

LIPOPROTEIN LIPASE: PHYSIOLOGY, BIOCHEMISTRY, AND MOLECULAR BIOLOGY

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1. ABSTRACT

Lipoprotein lipase (LpL) is the primary enzyme responsible for conversion of lipoprotein triglyceride into free fatty acids and monoglycerides. This permits their uptake into muscle and adipose. The roles of this enzyme in normal and altered physiology are reviewed. In addition, the relationship of LpL activity and genetic variations of LpL and human disease are summarized.

2. PHYSIOLOGICAL AND PATHOPHYSIOLOGICAL FUNCTIONS

Over fifty years ago, a short paper appeared in the journal *Science* describing experiments studying fat absorption in dogs. The investigator, Hahn, noted that injection of heparin led to the rapid clearance of chylomicrons from plasma (1). Heparin releases two triglyceride hydrolyzing enzymes, lipoprotein lipase (LpL) and hepatic triglyceride lipase (HL), into the bloodstream. LpL is the major enzyme responsible for lipolysis of circulating lipoproteins, thereby producing free fatty acids. This is believed to be the major route for fatty acid accumulation by tissues as intact triglyceride is unable to dissolve in plasma and is thought to be incapable of transport across the cell membrane. In contrast, fatty acids enter cells via direct diffusion or fatty acid transporters such as CD36 (2).

Delivery of calories in the form of triglyceride and other lipophilic substances such as cholesterol and fat-soluble vitamins is accomplished through the interactions of lipoprotein particles with cell surface receptors and with enzymes. On the luminal endothelial surface, lipoprotein triglyceride is hydrolyzed to free fatty acids that are taken-up by tissues and either used as energy or reassembled into triglyceride and stored (Figure 1). In tissues that do not have an intact endothelial cell barrier, or in situations in which the endothelial barrier permeability is altered it is likely that substantial amounts of these large lipoproteins leave the circulation and interact with parenchymal cells. While that is the conventional belief, studies of chylomicron uptake by tissues indicate that muscle and bone marrow may take up a significant amount of chylomicron core lipid (3). Several factors may alter the endothelial barrier function; one of these may be LpL generated free fatty acids. Endothelial barrier function *in vitro* (4, 5) and in perfused blood vessels (6) is disrupted by lipolysis products. Much of the LpL in tissues may be associated with the surface of LpL-expressing cells such as adipocytes and myocytes. Therefore if a substantial number of triglyceride-rich lipoproteins cross the endothelial barrier these LpLs could have significant physiological and pathophysiological effects.

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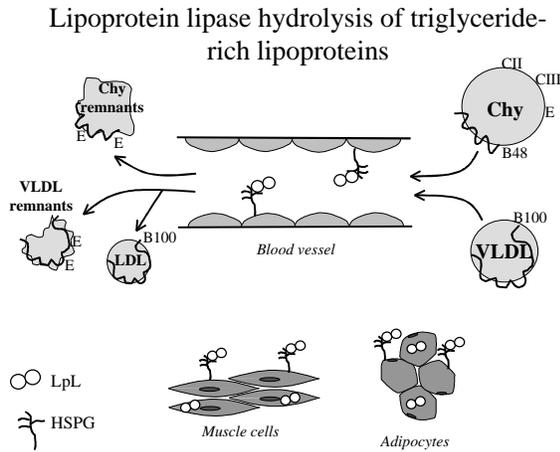


Figure 1. Lipoprotein lipase (LpL) shown as a dimer is thought to primarily hydrolyze circulating lipoproteins while it is associated with heparan sulfate proteoglycans (HSPG) on the luminal side of endothelial cells. This leads to conversion of VLDL to IDL and LDL and production of chylomicron remnants. In the process of this surface lipid and apoproteins dissociate from these particles and transfer to HDL. ApoCII on the triglyceride-rich lipoprotein is required to fully activate LpL. ApoCIII, apoCI, and perhaps apoE may inhibit this process. The origin of vascular LpL is the underlying parenchymal cells, primarily myocytes and adipocytes. Thus the enzyme must transfer from its site of synthesis on these cells to the endothelial cells and then must translocate from the abluminal to the luminal side of this cell.

In several tissues unlipolyzed particles must directly interact with parenchymal cells. These are tissues that have portal blood supplies, such as liver, adrenal, and bone marrow. In the bone marrow of some animals there appears to be a mechanism for direct cellular uptake of non-lipolyzed large triglyceride-rich lipoproteins (7). This appears to be a non-LpL requiring process. In contrast lipoprotein uptake into the liver is clearly increased by LpL expression in that tissue (8).

3. CALORIC AND VITAMIN DISTRIBUTION BY LpL

Exclusive of its actions to alter the circulating levels of lipoproteins, LpL affects the distribution of calories between tissues. As a marker for adipocyte differentiation and fat stores, LpL is correlated with obesity (9). After weight loss, LpL activity increases (10). A number of adipose genes that are stimulated by greater insulin sensitive are increased after weight loss (11, 12). Although it has been postulated that genetic regulation of adipose LpL might, in fact, modulate the propensity to weight gain, LpL is likely to be but one of many factors important in this respect. Humans and genetically manipulated mice that have no adipose LpL do not have a defect in fat development (13). Although less plasma lipoprotein free fatty acids are internalized in LpL deficient fat, more *de novo* fatty acids are produced from

carbohydrates. Mice that only excess LpL in muscles do have a decrease in weight gain when crossed onto the ob/ob background. Therefore, there appear to be conditions in animals, perhaps reproduced in humans, in which LpL may be limiting for fat accumulation.

Partitioning of more fatty acids into muscle occurs with exercise. This could increase fatty acid oxidation in muscle and modulate the development of obesity (14). Moreover, LpL-induced triglyceride accumulation that occurs in muscle LpL overexpressing mice leads to increased muscle triglyceride and fatty acids and a myositis that is akin to those associated with mitochondrial disorders (15). In addition, even lesser increases in muscle LpL and fat uptake will produce insulin resistance (16). Similarly, liver overexpression of LpL leads to hepatic resistance to insulin [16]. These types of animal experiments have shown that LpL modulation of the generation of fatty acids can play a central, but not necessarily essential, role in tissue fat and glucose metabolism.

The major fat-soluble vitamins that circulate in the bloodstream are vitamin A and vitamin E. Both vitamins are absorbed on chylomicrons; some of the chylomicron vitamin esters are delivery to peripheral tissues. For retinyl ester, the initial circulating form of vitamin A, that uptake is primarily into muscle and is modulated by the amount of LpL in the tissues (17). Retinyl ester that remains with the remnant particles arrives in the liver and is re-secreted as retinol bound to retinol binding protein (RBP). If RBP is knocked out in a mouse, the newborn pups are blind but develop sight presumably due to delivery of milk-derived vitamin A via the lipolysis route (17). LpL on the surface of cells will increase uptake of tocopherol (18). Moreover, mice that overexpress LpL in muscle have an increase in vitamin E (19). Like vitamin A, vitamin E also circulates in the bloodstream associated with a binding protein. Thus, the LpL mediated pathways for fat-soluble vitamin uptake may be physiologically important only under some conditions. In this regard, it should be noted that humans with a genetic deficiency of LpL are not clinically deficient in fat-soluble vitamins.

4. SYNTHESIS AND PROCESSING OF LIPASES

LpL is synthesized by a number of cells and tissues. The major sites of LpL synthesis are the skeletal and cardiac muscle and adipose; lesser amounts of LpL are made in the kidney, adrenal, brain, and macrophages (see below). LpL undergoes a series of intracellular processing events that control its activity; unglycosylated LpL is inactive. In addition, LpL is most active as a dimer. This dimerization process does not require the presence of heparan sulfate proteoglycans (20). Defects in LpL processing are the cause of severe hyperchylomicronemia and lack of LpL enzymatic activity in the *cld* (combined lipase deficiency) mouse (21).

Postheparin lipase enzymes must transfer from their cells of origin to the luminal surface of capillary endothelial cells that are exposed to the large triglyceride-

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rich lipoproteins contained in the blood. Regulation of LpL appears to involve this transfer process as major changes in LpL activity and actions occur without alterations in LpL gene expression or translation (22). In part, this may involve changes in LpL activity that occur as the protein is released from the adipocyte or myocyte and moves to the luminal side of the endothelial cell.

After its synthesis, LpL must undergo a series of extracellular movements to reach its site of physiological actions, on the luminal surface of endothelial cells. From tissue culture studies it appears that the newly synthesized protein is, at least in adipose, first associated with the surface of the cells. Some of this LpL is re-internalized and then degraded by the adipocytes (23, 24). The remainder is dissociated from the cell surface, perhaps via the actions of an endothelial cell heparanase (25). The newly released LpL, either alone or in tandem with a fragment of digested glycosaminoglycan, transfers to the endothelial cell. Aside from proteoglycans LpL also binds to members of the LDL-receptor superfamily. Therefore LpL transfer from the abluminal to the luminal side of endothelial cells could occur by moving around or non-specifically through the endothelial cells. Alternatively, a receptor like the VLDL receptor could be responsible for LpL movement across cells (26).

LpL association with the luminal endothelial surface and its release from these cells could affect its activity *in vivo*. Both LpL and hepatic lipase associate with highly negative charged molecules, heparan sulfate proteoglycans on the cell surface. In addition to heparan sulfate proteoglycans with specific sequences (27, 28). LpL associates with a number of other proteins including member of the LRP receptor family - including LRP (29-31) the VLDL receptor (32), gp330 (33) - and regions of apolipoprotein B (34). LpL will bind to a number of proteoglycans that are not associated with cell surfaces including perlecan, the major heparan sulfate in the subendothelial cell matrix (5, 35), and dermatan sulfate proteoglycans produced by macrophages and smooth muscle cells (36, 37). Perturbations of endothelium with tumor necrosis factor (38) and perhaps other cytokines, and lipolysis products (39) will release the bound LpL into the bloodstream. Some active LpL is found in the bloodstream associated with lipoproteins (40-42) and even more inactive LpL is present on lipoproteins in pre-heparin blood (41). Most of this LpL is rapidly removed by the liver (43, 44). Its uptake may be via LRP or proteoglycans. It is possible that by acting as a ligand for LRP, LpL will increase removal of associated lipoproteins (29).

5. LIPOPROTEINS AND REGULATION OF THE LIPOLYSIS REACTION

LpL controls the circulating levels of all classes of lipoproteins and is responsible for differences in size and composition of particles within the conventional lipoproteins classes. Although the hydrolysis of triglyceride within chylomicrons and VLDL is the most well known of the LpL actions, this is a complicated process that has only been partially reproduced by *in vitro* experiments.

The lipoproteins must physically come into contact with LpL for lipolysis to begin. The diameter of the vessel, its tortuosity, and the flow rate of the blood and any margination of the particles that allows them to contact the vessel wall must modulate this. Larger diameter particles are more likely to come into contact with the vessel wall and are also more likely to interact with multiple LpL molecules at once

LpL has enzymatic actions to hydrolyze triglyceride and phospholipids. Within the bloodstream, it is the essential enzyme required for clearance of chylomicrons. In addition, catabolism of larger VLDL and initiation of the conversion of VLDL to LDL requires LpL. VLDL and chylomicrons appears to compete for interaction with cell surface LpL, such that increases of VLDL above 5 umoles/ml, an amount that is near the saturation of the enzyme, will decrease both VLDL and chylomicron catabolism (45). In fact, lipolysis appears to require a number of steps that may represent the number of LpL proteins interacting with the lipoproteins or the number of separate associations of the lipoproteins with endothelial associated LpL. Thus, each triglyceride-rich lipoprotein has a competition between lipolysis and liver uptake of partially hydrolyzed lipoproteins. In the case of VLDL, this process determines the percent of VLDL that is converted to LDL; larger VLDL require more lipolysis and are less likely to be converted to LDL. A similar process is likely to occur for chylomicrons; smaller chylomicrons may generate more remnants that circulate in the postprandial period.

LpL will hydrolyze triglyceride and phospholipid on other circulating lipoproteins, LDL and HDL. Therefore it will convert triglyceride-rich LDL into smaller denser LDL. Triglyceride in HDL is also a substrate for LpL actions. Probably more importantly, removal of surface lipid from chylomicrons causes their transfer to HDL. This increases circulating HDL lipids. Moreover, larger, more lipid rich HDL are catabolized more slowly (46). For this reason, LpL activity is positively correlated with HDL (47-49). Although LpL will hydrolyze most triacylglycerols, its preferred fatty acid is oleate. Saturated fatty acids appear to be a less preferred substrate than unsaturated. Fatty acids in the 1 position of triglyceride and phospholipids are hydrolyzed in preference to those in the 2 position (50).

6. APOLIPOPROTEINS

Maximal activation of lipoprotein lipase requires the presence of apolipoprotein CII. Both triglyceride-rich lipoproteins and HDL contain apoCII. Since newly formed chylomicrons that are isolated from the lymph before their entry into the circulation contain very little apoCII, chylomicron CII in the bloodstream must have transferred from other lipoproteins, most likely from HDL. The apoCII is a component of the surface of the triglyceride rich lipoproteins and increases the V_{max} of the reaction (50).

Excess of a number of apolipoproteins inhibit LpL-mediated lipolysis either by displacing apoCII or by direct actions on the enzyme. This was first observed *in vitro* (51) and subsequently has been confirmed by studies in transgenic mice overexpressing apoCIII (52). ApoCIII

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also decreases uptake of remnant lipoproteins by blocking their interaction with the LDL receptor related protein (LRP). It had been thought that apoCIII overexpression led to larger triglyceride-rich lipoproteins by blocking the actions of apoE. This is not the case, as the apoCIII transgene also caused hypertriglyceridemia in apoE knockout mice (53). It may be that excess apoproteins will block lipolysis. ApoCI (54), apoAIV (55), and even apoCII (56), the LpL activator, when overexpressed in mice lead to hypertriglyceridemia. ApoE if expressed in low concentrations will increase removal of triglyceride-rich lipoproteins, however at high concentrations it will lead to hypertriglyceridemia (57, 58). Although in part this effect may result from changes in lipoprotein production by the liver (59, 60), excess apoE may affect lipolysis. Although the reasons for this are not clear, it may be that excess apoproteins coat the surface of the lipoprotein and prevent LpL from having access to any triglyceride that normally is near the surface of the particle.

7. NON-ENZYMATIC ACTIONS OF LIPOPROTEIN LIPASE

LpL interacts with both lipoproteins and cell and matrix proteoglycans; therefore it can form a molecular bridge between these molecules. When circulating triglyceride-rich lipoproteins are hydrolyzed by LpL, the enzyme must interact with lipoproteins while it also is associated with the endothelial surface. Thus, it must provide a molecular bridge between triglyceride-rich lipoproteins and the cell surface. However, lipoproteins that are not its usual substrates will also be anchored to proteoglycans by LpL. LpL associated with matrix proteoglycans will increase LDL and oxidized LDL association with subendothelial matrix (5, 36, 61, 62). This does not require the LpL to be enzymatically active. Moreover, the interaction appears to involve an association between LpL and a region in the amino-terminal 20% of apoB (34). The physiologic and pathophysiological importance of the non-enzymatic effects of the lipases is currently an area of active investigation.

Non-enzymatic, actions of LpL can increase cellular lipoprotein uptake. LpL mediated increased lipoprotein uptake by cells may occur via a number of mechanisms. 1) LpL increases the effective concentrations of lipoproteins on the surface of cells by serving as a bridge between the lipoproteins and cell surface proteoglycans. 2) Lipoproteins are internalized along with recycling of the proteoglycans, or because the LpL serves as a ligand for the LRP family of cell surface receptors. 3) By increasing the proximity of the lipoprotein and cell membrane lipids, a transfer of lipids could occur. Overexpression of enzymatically inactive LpL leads to uptake of lipids into muscle (63), thus inactive LpL can function *in vivo*. In part, this may have occurred because the inactive LpL binds circulating lipoproteins and approximates them near active LpL (64).

8. STRUCTURE-FUNCTION ANALYSIS OF LIPOPROTEIN LIPASE

LpL belongs to a gene family that includes hepatic lipase, pancreatic lipase, and a newly described endothelial

lipase. All members of this family have a similar active serine catalytic site. This site has been identified, mutated, and the inactive LpL has been used to create transgenic mice (see above). Difference in their substrates utilization is due to differences in the lipid binding regions of the proteins, e.g. substituting the hepatic lipase lid will cause the remaining LpL to function like hepatic lipase (65). This is a simplistic analysis and does not explain all the data. Monoclonal antibodies that are directly to the carboxyl terminal region of LpL also inhibit lipolysis (66). Therefore several regions may be required for full LpL activity or distant mutations or antibody interactions might alter the tertiary structure of the LpL sufficiently to affect its actions. In support of a role of the carboxyl-terminal region in LpL activity is the observation that a truncated form of LpL (serine 447 changed to a stop codon) is more active than the native lipase (see section 2).

LpL interaction with heparin plays a critical role in the metabolism and physiological actions of this enzyme. For this reason, the heparin-binding regions of LpL have been studied in some detail. There are a number of basic amino acid rich regions of LpL in both the amino and carboxyl terminal regions of the enzymes. Mutations in either site will decrease LpL interaction with heparin (67, 68). In an elegant study to determine why LpL has greater affinity for heparin than hepatic lipase, portions of LpL and hepatic lipase were interchanged. This study suggested that the carboxyl-terminal domains of the proteins modulate LpL high affinity interaction with heparin (69). The carboxyl terminal heparin-binding region of LpL appears to overlap with the region of LpL that binds to apoB (70). Recently a defective heparin-binding LpL has been produced in transgenic mice; the LpL was mutated in the carboxyl terminal heparin-binding region. This LpL lead to a greater amount of circulating LpL protein in the plasma and increased postprandial free fatty acids, presumably due to intravascular triglyceride lipolysis (71). Moreover, LpL that is defective in heparin binding is unstable. This confirms the previous observations that heparin association stabilizes LpL activity (20).

LpL is widely believed to be most active as a dimeric molecule that is composed of two identical subunits that are arranged in a head to tail configuration (72). When the molecule is allowed to monomerize, this leads to a decrease in heparin affinity and enzyme activity (73). The sites on the LpL protein that are involved in dimerization have not been identified. Moreover, the importance of monomerization per se versus the accompanying loss of heparin affinity has not been ascertained.

A final domain on LpL is that which interacts with apoCII. ApoCII activation is unique to LpL; hepatic lipase activity is not increased by apoproteins. In an *in vitro* assay, the addition of the detergent Triton will also increase LpL activity and negates the requirement for apoCII. It appears that apoCII may directly affect the interaction of the LpL and its substrates (50). The site on LpL that interacts with apoCII has not been defined.

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Table 1. Mutations in the LpL gene possible with clinical relevance in found in humans

Ex	Amino Acid	Nucleotide	Clinical importance	References
2	Asp9Asn	GAC->AAC	HTG, low HDL	(81, 116-118, 122, 143, 144)
3	Val69Leu	GTG->CTG	Chylomicronemia	(81, 92, 145)
3	Arg75Ser	AGA->AGT	Chylomicronemia*	(146)
3	Trp86Arg	TGG->CGG	Chylomicronemia*	(81, 147, 148)
3	Trp86Gly	TGG->GGG	Chylomicronemia	(102)
4	His136Arg	CAT->CGT	Chylomicronemia*	(81, 147)
4	Gly139Ser	GGC->AGC	Chylomicronemia	(81, 92, 149)
4	Gly142Glu	GGA->GAA	Chylomicronemia	(81, 150, 151)
5	Gly154Ser	GGC->AGC	Chylomicronemia	(81, 92)
5	Asp156Asn	GAT->AAT	Chylomicronemia *	(81, 152)
5	Asp156Gly	GAT->GGT	Chylomicronemia	(81, 152, 153)
5	Pro157Arg	CCA->CGA	Chylomicronemia	(81, 154)
5	Ala158Thr	GCT->ACT	Chylomicronemia	(102)
5	Ser172Cys	TCT->TGT	Chylomicronemia only in pregnancy	(81, 92, 155)
5	Ala176Thr	GCA->ACA	Chylomicronemia	(81, 156)
5	Asp180Glu	GAC->GAG	Chylomicronemia	(157)
5	His183Gln	CAC->CA?	Chylomicronemia*, unknown second Allele	(102)
5	His183Asp	CAC->GAC	Chylomicronemia	(158)
5	Gly188Glu	GGG->GAG	Chylomicronemia	(81, 102, 145, 147, 159-165)
5	Ser193Arg	AGC->?G?	Chylomicronemia*	(102)
5	Ile194Thr	ATT->ACT	Chylomicronemia	(81, 147, 166-169)
5	Asp204Glu	GAC->GAG	Chylomicronemia	(81, 171)
5	Gly195Glu	GGA->GAA	Chylomicronemia	(170)
5	Ile205Ser	ATT->AGT	Chylomicronemia	(81, 147)
5	Pro207Leu	CCG->CTG	Chylomicronemia*	(81, 102, 168, 172)
5	Cys216Ser	TGT->AGT	Chylomicronemia*	(81, 152)
5	Ile225Thr	ATT->ACT	Chylomicronemia*	(81, 173, 174)
6	Glu242Lys	GAG->AAG	Chylomicronemia*, unknown second Allele	(175)
6	Arg243His	CGC->CAC	Chylomicronemia	(81, 169, 171)
6	Arg243Cys	CGC->TGC	Chylomicronemia	(81, 170)
6	Ser244Thr	TCC->ACC	Chylomicronemia*	(81, 176)
6	Asp250Asn	GAC->AAC	Chylomicronemia*	(81, 172, 177, 178)
6	Ser251Cys	TCT->TGT	Chylomicronemia*	(81, 92, 172)
6	Leu252Val	CTG->GTG	Chylomicronemia	(179, 180)
6	Leu252Arg	CTG->CGG	Chylomicronemia	(179)
6	Ser259Gly	AGT->GGT	Chylomicronemia*	(160)
6	Ser259Arg	AGT->AGA	Chylomicronemia	(181)
6	Ala261Thr	GCC->ACC	Chylomicronemia	(81, 92)
6	Tyr262His	TAC->CAC	Chylomicronemia, combined with Asp9Asn	(81, 121, 143)
6	Asn291Ser	AAT->AGT	Heterozygous, FCHL, CAD	(88, 89, 103-112, 167, 182)
6	Met301Thr	ATG->ACG	Chylomicronemia*, unknown second Allele	(102)
6	Leu303Pro	CTG->CCG	Chylomicronemia	(102)
7	Ser323Cys	TCT->TGT	only heterozygous, HTG	(183)
7	Ala334Thr	GCC->ACC	Chylomicronemia	(184)
8	Leu365Val	CTA->GTA	Chylomicronemia	(185)
9	Cys418Tyr	TGT->TAT	Chylomicronemia*	(186)
9	Glu421Lys	GAG->AAG	only heterozygous, HTG in pregnancy	(99)
Nonsense mutations				
Exon	Amino Acid	Nucleotide	Clinical importance	References
1	Trp-14stop	TGG->Stop	mild Chylomicronemia	(187)
3	Tyr61stop	TAT->TAA	Chylomicronemia	(81, 171, 188)
3	Tyr73stop	TAC->TAA	Chylomicronemia*	(146)
3	Trp64stop	TCG->TAG	Chylomicronemia*	(81, 168)
3	Glu106stop	CAG->TAG	Chylomicronemia	(81, 189)
6	Cys239stop	TGA->TGA	heterozygous HTG	(190)
6	Tyr262stop	TAC->TAA/G	Chylomicronemia	(81)
6	Tyr302stop	TAC->TAA	Chylomicronemia	(191)
8	Trp382stop	TGG->TGA	Chylomicronemia	(81, 159, 171, 192)
9	Ser447stop	TCA->TGA	only heterozygous, lower TG, increased HDL	(81, 93, 153, 193, 194)

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Table 1. continued

Frameshift mutations and small insertions/deletions			Clinical importance	References
Exon	Amino Acid	Nucleotide		
2	Thr18del	ACC CCT GAA Gadel	Chylomicronemia*	(147)
2	Glu35ins	GAG->A+GAG	Chylomicronemia. (Uniparental disomy)	(195)
3	Thr101ins	ACC->ACT+GGGCT	Chylomicronemia	(81, 196)
5	Ala221del	GCT->CT	Chylomicronemia	(81, 188, 197, 198)
5	Gly229ins	GGA->GG+TAAATATT	Chylomicronemia	(81, 92)
6	Asn 291del	AAT->AT	Chylomicronemia*	(167)
6	Leu252del	CTG->2bp del	Chylomicronemia*	(102)
8	Ser396- Pro397 del	AGT CCCdel	linked to another mutation	(102)
Other mutations			Clinical importance	References
Location	Mutation			
6	2kb dupl		Chylomicronemia	(81, 102, 199, 200)
3-5	6kb del		Chylomicronemia	(81, 199)
9	3kb deletion		Chylomicronemia	(81)
intr. 1	-2 to -4 del, (skipping of exon 2)		Chylomicronemia	(158)
intr. 2	G->A (acceptor splice site)		Chylomicronemia*	(81, 176)
intr. 2	G->A (donor splice site)		Chylomicronemia	(81)
intr. 3	C->T (6bp 5' from acceptor)		Heterozygous, Hypertriglyceridemia	(81, 183, 187)
intr. 8	HIII Polymorphism (Linkage to Ser447Stop)		see Ser447Stop	(123, 201, 202)
Promoter				
Location	Clinical importance			References
-93T->G	Heterozygous FCHL and increased CAD; linkage to Asp9Asn			(118, 122, 131-133)
-53G->C	Decreased promoter activity, possible FCHL			(133, 203)
-39T->C	Decreased promoter activity, possibly FCHL			(133)
+13-+19	Insertion in 5' untranslated region: decreased promoter activity			(133)
CC				

HTG: Hypertriglyceridemia. *Found as compound heterozygote Genotype. Missense mutations

9. GENETIC VARIATION IN LIPOPROTEIN LIPASE

The LpL gene spans about 30 kb on chromosome 8p22 and is divided into 10 exons (74, 75). The cDNA for human LpL codes for a mature protein of 448 amino acids resulting in a calculated molecular weight of 50,394 Daltons (76), an additional 8 percent of carbohydrates is assumed (77). The catalytic center consists of three amino acids, Ser132, Asp156, and His241 (5-7).

About 80 naturally occurring mutations in the LpL gene have been described in humans, the majority of which are missense (Table 1). LpL mutations are spread over most exons; the most frequent sites of these mutations are in exons 5 and 6. Most of these mutations are rare and lead to LpL deficiency if they are present as homozygote or compound heterozygotes. However, for some mutations a linkage to increased triglycerides, decreased HDL-cholesterol, familiar combined hyperlipidemia (FCHL) and premature coronary artery disease (CAD) has been found in the heterozygous state.

10. HOMOZYGOTE LpL DEFICIENCY: THE FAMILIAR CHYLOMICRONEMIA SYNDROME

Homozygote or compound heterozygote mutations in the LpL gene leading to a complete loss of LpL activity result in the familiar chylomicronemia syndrome. Due to lack of plasma triglyceride hydrolysis, a dramatic increase of chylomicrons is found resulting in triglyceride levels far over

1000 mg/dl and extremely low HDL-cholesterol. Patients usually suffer from recurrent abdominal pain, pancreatitis, memory loss, xanthomas and/or dyspnea (81). Case reports with a wide range of severity of symptoms have been described, and occasionally patients present for the first time during pregnancy or following dietary excess (81). It has been suggested, that LpL deficiency can lead to premature atherosclerosis (82). The prevalence of this disease has been estimated to be 1:1,000,000 (83), however, considering the frequency of heterozygote LpL mutations (see below), many cases may have been missed due to inapparent symptoms.

If the disease is suspected, the diagnosis is made by measuring LpL activity in post heparin plasma (84); however, no standardized assay for LpL activity is available to date. LpL mass measured by ELISA (77) may be low, normal, or even increased, depending on whether the mutation alters LpL structure and production. Defects have been demonstrated or are proposed to affect catalytic activity, protein transport or translocation, heparin binding, or dimerization. The structure-function relationship of LpL has been extensively studied *in vitro*.

A disease to differentiate from primary LpL deficiency is a deficiency of apoCII, the apoprotein necessary for full LpL activity. Since the clinical features for this syndrome are less severe but the same as in LpL deficiency, the diagnosis can be made by using the patient's serum as an activator from a standard source of LpL (81), only if apoCII is present will full activity be found.

11. HETEROZYGOTE MUTATIONS IN THE LpL GENE AND ATHEROSCLEROSIS

Homozygous LpL deficiency can lead to a dramatic disease, chylomicronemia, however, the relation of mutations in the LpL gene and premature atherosclerosis may be of great importance for a broad range of populations in all cultures. Although it seems clear that a reduction of LpL activity should lead to increased triglycerides, decreased HDL and therefore possibly premature atherosclerosis (85), only a part of the clinical studies were able to show this connection, and sometimes the findings were contradictory. Generally, it seems to be accepted, that the presence or absence of LpL mutations is able to modulate the development of familiar combined hyperlipidemia and premature atherosclerosis, but LpL mutations fail to be a major defect directly leading to these diseases. Other factors - which are likely to be partially unknown genes, or factors like hyperinsulinemia, adiposity (86) or apo E2/E2 (87) - may modify the effects of LpL mutations.

The frequency of individual mutations differs widely between populations. It is expected, that the frequency of heterozygous LpL deficiency may be as high as 3-7% (82), with Asn291Ser most common, in some Caucasian populations (88, 89). In the French Canadian population, an especially high rate of LpL mutation carriers up to 17% of the population was found, with Pro207Leu, Gly188Glu, and Asp250Asn being the most abundant (90, 91). In other Caucasian groups, Gly188Glu is also widely present (92), however, Pro207Leu and Asp250Asn has rarely been found. Based on a recent meta-analysis, at least one mutation, Ser447Stop (93) seems to be beneficial in terms of lipid metabolism and CAD (94).

Mutations in the LpL gene have also been linked to other diseases: A recent population study shows a relation of LpL mutations to Alzheimer's disease [Ser447-Stop may prevent and Asn291Ser may contribute to its development (95)]. Although clinical studies found a linkage between hypertension and the LpL gene locus (96-98), the importance of this relationship is still unclear. Occasionally, severe hyperlipidemia due to heterozygote LpL mutations may develop during pregnancy [e.g. Glu421Lys (99), Gly188Glu (100)]. Furthermore, carriers of Asn291Ser or combined Asp9Asn/T-93G mutations in the LpL gene may have an increased risk of pre-eclampsia (101).

11.1. Asn291Ser

Asn291Ser is a common mutation in the LpL gene. Heterozygote frequency in the normal population has been estimated to be about 2-5% in Caucasian population (88, 89). This mutation was reported to be heterozygous in a patient with chylomicronemia and an unknown second allele (102). However, it is quite unlikely that the reduced LpL activity found in Asn291Ser-LpL (103) causes chylomicronemia alone; the high frequency of this mutation would lead to much more disease than is commonly found.

Heterozygosity for Asn291Ser was found widely in patients with FCHL and premature CAD (104-108).

Based on a meta-analysis, triglycerides were increased 31%, HDL-cholesterol was decreased 0.12 mmol/l (4.8 mg/dl), and a 1.2 fold increased risk in ischemic heart disease was found (94). Some data suggested that the Asn291Ser mutation affects especially postprandial lipemia (89, 105). An association with other genetic factors such as apoE-3 deficiency or familial hypercholesterolemia (FH) may increase the effect of this mutation on plasma lipids and coronary artery disease (88, 109, 110) and worsen the FCHL phenotype (107, 110-112).

11.2. Asp9Asn

Asp9Asn has been frequently linked to hypertriglyceridemia, low HDL, small dense LDL, FCHL and increased risk of CAD, especially if combined with other risk factors (113-119). Its heterozygous frequency has been estimated as being up to 4.5% (114, 117, 120). Homozygotes with Asn291Ser, Asp9Asn do not have chylomicronemia. However, a patient who was a compound heterozygote for Tyr262His and Asp9Asn had this disease and a 20% decrease in specific LpL activity (117, 121). According to a meta-analysis by Wittrup, triglycerides were increased 20%, HDL-cholesterol was decreased 0.8 mmol/l (3.2 mg/dl), and the risk of ischemic heart disease was 1.4 fold increased (94). However, in Caucasian populations Asp9Asn is strongly linked to the promoter mutation T-93G, which also leads to decreased LpL activity (118, 122). Unlike T-93G, the frequency of Asp9Asn did not differ between American Blacks and Hispanics (122). In the Copenhagen city heart study, double-heterozygous carrier status of both mutations was associated with elevated plasma triglycerides and an increased risk of CAD in men (120). However, the effect of the mutation Asp9Asn without additional promoter mutation has not been estimated at this time.

11.3. Gly188Glu

Although the Gly188Glu mutation is most frequent among French Canadians in Quebec, it is widely spread among populations (92). Heterozygote carriers have 78% increased triglycerides, 0.25 mmol (10 mg/dl) decreased HDL-cholesterol, and a 4.9 fold increased risk of coronary heart disease (94). A preliminary report also found higher systolic blood pressure in heterozygote carriers of Gly188Glu and Pro207Leu (97), however, these data have not yet been confirmed.

11.4. Ser447Stop

The Ser447Stop mutation is a common gene defect (up to 20% heterozygous carriers), resulting in a truncation of the LpL protein by two amino acids (EARS study, 123). The HindIII polymorphism of intron 8 in the LpL gene is associated with this mutation (123). Based on clinical data from the Framingham Offspring study, that this mutation in heterozygous carriers results in decreased plasma triglycerides and higher HDL, combined with a decreased risk of CAD (124). Other studies have supported these findings (93, 125-129). In a meta-study of 9 studies an 8% reduction of triglycerides, a slight (0.04 mmol/l = 1.6 mg/dl) increase in HDL cholesterol, and a 0.8 fold reduced risk in ischemic heart disease was found (94). Interestingly, the beneficial effect of the mutation seems to be most abundant in patients using beta-blockers (126).

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In vitro and *in vivo* studies found that the Ser447Stop-LpL leads a higher LpL activity due to higher LpL expression (126, 130). In addition, LpL bridging, dimer conformation or LpL lipid binding could be affected.

11.5. T-93G

The variant T-93G is a promoter variant. The highest frequency was found in South African Blacks (76.4%); it was less present in Caucasian population (1.7%, 131). Near complete linkage disequilibrium between the –93G and the Asp9Asn mutation was observed in the Caucasian population, but not in South African Blacks (118, 122, 131). Individuals homozygous for the G allele showed mildly decreased triglycerides compared with individuals homozygous for the T allele (131). It is suggested, that the –93T variant has a lower promoter activity than the –93G (132, 133).

12. ANIMAL MODELS OF GENETIC VARIANTS OF LpL

Several animal models of muted LpL have been established. The naturally combined lipase deficiency (cld/cld) mutation mouse line (134-136) as well as homozygote LpL deficiency in two independent mouse lines developed by homologous recombination (137, 138) result in a dramatic chylomicronemia, decreased HDL cholesterol and neonatal death after 1-2 days of life. LpL deficient cats also develop chylomicronemia; they have reduced body mass and lower growth rates. However, they survive until adulthood as do humans (139). Originally it was thought that chylomicronemia and obstruction of lung capillaries caused the neonatal demise of the LpL deficient mice (137). However, data from liver LpL expressing mice show that LpL deficient mice have an energy substrate deficiency and appear to die from hypoglycemia (140). Heterozygote LpL deficient mice suffered from mild hypertriglyceridemia and have impaired VLDL clearance (137). Based on data from these mice it has been suggested, that a reduction in endothelial LpL may be protective against atherosclerosis (141). Experiments in mice overexpressing mutated, inactive LpL (Asp156Asn-LpL) in the muscle revealed, that mutated LpL might still increase lipoprotein and cholesterol ester uptake into organs (142). Therefore, LpL mutations causing a complete destruction of one LpL gene may have different clinical implications than mutations causing complete LpL deficiency for instance by changing the catalytic center.

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