Resolving the taxonomic enigma of the iconic game fish, the hump backed mahseer from the Western Ghats biodiversity hotspot, India

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32 Abstract

34 Growing to lengths and weights exceeding 1.5 m and 45 kg, the hump-backed mahseer fish of the 35 Western Ghats biodiversity hotspot. India, is an iconic, mega-faunal species that is globally recognized as 36 a premier freshwater game fish. Despite reports of their high extinction risk, conservation approaches are 37 currently constrained by their lack of valid taxonomic identity. Using an integrative approach, 38 incorporating morphology, molecular analysis and historical photographs, this fish can now be revealed to 39 be conspecific with Tor remadevii, a species lacking a common name, that was initially, but poorly, 40 described in 2007 from the River Pambar, a tributary of the River Cauvery in Kerala. Currently known to 41 be endemic and restricted to the River Cauvery basin in the Western Ghats, T. remadevii is distinguished 42 from congeners by its prominent hump originating above the pre-opercle and extending to the origin of 43 the dorsal fin, a well-developed mandible resulting in a terminal or slightly superior mouth position, and 44 the dorsal orientation of the eyes. While body colouration varies (silver, bronze, greenish) and is not

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45 considered a reliable diagnostic character, orange coloration of the caudal fin (sometimes extending to all 46 fins) is considered a consistent characteristic. Having been first brought to the attention of the scientific 47 community in 1849, and the recreational angling (game fishing) community in 1873, it has taken over 150 48 years to finally provide this iconic fish with a valid scientific name. This taxonomic clarity should now 49 assist development and delivery of urgent conservation actions commensurate with their extinction risk. 50

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52 Keywords: Cyprinidae, freshwater fish, megafauna, River Cauvery, taxonomy, Tor remadevii

53 Introduction

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Freshwater megafauna (defined as species with adult body weights of at least 30 kg) occur in large rivers and lakes of every continent except Antarctica [1]. These megafauna comprise one of the world's most vulnerable groups of vertebrates to extinction, with 58 % of species at threat from stressors including overexploitation, habitat alteration and pollution [1-2]. Despite this, for many freshwater mega-fauna, knowledge on their taxonomy, natural history and threats remain incomplete, as despite their body sizes providing high anthropogenic interest, some species have only recently been described [3], while the identity of others remain to be elucidated [4].

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63 With validated body weights exceeding 45 kg [5], the hump-backed mahseer of the River Cauvery 64 (Western Ghats, India) represents the largest of all known mahseers of the Tor genus (Fig 1). Globally 65 recognized by recreational fishers as an iconic game fish for over a century [6], it was initially brought to their attention in 1873, under the nom de plume 'Barbus tor' [6], with documentation of a world record 66 67 specimen of 119 lbs (54 kg) captured in 1921 from the River Kabini, a tributary of the River Cauvery [7]. Following Indian independence in 1947, the fish was largely forgotten until a resurgence in recreational 68 69 angling interest and subsequent development of catch-and-release fisheries in the main River Cauvery in 70 the early 1970s [8-9]. These fisheries subsequently became world famous for the size of mahseer they 71 produced [8-9] and were also recognized for the socio-economic benefits afforded to poor rural 72 communities via ecotourism based employment opportunities [8].

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Fig 1. Adult Cauvery hump-backed mahseer, *Tor remadevii* captured by Martin Clark, 1978 [Photo Credit:
 Trans World Fishing Team].

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Despite this long-term interest in the species, the hump-backed mahseer continued to be erroneously known under the names *Barbus mussullah* and *Tor mussullah*, both in scientific [10-13] as well as in popular literature [14]. This continued until Knight and coworkers [15-16] stabilized the use of the name 'mussullah' to a species of the cyprinid genus *Hypselobarbus*. However, this taxonomic revision continued to leave the hump-backed mahseer without a valid scientific identity, thus denying the formal recognition required to undertake IUCN Red List assessment and afford protection commensurate with their apparent high extinction risk [5].

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A new species of mahseer, *Tor remadevii* was described in 2007 from the River Pambar, the southernmost tributary of the River Cauvery [17]. This was based on the examination of 19 juvenile specimens (lengths 113.64mm to 331.82mm) [17]. However, neither a photograph of a live/preserved specimen, nor an illustration, accompanied the description, with no comparison to material from congeners. The description thus relied entirely on morphological measurements and counts available in the literature [17].

90 Despite these issues and the limited sample size, many of the characters were consistent with those 91 observed from images of the hump-backed mahseer caught by recreational fishers in the River Cauvery 92 (e.g. body shape: "dorsal profile has a moderate to prominent hump between the head region and the 93 dorsal fin"), colouration: ("fins reddish with black patches"; "younger specimens with red orange fins") and 94 a "distinctively longer mandible than other Southern Indian Tor species, resulting in a terminal/posterior 95 and slightly upturned mouth"). Consequently, given the outstanding requirement to resolve the taxonomic 96 identity and assist the conservation of the hump-backed mahseer, the aim of this study was to 1) apply 97 morphological and molecular analyses to test whether the hump-backed mahseer is distinct from the 98 currently known South Indian Tor species, and whether it is conspecific with T. remadevii, 2) provide 99 definitive morphological characters which can be reliably used to identify this species from congeners in 100 the field, and 3) provide notes on current knowledge relating to distribution and habitat utilization.

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103 Materials and methods

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105 Ethics Statement

106 Samples for the present study originated from three sources: (1) tissue samples (as fin-clips) for 107 molecular analyses obtained from cast-net sampling and catch-and-release angling, where the specimens were released back in the wild. (2) voucher specimens collected from inland fish markets 108 109 (from where dead specimens were purchased), and (3) voucher specimens collected from stream 110 habitats inside protected areas. Permissions for collecting specimens inside protected areas were issued by the Department of Forests and Wildlife, Government of Kerala to Rajeev Raghavan (WL12-8550/2009) 111 112 and Government of Tamil Nadu (WL5 (A) /26789/2017) to A. Manimekalan. Immediately upon capture 113 using a cast net or rod-and-line, specimens were euthanized (anesthetic overdose; tricaine 114 methanesulfonate, MS222; following the guidelines developed by the American Society of Ichthyologists 115 and Herpetologists (ASIH) (http:// www.asih.org/pubs/; issued 2013)). Samples of pelvic fin tissue were 116 taken and stored in absolute ethanol. Voucher specimens were preserved whole in either 5% formalin or 117 70% ethanol. Institutional ethics committee of Mahseer Trust approved the design and implementation of 118 the study (MTE/ 17/01). In-country (India) ethical approvals were not required as no experimentation or 119 manipulations were carried out. All molecular genetic work was completed within India and no specimens 120 or fish tissues were taken out of the country. Voucher specimens were primarily deposited in national 121 and/or regional repositories. Individual participants who appear in the Figures in this manuscript have 122 given written informed consent (as outlined in PLOS consent form) to publish these case details. Individual participants appearing in Figs 1. 6 and 7 in this manuscript have given written informed consent (as 123 124 outlined in PLOS consent form) to publish these case details. 125

126 Specimen collection and vouchers

127 Topotypic specimens of mahseer species were collected from various rivers in India: Tor khudree from 128 River Krishna and its tributaries in Maharashtra, Tor malabaricus from River Chaliyar in Kerala, T. remadevii from River Pambar in Kerala, and the hump-backed mahseer from River Moyar in Tamil Nadu. 129 130 The fishes were preserved in 10% formaldehyde and transferred to 5% formaldehyde or 70% ethanol for 131 long-term storage. Fin clips from topotypic Tor putitora from River Teesta in West Bengal, and hump-132 backed mahseer from the River Cauvery at Dubare, Karnataka and River Moyar in Tamil Nadu were 133 taken. In addition, fin clips from a yet-to-be identified mahseer species from River Vaitarna, Harkul 134 Reservoir, Krishna River in Maharashtra and Forbes Sagar Lake in Karnataka (see Tor sp 1 in Fig 2) 135 were also collected following their sampling by catch-and-release angling. Tissue samples were 136 preserved in absolute ethanol. Voucher specimens are in the museum collections of the Zoological 137 Survey of India, Kolkata (ZSI); Zoological Survey of India - Southern Regional Center, Chennai, India (ZSI-SRC); Zoological Survey of India - Western Regional Center, Pune, India (ZSI-WGRS); Kerala 138 139 University of Fisheries and Ocean Studies, Kochi, India (KUFOS); Department of Aquatic Biology and 140 Fisheries, University of Kerala, Thiruvananthapuram, Kerala (DABFUK); and in the private collections of J.D. Marcus Knight (MKC). 141

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143 Comparative material examined for morphometric analysis

144 *Tor malabaricus*: 5 ex, MKC 450, 196.6–231.7mm SL, Ivarnadu, Payaswini River, Karnataka, India 145 (12.522°N & 75.425°E); collected by A Rai, August 2014.

146 Tor kulkarnii: Holotype, ZSI F2710, 220.0mm SL, Nashik, Darna River, between Sawnuri and Beladgaon,

- 147 Deolali, Maharashtra, India (19.929°N & 73.856°E); collected by AGL Fraser, 29 April 1936; paratypes,
- 148 ZSI F2711, 3 ex., 103.2–197.0mm SL, same data as holotype.
- 149 Tor khudree: ZSI-WRC P/2451, 1 ex, 121.9mm SL, Neera River, Bhor, Pune, Maharashtra, India 150 (18.152°N & 73.829°E); collected by N Dahanukar and M Paingankar, 20 August 2010; ZSI-WRC P/3067, 151 6 ex. 106.1–171.2mm SL, Krishna River, Wai, Satara, Maharashtra, India (17.991°N & 73.786°E); 152 collected by N Dahanukar and M Paingankar, 2 February 2011; ZSI-WRC P/3072, 5 ex. 77.4-151.2mm 153 SL, Krishna River, Wai, Satara, Maharashtra, India (17.991°N & 73.786°E); collected by N Dahanukar 154 and M Paingankar, 18 February 2011; ZSI-WRC P/3071, 7 ex. 51.5-66.7mm SL, Koyna River, Patan, 155 Satara, Maharashtra, India (17.367°N & 73.903°E); collected by N Dahanukar and M Paingankar, 1 July 156 2007.
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158 Morphometric analysis

Point to point measurements were made using digital calipers, to the nearest 0.1 mm, based on standard methods employed for cyprinid fishes [18] and *Tor* mahseer [19]. Morphometric data used in the study is available online on figshare (<u>https://doi.org/10.6084/m9.figshare.6085982</u>). Statistical analysis of the 162 morphometric data was performed on size-adjusted measurements of subunits of the body expressed as 163 proportions of standard length and subunits of head expressed as proportions of head length. The null 164 hypothesis that the data were multivariate-normal was checked [20]. Multivariate Analysis of Variance 165 (MANOVA) was performed to test whether the populations of different species (see comparative material 166 examined) formed significantly different clusters [21] using Pillay's trace statistic [22]. Mahalanobis 167 distances [22] between pairs of individuals were calculated and used for computing Fisher's distances 168 (distance between the centroids of the clusters, divided by the sum of their standard deviations) between 169 two clusters to check if the species clusters were significantly different from each other. Statistical 170 analyses were performed in PAST 3.16 [23].

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172 Molecular analysis

173 DNA extraction, PCR amplification for cytochrome oxidase subunit 1 (cox1) gene and sequencing 174 protocols were as per [24]. Sequences were checked using BLAST [25] and the sequences generated as 175 part of this work deposited in GenBank under the accession numbers MG769028 to MG769056 (S1 176 Table). Neolissochilus species were used as outgroup based on earlier study [26]. Gene sequences were 177 aligned using MUSCLE [27], and raw (p) distances for cox1 between pairs of sequences were calculated 178 in MEGA 7 [28]. The best-fit partition model and the substitution model was found using the IQTree 179 software [29] based on the Bayesian Information Criterion (BIC) [30-31]. Maximum likelihood analysis based on best partition scheme was performed in IQ-Tree [28] with ultrafast bootstrap support for 1000 180 181 iterations [32]. The phylogenetic tree was edited in FigTree v1.4.2 [33].

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184 **Results**

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186 Molecular analysis

The results suggested that the best partition scheme was Tamura & Nei's [34] model with invariant sites (TN+I, BIC = 3622.967, InL = -1580.211, df = 71) for combined partition of all three codon positions. Topotypic *T. remadevii* formed a monophyletic clade with the hump-backed mahseer collected from widely distributed populations from within the Cauvery River system (Fig 2; Table 1). Genetic distance between *T. remadevii* and other species of *Tor* from peninsular India ranged between 2.3 and 4.6% (Table 1).

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194 Table 1. Pairwise percentage raw (p) genetic distances between *Tor* species.

Tor malabaricus [2]	2.3 - 2.8	0.3-0.3				
Tor khudree [3]	2.7 - 3.2	1.6-2.0	0.0 - 0.0			
Tor putitora [4]	2.7-4.3	2.0-3.5	2.2 - 3.0	0.0 - 1.0		
<i>Tor</i> sp2 [5]	3.3-4.6	2.1-3.4	3.1-3.8	1.1-2.2	0.0-0.4	
<i>Tor</i> sp1 [6]	2.8-3.6	1.8-3.0	2.8-3.3	2.4-2.9	2.8-3.4	0.0-0.0

Fig 2. Maximum likelihood phylogenetic tree based on cox1 sequences of mahseer species occurring in India (Tor sp 1 represent individuals not matching any of the described species from India and could potentially comprise new species, Tor sp. 2 are sequences available in GenBank with uncertain identities, i.e. under different species names). Species of Neolissochilius are used as outgroup. Values along the nodes are percentage bootstraps for 1000 iterations.

Morphometrics

Morphometric data were multivariate normal (Doornik and Hansen omnibus, Ep = 55.11, P = 0.168). The four peninsular Indian species of Tor formed distinct clusters (Fig 3), with T. remadevii distinguished based on comparatively larger pre-anal length, head length, pre-ventral length, pre-pectoral length and pre-dorsal length, and comparatively smaller dorsal to caudal length, head length and inter-orbital length (Table 2). The specimens that make up the T. remadevii group/clade includes the type material of the species (ZSI-WGRS V/F 13119a and 13119b) as well as freshly collected specimens from the River Moyar (see section on comparative material below; Table 3) (ZSI-SRS F 9145, 9148, 9149, 9150).

Table 2. Factor loading on the first two axes of discriminant analysis.

Character	Axis 1	Axis 2
Head length	-0.19	0.08
Snout length	0.08	-0.12
Inter orbital length	0.32	0.11
Eye diameter	0.18	0.06
Head depth	0.09	-0.22
Head width	0.41	-0.40
Pre-dorsal length	-0.11	-0.02
Dorsal to caudal distance	0.64	0.07
Pre-pectoral length	-0.16	0.01
Pre-ventral length	-0.18	0.00
Pre-anal length	-0.22	0.05
Caudal-peduncle length	-0.03	-0.07
Caudal-peduncle depth	0.03	0.01
Dorsal-fin length	-0.07	-0.01
Dorsal-fin base	0.01	-0.02
Pectoral-fin length	-0.01	0.16
Ventral-fin length	-0.01	0.13
Anal-fin length	-0.02	0.21
Anal-fin base	-0.01	0.06
Body depth (D)	0.05	-0.08

218	Body depth (A)0.00Body width (D)-0.01Body width (A)0.01) -	-0.03 0.14 0.04			
219 220 221						
222 223 224 225	Fig 3. Discriminant analysis of th (blue cells) and associated p v percentage variation explained by	e four alues / each	r peninsular Indian <i>Tor</i> (red cells) are provie n discriminant axis.	species. Fisher's di ded in inset. Value	istances between cluster is in parenthesis are the	s e
226	Taxonomy					
227 228 229 230	<i>Tor remadevii</i> Kurup & Radhakris (Figs 1 and 4 - 6)	hnan	2007			
231 232 233	Fig 4. Lateral (A), dorsal (B) and from the River Moyar, India.	d vent	tral (C) view of <i>Tor re</i>	emadevii (ZSI F-915	50, 487 mm SL) collecte	d
234 235 236	Fig 5. Lateral (A), ventral (B) an mm SL) collected from the River	d dors Moyar	sal (C) view of the he r, India.	ad region of <i>Tor rer</i>	<i>madevii</i> (ZSI F-9150, 48	7
237 238 239	Fig 6. Freshly caught adult <i>Tor</i> coloured fins	remad	<i>devii</i> from the River Mo	oyar, India, showing	ι the characteristic orang	е
240	Material Examined					
241 242 243 244 245 246 247 248	Type material: ZSI-WGRS V/F 1 River Pambar, Champakkad, Ker Additional material: ZSI-SRS Thengumarahada, Tamil Nadu, I 7 October 2017; KUFOS-PK-20 Wildlife Sanctuary, Kerala, India October 2016.	3119a ala, Ir F 914 ndia (* 16.100 r (10.3	a (holotype) and 13119 ndia; collected by KV F 45, 9148, 9149, 91 11.614°N & 76.740°E; 0.1, 1ex, 84mm SL, F 353°N, 77.216ºE, 454	9b (paratypes), 3 ex Radhakrishnan, 18 M 50, 4ex, 356–487 474m ASL); collect Pambar River, Chin 1m ASL); collected	к, 168.00-217.063mm SL Vay 2004. 7mm SL, River Moya ted by A Manimekalan, 6 nar Check Post, Chinna I by P. Krishnankutty, 12	-, r, ir 2

Diagnosis

Tor remadevii can be distinguished from all its congeners by the following combination of characters:
 large adult body size (≥1500mm Total Length/TL and 45kg), dorsal orientation of eyes not visible from
 ventral aspect, shorter inter-orbital distance (7.1–9.6% of Standard Length/SL), a distinctive kink in the

- 253 profile of the pre-opercle and a well-developed mandible extending to either equal distance or anterior of
- the maxilla, resulting in a terminal or slightly superior mouth position (Fig 5).
- 255

256 **Description**

A large sized *Tor* attaining a maximum size of 1500mm TL. For general shape and appearance see Figs
1 - 2 and 4 - 6. Morphometric data are provided in Table 3.

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260 Table 3. Morphometric data of *Tor remadevii* type and comparative material.

		Paratypes		Comparative material (ZSI-SRS)			
Characters	Holotype	#1	#2	F9148	F9149	F9150	F9145
Standard length (SL, mm)	217.1	194.1	168.0	356.0	369.0	487.0	572.0
Head length (HL, mm)	66.0	63.0	60.5	112.8	117.2	159.0	182.4
%SL							
Head length	30.4	32.5	36.0	31.7	31.8	32.6	31.9
Pre-dorsal length	54.4	52.1	57.1	56.2	51.5	55.0	54.9
Dorsal to caudal distance	30.4	33.0	33.3	33.7	36.3	36.3	32.3
Pre-pectoral length	29.0	31.4	34.0	30.9	29.6	30.3	30.2
Pre-ventral length	53.5	56.8	58.3	58.4	58.3	57.7	56.5
Pre-anal length	82.5	88.8	82.2	84.3	84.6	84.2	81.3
Caudal-peduncle length	19.8	24.2	24.1	17.9	16.7	18.3	15.4
Caudal-peduncle depth	12.0	12.4	13.1	10.8	9.1	10.4	9.9
Dorsal-fin length	27.2	29.4	30.4	23.6	23.3	21.1	21.0
Dorsal-fin base	14.7	15.0	14.3	12.5	12.6	11.3	12.6
Pectoral-fin length	21.2	21.1	20.3	18.5	19.3	19.5	20.1
Ventral-fin length	18.9	18.6	19.1	17.0	17.2	17.2	16.6
Anal-fin length	20.8	20.7	19.7	16.0	18.3	17.6	18.2
Anal-fin base	5.6	7.3	7.2	7.7	7.2	7.2	7.1
Body depth (D)	26.7	28.9	31.6	25.9	26.5	24.5	24.8
Body depth (A)	17.1	19.1	19.1	17.4	16.1	15.9	15.8
Body width (D)	14.0	14.4	13.7	14.6	14.2	15.1	16.2
Body width (A)	9.7	8.8	8.4	8.6	8.3	9.6	11.7
% HL							
Snout length	30.4	32.7	31.5	32.0	29.0	30.6	29.3
Inter-orbital length	28.9	20.7	28.2	24.0	22.6	21.7	23.5
Eye diameter	21.3	19.1	19.9	14.1	14.5	12.2	11.9
Head depth	57.6	50.8	52.9	71.4	76.1	69.9	75.6
Head width	41.0	36.5	33.7	43.0	41.6	46.3	48.2

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266 Consistent with the common name, the dorsal profile of *T. remadevii* exhibits a prominent hump 267 originating above the pre-opercle and extending to the origin of the dorsal fin. Dorsal fin with 4

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unbranched and 9 branched rays, the fourth unbranched ray forming a strong smooth spine. Dorsal-fin origin directly above the pelvic-fin origin. Pelvic fin with one un-branched and 7–8 branched rays. Anal fin with two un-branched and five branched rays. Pectoral fin with one un-branched and 14–15 branched rays. Lateral line complete, with 24–29 scales. Transverse scales from dorsal-fin origin to ventral-fin origin ½3/1/2½. Pre-dorsal scales 7–8. In contrast with the description [17], dorsal-fin height less than and not exceeding 91% of dorsal body-depth. Consistent with other species of *Tor*, pharyngeal teeth display a

- 274 5,3,2:2,3,5 ratio.
- 275

276 Colouration

Live specimens of *T. remadevii* from the River Moyar display contrasting dorsal and lateral body colouration, from deep bronze to metallic greens. Bright orange fins (Fig 6) were consistent in all specimens examined. Photographic records captured by anglers from the main stem of the River Cauvery exhibit body colouration ranging from silver to deep bronze, with orange colouration of fins always evident in caudal fin as a minimum. Colour of the remaining fins range between deep orange and bluish grey. With the exception of fin-colour, observed variations suggest that body colouration may not be a reliable diagnostic character.

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285 **Distribution**

Tor remadevii is currently known only from the eastward flowing River Cauvery and its tributaries
 including the Moyar, Kabini, Bhavani and the Pambar, in the Western Ghats Hotspot of peninsular India
 (Fig 7).

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Fig 7. Collection locations of *Tor remadevii* from the tributaries of the River Cauvery, India

292 Habitat

While functional habitats are yet to be elucidated, *T. remadevii* inhabits the middle to upper reaches of the
River Cauvery and some of its tributaries. Mesohabitat utilization is known to incorporate shallow high
velocity rapids to deep, slow flowing pools, with substrates typically composed of bedrock and boulders
(Fig 8).

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- 298 **Fig 8.** Typical habitat of *Tor remadevii* in the River Moyar, India
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- 300 **Discussion**
- 301

302 These results confirm that the hump-backed mahseer, an iconic species that can be classed as mega-303 fauna on account of its large body size, is genetically distinct from other South Indian Tor fishes and is 304 conspecific with T. remadevii. In addition to their potentially large adult body sizes, they can be 305 distinguished from other Tor fishes by definitive morphological characters including their inter-orbital 306 distances, distinctive kink in the pre-opercle, a well-developed mandible and orange colouration of the 307 caudal fin. These results also reveal that T. remadevii only occurs in the River Cauvery basin, and thus 308 appears to be endemic with a limited distribution. Given the on-going threats to their populations in the 309 Cauvery [5], these results highlight that despite their iconic status, T. remadevii is imperiled and urgent 310 conservation assessments and actions are needed forthwith.

311

The first documented record of the hump-backed mahseer in scientific literature dates back to 1849, when British naturalist Thomas Jerdon [35] mentioned collecting from Seringapatanam (=Srirangapatanam) in the River Cauvery, a juvenile specimen of a mahseer that grows to enormous sizes, which he identified as *Barbus megalepis*. Later, in a classical work on angling in India [6], Henry Sullivan Thomas characterized this fish as having a deeper body and higher back and called it the Bawwany mahseer, or 'Barbus tor'. Subsequent workers [10-13] considered Jerdon's and Thomas' fish to be synonymous with *Barbus mussullah* Sykes, and called it the hump-backed mahseer [36].

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320 The identity and generic placement of Barbus mussullah Sykes, which was long unclear, having been 321 considered a synonym of Cyprinus curmuca Hamilton, or a species of Tor Gray, was clarified to be a 322 species of Hypselobarbus Bleeker and the identity stabilized by the designation of a neotype [15-16]. 323 However, Knight et al. [15-16] also brought attention to the fact that the identity of Barbus (Tor) mussullah 324 sensu Hora [10-11] still remained to be elucidated. Hora's use of coloration and local knowledge 325 (including local names) to characterize this species [10] was unreliable, as fishes often have a greater 326 variety of local names than any other group of animals [37], with the same name being used for different 327 species and different names being used for the same species. Although there was uncertainty in the use 328 of vernacular names, Hora [10] distinguished the high-backed species, which he called T. mussullah, 329 from T. khudree sensu Sykes.

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In their work, Knight et al. [15-16] also drew attention to a *Tor* specimen in the unregistered, reserve collections in the Zoological Survey of India, Southern Regional Center, Chennai (ZSI-SRS), labeled *Tor neilli* and originating from the River Krishna at Satara, Maharashtra with a characteristic high back and 24 scales in the lateral series. Knight et al. [15] speculated that this could be the species which Hora [10] considered as *T. mussullah*. Quoting Day's description of *T. neilli* from the River Tungabhadra at Kurnool [38], part of the Krishna River basin (from where Hora [10] collected his *T. mussullah*), as a large species of mahseer with tubercles on its snout. His illustration of quite a deep-bodied fish, and opinion that this species sometimes has reddish fins, Knight et al [15] suggested that in the event of *T. mussullah* sensu
Hora [10-11] is found to be a valid, the name *T. neilli* should be considered for it.

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341 Comparison of topotypic specimens and/or type material of valid mahseer species of peninsular India (T. 342 malabaricus, T. khudree and T. remadevii) with specimens of the hump-backed mahseer collected from 343 River Cauvery and its tributaries revealed striking similarities between the hump-backed mahseer and T. 344 remadevii in morphometrics, meristics and mitochondrial DNA (cox1). The Tor specimens from the 345 Tungabhadra, a tributary of the Krishna matched topotypic T. khudree and not the specimens collected in 346 the various tributaries of the Cauvery in their genetic make-up. Tor neilli is therefore treated as a junior 347 synonym of T. khudree, while T. remadevii is considered as a valid species restricted to the Cauvery 348 River system including its northern and southern tributaries. The name 'Tor moyarensis' propagated in 349 popular literature is a 'nomen nudum' [39].

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351 The first mention of the name Tor remadevii was made in 2007, when Kurup & Radhakrishnan's 352 description was published in the proceedings of a global mahseer symposium held in Malaysia [17]. 353 Perhaps, because of the limited circulation of this publication, the description went unnoticed, and the 354 same authors published a second paper in the year 2011 [40] reproducing the bulk of the original text. 355 probably with a view to make a 'formal description' in a peer reviewed journal. However, the description 356 made in 2007, satisfies all the 'criteria of availability' as per the International Code on Zoological Nomenclature (ICZN) (Articles 10, 11, 13 and 16), and therefore the paper published in 2011 [40] is 357 358 merely a re-description and irrelevant to nomenclature. The original year of publication is 2007, from 359 when the name *T. remadevii* became available.

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The Catalog of Fishes [41] mentions that the species epithet should be 'remadeviae' and not 'remadevii' because of the reason that the species was named for K. Rema Devi, (a feminine name). However, the ICZN in its Article 31.2.3 states "If a species-group name (or, in the case of a compound species-group name, its final component word) is not a Latin or latinized word [Articles 11.2, 26], it is to be treated as indeclinable for the purposes of this Article, and need not agree in gender with the generic name with which it is combined (the original spelling is to be retained, with ending unchanged; also see Article 34.2.1)". Therefore, the correct usage should be *Tor remadevii*.

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Having been first brought to the attention of the scientific community in the year 1849 [34], and the recreational angling community in the year 1873 [6], a century and half has since passed before the iconic hump-backed mahseer is afforded a scientific name. With the name now assigned to *T. remadevii* and the previously reported imperiled status of this mega-fauna [5], there is an immediate urgency to assess its extinction risk based on the IUCN Red List Categories and Criteria, with a view to affording this iconic species appropriate protection and accelerating the conservation agenda to secure the futuresustainability of remaining populations from severe and escalating anthropogenic threats [8].

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540 Supporting information

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542	S1 Table. List of specimens used for the molecular analysis in Fig 3.