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REVIEW

Vertebrate hepatic lipase genes and proteins: a review supported by bioinformatic studies

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Abstract: Hepatic lipase (gene: *LIPC*; enzyme: HL; E.C.3.1.1.3) is one of three members of the triglyceride lipase family that contributes to vascular lipoprotein degradation and serves a dual role in triglyceride hydrolysis and in facilitating receptor-mediated lipoprotein uptake into the liver. Amino acid sequences, protein structures, and gene locations for vertebrate *LIPC* (or *Lipc* for mouse and rat) genes and proteins were sourced from previous reports and vertebrate genome databases. *Lipc* was distinct from other neutral lipase genes (*Lipg* encoding endothelial lipase and *Lpl* encoding lipoprotein lipase [LPL]) and was located on mouse chromosome 9 with nine coding exons on the negative strand. Exon 9 of human *LIPC* and mouse and rat *Lipc* genes contained "stop codons" in different positions, causing changes in C-termini length. Vertebrate HL protein subunits shared 58%–97% sequence identities, including active, signal peptide, disulfide bond, and N-glycosylation sites, as well as proprotein convertase ("hinge") and heparin binding regions. Predicted secondary and tertiary structures revealed similarities with the three-dimensional structure reported for horse and human pancreatic lipases. Potential sites for regulating *LIPC* gene expression included CpG islands near the 5"-untranslated regions of the mouse and rat *LIPC* genes. Phylogenetic analyses examined the relationships and potential evolutionary origins of the vertebrate *LIPC* gene family with other neutral triglyceride lipase gene families (*LIPG* and *LPL*). We conclude that the triglyceride lipase ancestral gene for vertebrate neutral lipase genes (*LIPC*, *LIPG*, and *LPL*) predated the appearance of fish during vertebrate evolution.

Keywords: vertebrates, amino acid sequence, hepatic lipase, evolution, gene duplication

Introduction

Hepatic lipase (HL; gene *LIPC*; E.C.3.1.1.3) is one of three members of the triglyceride lipase family that contributes to lipoprotein degradation within the circulation system.[1–3] HL also regulates the metabolism of low-density lipoprotein, intermediate-density lipoprotein, and high-density lipoprotein particles and is capable of catalyzing the hydrolysis of phospholipids, triglycerides, and acyl-CoA thioesters.[4,5] Endothelial lipase (EL; gene *LIPG*; E.C.3.1.1.3) is a related family member that plays a major role in high-density lipoprotein cholesterol metabolism in the body, catalyzing phospholipase and triglyceride lipase activities[6–8] and lipoprotein lipase (LPL; gene *LPL*; E.C.3.1.1.34) functions in the hydrolysis of triglycerides of circulating chylomicrons and very low-density lipoproteins.[9–11] These enzymes share sequence similarities (38%–44% identities) and are usually referred to as the vascular lipase gene family[7,12,13] because of their contributions to plasma lipoprotein, cholesterol, and triglyceride phenotypes and to the development of coronary heart diseases in human and animal populations.[14–21]

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The human *LIPC* gene is located on chromosome 15 and comprises 158.3 kb nucleotides on the direct strand with nine exons and eight introns and encodes a 449 amino acid protein subunit.[3,22] Genetic variants have been described that cause HL deficiency and associated hyperlipidemia.[23] Several promoter polymorphisms in linkage disequilibrium have also been identified, and the more frequent –250G > A substitution in the *LIPC* promoter region is associated with changes in plasma lipid concentrations and the risk of coronary artery disease in some ethnic groups.[24] *LIPC* is expressed predominantly in the liver, where the enzyme contributes significantly to the determination of lipoprotein levels, structure, and metabolism.[1–3] Studies of *Lipc*$^{-}$/*Lipc*$^{-}$ knockout mice have supported multiple roles for HL in vascular lipoprotein metabolism, including a lipolytic role and a ligand binding function facilitating lipoprotein uptake, which influence lipoprotein particle size in the circulation.[17] Following synthesis in the liver endoplasmic reticulum, rat HL is processed by the hydrolysis of the N-terminal leader peptide and acquisition of oligosaccharides within the Golgi and is then rapidly secreted and subsequently bound to heparin sulfate proteoglycans on the surface of hepatocytes.[25] HL forms a dimeric subunit structure[26] exhibiting similarities with EL, which behaves as a homodimer with a proposed head-to-tail conformation,[27] and is subject to proprotein convertase cleavage at a site in the "hinge" region separating the N- and C-terminal enzyme domains.[28] Three-dimensional studies of a related mammalian lipase (LIPP, pancreatic lipase)[29,30] have enabled identification of three major structural domains for the mammalian neutral lipase family, including an N-terminal domain with a catalytic triad of serine, aspartate, and histidine residues; a "lid" domain that covers the active site and contributes to the specificity for triglyceride and phosphoglyceride substrates; and a C-terminal or "plat" domain, which contributes to lipid binding and specificity.[31,32]

This paper examines and reviews the gene structures and amino acid sequences for several vertebrate *LIPC* genes and proteins; the predicted secondary and tertiary structures for vertebrate HL enzymes; and the structural, phylogenetic, and evolutionary relationships for these genes and enzymes with those for human and mouse lipase neutral lipase gene families, *LIPG* (encoding endothelial lipase), and *LPL* (encoding lipoprotein lipase).

Methods

Vertebrate *LIPC* gene and HL identification

Protein BLAST (Basic Local Alignment Search Tool) analyses generated several vertebrate HL amino acid sequences from the National Center for Biotechnology Information (NCBI) database (http://blast.ncbi.nlm.nih.gov/Blast.cgi)[33] (Table 1). Nonredundant protein sequence databases for vertebrate genomes were examined using the blastp algorithm, including human (*Homo sapiens*),[34] chimpanzee (*Pan troglodytes*),[35] orangutan (*Pongo abelii*) (http://genome.wustl.edu), rhesus monkey (*Macaca mulatta*),[36] cow (*Bos taurus*) (http://hgsc.bcm.tmc.edu/projects/bovine), mouse (*Mus musculus*),[37] rat (*Rattus norvegicus*),[38] rabbit (*Oryctolagus cuniculus*) (http://www.broadinstitute.org/science/projects/mammals-models/rabbit/rabbit-genome-sequencing-project), opossum (*Monodelphis domestica*),[39] chicken (*Gallus gallus*),[40] frog (*Xenopus tropicalis*) (http://genome.jgi-psf.org/Xentr3/Xentr3.home.html), and zebrafish (*Danio rerio*) (http://www.sanger.ac.uk/Projects/D_rerio/). Predicted or previously reported vertebrate HL-like protein sequences were then subjected to analyses of protein and gene structures (Table 1).

BLAT (BLAST-like Alignment Tool) analyses were subsequently undertaken for each of the predicted HL amino acid sequences using the University of California, Santa Cruz genome browser (http://genome.ucsc.edu/cgi-bin/hgBlat)[41] with the default settings to obtain the predicted locations for each of the mammalian *LIPC* genes, including predicted exon boundary locations and gene sizes. BLAT analyses were also undertaken for human *LPL* (encoding lipoprotein lipase)[9] and *LIPG* (encoding endothelial lipase)[6–8] (see Table 1). Structures for human, mouse, and rat isoforms (splicing variants) were obtained using the AceView website to examine predicted gene and protein structures[42] (http://www.ncbi.nlm.nih.gov/IEB/Research/Acembly/index.html?human).

Predicted structures and properties of vertebrate hepatic lipases

Secondary and tertiary structures for human and other vertebrate HL-like proteins were predicted using Web tools from PSIPRED v2.5 (http://bioinf.cs.ucl.ac.uk/psipred/) and SWISS MODEL (http://swissmodel.expasy.org), respectively.[43,44] The structure for the human pancreatic lipase–colipase complex[45] served as a reference for the predicted horse LIPP (pancreatic lipase) structure (previously reported by Bourne et al[30]) and the human, opossum and zebrafish LIPC tertiary structures, with modeling ranges of residues 18–465, 25–471, 4–448 and 25–485, respectively. Theoretical isoelectric points and molecular weights (http://au.expasy.org/tools/pi_tool.html), location of signal peptide cleavage sites (http://www.cbs.dtu.dk/services/SignalP/),[46] and potential N-glycosylation sites (http://www.cbs.dtu.dk/services/NetNGlyc/) for vertebrate LIPC proteins were obtained using Web tools.

Table 1 Vertebrate hepatic lipase (*LIPC*), human and mouse endothelial lipase (*LIPG*) and lipoprotein lipases (*LPL*), horse pancreatic lipase (*LIPP*), and sea squirt lipase genes and proteins

Hepatic lipase Gene *LIPC*	Species	RefSeq ID [1]Ensembl (predicted)	GenBank ID	UNIPROT ID	Amino acids	Chromosome location	Exons (strand)	Gene size bps	pI	Subunit MW	Signal peptide (cleavage site)
Human	*Homo sapiens*	NM_000236.2	BC146659	P11150	499	15:56,511,524-56,648,315	9 (+ve)	136,792	9.22	55,914	1-24 [LG-QS]
Chimpanzee	*Pan troglodytes*	[1]XP_001172241.1	[2]	[2]	499	15:55,899,209-56,038,386	9 (+ve)	139,178	9.27	56,024	1-24 [LG-QS]
Orangutan	*Pongo abelii*	[4]	[2]	[2]	499	15:55,440,202-55,470,553	9 (+ve)	[4]30,352	[4]9.16	[4]56,012	[4]
Rhesus	*Macaca mulatta*	[1]XP_001095252.1	[2]	[2]	499	7:36,761,876-36,903,612	9 (+ve)	141,737	9.36	56,023	1-24 [HG-QS]
Mouse	*Mus musculus*	NM_008280.2	BC021841	P27656	510	9:70,645,935-70,782,615	9 (–ve)	136,681	8.34	57,389	1-22 [AC-GQ]
Rat	*Rattus norvegicus*	NM_012597	BC088160	P07867	494	8:75,323,443-75,450,353	9 (–ve)	126,911	8.49	55,752	1-22 [AC-GQ]
Rabbit	*Oryctolagus cuniculus*	NM_001082032.1	AF041202	[2]	499	17:13,811,866-13,970,782	9 (–ve)	158,863	9.08	55,857	1-23 [HG-QS]
Cow	*Bos taurus*	NM_001035410.1	BC103072	Q3SZ79	500	10:52,220,965-52,415,726	[2,3]	194,762	9.09	56,826	1-23 [HG-QS]
Dog	*Canis familaris*	[1]XP_535495.2	[2]	[2]	502	30:26,546,842-26,574,268	9 (+ve)	[4]27,427	8.53	56,594	1-24 [VG-SP]
Opossum	*Monodelphis domestica*	[1]XP_001377665.1	[2]	[2]	[4]460	[4]1:162,290,356-162,337,323	[4]8 (–ve)	[4]46,968	[4]	[4]	[4]
Chicken	*Gallus gallus*	[1]XP_425067.2	[2]	[2]	[4]474	[4]10:7,955,298-7,967,646	[4]8 (–ve)	[4]12,349	[4]	[4]	[4]
Frog	*Xenopus tropicalis*	NM_001114259.1	BC158363	B0BMB8	496	[5]sc301:941,950-1,004,887	9 (–ve)	62,938	8.47	56,687	1-21 [LT-QK]
Zebrafish	*Danio rerio*	NM_201022.1	BC053243	Q7T359	514	7:33,180,131-33,193,766	9 (–ve)	13,636	8.50	57,933	1-20 [DG-AT]
Other lipase gene											
Horse *LIPP*	*Equus caballus*	NM_001163949	X66218	P29183	465	1:15,534,773-15,551,621	12 (–ve)	16,849	5.46	54,435	1-16 [VG-NE]
Human *LIPG*	*Homo sapiens*	NM_006033.2	BC060825	Q9Y5X9	500	18:45,342,677-45,367,216	10 (+ve)	24,540	8.1	56,795	1-20 [AG-SP]
Mouse *LIPG*	*Mus musculus*	NM_010720.3	BC020991	Q9WVG5	500	18:75,102,996-75,120,628	10 (–ve)	17,633	8.79	56,629	1-20 [AG-SI]
Human *LIPL*	*Homo sapiens*	NM_000237.2	BC011353	P06858	475	8:19,841,232-19,864,008	9 (+ve)	22,777	8.4	53,163	1-27 [AA-AD]
Mouse *LIPL*	*Mus musculus*	NM_008509.2	BC003305	P11152	474	8:71,404,652-71,426,282	9 (+ve)	21,631	8.0	53,109	1-27 [AA-AD]
Sea squirt *LIP*	*Ciona intestinalis*	[1]ENSCINT00000009034	[2]	[2]	460	07q:1,148,429-1,153,888	11 (–ve)	5460	4.57	51,184	1-18 [NC-DT]

Notes: [1]Predicted Ensembl amino acid sequence; [2]not available; [3]exon 1 missing; [4]incomplete sequence available; [5]scaffold of DNA used in sequencing frog genome. GenBank IDs are derived from NCBI sources http://www.ncbi.nlm.nih.gov/genbank/; Ensembl ID was derived from Ensembl genome database http://www.ensembl.org; UNIPROT refers to UniprotKB/Swiss-Prot IDs for individual acid lipases (http://kr.expasy.org); bps refers to base pairs of nucleotide sequences; pI refers to theoretical isoelectric points; the number of coding exons is listed.

Abbreviation: RefSeq, the reference amino acid sequence.

Phylogenetic studies and sequence divergence

Alignments of vertebrate HL with human and mouse EL and LPL sequences were assembled using BioEdit v.5.0.1 and the default settings.[47] Alignment ambiguous regions, including the amino and carboxyl termini, were excluded prior to phylogenetic analysis, yielding alignments of 395 residues for comparisons of vertebrate HL, human and mouse EL, and LPL sequences with the sea squirt (*Ciona intestinalis*) lipase sequence (Table 1). Evolutionary distances were calculated using the Kimura option[48] in TREECON.[49] Phylogenetic trees were constructed from evolutionary distances using the neighbor-joining method[50] and rooted with the sea squirt lipase sequence. Tree topology was re-examined by the bootstrap method (100 bootstraps were applied) of resampling and only values that were highly significant (≥90) are shown.[51]

Results and discussion

Alignments of vertebrate HL amino acid sequences

The deduced amino acid sequences for dog, frog, and zebrafish HL are shown in Figure 1 together with previously reported sequences for human HL,[3,22] mouse HL,[52] rat HL,[53,54] and horse pancreatic lipase (LIPP)[30] (Table 1). Alignments of human and other vertebrate HL sequences examined showed between 49% and 98% identities, suggesting that they are products of the same family of genes, whereas comparisons of sequence identities of vertebrate HL proteins with human and mouse EL and LPL and horse LIPP exhibited lower levels of sequence identities, EL (38% and 42%, respectively), LPL (44% and 45%, respectively), and LIPP (25%), indicating that they are members of distinct but related neutral lipase families (Table 2).

The amino acid sequences for human, chimp, orangutan, rhesus monkey, and rabbit HL contained 499 residues whereas mouse, rat, cow, dog, and frog HL contained 510, 494, 500, 502, and 496 amino acids, respectively (Table 1; Figure 1). Previous three-dimensional studies of horse pancreatic lipase (LIPP)[30] and modeling studies of human EL[29] have enabled predictions of key residues for vertebrate HL amino acid sequences (numbers refer to human HL). These included the catalytic triad for the active site (Ser168, Asp194, and His279); the hydrophobic N-terminus signal peptides (see also Table 1), which facilitate enzyme secretion into the

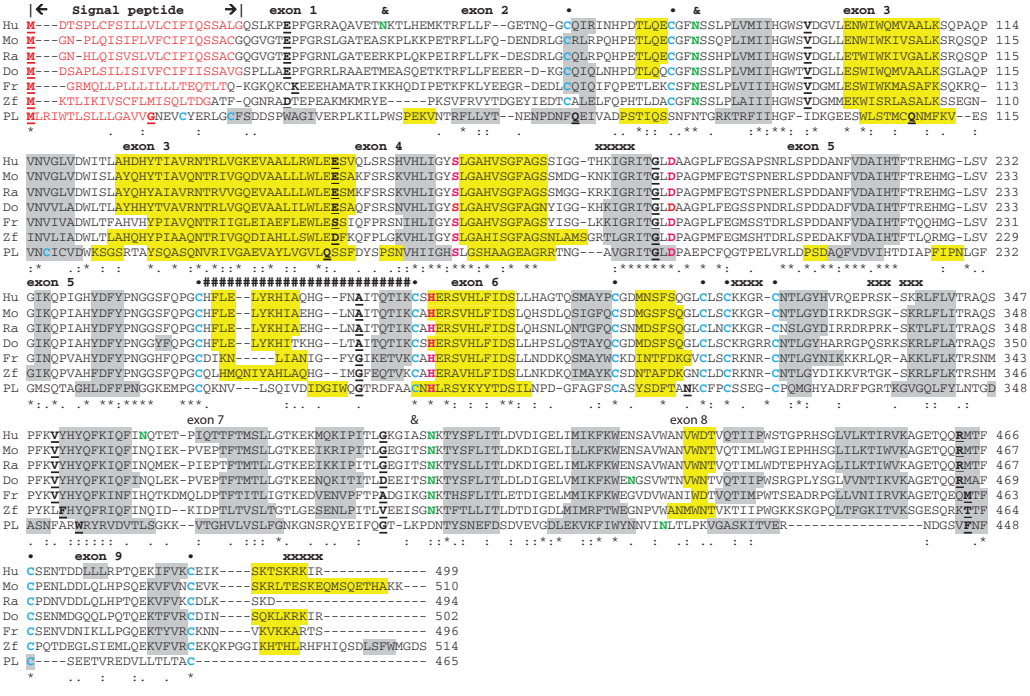

Figure 1 Amino acid sequence alignments for vertebrate hepatic lipase (HL) and horse pancreatic lipase (LIPP) sequences. See Table 1 for sources of HL and horse LIPP sequences.

Notes: *shows identical residues for lipase subunits; similar alternative residues; dissimilar alternative residues; residues involved in N-signal peptide formation are shown in red; N-glycosylated (marked as and for human HL) and potential N-glycosylated Asn sites are in green bold; active site triad residues Ser (S), Asp (D), and His (H) are in pink bold; predicted disulfide bond Cys residues are shown in blue bold (•); α-helix for horse LIPP or predicted for vertebrate HL is in shaded yellow; β-sheet for horse LIPP or predicted for vertebrate HL is in shaded grey; bold underlined font shows residues corresponding to known or predicted exon start sites; exon numbers refer to human *LIPC* gene exons; **####** refers to residues that correspond to the horse LIPP "lid" region; **xxxxx** refers to the four predicted "heparin binding" regions for human HL.

Abbreviations: Do, dog HL; Fr, frog HL; Hu, human HL; Mo, mouse HL; PL, horse pancreatic lipase; Ra, rat HL; Zf, zebrafish HL.

Table 2 Percentage identities for vertebrate hepatic lipases, human and mouse endothelial and lipoprotein lipases, horse pancreatic lipase, and sea squirt lipase amino acid sequences[a]

Lipase gene	Human HL	Chimp HL	Rhesus HL	Mouse HL	Rat HL	Rabbit HL	Cow HL	Opossum HL	Chicken HL	Frog HL	Zebrafish HL	Human EL	Mouse EL	Human LPL	Mouse LPL	Horse LIPP	Sea squirt LIP
Human HL	100	98	94	74	74	79	77	66	64	57	49	38	37	41	42	25	21
Chimp HL	98	100	95	75	75	80	78	66	65	57	50	39	37	41	42	25	21
Rhesus HL	94	95	100	74	75	80	77	66	64	56	49	40	38	42	43	24	21
Mouse HL	74	75	74	100	89	75	70	64	61	56	50	42	40	44	43	29	25
Rat HL	74	75	75	89	100	74	68	64	60	54	51	41	39	43	42	28	25
Rabbit HL	79	80	80	75	74	100	76	68	64	56	50	39	38	41	40	25	21
Cow HL	77	78	77	70	68	76	100	63	62	54	49	40	37	40	40	23	23
Opossum HL	66	66	66	64	64	68	63	100	68	63	56	43	42	43	42	27	23
Chicken HL	64	65	64	61	60	64	62	68	100	70	57	44	43	44	44	24	23
Frog HL	57	57	56	56	54	56	54	63	70	100	55	41	41	45	42	24	24
Zebrafish HL	49	50	49	50	51	50	49	56	57	55	100	40	42	42	41	23	23
Human EL	38	39	40	42	41	39	40	43	44	41	40	100	80	44	45	25	25
Mouse EL	37	37	38	40	39	38	37	42	43	41	42	80	100	45	46	25	25
Human LPL	41	41	42	44	43	41	40	43	44	45	42	44	45	100	93	24	25
Mouse LPL	42	42	43	43	42	40	40	42	44	42	41	45	46	93	100	26	25
Horse LIPP	25	25	24	29	28	25	23	27	24	24	23	25	25	24	26	100	35
Sea squirt LIP	21	21	21	25	25	21	23	23	23	24	23	25	25	25	25	35	100

Note: [a]Numbers show the percentage of amino acid sequence identities.

Abbreviations: EL, endothelial lipase; HL, hepatic lipase; LIP, sea squirt lipase; LIPP, pancreatic lipase; LPL, lipoprotein lipase.

circulation system;[25] five disulfide bond-forming residues (Cys62/Cys75, Cys254/Cys277, Cys302/Cys313, Cys316/Cys321, and Cys467/Cys487); the predicted "lid" region (255–276), which covers the active site and participates in lipid substrate binding in analogous lipases;[31,32] and a predicted "hinge" region for vertebrate HL (332Arg-333Ser-334Lys-335Ser) (based on sequence similarity with human EL [327Arg-328Asn-329Lys-330Arg], which contains a proprotein convertase proteolytic cleavage site).[29–32] With the exception of the N-terminus signal peptides, the vertebrate HL sequences were strictly conserved or underwent conservative substitutions, which may reflect the essential nature of these residues in contributing to HL structure and function. The N-terminal region (residues 1–63) underwent major changes in the number and sequence of amino acid residues but retained a predicted signal peptide property in each case (Figure 1; Table 1). The horse LIPP sequence shared the catalytic triad residues, four of the five disulfide bonds predicted for the vertebrate HL sequences, and an N-signal peptide sequence property; however, other sequences were distinct with only 25% identical residues observed for horse LIPP and human HL.

Figure 2 compares vertebrate HL sequences for four putative heparin binding sites described for human HL, which contain clusters of basic amino acid residues with different consensus sequences.[56–59] These sites are apparently responsible for HL binding to heparin sulfate proteoglycans on the surface of parenchymal cell microvilli where the enzyme functions in liver lipoprotein catabolism.[58,59] Several vertebrate HL sequences have also been compared with human LPL and EL putative heparin binding sites, as well as those for human apolipoproteins APOB and APOE, the major proteins of chylomicrons, low-density lipoprotein, and very low-density lipoprotein, which function as recognition signals for the cellular binding and internalization of low-density lipoprotein particles.[60] Several differences from heparin binding consensus sequences were observed. For consensus sequence 1 (XBBBXXBX where B refers to a basic amino acid and X to any other amino acid), human, rhesus, and mouse HL and human LPL sequences lacked the first basic amino acid, and human EL contained only two of four basic amino acids. Consensus sequence 2 (XBBXBX) showed consistency for all vertebrate HL, human LPL and EL, and APOB sequences examined with the exception of rabbit HL, which lacked one of the B residues, and dog HL, which contained an extra B residue. Several differences were observed for consensus sequence 3 (XBXBBX), including rat and dog HL and human EL and LPL. The C-terminal

Gene	Protein	Vertebrate	Consensus Heparin Binding Sequences 1	2	3	4 (C-terminal)
			XBBBXXBX	XBBXB-X	X-BXBBX	BXBXXBBBXB
LIPC	HL	Human	183GTHKIGRI	316CKKGR-C	334S-KSKRL	489KSKTSKRKIR
		Rhesus	183GTRKIGRI	316CKKGR-C	334S-KNKKL	489KSKTSKRQIR
		Mouse	184GTNKIGRI	317CKKGR-C	335G-KSKRL	490KSKRLTESKEQMSQETHAKK
		Rat	184GKRKIGRI	317CKKGR-C	335R-KSKTL	490KSKD
		Rabbit	183GKHKIGRI	316CTKGR-C	334S-KGKRL	489NPKKLKLKIK
		Dog	184GKHKIGRI	317CKRGRRC	338SRKSKRL	492NSQKLKRKIR
		Opossum	144GTNKIGRI	277CKKGR-C	295Q-KSKKL	450GSKPQNQRLR
		Chicken	160GTNKIGRI	292CRKNR-C	310P-KSRKL	466RLRQHERK
		Frog	182GLKKIGRI	312CRKNR-C	330Q-RAKKL	486NVKVKKARTS
LPL	LPL	Human	174TNKKVNRI	305CRKNR-C	323K-RSSKM	467KSLNKKSG
LIPG	EL	Human	184VKGTVGRI	311CRKNR-C	329K-RNSKM	485GWRMKNETSPTVELP
APOB	ApoB	Human	3388TRKRGLKL	113LKKTK-N	2145T-KKYRI	
APOE	ApoE	Human	158LRKRLLRD			

Figure 2 Comparative amino acid sequences for predicted heparin binding sequences for vertebrate hepatic lipase (HL) and human lipoprotein lipase (LPL), endothelial lipase (EL), apolipoprotein B (APOB), and apolipoprotein E (APOE) sequences. Four predicted heparin binding sites are shown based on previous studies[56–60] and the predicted vertebrate HL sequences reported in this paper.
Abbreviations: B, basic amino acid; K, lysine; R, arginine; X, any other amino acid residue.

heparin binding site (consensus sequence 4) showed major differences among the HL sequences examined, especially for mouse and rat HL, which lacked this motif. This may explain why mouse HL is predominantly found in the circulation system as compared with human HL, which is released into the circulation following heparin administration.[61]

Four N-glycosylation sites have previously been reported for human HL at 42Asn-43Lys-44Thr, 78Asn-70Ser-71Ser, 362Asn-363Gln-364Thr, and 397Asn-398Lys-399Thr.[62,63] A comparative analysis of potential N-glycosylation sites for vertebrate HL has shown that there are seven sites overall, although only two of these have been predominantly retained for the 13 vertebrate HL sequences examined (designated as sites 3 and 7) (Table 3). Site-directed mutagenesis studies of site 3 (human HL 78Asn) have demonstrated that this N-glycosylation site is required for the efficient secretion of this liver enzyme.[64,65]

Predicted secondary and tertiary structures for vertebrate hepatic lipases

Predicted secondary structures for vertebrate HL sequences were compared with the previously reported secondary structure for horse LIPP (pancreatic lipase)[30] (Figure 1). α-Helix and β-sheet structures for the vertebrate HL protein sequences were examined and found to be similar for several regions with the horse LIPP secondary structures. Consistent structures were predicted near key residues or functional domains, including the β-sheet and α-helix structures near

Table 3 Predicted N-glycosylation sites for vertebrate hepatic lipases. Numbers refer to amino acids in the acid sequences, including N-asparagine, K-lysine, I-isoleucine, M-methionine, H-histidine, S-serine, R-arginine, T-threonine, Q-glutamine, and V-valine. Note that seven potential sites were identified, including four confirmed sites for human LIPC (HL) (sites 1, 3, 5, and 7). High- (yellow highlighted) and lower probability N-glycosylation sites were identified using the NetNGlyc 1.0 Web server (http://www.cbs.dtu.dk/services/NetNGlyc/)

Vertebrate	Species	Site 1	Site 2	Site 3	Site 4	Site 5	Site 6	Site 7	No. of sites
Human	*Homo sapiens*	42NKT		78NSS		362NQT		397NKT	4
Chimpanzee	*Pan troglodytes*	42NKT		78NSS		362NQT		397NKT	4
Orangutan	*Pongo abelii*	42NKT		78NSS		362NQT			3
Rhesus	*Macaca mulatta*	42NKT		78NSS		362NQT		397NKT	4
Mouse	*Mus musculus*			79NSS				398NKT	2
Rat	*Rattus norvegicus*			79NSS				398NKT	2
Rabbit	*Oryctolagus cuniculus*			78NSS				397NKT	2
Cow	*Bos taurus*		67NHS	78NSS		363NQT		398NET	4
Dog	*Canis familaris*			79NSS				400NKT	2
Opossum	*Monodelphis domestica*	39NSS			143NGT	358NKT	378NFT		4
Chicken	*Gallus gallus*		55NAS				374NKT		2
Frog	*Xenopus tropicalis*			78NES				394NKT	2
Zebrafish	*Danio rerio*			75NSS				395NKT	2

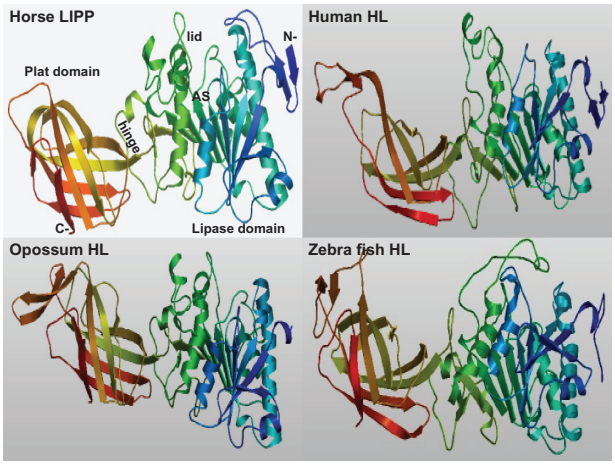

Figure 3 Predicted Tertiary Structures for Horse LIPP and for Human, Opossum and Zebrafish LIPC Predicted horse LIPP and human, opossum and zebrafish LIPC tertiary structures were obtained using SWISS MODEL methods; the rainbow color code describes the tertiary structures from the N- (blue) to C-termini (red color); the horse LIPP tertiary structure shows the N- and C-termini, the 'lipase', 'lid' (in yellow) and 'plat' domains which are separated by a 'hinge' region; and the active site region (AS) for horse LIPP is identified (based on the horse LIPP structure reported by Bourne et al.[30]).

the active site residues (human HL numbers used) Ser168, Asp 194, and His279; the "lid" domain (residues 255–276); and the "hinge" region, which commences with an α-helix and concludes with a β-sheet (residues 333–339). Figure 3 describes predicted tertiary structures for human, opossum, and zebrafish HL protein sequences and shows significant similarities for these polypeptides with horse pancreatic lipase (LIPP).[30] The three LIPP and HL domains were readily apparent, including the N-terminal "lipase" domain with the active site triad residues buried under the "lid" domain observed for horse LIPP. The "lid" has previously been shown to contribute to the preference for triglyceride and phopholipid substrates of vascular lipases HL and LPL.[31,65] A "hinge" region was also observed for these vertebrate HL proteins, separating the "lipase" and "plat" domains, with the latter having a "sandwich-like" β-pleated sheet structure. The "plat" domain for HL and LPL has been shown to be essential for binding these enzymes to lipoprotein micelles and also contributes to preferences in lipoprotein binding.[29] These comparative studies for other vertebrate HL proteins suggest that these properties and key sequences are substantially retained for all of the vertebrate sequences examined.

Predicted gene locations and exonic structures for vertebrate *LIPC* genes

Table 1 summarizes the predicted locations for vertebrate *LIPC* genes based on BLAT interrogations of several vertebrate genomes using the reported sequences for human,[6,7] mouse,[66] and rat HL[38] and the University of California, Santa Cruz genome browser.[41] The predicted primate *LIPC* genes were transcribed on the positive strand, whereas other vertebrate *LIPC* genes were transcribed on the negative strand. Figure 1 summarizes the predicted exonic start sites for vertebrate *LIPC* genes with each having nine coding exons, in identical or similar positions to those predicted for the human *LIPC* gene.[67]

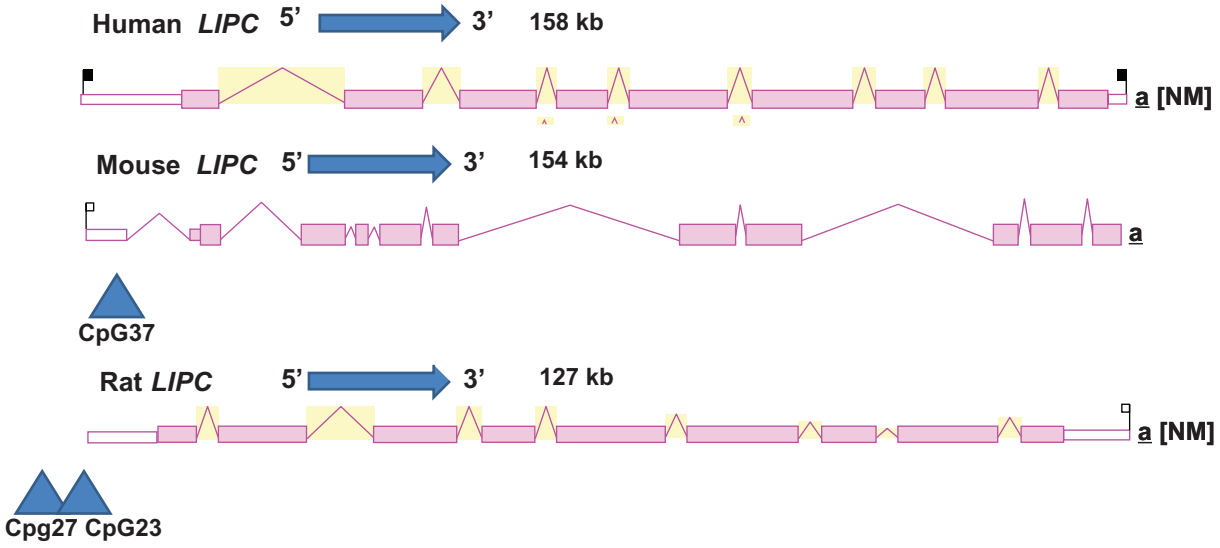

Figure 4 Gene structures and major splicing variant for the human, mouse, and rat *LIPC* transcripts. Derived from the AceView website[42] http://www.ncbi.nlm.nih.gov/IEB/Research/Acembly/. Mature isoform variants (a) are shown with capped 5"- and 3"- ends for the predicted mRNA sequences; NM refers to the NCBI reference sequence; exons are in pink; the directions for transcription are shown as 5" → 3"; blue triangles show predicted CpG island sites at or near the 5"untranslated regions of the gene; sizes of mRNA sequences are shown in kilobases (kb).

```
Human LIPC Exon 9 C-Terminus
TGTGAAATAAAGTCTAAAACATCAAA----GCGAAAGATCAGATGAGATTTAATGAAGACCCAGTGTAAAGAA
CysGluIleLysSerLysThrSerLy    sArgLysIleArg Ter

Mouse LIPC Exon 9 C-terminus
TGTGAAGTGAAGTCAAAAAGACTGACTGAATCGAAAGAGCAGATGAG---TCAAGAGACCCATGCAAAAAAAA
CysGluValLysSerLysArgLeuThrGluGlnMetSerGlnGluTh   rHisAlaLysLys Ter

Rat LIPC Exon 9 C-terminus
TGTGACCTGAAGTCAAAA-GACTGAA-GAAGCAAAAGAGCAGATGAG---TCAAGAGACCCAAGCACAAAATA
CysAspLeuLysSerLys AspTer
*****  * ***** ***  *   *      * ***** ********   * * **   **  *   ***  * nt identity
 *        *  *  *                                                          aa identity
```

Figure 5 Nucleotide and amino acid sequence alignments for human, mouse, and rat *LIPC* genes and hepatic lipase proteins: predicted c-termini and exon 9 sequences. Identical nucleotide (nt) and amino acid (aa) sequences are shown (*). Ter (in red) refers to predicted terminating codons.

Figure 4 illustrates the predicted structures of mRNA for human, mouse, and rat *LIPC* transcripts for the major transcript isoform in each case.[42] The transcripts were 127–158 kbs in length with nine introns present for these *LIPC* mRNA transcripts. Figure 5 examines the predicted amino acid and nucleotide sequence for the C-terminus end of exon 9 human, mouse, and rat *LIPC* sequences. It is proposed that exon 9 has undergone nucleotide substitutions or deletions/insertions that have introduced a termination codon for the rat *LIPC* gene encoding an incomplete C-terminus for rat HL and an extended C-terminus for mouse HL. The significance of these differences in rodent *LIPC* structure has been previously discussed in terms of the observed changes in HL binding to heparin sulfate proteoglycans on liver parenchymal cells where the enzyme functions in liver lipoprotein catabolism.[57–59]

Phylogeny and divergence of hepatic lipase and other vertebrate lipase sequences

A phylogenetic tree (Figure 6) was calculated by the progressive alignment of 12 vertebrate LIPC amino acid sequences with human and mouse LIPL and LIPG sequences that was "rooted" with the *Ciona intestinalis* (sea squirt) lipase

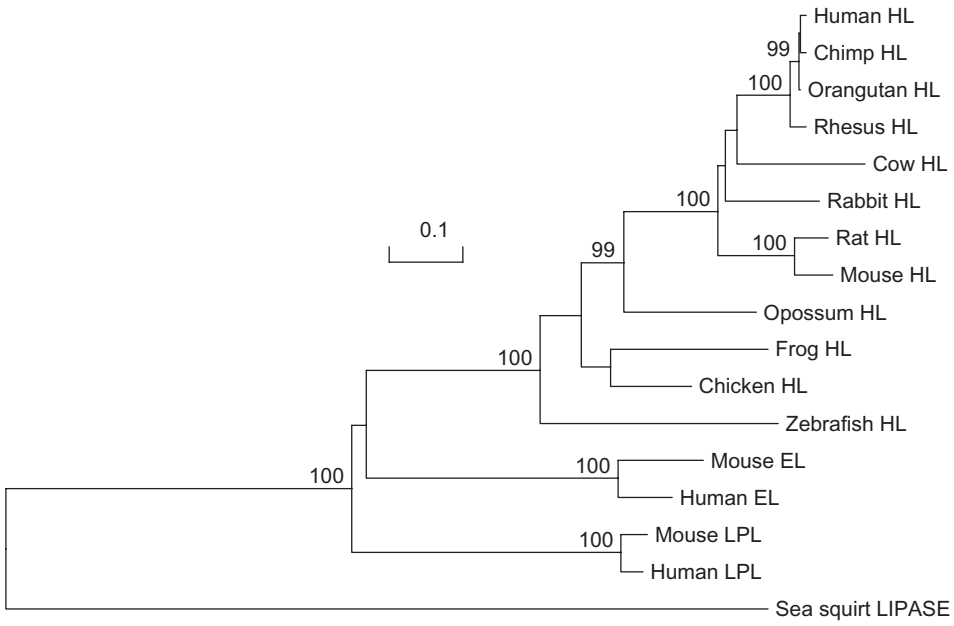

Figure 6 Phylogenetic tree of vertebrate hepatic lipase (HL), human and mouse lipoprotein lipase (LPL) and endothelial lipase (EL), and sea squirt lipase amino acid sequences. The tree is labeled with the lipase name and the name of the animal and is "rooted" with the *Ciona intestinalis* (sea squirt) lipase sequence. Note the major cluster of vertebrate HL sequences, which is distinct from the human and mouse LPL and EL and the sea squirt lipase sequences. A genetic distance scale is shown. The number of times a clade (sequences common to a node or branch) occurred in the bootstrap replicates are shown. Only replicate values of 90 or more that are highly significant are shown, with 100 bootstrap replicates performed in each case. Note the significant separation of clades for the three human vascular lipases (LPL, EL, and HL).

sequence (see Table 1). The phylogram showed clustering of the LIPC sequences into groups that were consistent with their evolutionary relatedness as well as distinct groups for human and mouse LIPL and LIPG sequences, which were distinct from the sea squirt lipase sequence. These groups were significantly different from each other (with bootstrap values of ~100/100). It is apparent from this study of vertebrate LIPC genes and proteins that this is an ancient protein for which a proposed common ancestor for the *LIPC*, *LIPG*, and *LIPL* neutral lipase genes may have predated the appearance of bony fish, which occurred >500 million years ago.[68] This proposal is consistent with a previous report from Cohen,[69] which described predicted amino acid sequences for human and pufferfish (*Takifugu rubripes*) LIPG, LIPL, and LIPC.

Conclusion

These results indicate that vertebrate *LIPC* genes and encoded HL enzymes represent a distinct gene and enzyme family of neutral lipases that share key conserved sequences that have been reported for other neutral lipases previously studied.[6–11] This enzyme has a distinct property among the neutral lipases studied in being the major liver lipase and playing a major role in the catabolism of lipoproteins in the circulation system.[1–3] HL is encoded by a single gene for the vertebrate genomes studied and usually contains nine coding exons. The rat *LIPC* gene encoded a shorter form of this enzyme (494 residues compared with 499 amino acids for most mammalian HL sequences) due to the presence of a termination codon located in exon 9. Predicted secondary structures and tertiary structures for vertebrate HL proteins showed a strong similarity with human and horse pancreatic lipases (LIPP).[29,30] Three major structural domains were apparent for vertebrate HL, including the "lipase" domain containing the catalytic triad residues; the "lid", which covers the active site and may contribute to the substrate specificities of neutral lipases;[31,64] and the "plat" domain, which contributes to lipoprotein binding.[65] Phylogenetic studies using amino acid sequences for 13 vertebrate HL lipases, human and mouse LPL and EL, and an invertebrate lipase indicated that the *LIPC* gene has appeared early in vertebrate evolution, probably prior to the appearance of bony fish more that 500 million years ago.

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Disclosure

The authors report no conflicts of interest in this work.

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