

Table S1. List of Countries, Number of Sequences (NS), and their accession numbers of GenBank

Country	NS	Sequences reference number	Population Design and References
Uganda (Lake Edward basin)	25	MT523757, MT523756, MT523699, MT523697, MT523625, MT523618, MT523617, MT523614, MT523604, MT523603, MT523556, MT523555, MT523554, MT523546, MT523545, MT523544, MT523526, MT523525, MT523519, MT523518, MT523517, MT523516, MT523500, MT523250, MT523249,	Fishes were collected during four expeditions (2016–2019) to the Ugandan part of the Lake Edward/George system [1].
India	20	KF742418, JQ699203, JQ699202, JQ699201, JQ699200, KR063237, KR047790, OK605095, ON032576, MW167121, MW167120, OK001827, MW506812, MH197226, MH197225, MH197194, MH197182, KX946613, JX260853, MF189951	Fishes were collected from fifteen different river sites in the southern part of the northern Western Ghats region. A total of 343 Fish specimens were captured using gill nets, cast nets, and hand nets during 2013–2016. 1–3 or >3 specimens per species were collected from each sampling site [2].
Turkey	21	KC500432, KC500431, KC500430, KC500429, KC500428, KC500427, KC500426, KC500425, KC500423, KC500424, KC500422, KC500421, KC500420, KC500419, KC500418, KC500417, KC500416, KC500415, KC500414, KC500413, JQ623925,	A sampling of 89 commercially important fish species was made from 2006 to 2011 from 26 sites around Turkey. Samples were collected with the help of local commercial traders and local fishermen using push nets or gillnets. Major fish markets (Ankara, Antalya, Istanbul, Iskenderun, Izmir, Mersin, Sinop, and Trabzon) were also visited for specimen collection [3].
Nigeria	21	HM882831, HM882830, HM882828, HM882827, HM882826, HM882825, HM882824, HM882823, HM882821, HM882820, HM882817, HM882814, HM882813, HM882812, HM882811, HM882810,	Iyiola et al. [4] collected one hundred thirty-six (136) freshwater fish samples belonging to 53 species between 2016 and 2017. Their sampling covered nine (9) inland water bodies.

		HM882809, MG824583, MG824582, MG824581, MG824580,	Nwani et al. [5] sampled 366 fish specimens, representing 70 species, 38 genera, and 20 families. Samples were collected from three different sites at three rivers (Afikpo, Anambra, and Ebonyi) in southeastern Nigeria between February 2008 and March 2010. The number of specimens per species collected at each site ranged from 1 to 15, with a mean of 3.5. All specimens were caught in the wild.
Thailand	13	MZ407829, MZ407785, JF292320, JF292319, JF292318, JF292317, JF292316, JF292315, JF292314, JF292313, JF292312, JF292311, JF292310.	<p>Fifty-four fish fillet products belonging to 22 distinct manufacturers were purchased from several supermarkets in Thailand between March 2018 and September 2020. All products were photographed, and the details appeared on the labels, such as the common/market/scientific names, product names, and source of origin (cultured/wild caught). The source for all the samples for <i>Clarias gariepinus</i> was cultured [6].</p> <p>A total of 173 individual samples representing 9 catfish species and an Ictalurid hybrid were used in this study. <i>Clarias gariepinus</i> catfish fin clips were obtained from the Department of Aquaculture, Faculty of Fisheries, Kasetsart University, Thailand (Nakhon Ratchasima Province) [7].</p>
Cameroon	13	OP555285, OP555284, OP555283, OP555282, OP555281, OP555280, OP555274, OP555275, OP555279, OP555278, OP555277, OP555276, OP555273.	A total of 63 <i>Clarias</i> specimens were collected from three different localities in the Nyong River from Cameroon during July 2019 to November 2020. The specimens were captured by using a standard cast net. The specimens were identified as <i>C. gariepinus</i> (n = 13) [8].
D.R. Congo	10	KT193492, KT193491, KT193046, KT193045, MK074109, MK074108, MK074107, MK074106, MK074105, MK074104,	The fish samples were collected during five expeditions between 2009 and 2011 in the Kisangani area downstream and upstream of the Wageniarapids and on the north-eastern affluents of the Congo Basin [9].

			Sonet et al. [10] sampled a total of 741 specimens during four field campaigns carried out between 2004 and 2007 in the Democratic Republic of the Congo (DRC). A total of 496 specimens were collected in the Lower Congo and the Middle Congo. A total of 245 specimens were caught in three major drainage systems. Fishes were caught using gill nets.
Egypt	7	MK335913, MK335912, MK335911, MK335910, MK335909, LC487119, LC487118	Geba et al., 2018, Unpublished
Brazil	5	GU701829, GU701828, GU701827, GU701826, GU701825,	A total of 1,244 fishes were collected at 208 different sites along the Upper Parana River basin [11].
Philippines	5	KF604661, KF604660, KF604659, KF604658, KF604657	Quilang et al., 2013, Unpublished
Indonesia	6	KX619412, HM345934, HM345933, KU692441, KU692440, KU692439,	Widyastuti et al., 2016, Unpublished
Algeria	4	ON643478, ON643477, ON643476, ON643475	Eighty-four samples of <i>C. gariepinus</i> were caught in October 2019 at the Oued Takhamalte of the Saharan rural area, which is located 60 km from the capital of the willaya of Illizi in Southeast Algeria. Fish were collected using an artisanal method practiced by the region's inhabitants [12].
Zimbabwe	4	OL311811, OL311810, OL311809, OL311814	Chakona, 2021, Unpublished
Bangladesh	3	KX657715, KU958020, MG988400,	Ahmed et al., 2016, Unpublished
China	2	MT571809, KM610469,	For this study, sample collections were performed in the NR basin in Yunnan province because the majority of the reported species are

			present there. A total of 1139 specimens were collected during March and October 2012 and May and June 2013 from localities in the upper-middle NR [13]
Malaysia	2	MW591039, KT001047,	Jamaluddin et al., 2021, Unpublished
Syria	1	KJ552903	The Mediterranean BH includes all areas of the Mediterranean floral zone, therefore including Portugal and the Atlantic parts of Spain and Morocco, as well as the Macaronesian islands. The geographical area considered for this study [14].
Ethiopia	1	KF929769	Bentley et al., 2013, Unpublished
Sudan	1	OL804284	Hamza et al., 2021, Unpublished

Table S2. Nucleotide sites indicate each haplotype (17 haplotypes) in *Clarias gariepinus*

	-----GCCCTGATATAGCATTCCCACGAATAAATA-----ATATAAGCTTCTG----- ACTACTACCCCATCATTCTATTGCTAC-TCGCCTCATCAGGTGTTGAAGCAGGGGCTGGGACAGGGTGAACAG----- Hap_1 TATATCCACCCCTTGCAGGAAACCTCGCACATGCAGGAGCTTCCGTAGATTAACTATTTTCTCCCTACATCTAGCAGGTGTCTCATCAATTCT TGCATCTATTAATT----- TCATTACAACTATTATTAATATGAAACCCCCAGCTATTTTCAATATCAAACACCTTTATTTGTCTGATCAGTAATGATTACAGCAGTACTCC-- TACTGCTTTCCTCCCGTACTAGCA-----GCAGGAATT
Hap_2	-----GCCCTGATATAGCATTCCCACGAATAAATA-----ATATAAGCTTCTG--- -----ACTACTACCCCATCATTCTATTGCTAC-TCGCCTCATCAGGTGTTGAAGCAGGGGCTGGGACAGGGTGAACAG----- TATATCCACCCCTTGCAGGAAACCTCGCACATGCAGGAGCTTCCGTAGATTAACTATTTTCTCCCTACATCTAGCAGGTGTCTCATCAATTCT

	TGCATCTATTAATT-----
	TCATTACAAC TATTATTAATATGAAACCCCCAGCTATTTT CACAATATCAAACACCTTTATTTGTCTGATCAGTAATGATTACAGCAGTACTCC---
	TACTGCTCTCCCTCCCCG TACTAGCA-----GCAGGAATT-----
	-----GCCCCTGATATAGCATTCCCACGAATAAATA-----ATATAAGCTTCTG-----
	ACTACTACCCCCATCATTCTATTGCTAC-TCGCCTCATCAGGTGTTGAAGCAGGGGCTGGGACAGGGTGAACAG-----
Hap_3	TATATCCGCCCCCTTGCAGGAAACCTCGCACATGCAGGAGCTTCCGTAGATTTA ACTATTTTCTCCCTACATCTAGCAGGTGTCTCATCAATTCT
	TGCATCTATTAATT-----
	TCATTACAAC TATTATTAATATGAAACCCCCAGCTATTTT CACAATATCAAACACCTTTATTTGTCTGATCAGTAATGATTACAGCAGTACTCC---
	TACTGCTTTCCCTCCCCG TACTAGCA-----GCAGGAATT-----
	-----GCTCCTGATATAGCATTCCCACGAATGAATA-----ACATAAGCTTCTG-----
	ACTACTTCCCCCATCATTCTATTGCTAC-TCGCCTCATCAGGTGTTGAAGCAGGGGCTGGGACAGGGTGAACAG-----
Hap_4	TATATCCACCCCCTTGCAGGAAACCTCGCACATGCAGGAGCTTCCGTAGATTTA ACTATTTTTTCCCTACATCTAGCAGGTGTCTCATCAATTCTT
	GCATCTATTAATT-----
	TCATTACAAC TATTATTAATATGAAACCCCCAGCTATTTT CACAATATCAAACACCTTTATTTGTCTGATCAGTAATGATTACAGCAGTACTCC---
	TACTGCTCTCCCTCCCCG TACTAGCA-----GCAGGAATT-----
	-----GCTCCTGATATAGCATTCCCACGAATAAATA-----ACATAAGCTTCTG-----
	ACTACTTCCCCCATCATTCTATTGCTAC-TCGCCTCATCAGGTGTTGAAGCAGGGGCTGGGACAGGGTGAACAG-----
Hap_5	TATATCCACCCCCTTGCAGGAAACCTCGCACATGCAGGAGCTTCCGTAGATTTA ACTATTTTTTCCCTACATCTAGCAGGTGTCTCATCAATTCTT
	GCATCTATTAATT-----
	TCATTACAAC TATTATTAATATGAAACCCCCAGCTATTTT CACAATATCAAACACCTTTATTTGTCTGATCAGTAATGATTACAGCAGTACTCC---
	TACTGCTCTCCCTCCCCG TACTAGCA-----GCAGGAATT-----
	GCTCCTGATATAGCATTCCCACGAATAAATA-----ACATAAGCTTCTG-----ACTACTTCCCCCATCATTCTATTGCTAC-
	TCGCCTCATCAGGTGTTGAAGCAGGGGCTGGGACAGGGTGAACAG-----
Hap_6	TATATCCACCCCCTTGCAGGAAACCTCGCACATGCAGGAGCTTCCGTAGATTTA ACTATTTTTTCCCTACATCTAGCAGGTATCTCATCAATTCTT
	GCATCTATTAATT-----
	TCATTACAAC TATTATTAATATGAAACCCCCAGCTATTTT CACAATATCAAACACCTTTATTTGTCTGATCAGTAATGATTACAGCAGTACTCC---
	TACTGCTCTCCCTCCCCG TACTAGCA-----GCAGGAATT-----
	-----GCCCCTGATATAGCATTCCCACGAATAAATA-----ATATAAGCTTCTG-----
Hap_7	ACTACTACCCCCATCATTCTATTGCTAC-TCGCCTCATCAGGTGTTGAAGCAGGGGCTGGGACAGGGTGAACAG-----

	TATATCCGCCCTTGCAGGAAACCTCGCACATGCAGGAGCTTCCGTAGATTAACTATTTTCTCCCTACATCTAGCAGGTGTCTCATCAATTCT
	TGCATCTATTAATT-----
	TCATTACAACCTATTATTAATATGAAACCCCCAGCTATTTTACAATATCAAACACCTTTATTTGTCTGATCAGTAATGATTACAGCAGTACTCC--
	TACTGCTCTCCCTCCCCGTACTAGCA-----GCAGGAATT-----
	-----GCTCCTGATATAGCATTCCCACGAATAAATA-----ACATAAGCTTCTG-----
	ACTACTTCCCCCATCATTCCTATTGCTAC-TCGCCTCATCAGGTGTTGAAGCAGGGGCTGGAACAGGGTGAACAG-----
Hap_8	TATATCCACCCCTTGCAGGAAACCTCGCACATGCAGGAGCTTCCGTAGATTAACTATTTTTCTCCCTACATCTAGCAGGTGTCTCATCAATTCTT
	GCATCTATTAATT-----
	TCATTACAACCTATTATTAATATGAAACCCCCAGCTATTTTACAATATCAAACACCTTTATTTGTCTGATCAGTAATGATTACAGCAGTACTCC--
	TACTGCTCTCCCTCCCCGTACTAGCA-----GCAGGAATT-----
	-----GCCCTGATATAGCATTCCCACGAATAAATA-----ATATAAGCTTCTG-----
	ACTACTACCCCATCATTCCTATTGCTAC-TCGCCTCATCAGGTGTTGAAGCAGGGGCTGGGACAGGGTGAACAG-----
Hap_9	TATATCCACCCCTTGCAGGAAACCTCGCACATGCAGGAGCTTCCGTAGATTAACTATTTTCTCCCTACATCTAGCAGGTGTCTCATCAATTCT
	TGCATCTATTAATT-----
	TCATTACAACCTATTATTAATATGAAACCCCCAGCTATTTTACAATATCAAACACCTTTATTTGTCTGATCAGTAATGATTACAGCAGTACTCC--
	TACTGCTTTCCCTCCCCGTACTAGCA-----GCAGGAATT-----
	-----GCTCTTGATATAGCATTCCCACGAATGAATA-----ACATAAGCTTCTG-----
	ACTTCTTCCCCCATCATTCCTATTGCTAC-TTGCCTCATCAGGTGTTGAAGCAGGGGCTGGGACAGGGTGAACAG-----
Hap_1 0	TATATCCACCCCTTGCAGGAAACCTCGCACATGCAGGAGCTTCCGTAGATTAACTATTTTTCTCCCTACATCTAGCAGGTGTCTCATCAATTCTT
	GCATCTATTAATT-----
	TCATTACAACCTATTATTAATATGAAACCCCCAGCTATTTTACAATATCAAACACCTTTATTTGTCTGATCAGTAATGATTACAGCAGTACTCC--
	TACTGCTCTCCCTCCCCGTACTAGCA-----GCAGGAATT-----
	-----GCTCCTGATATAGCATTCCCACGAATAAATA-----ACATAAGCTTCTG-----
	ACTACTACCCCATCATTCCTATTGCTAC-TCGCCTCATCAGGTGTTGAAGCAGGAGCTGGAACAGGATGAACAG-----
Hap_1 1	TATATCCACCCCTTGCAGGAAACCTCGCACATGCAGGAGCTTCCGTAGATTAACTATTTTTCTCCCTACATCTAGCAGGTGTCTCATCAATTCTT
	GCATCTATTAATT-----
	TCATTACAACCTATAATTAATATGAAACCCCCAGCTATTTTACAATACCAAACACCTTTATTTGTCTGATCAGTAATGATTACAGCAGTACTCC--
	-TGCTGCTCTCCCTCCCCGTACTAGCA-----GCAGGAATT-----

-----GCTCCTGATATAGCATTCCCACGAATAAATA-----ACATAAGCTTCTG-----
 ACTACTACCCCCATCATTCTATTGCTAC-TCGCCTCATCAGGTGTTGAAGCAGGAGCTGGAACAGGATGAACAG-----
 Hap_1
 2 TATATCCACCCCTTGCAGGAAACCTCGCACATGCAGGAGCTCCGTAGATTAACTATTTTTCCCTACATCTAGCAGGTGTCTCATCAATTCTT
 GCATCTATTAATT-----
 TCATTACAACCTATTATTAATATGAAACCCCCAGCTATTTTACAATACCAAACACCTTTATTTGTCTGATCAGTAATGATTACAGCAGTACTCC--
 TGCTGCTCTCCCTCCCCGTACTAGCA-----GCAGGAATT-----

-----GCTCCTGATATAGCATTCCCACGAATAAATA-----ACATAAGCTTCTG-----
 ACTACTACCCCCATCATTCTATTGCTAC-TCGCCTCATCAGGTGTTGAAGCAGGAGCTGGAACAGGGTGAACAG-----
 Hap_1
 3 TATATCCACCCCTTGCAGGAAACCTCGCACATGCAGGAGCTCCGTAGATTAACTATTTTTCCCTACATCTAGCAGGTGTCTCATCAATTCTT
 GCATCTATTAATT-----
 TCATTACAACCTATTATTAATATGAAACCCCCAGCTATTTTACAATACCAAACACCTTTATTTGTCTGATCAGTAATGATTACAGCAGTACTCC--
 TACTGCTCTCCCTCCCCGTACTAGCA-----GCAGGAATT-----

-----GCTCCTGATATAGCATTCCCACGAATAAATA-----ACATAAGCTTCTG-----
 ACTACTACCCCCATCATTCTATTGCTAC-TCGCCTCATCAGGTGTTGAAGCAGGAGCTGGAACAGGGTGAACAG-----
 Hap_1
 4 TATATCCACCCCTTGCAGGAAACCTCGCACATGCAGGAGCTCCGTAGATTAACTATTTTTCCCTACATCTAGCAGGTGTCTCATCAATTCTT
 GCATCTATTAATT-----
 TCATTACAACCTATTATTAATATGAAACCCCCAGCTATTTTACAATACCAAACACCTTTATTTGTCTGATCAGTAATGATTACAGCAGTACTCC--
 TGCTGCTCTCCCTCCCCGTACTAGCA-----GCAGGAATT-----

-----GCTCCTGATATAGCATTCCCACGAATAAATA-----ACATAAGCTTCTG-----
 ACTACTACCCCCATCATTCTATTGCTAC-TCGCCTCATCAGGTGTTGAAGCAGGAGCCGGAACAGGATGAACAG-----
 Hap_1
 5 TATATCCACCCCTTGCAGGAAACCTCGCACATGCAGGAGCTCCGTAGATTAACTATTTTTCCCTACATCTAGCAGGTGTCTCATCAATTCTT
 GCATCTATTAATT-----
 TCATTACAACCTATTATTAATATGAAACCCCCAGCTATTTTACAATACCAAACACCTTTATTTGTCTGATCAGTAATGATTACAGCAGTACTCC--
 TGCTGCTCTCCCTCCCCGTACTAGCA-----GCAGGAATT-----

-----GCCCTGATATAGCATTCCCACGAATAAATA-----ATATAAGCTTCTG-----
 ACTACTACCCCCATCATTCTATTGCTAC-TCGCCTCATCAGGTGTTGAAGCAGGGGCTGGGACAGGGTGAACAG-----
 Hap_1
 6 TATATCCACCCCTTGCAGGAAACCTCGCACATGCAGGAGCTCCGTAGATTAACTATTTCTCCCTACATCTAGCAGGTGTCTCATCAATTCTT
 TGCATCTATTAATT-----

TCATTACAACCTATTATTAATATGAAACCCCCAGCTATTTTACAATATCAAACACCTTTATTTGTCTGATCAGTAATGATTACAGCAGTACTCC---
TACTGCTTTCCCTCCCAGTACTAGCA-----GCAGGAATT-----

-----GCTCCTGATATAGCATTCCCACGAATAAATA-----ACATAAGCTTCTG-----

Hap_1
7 ACTACTTCCCCCATCATTCTATTGCTAC-TCGCCTCATCAGGTGTTGAAGCAGGGGCTGGGACAGGGTGGACAG-----
TATATCCACCCCTTGCAGGAAACCTCGCACATGCAGGAGCTTCCGTAGATTTAACTATTTTTTCCCTACATCTAGCAGGTGTCTCATCAATTCTT
GCATCTATTAATT-----

TCATTACAACCTATTATTAATATGAAACCCCCAGCTATTTTACAATATCAAACACCTTTATTTGTCTGATCAGTAATGATTACAGCAGTACTCC---
TGCTGCTCTCCCTCCCCGTACTAGCA-----GCAGGAATT-----

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MATRIX
[
      10      20
      *      *
'Hap_1' CCATAACGTGGAACGTTATCAT
'Hap_2' .....C...
'Hap_3' .....G.....
'Hap_4' T.GC.T.....T....C...
'Hap_5' T..C.T.....T....C...
'Hap_6' T..C.T.....TA...C...
'Hap_7' .....G.....C...
'Hap_8' T..C.T...A...T....C...
'Hap_9' .....GA
'Hap_10' TTGCTTT.....T....C...
'Hap_11' T..C...A.AA..T.ACGC...
'Hap_12' T..C...A.AA..T..CGC...
'Hap_13' T..C...A.A...T..C.C...
'Hap_14' T..C...A.A...T..CGC...
'Hap_15' T..C...ACAA..T..CGC...
'Hap_16' .....A..
'Hap_17' T..C.T.....G.T...GC...

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Figure S1. Nucleotide sites indicate each haplotype (17 haplotypes) in *Clarias gariepinus*

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