All these strains showed a relatively fast growing on PDA, reaching a colony size of $75 \pm$
 5 mm diameter after 7 days of incubation at $26 \pm 1^\circ\text{C}$.
 In order to assign a taxonomic designation to the isolates and to confirm previous results, a molecular
 approach, consisting in the amplification and sequencing of Tef1- α regions was performed. Sequence
 analysis allowed confirming the identity of our isolates as members of the FSSC *sensu* O'Donnell et
 al. (2022) or *Neocosmospora* spp. *sensu* Crous et al. (2021), *F. oxysporum sensu* O'Donnell et al.
 (2022) or FO SC *sensu* Crous et al. (2021) and *F. nodosum* (Table 2). Specifically, at the Rocchette
 sites, a total of 14 different isolates (t7, t2, t6, 1A, 1B, 1C, 2A, 2B, 2C1, 2C2, 3A, 3B, 3C), belonging
 to different lineages of the FSSC / *Neocosmospora* spp., FO SC and *F. nodosum* (sambucinum species
 complex), were isolated from eggs collected before hatching (ID 2080970), while only two isolates
 (t21, t5; FSSC / *Neocosmospora* spp.) were found in samples taken after hatching (ID 20106236). A
 total of eight isolates were found from samples collected at the Rocca a Mare site (ID 20106837):
 five of these were found to be FO SC (t11, t12, t14, t19, t22), while the remaining three to the FSSC
 / *Neocosmospora* spp. (t16, t13, t18). The last nine isolates were collected from the Riva del Sole
 sampling site (ID 20106864), and they included five isolates of the FSSC / *Neocosmospora* spp. (t3,
 t8, t9, t10, t15) and three of FO SC (t1, t4, t17, t20). Overall, 18 strains of FSSC / *Neocosmospora*
 spp. (56%), 12 of FO SC (38%) and two of *F. nodosum* (6%) were identified (Figure 1).



225 Figure 1. Phylogenetic tree of TEF1 sequences of *Fusarium* strains isolated from *Caretta caretta*'s eggs in this study
 226 (highlighted in blue and bold), reference isolates retrieved from the FUSARIOID-ID database (<https://www.fusarium.org>)
 227 and from the FUSARIUM-ID v.3.0 (Torres-Crus et al., 2022) and of isolates associated with sea water and fresh water
 228 turtle (highlighted in bold) retrieved from previously published works (García-Martín et al., 2021; Greeff-Laubscher and
 229 Jacobs, 2022; Sidique et al., 2017; Zhang et al., 2006). Support values (above 50%) are shown at the nodes while the
 230 thickened nodes represent support values equal or higher than 90%.

231

232 Table 2. Identification of *Fusarium* spp. isolates, according to Tef1- α DNA sequence, collected from sea turtle eggshells
 233 and the corresponding Accession number (NCBI). Abbreviation: Egg ID, identification number of nest site and unhatched
 234 egg number (nest | egg); Sample ID, identification number of fungal isolates; FSSC, *Fusarium solani* species complex.

Egg ID (nest egg)	Sample ID	Species	Accession number
2080970 70	t7	<i>FOSC / F. oxysporum</i>	OQ053309
2080970 70	t2	<i>Fusarium nodosum</i>	OQ053304
2080970 70	t6	<i>FSSC / Neocosmospora spp.</i>	OQ053308
2080970 1	1AF	<i>FSSC / Neocosmospora spp.</i>	OQ054992
2080970 1	1BF	<i>FSSC / Neocosmospora spp.</i>	OQ053293
2080970 1	1CF	<i>FSSC / Neocosmospora spp.</i>	OQ053294
2080970 2	2AF	<i>FSSC / Neocosmospora spp.</i>	OQ053295
2080970 2	2BF	<i>Fusarium nodosum</i>	OQ053296
2080970 2	2C1F	<i>FOSC / F. oxysporum</i>	OQ053297
2080970 2	2C2F	<i>FOSC / F. oxysporum</i>	OQ053298
2080970 2	2DF	<i>FOSC / F. oxysporum</i>	OQ053299
2080970 3	3AF	<i>FSSC / Neocosmospora spp.</i>	OQ053300
2080970 3	3BF	<i>FSSC / Neocosmospora spp.</i>	OQ053301
2080970 3	3CF	<i>FSSC / Neocosmospora spp.</i>	OQ053302
20106836 16	t21	<i>FSSC / Neocosmospora spp.</i>	OQ053322
20106836 18	t5	<i>FSSC / Neocosmospora spp.</i>	OQ053307
20106837 1	t14	<i>FOSC / F. oxysporum</i>	OQ053316
20106837 1	t22	<i>FOSC / F. oxysporum</i>	OQ053323
20106837 2	t16	<i>FSSC / Neocosmospora spp.</i>	OQ053318
20106837 2	t19	<i>FOSC / F. oxysporum</i>	OQ053320
20106837 3	t18	<i>FSSC / Neocosmospora spp.</i>	OQ053319
20106837 4	t11	<i>FOSC / F. oxysporum</i>	OQ053313
20106837 5	t12	<i>FOSC / F. oxysporum</i>	OQ053314
20106837 5	t13	<i>FSSC / Neocosmospora spp.</i>	OQ053315
20106864 18	t10	<i>FSSC / Neocosmospora spp.</i>	OQ053312
20106864 19	t1	<i>FOSC / F. oxysporum</i>	OQ053303
20106864 92	t8	<i>FSSC / Neocosmospora spp.</i>	OQ053310
20106864 92	t9	<i>FSSC / Neocosmospora spp.</i>	OQ053311
20106864 93	t15	<i>FSSC / Neocosmospora spp.</i>	OQ053317
20106864 93	t3	<i>FSSC / Neocosmospora spp.</i>	OQ053305
20106864 93	t4	<i>FOSC / F. oxysporum</i>	OQ053306
20106864 104	t20	<i>FOSC / F. oxysporum</i>	OQ053321

235

236

237 **Pathogenicity tests**

238 All inoculated plants were constantly monitored for the specific symptoms caused by each of the
239 potential pathogens used for pathogenicity tests.

240 After two weeks from inoculation, wheat spikes started to show a premature bleaching, firstly on
241 single spikelets and after spread all over the spike, thus confirming the pathogenicity of *F. nodosum*.

242 This last was confirmed also by plating spikelets portions on PDA + streptomycin: colony
243 morphologically similar to that of *F. nosodum* were observed.

244 With respect to all the other artificial inoculations, any of the plants inoculated with the isolate
245 belonging to the FSSC or with FOOSC showed the typical symptoms of the corresponding disease,
246 thus not allowing us to confirm the pathogenicity of the isolates belonging to the FSSC /
247 *Neocosmospora* spp. and, in the case of FOOSC / *F. oxysporum*, to assign our isolate to one of the
248 specific *formae speciales* of the hosts here tested.

249

250 **Discussion**

251 In the last decades, there has been an increasing number of reports concerning sea turtles (*Caretta*
252 *caretta*) infected by Ascomycota fungi belonging to *Fusarium* genus, with, among the first,
253 Wynecken and collaborators who described natural and artificial nests of *C. caretta* containing
254 diseased eggs failing in hatching (Wynecken et al., 1988). Several other reports at global level have
255 followed, all indicating *Fusarium* spp. as constantly associated with hatching failure loggerhead sea
256 turtle eggs as well as mass mortalities in nests (Sarmiento-Ramirez et al., 2010; Garcia-Hartman et

257 el. 2016). Due to the incidence of *Fusarium* spp. associated with the affected eggs/turtles, the apparent
258 disease is generally indicated as STEF. As listed by Gleason et al. (2020), Australia is the main
259 country in terms of STEF occurrence, while North and South America, Asia and Europe have only
260 few reports. With respect to Italy, very few studies are available such as that by Gambino and co-
261 authors where microbial diversity associated with turtle nests from the coastlines of Sicily and the
262 evaluation of the presence of *Fusarium* spp. have been investigated, providing key information on
263 potential pathogens that may affect hatching success (Gambino et al., 2019). More recently, two
264 northernmost worldwide loggerhead sea turtle nests were monitored along the Northern Adriatic
265 coastline (Veneto, Italy), where STEF deeply compromised the hatching success (Pietrolungo et al.,
266 2023). In this contest, the present work represents the first report of STEF on Tuscan coast. Although
267 Tuscany does not represent a primary nesting area of *C. caretta* in Italy and in the Mediterranean
268 area, the record of the disease on this coastline, in line with what recorded across the globe, confirms
269 that STEF may represent a major risk for the conservation of the loggerhead sea turtles also in this
270 region, especially considering how natural systems can be affected by the present climate change
271 perspective (Gleason et al., 2020; São Miguel et al., 2022).

272 Global climate change played an important role on the occurrence of emerging pathogens in new
273 environments and geographic areas (Fisher et al., 2012; Groner et al., 2016), thus resulting in an
274 increase of environmental stress conditions and, consequently, of fungal infection diseases also in the
275 marine ecosystems (Gleason et al., 2020), whose biodiversity is continuously threatened (Lafferty,
276 2009; Fisher et al., 2012, 2016). Climatic factors, alone and in combination with anthropogenic ones,
277 are considered as stressors that exasperated the impact of diseases since climate changes, such as

278 warming temperatures or changes in precipitation, may alter marine disease dynamics (Harvell et al.
279 2009). In addition to be perceived by living organisms as a source of stress, even if not demonstrated
280 yet specifically for sea turtles, these climatic factors can alter host-pathogen interactions in terms of
281 either alteration of pathogens' virulence that by compromising host's immune systems, as described
282 for several other marine species (Burge et al., 2014).

283 Members of the FSSC / *Neocosmospora* spp., such as *F. keratoplasticum*, *F. falciforme*, and *F.*
284 *oxysporum* were already associated with *C. caretta* eggs showing symptoms of fungal infection
285 (Candan et al., 2021; Greeff-Laubscher and Jacobs, 2022; Sarmiento-Ramírez et al., 2010, 2014a,
286 2014b). This is in line with the results here presented, where the two main fungal species isolated
287 from the three Tuscany sampling locations were identified as members of the FSSC / *Neocosmospora*
288 spp. and FOSC / *F. oxysporum*, both before and after eggs hatching. These two species are globally
289 recognized as among the most important plant pathogenic fungi, causing severe diseases on several
290 cultivated and spontaneous plants, thus representing a significant threat to human food supply and
291 agricultural biosecurity (O'Donnell et al., 2022). Despite the *Fusarium solani* species complex
292 (FSSC) has been considered as responsible for hatching failure in sea turtles worldwide, in 2021
293 (Carranco et al., 2022) it has also been associated with high hatching failure in eggs symptomatic of
294 fusariosis in *Podocnemis unifilis*, the yellow-spotted Amazon River turtle, thus highlighting its wide
295 dissemination among the Testudines not limited to sea environments.

296 Several *Fusarium* species can synthesize dangerous specialized secondary metabolites, defined
297 mycotoxins, that can cause adverse effects on human and animal health (D'Mello et al., 1999; Perrone
298 et al., 2020; Sarrocco et al., 2019, Pisuttu et al., 2023). It is the case of *F. nodosum* that, as far as we

299 know, has been here isolated for the first time from affected *C. caretta* eggs. *F. nodosum* is a
300 mycotoxigenic plant-pathogenic fungus, belonging to the complex of *Fusarium* species causing FHB
301 of wheat (Fusarium Head Blight Species Complex), recently reported for the first time in Italy on
302 *Triticum durum* (Felici et al., 2021). As already discussed by Gleason et al. (2020), the presence of
303 mycotoxigenic fungi on eggshell could represent a threaten for the animal since mycotoxins may
304 diffuse into embryo's tissues thus affecting its development and causing its death (Gleason et al.,
305 2020).

306 Tests here made on plants, even if performed on a limited number of fungal isolates, resulted in a lack
307 of pathogenicity of the strains included in the FSSC and of FOOSC / *F. oxysporum* when inoculated
308 on some of the main plant hosts for these pathogen. The lack of pathogenicity of FOOSC / *F. oxysporum*
309 here isolated is in favour of the hypothesis these isolates are included within a different *forma*
310 *specialis* than those here supposed or belong to saprotrophic populations occurring on sea turtle
311 affected eggs. The ability to infect and cause a premature blenching of wheat spikes, instead,
312 confirmed the plant pathogenic potentiality of the *F. nodosum* isolate and reinforced the trend of the
313 transmission of emerging pathogens into new environment (Groner et al., 2016). Results here reported
314 confirm a global occurrence of the problem and the need for further studies concerning the biology
315 and ecology of the pathogenic agents, as well as the aetiology and epidemiology of the disease.

316 Since fungal pathogens and associated diseases are spreading in marine environment (Pang et al.,
317 2021), it is critical to identify the biological and ecological components that could contribute to
318 disease epidemic outbreak and severity. In addition to the isolation and identification of the potential
319 causal agents of the diseases, as done in the present and several other works, other investigation are

320 needed, including histopathological examination. A standardize diagnostic approach appears to be
321 essential to harmonize results in order to tackle an emergent infectious disease, as suggested by Di
322 Nicola et al., (2022). Even if specifically referred to *O. ophidiicola* detection and infection in snakes,
323 this paper should be considered as a guideline to be followed during investigation concerning
324 emergent diseases potentially affecting biodiversity, in order to better discriminate among the
325 presence of the pathogen, apparent disease and confirmed disease.
326 Further studies focused on pathogen phylo-biogeography, mechanisms of dispersion and colonization
327 of coastal habitats, and environmental and physiological parameters for infection are needed. For
328 these reasons, isolation and characterization of fungal pathogens will help us to reveal their biology
329 and epidemiology and will allow a better management of disease and to better understand the current
330 and future impact of STEF on sea turtles' conservation worldwide.

331

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336 **References**

337

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Highlights

- Fungal infectious diseases have dramatically increased in marine ecosystems
- STEF represent one of the main threats to *Caretta caretta* in Mediterranean region
- A total of 32 strains of *Fusarium* strains were identified
- Phylogenetic relationships of *Fusarium* isolates have been reconstructed
- For the first time strains of *F. nodosum* were isolated from infected eggs

Declaration of interests

☒ The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Riccardo Baroncelli

Cristina Nali

Samuele Risoli

Sabrina Sarrocco

Giuliana Terracciano

Luana Papetti