

The Teleostei Immunoglobulin Heavy IGH Genes

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Key Words

Teleostei · IMGT · Immunoglobulin · Heavy variable genes · Heavy joining genes · Heavy constant genes

Abstract

'Teleostei Immunoglobulin Heavy IGH Genes', the eleventh report of the 'IMGT Locus in Focus' section, comprises four tables: (1) 'Teleostei IGHV genes'; (2) 'Teleostei germline IGHJ genes'; (3) 'Teleostei IGHC genes and alleles'; (4) 'FR-IMGT and CDR-IMGT length of the Teleostei IGHV genes'. These tables are available at the IMGT Marie-Paule page from **IMGT**, the international ImMuNoGeneTics database (<http://imgt.cines.fr:8104>) created in 1989 by Marie-Paule Lefranc, Université Montpellier II, CNRS, France.

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Introduction

'Teleostei Immunoglobulin Heavy IGH Genes' is the 11th report of the 'IMGT Locus in Focus' section launched in the April 1998 issue of *Experimental and Clinical Immunogenetics* [1]. We have previously reported the

complete repertoire of the human germline V and J genes of the immunoglobulin IGK and IGL and of the T cell receptor TRA loci [2–6], and that of the human germline V, D and J genes of the immunoglobulin IGH and of the T-cell receptor TRB loci [6–10]. This eleventh report on Teleostei Immunoglobulin Heavy IGH Genes describes the current data for 11 species of teleost fishes whose sequences are found in IMGT/LIGM-DB (fig. 1). It comprises four tables: (1) 'Teleostei IGHV genes'; (2) 'Teleostei germline IGHJ genes'; (3) 'Teleostei IGHC genes and alleles'; (4) 'FR-IMGT and CDR-IMGT length of the Teleostei IGHV genes'. These tables are available at the IMGT Marie-Paule page from **IMGT**, the international ImMuNoGeneTics database (<http://imgt.cines.fr:8104>) created in 1989 by Marie-Paule Lefranc, Université Montpellier II, CNRS, France [11, 12]. Teleostei IGH genes have a temporary designation based on the IMGT gene name nomenclature rules for the unmapped genes, the incomplete loci, or the cDNAs in the absence of germline genes. Descriptions of functionality (functional, open reading frame, pseudogene) are according to the IMGT Scientific chart [11, 12], available at the IMGT Marie-Paule page.

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Table 1. Teleostei IGHV genes

Fct: FUNCTIONALITY
F: Functional
P: Pseudogene
ORF: Open Reading Frame
Vg: Vestigial
R: Rearranged
T: Transcribed
Pr: Translated into protein

"+" or "-" indicates if the gene sequences have been found (+) or not been found (-) rearranged (R), transcribed (T), and/or translated into protein (Pr). Functionality is shown between parentheses when the accession number refers to a cDNA sequence and the corresponding genomic gene has not yet been isolated. Except if indicated, there is no correspondence between IGHV subgroups and IGHV gene names between taxons.

Taxon	IGHV subgroup	IGHV gene name (1)	Fct	R	T	Pr	Reference sequences	Accession numbers	Sequences from the literature
Antarctic fish (<i>Trematomus bernacchii</i>)	1	1S1	(F)	+	+		2C2	AF094531 [8] #c	
	1	1S1	(F)	+	+		cACVH4	AJ000361 [5] #c	
		1S2	(F)	+	+		cACVH9	AJ000367 [5] #c	
	2	2S1	(F)	+	+		cACVH3	AJ000360 [5] #c	
		2S2	(F)	+	+		cACVH27	AJ000363 [5] #c	
	3	3S1	(F)	+	+		cACVH124	AJ000366 [5](2) #c	
	4	4S1	(F)	+	+		cACVH8	AJ000368 [5] #c	
	5	5S1	(F)	+	+		cACVH1	AJ000359 [5] #c	
		5S2	(F)	+	+		cACVH2	AJ000358 [5] #c	
	6	6S1	(F)	+	+		cACVH31	AJ000364 [5] #c	
		6S2	(F)	+	+		cACVH6	AJ000369 [5] #c	
8	8S1	(F)	+	+		cACVH10	AJ000370 [5] #c		
	8S1	(F)	+	+		cACVH5	AJ000362 [5] #c		
11	11S1	(F)	+	+		cACVH130	AJ000365 [5] #c		
Atlantic cod (<i>Gadhus morhua</i>)	1	1S1	(F)	+	+		cSg 5.1	X58870 [6] #c	
	2	2S1	(F)	+	+		112-12	X76510 [7] #c	
		3S1	(F)	+	+		112-4	X76512 [7] #c	
	3	3S2	(F)	+	+		112-22	X76511 [7] #c	
		3S3	(F)	+	+		112-5	X76514 [7](4) #c	
	3S4	(F)	+	+		S2A	X76516 [7](5) #c		
	3S5	(F)	+	+		101-11	X76507 [7] #c		
	3S6	(F)	+	+		112-25	X76513 [7] #c		
	3S7	(F)	+	+		112-1	X76509 [7] #c		
	3S8	(F)	+	+		3.3	X76515 [7](6) #c		
	3S9	(F)	+	+		101-14	X76508 [16] #c		
Atlantic salmon (<i>Salmo salar</i>)	1	1S1	F				g1.1 (10)	Y12452 [10]	
	1S2	P(7)					g12.2 (10)	Y12454 [10]	
	1S3	P(8)					g11.5 (10)	Y12453 [10]	
	1S4	P(9)					g11.5 (10)	Y12455 [10]	

Table 1 (continued)

Channel catfish (<i>Ictalurus punctatus</i>)	1	151	F			VH1.1	U09719 [15]
		152	IF1			NG70	M27230 [23] #c
	2	251	P111			VH2.1	U09720 [15]
		252	IF1			NG41	M58671 [24] #c
	3	351	F			VH3.1	U09721 [15]
		352	IF1			NG54	M58672 [24] #c
		451	F			VH4.1	U09722 [15]
5	452	IF1			NG10	M58668 [24] #c	
		551	P112		VH5.1	U09723 [15]	
		552	IF1		NG66	M58674 [24] #c	
	6	651	F		VH6.1	U09724 [15]	
		652	IF1			M64400 [25] #c	
7	751	P113			VH7.1	U34412 [16]	
	752	IF1			cVH7c	U34411 [16] #c	
Fugu (<i>Fugu rubripes</i>)	1	151	F			F-Vh1	AF108421 [12]
		152	F			F-Vh3	AF108421 [12]
		153	F			F-Vh5	AF108421 [12]
		154	F			F-Vh6	AF108422 [12]
		155	F			F-Vh7	AF108423 [12]
	2	251	ORF14			F-Vh2	AF108421 [12]
		252	ORF14			F-Vh4	AF108421 [12]
253	253	ORF14			F-Vh8	AF108423 [12]	
	254	ORF14			F-Vh9	AF108422 [12] [15]	
Goldfish (<i>Carassius auratus</i>)	1	151	F			V3	J03616 [17] [18] [16]
	2	251	ORF17			99A	X61312 [19]
		252	P118			6X	X65266 [19]
	3	351	P119			99B	X61313 [19]
Ladyfish (<i>Elops saurus</i>)	1	151	IF1	+	+		M26182 [1] #c
		152	P111				M26580 [1]
		153	P118				M29586 [1]
	2	251	IF1	+	+		M26579 [1] #c
Rainbow trout (<i>Oncorhynchus mykiss</i>) (20)	1	151	F			RTVH431	M57442 [11]
		152	F			RTVH253	X92501 [2]
		153	IF1	+	+	cRTVH50	S63348 [3] #c
		154	IF1	+	+	cRTVH3	X81490 [4] #c
		155	IF1	+	+	lgh-V4	L28741 [13] #c
		156	IF1	+	+	TD1255	X81484 [4] #c
		157	IF1	+	+	cRTVH31	Y08597 [22] #c
	2	251	IF1	+	+	cRTVH12	X81509 [4] #c
		252	IF1	+	+	ris.155	X65262 [2] #c
		253	IF1	+	+	TD1271	X81512 [4] #c
		351	IF1	+	+	cRTVH19	X81510 [4] #c
		352	IF1	+	+	lgh-V5.1	L28742 [13] #c
		353	IF1	+	+	lgh-V5.2	L28805 [13] #c
354	354	IF1	+	+	cRTVH29	Y08595 [22] #c	
	451	IF1	+	+	lgh-V6	L28744 [13] #c	

Taxon	IGHV subgroup	IGHV gene name (1)	Fct	R	T	Pr	Reference sequences	Accession numbers	Sequences from the literature
	5	5S1	(F)	+	+	+	cRTVH6	X81513 [4] #c	
		5S2	(F)	+	+	+	Igh-V7	L28745 [13] #c	
		5S3	(F)	+	+	+	RBTIGTM1	U04616 [20] #c	
		5S4	(F)	+	+	+	RBTIGTM2	U04615 [20] #c	
		5S5	(F)	+	+	+	cRTVH28	X81493 [4] #c	
		5S6	(F)	+	+	+	cRTVH25	X81492 [4] #c	
		5S7	(F)	+	+	+	cRTVH8	X81491 [4] #c	
		5S8	(F)	+	+	+	cRTVH30	Y08596 [22] #c	
		5S9	(F)	+	+	+	cRTVH32	Y08599 [22] #c	
		6S1	(F)	+	+	+	cRTVH1	X81481 [4] #c	
		6S2	(F)	+	+	+	Igh-V8	L28746 [13] #c	
6S3	(F)	+	+	+	cRTVH18	X81496 [4] #c			
6S4	(F)	+	+	+	cRTVH5	X81494 [4] #c			
6S5	(F)	+	+	+	cRTVH23	X81497 [4] #c			
6S6	(F)	+	+	+	cRTVH26	X81487 [4] #c			
6S7	(F)	+	+	+	cRTVH5.1	X81486 [4] #c			
6S8	(F)	+	+	+	cRTVH7	X81485 [4] #c			
6S9	(F)	+	+	+	cRTVH14	X81495 [4] #c			
6S10	(F)	+	+	+	cRTVH33	Y08600 [22] #c			
6S11	(F)	+	+	+	cRTVH37	Y08602 [22] #c			
7S1	(F)	+	+	+	Igh-V9	L28747 [13] #c			
8S1	(F)	+	+	+	cRTVH2	X81482 [4] #c			
8S2	(F)	+	+	+	cRTVH11	X81501 [4] #c			
8S3	(F)	+	+	+	cRTVH24	X81503 [4] #c			
8S4	(F)	+	+	+	cRTVH9	X81499 [4] #c			
8S5	(F)	+	+	+	cRTVH17	X81488 [4] #c			
8S6	(F)	+	+	+	cRTVH15	X81498 [4] #c			
8S7	(F)	+	+	+	cRTVH16	X81502 [4] #c			
8S8	(F)	+	+	+	cRTVH10	X81500 [4] #c			
8S9	(F)	+	+	+	cRTVH2.1	X81483 [4] #c			
8S10	(F)	+	+	+	cRTVH34	Y08601 [22] #c			
8S11	(F)	+	+	+	cRTVH41	Y08889 [22] #c			
9S1	(F)	+	+	+	cRTVH21	X81505 [4] #c			
9S2	(F)	+	+	+	cRTVH20	X81504 [4] #c			
9S3	(F)	+	+	+	cRTVH27	X81507 [4] #c			
9S4	(F)	+	+	+	cRTVH22	X81506 [4] #c			
9S5	(F)	+	+	+	cRTVH39	Y08603 [22] #c			
9S6	(F)	+	+	+	cRTVH40	Y08604 [22] #c			
10S1	(F)	+	+	+	cRTVH4	X81508 [4] #c			
10S2	(F)	+	+	+	cRTVH4.1	X81489 [4] #c			
11S1	(F)	+	+	+	cRTVH13	X81511 [4] #c			
Spotted wolffish (<i>Anarhichas minor</i>) #c: Rearranged cDNA.	1	1S1	(F)	+	+		AF138958 [9] #c		

Table 1 (continued)**IMG T notes:**

- (1) Teleostei genes are designated by a number for the subgroup, following by the letter S and a number. Rainbow trout subgroup is according to [10].
- (2) Partial V-REGION: CDR3-IMG T is partial.
- (3) The designation of the Arctic charr (*Salvelinus alpinus*) IGHV subgroups is according to that of the Rainbow trout (*Oncorhynchus mykiss*) IGHV subgroups [14]. Representatives of the IGHV7, IGHV9, and IGHV10 subgroups have not yet been found in the Arctic charr.
- (4) Partial V-REGION: partial FR1-IMG T in 5' (AA 1 to 6 are absent).
- (5) Partial V-REGION: partial FR1-IMG T in 5' (AA 1 to 17 are absent).
- (6) Partial V-REGION: partial FR1-IMG T in 5' (AA 1 to 14 are absent).
- (7) In frame STOP-CODON in the CDR3-IMG T.
- (8) Frameshift in CDR2-IMG T.
- (9) In frame STOP-CODON in the FR2-IMG T.
- (10) In this column are shown the names of the lambda phages from which are derived the Reference sequences.
- (11) Frameshift in FR3-IMG T.
- (12) Frameshift in CDR1-IMG T and FR3-IMG T.
- (13) Frameshift in FR2-IMG T.
- (14) Non canonical V-HEPTAMER: CACAATA instead of CACAGTG.
- (15) Partial V-REGION: AA 1 to 89 are absent (no FR1-IMG T, no CDR1-IMG T, no FR2-IMG T, no CDR2-IMG T, partial FR3-IMG T).
- (16) J0317 originally assigned to *Carassius auratus* has been shown to be a human sequence (see [17] and [18]).
- (17) Non canonical V-HEPTAMER: CACTGTT instead of CACAGTG.
- (18) In frame STOP-CODONS in FR1-IMG T.
- (19) In frame STOP-CODONS in FR1-IMG T and in CDR1-IMG T.
- (20) Rainbow trout (*Oncorhynchus mykiss*) subgroups are according to [14].

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Table 2. Teleostei germline IGHJ genes

Fct: FUNCTIONALITY

F: Functional

P: Pseudogene

ORF: Open Reading Frame

vg: Vestigial

R: Rearranged

T: Transcribed

Pr: Translated into protein

"+" or "-": indicates if the gene sequences have been found (+) or not been found (-) rearranged (R), transcribed (T), and/or translated into protein (Pr).

Taxon	IGHJ name	Fct	R	T	Pr	Reference sequences	Accession numbers	Sequences from the literature
Atlantic salmon (<i>Salmo salar</i>)	IGHJ1-1	F				JHA-1	Y12391 [3]	
	IGHJ1-2	F				JHA-2	Y12391 [3]	
	IGHJ1-3	F	+ [1]			JHA-3	Y12391 [3]	
	IGHJ1-4	F				JHA-4	Y12391 [3]	
	IGHJ1-5	ORF (1)				JHA-5	Y12391 [3]	
	IGHJ2-1	F				JHB-1	Y12392 [3]	
	IGHJ2-2	F	+ [1]			JHB-2	Y12392 [3]	
	IGHJ2-3	F				JHB-3	Y12392 [3]	
	IGHJ2-4	F				JHB-4	Y12392 [3]	
	IGHJ2-5	ORF (1)				JHB-5	Y12392 [3]	
Channel catfish (<i>Ictalurus punctatus</i>)	IGHJ1	F	+	+		JH1	L22340 [4]	
	IGHJ2	F	+	+		JH2	L22340 [4]	
	IGHJ3	F	+	+		JH3	L22340 [4]	
	IGHJ4	F	+	+		JH4	L22340 [4]	
	IGHJ5	F				JH5	L22340 [4]	
	IGHJ6	F				JH6	L22340 [4]	
	IGHJ7	F	+	+		JH7	L22340 [4]	
	IGHJ8	F	+	+		JH8	L22340 [4]	
	IGHJ9	F	+	+		JH9	M74041 [5] [X79482][2], [X65182][6]	
Ladyfish (<i>Elops saurus</i>)	IGHJ1	F					M26578 [1]	

IMGT note: (1) Non canonical J-HEPTAMER, CACAGCT instead of CACTGTG, however rearrangement is not excluded (see [1]).

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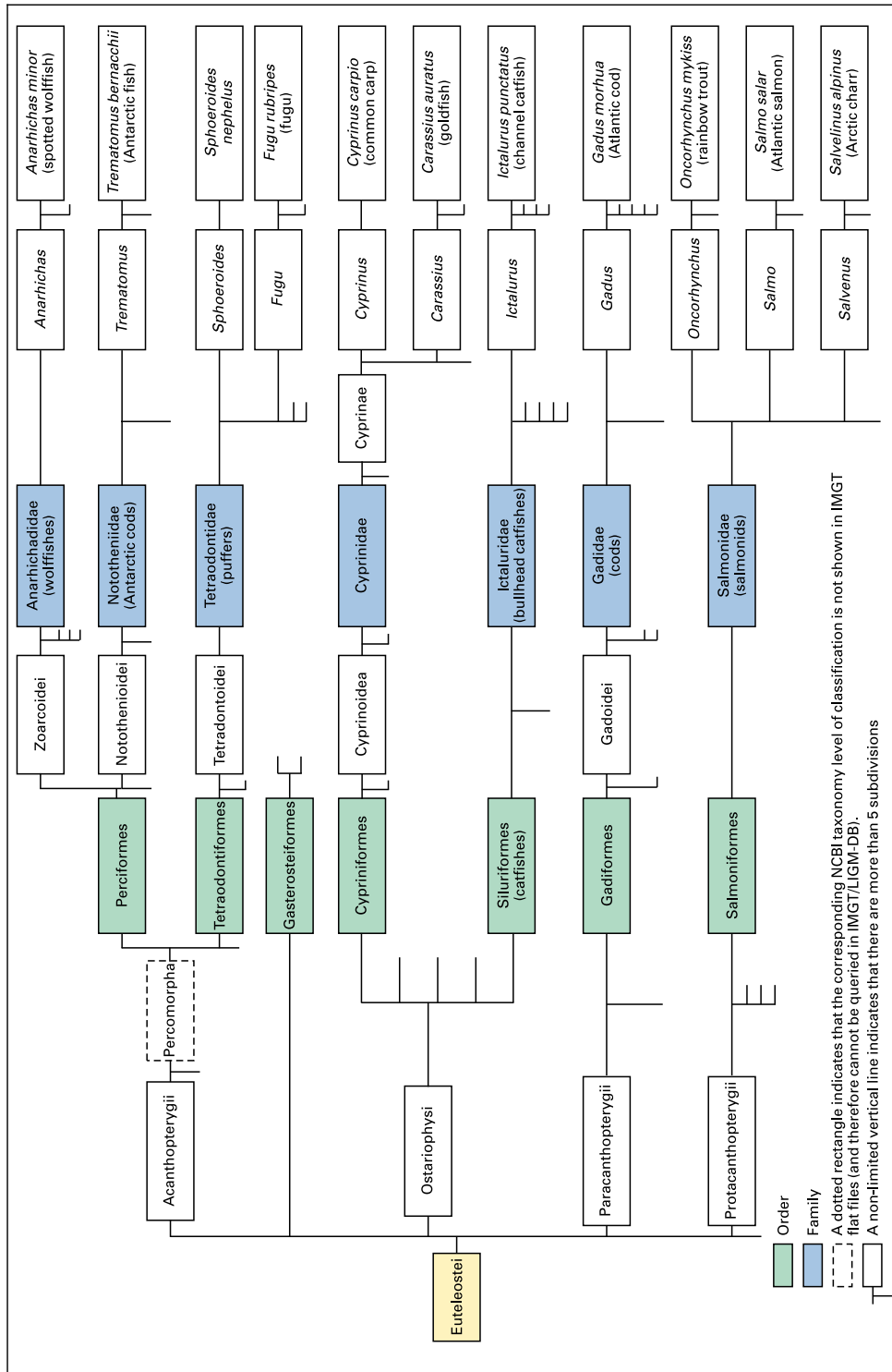


Fig. 1. IMGT taxonomy tree of the Euteleostei present in IMGT/LIGM-DB. Note that the Ladyfish (*Elops saurus*) which does not belong to the Euteleostei but to the Elopomorpha [Order: Elopiformes; Family: Elopidae (tenpounders)] is not shown in that figure. T cell receptor sequences, but no immunoglobulin sequences, have been so far described for *Sphoeroides nephelus*.

Table 3. Teleostei IGHC genes and alleles

Fct: FUNCTIONALITY

F: Functional

P: Pseudogene

ORF: Open Reading Frame

Taxon	IGHC gene name	IGHC allele name	Fct	Exons	Reference sequences	Accession numbers	Sequences from the literature
Antarctic fish (<i>Trematomus bernacchii</i>)	IGHM	IGHM*01	F	CH1		AF094531 [6] c (s)	
				CH2		AF094531 [6] c (s)	
				CH3(10)		AF094531 [6] c (s)	
				CH4(10)		AF094531 [6] c (s)	
				M1(10)			
				M2			
Arctic charr (<i>Salvelinus alpinus</i>)	IGHM	IGHM*01	F	CH1	gACIgm	X83373 [3] (2)	
				CH2	gACIgm	X83373 [3]	
				CH3(1)	gACIgm	X83373 [3]	
				CH4(1)	gACIgm	X83373 [3] (3)	
				M1(1)			
				M2			
Atlantic cod (<i>Gadus morhua</i>)	IGHM	IGHM*01	F	CH1	cSg 5.1	X58870 [5] c (s)	
				CH2	cSg 5.1	X58870 [5] c (s)	
				CH3(1)	cSg 5.1	X58870 [5] c (s)	
				CH4(1)	cSg 5.1	X58870 [5] c (s)	
				M1(1)			
				M2			
	IGHM*02	F	CH1				
			CH2				
			CH3(1)(4)	cSg F.1	X58871 [5] c (m)		
			M1(1)	cSg F.1	X58871 [5] c (m)		
			M2	cSg F.1	X58871 [5] c (m)		
Atlantic salmon (<i>Salmo salar</i>)	IGHM1	IGHM1*01	F	CH1	lambda 6.3 (5)	Y12391 [12]	
				CH2	lambda 6.3 (5)	Y12391 [12]	
				CH3(1)	lambda 6.3 (5)	Y12391 [12]	
				CH4(1)	lambda 6.3 (5)	Y12391 [12]	
				M1(1)	lambda 6.3 (5)	Y12391 [12]	
				M2	lambda 6.3 (5)	Y12391 [12]	
	IGHM1*02	F	CH1	7.3 (5)	Y12456 [12] c (s)		
			CH2	7.3 (5)	Y12456 [12] c (s)		
			CH3(1)	7.3 (5)	Y12456 [12] c (s)		
			CH4(1)	7.3 (5)	Y12456 [12] c (s)		
			M1(1)	7.1 (5)	S48658 [11] c (m)		
			M2	7.1 (5)	S48658 [11] c (m)		

Table 3 (continued)

Atlantic salmon (<i>Salmo salar</i>)	IGHM2	IGHM2*01	F	CH1	lambda 5.1 (5)	Y12392 [12]					
				CH2	lambda 5.1 (5)	Y12392 [12]					
				CH3(1)	lambda 5.1 (5)	Y12392 [12]					
				CH4(1)	lambda 5.1 (5)	Y12392 [12]					
				M1(1)	lambda 5.1 (5)	Y12392 [12]					
				M2	lambda 5.1 (5)	Y12392 [12]					
				CH1	g 5.1 (5)	S48652 [11] c (s)					
				CH2	g 5.1 (5)	S48652 [11] c (s)					
				CH3(1)	g 5.1 (5)	S48652 [11] c (s)					
				CH4(1)	g 5.1 (5)	S48652 [11] c (s)					
				M1(1)							
				M2							
				CH1	7.2 (5)	Y12457 [12] c (m)					
				CH2	7.2 (5)	Y12457 [12] c (m)					
				CH3(1)	7.2 (5)	Y12457 [12] c (m)					
M1(1)	7.2 (5)	Y12457 [12] c (m)									
M2	7.2 (5)	Y12457 [12] c (m)									
Channel catfish (<i>Ictalurus punctatus</i>)	IGHM	IGHM*01	F	CH1	12c (5)	X52617 [17]/X79482 [14]	C7[M*404] [16] (2), NG70[M27230] [9] c (s)				
				CH2	12c (5)	X52617 [17]/X79482 [14]	NG70[M27230] [9] c (s), HG103[M23733] [8] (8) c (s)				
				CH3(1)	12c (5)	X52617 [17]/X79482 [14]	NG70[M27230] [9] c (s), HG103[M23733] [8] c (s)				
				CH4(1)	12c (5)	X52617 [17]/X79482 [14]	NG70[M27230] [9] c (s), HG103[M23733] [8] c (s)				
				M1(1)	12c (5)	X52617 [17]/X79482 [14]					
				M2	12c (5)	X52617 [17]/X79482 [14]					
				CH1	12c (5)	X79482 [14]					
				CH2	12c (5)	X79482 [14] (9)					
				Common carp (<i>Cyprinus carpio</i>)	IGHM1	IGHM1*01	F	CH1(6)	Cp1, CpM	AB004105 [15] c (s), AB004106 [15] c (m)	
								CH2	Cp1, CpM	AB004105 [15] c (s), AB004106 [15] c (m)	
								CH3(1)	Cp1, CpM	AB004105 [15] c (s), AB004106 [15] c (m)	
								CH4(1)	Cp1	AB004105 [15] c (s)	
								M1(1)	CpM	AB004106 [15] c (m)	
								M2	CpM	AB004106 [15] c (m)	
								CH1(6)	Cp3	AB004107 [15] c (s)	
CH2	Cp3	AB004107 [15] c (s)									
CH3(1)	Cp3	AB004107 [15] c (s)									
CH4(1)	Cp3	AB004107 [15] c (s)									
M1(1)		AB004107 [15] (7) c (s)									
M2											
CH1(6)	Cp4	AB004108 [15] c (s)									
CH2	Cp4	AB004108 [15] c (s)									
CH3(1)	Cp4	AB004108 [15] c (s)									
CH4(1)	Cp4	AB004108 [15] (7) c (s)									
M1(1)											
M2											

Taxon	IGHC gene name	IGHC allele name	Fct	Exons	Reference sequences	Accession numbers	Sequences from the literature
Ladyfish (<i>Elops saurus</i>)	IGHM	IGHM*01	F	CH1	gRTIgM	X83372 [3] [2]	
				CH2	gRTIgM	X83372 [3]	
				CH3(1)	gRTIgM	X83372 [3]	
				CH4(1)	gRTIgM	X83372 [3] [7]	
				M1(1)		(11)	
				M2			
Rainbow trout (<i>Oncorhynchus mykiss</i>)	IGHM	IGHM*02	F	CH1	lambda RT15	X65262 [13] (12) c (s), X65261 [13] (2) c (s)	lambda RT15C1[X677:3] [2] (12)
				CH2	lambda RT15	X65261 [13] c (s)	lambda RT15m[X65263] [13] (9) c (m)
				CH3(1)	lambda RT15	X65261 [13] c (s)	lambda RT15m[X65263] [13] c (m)
				CH4(1)	lambda RT15	X65261 [13] c (s)	
				M1(1)	lambda RT15m	X65263 [13] c (m)	
				M2	lambda RT15m	X65263 [13] c (m)	
				CH1	cRTVH50	S63348 [2] c (s)	cRTVH50C-H[Y08598] [4] c (s)
				CH2	cRTVH50	S63348 [2] c (s)	cRTVH50C-H[Y08598] [4] c (s)
				CH3(1)	cRTVH50	S63348 [2] c (s)	cRTVH50C-H[Y08598] [4] c (s)
				CH4(1)	cRTVH50	S63348 [2] c (s)	cRTVH50C-H[Y08598] [4] c (s)
		M1(1)					
		M2					
		IGHM*04	F	CH1	RBTIGTM2	U04615 [10] c (m)	
				CH2	RBTIGTM2	U04615 [10] c (m)	
				CH3(1)	RBTIGTM2	U04615 [10] c (m)	
				M1(1)	RBTIGTM2	U04615 [10] c (m)	
				M2	RBTIGTM2	U04615 [10] c (m)	
				CH1	RBTIGTM1	U04616 [10] c (m)	
				CH2	RBTIGTM1	U04616 [10] c (m)	
				CH3(1)	RBTIGTM1	U04616 [10] c (m)	
M1(1)	RBTIGTM1			U04616 [10] c (m)			
M2	RBTIGTM1			U04616 [10] c (m)			
Spotted wolffish (<i>Anarhichas minor</i>)	IGHM	IGHM*01	F	CH1		AF138958 [7] c (s)	
				CH2		AF138958 [7] c (s)	
				CH3(10)		AF138958 [7] c (s)	
				CH4(10)		AF138958 [7] c (s)	
				M1(10)			
				M2			

c: cDNA sequence.

(s) Transcript of a secreted chain.

(m) Transcript of a membrane chain.

Table 3 (continued)**IMGT notes:**

- (1) CH3 is spliced to CH4 in secretory mu cDNA, whereas it is spliced to the M1 exon in membrane mu cDNA.
 (2) Partial C-GENE: partial CH1 in 5'.
 (3) Partial C-GENE: partial CH4 in 3'. M1 and M2 exons are missing.
 (4) Partial C-GENE: partial CH3 in 5'.
 (5) In this column are shown the names of the phages from which are derived the Reference sequences.
 (6) The last ten amino acids of CH1, rich in prolin, suggest the existence of a region with hinge-like characteristics.
 (7) Partial C-REGION: partial CH4 in 3'.
 (8) Partial C-GENE: partial CH2 in 5'.
 (9) Partial C-GENE: only CH1 and CH2 are present.
 (10) By homology with other Teleostei, the CH3 is spliced to CH4 in secretory mu cDNA, whereas it is probably spliced to the M1 exon in membrane mu cDNA.
 (11) Partial C-GENE: partial in 3', M1 and M2 exons are missing.
 (12) Partial C-GENE: partial CH1 in 3'.

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Table 4. FR-IMG1 and CDR-IMG1 length of the Teleostei IGHV genes

Only FUNCTIONAL and ORF V-GENES are shown. The proteolytic cleavage site between the leader peptide and the V-REGION is putative and the assignment of amino acid 1 to one or the other region is uncertain.

Taxon	IGHV subgroup	FR1-IMG1 1 to 26 (25)	CDR1-IMG1 27 to 38 (8)	FR2-IMG1 39 to 55 (17)	CDR2-IMG1 56 to 65 (7)	FR3-IMG1 66 to 104 (38)	CDR3-IMG1 105 to 115 (2) [1]	
Antarctic fish (<i>Trematomus bernacchii</i>)	1	-1 (aa 10)	8			-1 (aa 73)	2 [1]	
	Arctic charr (<i>Salvelinus alpinus</i>)	1	(24 to 27)	(7,8,10)	(17)	(6 to 8)	(35 to 38)	(2) [1]
			-1 (aa 10)	7		7	-1 (aa73)	2 [1]
		2	-1 (aa 10) +2 (aa 6A,6B)	8		6.8	-1 (aa73)	2 [1]
		3	-1 (aa 10)	10		7	-1 (aa73)	2 [1]
		4	-1 (aa 10)	8		6	-1 (aa73)	2 [1]
		5	-1 (aa 10)	8		6.8	-1 (aa73)	2 [1]
		6	-2 (aa 1,10)	7		6.7	-1 (aa73)	2 [1]
		8		8		7	-3 (aa73,81,82)	2 [1]
		11	-1 (aa 10)	8		7	-2 (aa73,82)	2 [1]
		Atlantic cod (<i>Gadus morhua</i>)	1	(25)	(6,7,12)	(17)	(6,7)	(38)
2	-1 (aa 10)		12		7	-1 (aa73)	2 [1]	
3	-1 (aa 10)		6,7		6	-1 (aa73)	2 [1]	
Atlantic salmon (<i>Salmo salar</i>)	1	(25)	(8)	(17)	(7)	(38)	(3)	
		-1 (aa 10)	8		7	-1 (aa 73)	3	
Channel catfish (<i>Ictalurus punctatus</i>)	1	(25)	(8,10,12)	(17)	(6 to 8)	(38)	(3)	
	2	-1 (aa 10)	8		7	-1 (aa 73)	3	
	3	-1 (aa 10)	7		7	-1 (aa 73)	3 [1]	
	4	-1 (aa 10)	8		6.8	-1 (aa 73)	3	
	5	-1 (aa 10)	10		7	-1 (aa 73)	3	
	6	-1 (aa 10)	12		7	-1 (aa 73)	3 [1]	
	7	-1 (aa 10)	8		8	-1 (aa 73)	3 [1]	
Fugu (<i>Fugu rubripes</i>)	1	(25)	(7,8)	(17)	(7,8)	(38)	(2,3)	
	2	-1 (aa 10)	8		7.8	-1 (aa 73)	3	
		-1 (aa 10)	7		7.8	-1 (aa 73)	2	

Table 4 (continued)

Goldfish <i>(Carassius auratus)</i>		(25)	(8)	(17)	(6,7)	(38)	(2,3)
	1	-1 (aa 10)			7	-1 (aa 73)	2
	2	-1 (aa 10)			6	-1 (aa 73)	3
Ladyfish <i>(Elops saurus)</i>		(25)	(8,1)	(17)	(7,8)	(38)	(2) [1]
	1	-1 (aa 10)	8		8	-1 (aa 73)	2 [1]
	2	-1 (aa 10)	10		7	-1 (aa 73)	2 [1]
Rainbow trout <i>(Oncorhynchus mykiss)</i>		(24 to 27)	(7,8,10,12)	(17)	(6 to 9)	(36 to 38)	(2)
	1	-1 (aa 10)	7,8		7,8,9	-1 (aa 73)	2
	2	-1 (aa 10)	8		6	-1 (aa 73)	2 [1]
		+2 (aa 6A,6B)					
	3	-1 (aa 10)	10		7	-1 (aa 73)	2 [1]
	4	-2 (aa 1,10)	8		9	-1 (aa 73)	2 [1]
	5	-1 (aa 10)	8		8	-1 (aa 73)	2 [1]
	6	-2 (aa 1,10)	7		6	-1 (aa 73)	2 [1]
	7	-1 (aa 10)	12		7	-1 (aa 73)	2 [1]
	8	-2 (aa 10,11)	8		7	-3 (aa 73,82,83)	2 [1]
		-1 (aa 10)					
9	-1 (aa 10)	8		7	-1 (aa 73)	2 [1]	
10	-1 (aa 10)	8		6	-1 (aa 73)	2 [1]	
11	-1 (aa 10)	8		7	-2 (aa 73,82)	2 [1]	
Spotted wolffish <i>(Anarhichas minor)</i>		(25)	(7)	(17)	(6)	(38)	(2) [1]
	1	-1 (aa 10)	7		6	-1 (aa 73)	2 [1]

IMG1 note: [1] Probable CDR3-IMG1 length but needs to be confirmed with germline sequences.

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