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Novel Mutations in the *GPIHBP1* Gene Identified in Two Patients with Recurrent Acute Pancreatitis

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# Title page

## NOVEL MUTATIONS IN THE *GPIHBP1* GENE IDENTIFIED IN TWO PATIENTS WITH RECURRENT ACUTE PANCREATITIS

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**ABSTRACT**

**Background:** Glycosylphosphatidylinositol-anchored high-density lipoprotein-binding protein 1 (GPIHBP1) has been demonstrated to be essential for the *in vivo* function of Lipoprotein Lipase (LPL), the major triglyceride (TG) hydrolyzing enzyme involved in the intravascular lipolysis of TG-rich lipoproteins. Recently loss of function mutations of *GPIHBP1* have been reported as the cause of Type I hyperlipoproteinemia in several patients.

**Methods:** Two unrelated patients were referred to our Lipid Units because of a severe hypertriglyceridemia and recurrent pancreatitis. We measured LPL activity in post-heparin plasma and serum ApoCII and sequenced *LPL*, *APOC2* and *GPIHBP1*.

**Results:** The two patients exhibited very low LPL activity not associated with mutations in *LPL* gene or with ApoCII deficiency. The sequence of *GPIHBP1* revealed two novel point mutations. One patient (Proband 1) was found to be homozygous for a C>A transversion in exon 2 resulting in the conversion of threonine to lysine at position 80 (p.Thr80Lys). The other patient (Proband 2) was found to be homozygous for a G>T transversion in the third base of the ATG translation initiation codon in exon 1, resulting in the conversion of methionine to isoleucine (p.Met1Ile).

**Conclusion:** In conclusion, we have identified two novel *GPIHBP1* missense mutations in two unrelated patients as the cause of their severe hypertriglyceridemia.

**Keywords:** Glycosylphosphatidylinositol-anchored high-density lipoprotein-binding protein 1 (GPIHBP1), severe hypertriglyceridemia, recurrent pancreatitis, lipoprotein lipase activity.

## 87 1. Introduction

88 Type I and V hyperlipoproteinemia are characterized by high concentrations of chylomicrons in  
 89 the fasting state, a condition which increases the risk of acute pancreatitis<sup>1</sup>. Monogenic forms of  
 90 familial hyperchylomicronemia are due to defects in the lipolytic cascade of triglyceride (TG)  
 91 rich lipoproteins that may result from mutations in at least five different genes: *LPL*, encoding  
 92 the enzyme lipoprotein lipase (LPL; OMIM #238600) and involved in the majority of cases of  
 93 chylomicronemia<sup>2,3</sup>; *APOC2*, encoding the Apolipoprotein CII, the activator of LPL (ApoCII;  
 94 OMIM #207750)<sup>4</sup>; *APOA5*, encoding the Apolipoprotein AV, also an activator of LPL (ApoAV;  
 95 OMIM #144650)<sup>5</sup>; *LMF1*, encoding the Lipase Maturation Factor 1, a tissue factor which allows  
 96 the secretion of functional LPL and Hepatic Lipase (HL; OMIM #611761)<sup>6</sup> and *GPIHBP1*,  
 97 encoding the Glycosylphosphatidylinositol-anchored high-density lipoprotein-binding protein 1,  
 98 the molecular platform for LPL on the endothelial surface of capillaries, (*GPIHBP1*; OMIM  
 99 #612757)<sup>7,8</sup>.

100  
 101 *GPIHBP1* is a 184 aa endothelial cell protein which acts as a transporter for LPL across the  
 102 endothelial cells to the capillary lumen and appears to be the main binding site for LPL on the  
 103 endothelial surface<sup>9</sup>. *GPIHBP1* belongs to the Ly6 protein family<sup>10,11</sup>, so called because of a  
 104 lymphocyte antigen 6 domain that contains 10 cysteine residues forming disulfide bonds and  
 105 creating a characteristic three-finger structural motif. The Ly6 domain is crucial because it is  
 106 involved in the binding to LPL and allows the interactions of LPL with ApoCII, ApoAV and TG-  
 107 rich lipoproteins on the endothelial surface.

108  
 109 Most missense mutations found in *GPIHBP1* causing type I hyperlipoproteinemia are located in  
 110 the Ly6 domain and many of them affect a cysteine residue<sup>12-14</sup>. Interestingly, it has been  
 111 recently described that many amino acid substitutions in this domain lead to the formation of  
 112 disulfide-linked dimers and multimers. The formation of multimers explains the loss of function  
 113 of *GPIHBP1* as *GPIHBP1* monomers are capable of binding LPL<sup>15</sup>. In addition, a mutation  
 114 affecting the C-terminal domain has been shown to impair *GPIHBP1* trafficking to the  
 115 endothelial cell surface<sup>16</sup>. Finally, nonsense/frameshift mutations and large exon deletions in  
 116 this gene have also been described in some patients with Type I hyperlipoproteinemia<sup>17-19</sup>.

117  
 118 In this study we report two novel *GPIHBP1* missense mutations identified in two unrelated  
 119 patients as the cause of their severe hypertriglyceridemia.

120

## 121 2. Materials and methods

### 122 2.1. Subjects

123 Clinical, demographic, anthropometric and laboratory data were retrieved from clinical records  
 124 of two patients who attended the outpatient clinic at Hospital La Paz (Madrid) and Hospital de  
 125 Reus (Tarragona) respectively. Informed written consent has been obtained from the patients  
 126 and their relatives participating to the study. The study was approved by the Ethic Committee of  
 127 the participating institutions.

### 128 2.2. Plasma lipid analyses

129 Serum samples were obtained after an overnight fasting. Cholesterol and triglycerides were  
 130 determined by automated end-point enzymatic methods. Serum ApoCII was quantified by  
 131 immunoturbidimetry in a Mindray Bs-380 Clinical Autoanalyzer (Mindray. zhensheng. China)  
 132 using commercial assays (Spinreact. Barcelona, Spain).

133

### 2.3. LPL activity assay

A blood sample was drawn from each proband 15 minutes after the intravenous injection of sodium heparin (100 units/kg) in order to measure post-heparin plasma LPL activity. LPL activity was measured using a lipid emulsion containing triolein [9,10-3H(N)] (Perkin Elmer NET431) as a substrate according to Olivecrona *et al.*<sup>20</sup>.

### 2.4. Genetic analyses

Genomic DNA was isolated from frozen whole blood in EDTA using an EZ1 BioRobot® (QIAGEN, Hilden, Germany) with the appropriate reagents. The genotyping of common polymorphisms in *APOE* (rs429358, rs7412) and *APOA5* (rs3135506, rs662799) was performed using TaqMan assays in a real-time thermal cycler CFX96™ (BioRad, California, USA), the iQ™ Supermix and the allele discrimination mode of the CFX96™ software, as described previously<sup>21</sup>.

The sequencing of the *LPL*, *APOC2* and *GPIHBP1* exons and splice junctions was carried out as previously described<sup>19</sup>. The mutations were designated according to the Human Genome Variation Society, 2012 version (<http://www.hgvs.org/mutnomen/recs-DNA.html>). *GPIHBP1* protein sequence variants were designated according to <http://www.hgvs.org/mutnomen/recs-prot.html>.

The biological impact of the novel missense mutations found in the probands were tested *in silico* with two algorithms: SIFT (Sort Intolerant From Tolerant). [sift.jcvi.org](http://sift.jcvi.org) and Polyphen 2; [genetics.bwh.harvard.edu/pph2/](http://genetics.bwh.harvard.edu/pph2/).

The two novel *GPIHBP1* mutations found in the probands were screened in 200 normolipidaemic controls using two independent High Resolution Melting (HRM) assays.

## 3. Results

Proband 1, a 39-year-old Pakistani male, was referred to the Lipid Unit of the University Hospital San Joan (Reus, Spain) when he presented with the fifth episode of acute pancreatitis. After that episode he developed insulin dependent diabetes. This patient had had the first episode of pancreatitis at the age of 23. The highest recorded TG level was 4489 mg/dL. During the last year, the patient has been treated with a low-fat diet supplemented with medium chain triglycerides (SHS, Nutricia) 30 mL/day, plus atorvastatin 10 mg, fenofibrate 145 mg and 3 g of omega-3 fatty acids. This treatment however, did not improve his clinical conditions nor did it reduce plasma TG levels below 1000 mg/dL. He did not show eruptive xanthomas, hepatosplenomegaly or lipemia retinalis. No family members were available for study although we could confirm that his parent were first cousins and he has four brothers (Figure 1).

Proband 2 is a 25-year-old female from Ecuador born from consanguineous parents (first cousins). She attended the hospital La Paz (Madrid, Spain) for follow up when she started treatment with low-fat diet supplemented with medium-chain triglycerides (Nutrición Médica, Madrid, Spain) 20 mL/day, plus fenofibrate 145 mg, 2 g of omega-3 fatty acids and 600 mg of crystalline niacin. No beneficial effects were obtained in clinical or biochemical terms. Since the age of 15 she had had 12 episodes of acute pancreatitis. The highest recorded TG level was 3820 mg/dL. The lowest TG level reported was 343 mg/dL when she managed to follow a strict vegetarian diet and do sport every day. Proband 2 is the eldest of four healthy siblings which were available for the study together with their mother (Figure 1). Eruptive xanthomas, hepatosplenomegaly or lipemia retinalis were not observed in this patient. There was no known family history of pancreatitis.

The biochemical and genetic data are shown in Table 1. At the time of the molecular diagnosis both probands had triglycerides levels above 1000 mg/dL. Both patients exhibited very low levels of post-heparin plasma LPL activity compared with hypertriglyceridaemic patients without LPL deficiency (92 mU/mL  $\pm$  44 mU/mL)<sup>22</sup>. Plasma ApoCII level was in the range found in our series of patients with severe hypertriglyceridemia<sup>23</sup>.

In both probands the sequence of the *LPL* as well as the sequence of the *APOC2* gene did not reveal the presence of rare variants nor polymorphisms that could account for the very low LPL activity (Supplementary table S1). The sequencing of *GPIHBP1* revealed two novel point mutations (Figure 2). Proband 1 was found to be homozygous for a C > A transversion in exon 2 resulting in the conversion of threonine to lysine at position 80 (p.Thr80Lys, p.T80K). Proband 2 was found to be homozygous for a G>T transversion in the third base of the ATG translation initiation codon in exon 1 resulting in the conversion of methionine to isoleucine (p.Met1Ile, p.M1I).

According to *in silico* analysis (PolyPhen-2) the Thr80Lys mutation was predicted to be possibly damaging and the Met1Ile probably damaging. According to SIFT algorithm both mutations were predicted to be damaging.

The sequencing of the first exon of *GPIHBP1* in the relatives of Proband 2 revealed that the mother (B.I-2, Figure 1) and the youngest brother (B.II-4) of the proband were heterozygous carriers of the mutation (Table 1).

None of the two *GPIHBP1* mutations was found in the public data base from the National Center of Biotechnology, (<http://www.ncbi.nlm.nih.gov/>); from the Human Gene Mutation Database (<http://www.hgmd.cf.ac.uk/ac/index.php>) nor from the 1000 Genomes Catalog of Human Genetic Variation (<http://browser.1000genomes.org/index.html>). In addition, no carriers of the mutations were identified in a group of normolipidaemic Spanish workers<sup>21</sup>. A summary of the mutations in *GPIHBP1* found in severe hypertriglyceridaemic patients so far is displayed in Table 2.

Additionally to the *GPIHBP1* mutation, Proband 2 was homozygous for the rare allele of the common SNP in *APOA5*: rs3135506 (p.Ser19Trp), while her mother (B.I-2) was heterozygous and one of her brothers (B.II-2) was homozygous for this SNP (Table 1). Moreover, the youngest brother (B.II-4) was heterozygous not only for p.Ser19Trp variant but also for another SNP (rs662799; c.-1131C>T) in the *APOA5* gene. In all subjects the *APOE* genotype was  $\epsilon 3\epsilon 3$ .

#### 4. Discussion

*GPIHBP1* has been demonstrated to be an essential factor for intravascular lipolysis of TG-rich lipoproteins mediated by LPL<sup>2</sup>. Recently different *GPIHBP1* missense mutations have been found in patients with Type I hypertriglyceridaemia. In the present study we describe two novel rare variants of *GPIHBP1* gene found in homozygous state in two patients with severe hypertriglyceridemia associated with extremely low LPL activity in post-heparin plasma.

The clinical features of our patients were similar to those of other adult patients with *GPIHBP1* mutations reported so far (Table 2). Our patients showed persistently elevated plasma TG that did not respond to lipid lowering treatment and had partial response to diet<sup>24,12-14,16,25-27</sup>. Most patients with severe hypertriglyceridemia carrying mutations in *GPIHBP1* suffer from pancreatitis bouts (62% of cases described in Table 2 with these data available), including very young children<sup>16,28,29</sup> and, like in our probands, in some patients pancreatitis is reported to be recurrent<sup>13,16,17,24</sup>. On the other hand, we haven't observed in our patients other associated symptoms such as eruptive xanthomas, lipemia retinalis or hepatosplenomegaly (45% of cases in Table 2). Finally, CHD is reported just in the two oldest patients described in Table 2<sup>13,24</sup>.



Proband 1 (Table 1) is homozygous for a non-conservative amino acid substitution (p.Thr80Lys) located in Finger 1 of the Ly6 domain of the GPIHBP1 protein. This is the first naturally occurring mutation in Finger 1 that does not affect a cysteine residue. The threonine residue at position 80 belongs to a N-glycosylation consensus sequence and is close to the cysteine residue at position 83. The substitution of an uncharged polar amino acid (threonine MW 119.13) with a positively charged polar amino acid that is larger in size (lysine MW 146.19) is expected to disrupt the sequence of Finger 1 domain and to be deleterious. This prediction is supported by *in vitro* mutagenesis studies which demonstrated that p.Thr80Lys GPIHBP1 mutant, when expressed in CHOK1 cells, showed a reduced expression on the cell surface (suggesting an impaired intracellular transport) as well as a markedly reduced binding of LPL (> 90% reduction)<sup>30</sup>. In view of these findings we can reasonably conclude that p.Thr80Lys substitution is the cause of LPL deficiency in our patient.

The ATG (AUG) to ATT (AUU) conversion (leading to p.Met1Ile substitution) in the translation initiation codon found in Proband 2 is the first mutation affecting the *GPIHBP1* translation initiation codon described so far. Mutations affecting the translation initiation codon in human genes are relatively uncommon as compared to other exonic mutations and usually are considered deleterious. Interestingly, this type of mutation has been reported in other genes involved in intravascular lipolysis of TG-rich lipoproteins such as *LPL*<sup>31,32</sup> and *APOC2*<sup>33</sup>.

The effect of the conversion of the ATG (AUG) initiation codon to ATT (AUU) may have a variable effect on the efficiency of translation. The mutation can result in: i) a complete block of translation initiation with no production of GPIHBP1; ii) a reduced efficiency of translation initiation by the mutant translation initiation codon (with a parallel reduction of the synthesis of Met1Ile mutant GPIHBP1); iii) an activation of one or more alternative translation initiation codons along the mRNA sequence with a variable translation efficiency. The visual inspection of GPIHBP1 mRNA sequence reveals the presence of ATG triplets at 106, 125, 130, 253 and 381 nucleotides downstream from the position +1 (corresponding to the Adenine of the canonical ATG). These ATG triplets might be regarded as possible translation initiation sites, if embodied in a nucleotide sequence similar to Kozak consensus initiation sequence [(GCC) GCC -3 A/GCC ATG +4 G]<sup>34</sup>. However, the activation of alternative translation initiation sites at position 106, 125 or 130 is out of frame with respect to the canonical ATG initiation site and would lead to the insertion of a premature termination codon (TGA at position 231).

Regardless of the possible effect of the ATG->ATT mutation on the translation process, Proband 2 showed a dramatic reduction of LPL activity suggesting either a very low production of the mutant GPIHBP1 carrying the Met1Ile mutation (due to a residual initiation translation efficiency) or the production of a structurally abnormal GPIHBP1 protein devoid of function.

As expected, plasma TG levels observed in the heterozygous relatives of proband 2 were in a normal range in agreement with many other cases described in the literature<sup>16-18,26</sup>. A stringent follow up of these subjects is highly recommended as they (like heterozygotes for *LPL* or *APOA5* gene mutations) may be prone to develop hypertriglyceridemia and be at risk of pancreatitis, when secondary factors such as diabetes, obesity, alcohol abuse or pregnancy should occur<sup>2</sup>. In this context it is especially interesting the case of the youngest brother of proband 2 who has a normal TG level in spite of being not only a carrier of the *GPIHBP1*-Met1Ile mutation but also of two common *APOA5* SNPs known to be associated with hypertriglyceridemia in adults<sup>21,35</sup> as well as in children<sup>36,37</sup>.

Our results highlight the importance of sequencing the *GPIHBP1* gene in those patients with severe hypertriglyceridemia negative for mutations in *LPL* and *APOC2*. The number of *GPIHBP1* mutations found in these patients has increased during the last few years suggesting that the *GPIHBP1* gene mutations may be more frequent than previously assumed.

272

273 **Authors' contributions**

274 MJA contributed to the study design, participated in the genetic analyses and drafted the  
 275 manuscript. PLMH, DI, CGA and NP were in charge of the patient's management and carried  
 276 out the data collection. MJA and CR performed the sequencing of the GPIHBP1 gene and the *in*  
 277 *vitro* analyses of the mutations. PT and SC participated in the design and coordination of the  
 278 study and helped to draft the manuscript. JR carried out the plasma lipid analysis and the LPL  
 279 activity assays. GO contributed to the LPL activity assays and helped to draft the manuscript.  
 280 PV conceived the study, participated in its coordination and helped to draft the manuscript. All  
 281 authors read and approved the final version of the manuscript

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422

423 **Title and legend to figures**

424 **Figure 1. Pedegrees of proband 1 (A) and proband 2 (B).** Probands are designated with filled  
425 symbols. The question marks (?) denote individuals who could not be studied.

426 **Figure 2. *GPIPHBP1* sequences showing the mutations found in our patients.** Panel 1.a shows  
427 the normal sequence and 1.b the homozygous C>A transversion at the second base of codon  
428 80 in exon 3, resulting in a conversion of threonine to lysine found in proband 1. Panel 2.a  
429 shows the normal sequence and 2.b the homozygous G>T transversion at the third base of  
430 codon 1 in exon 1, resulting in a conversion of the first methionine to isoleucine found in  
431 proband 2. The sequence in panel 2.c corresponds to the youngest brother of proband 2 who  
432 is heterozygous for the mutation.

433

Table 1. Anthropometric, biochemical and genetic data

Subject	Age	BMI (Kg/m <sup>2</sup> )	TC (mg/dL)	HDL-C (mg/dL)	TG (mg/dL)	Max. TG (mg/dL)	ApoCII (mg/dL)	LPL activity (mU/mL)	Mutation in GPIHBP1	SNPs
P1 (A.II-1)	39	26,6	119	15	1270	4489	29,9	3.7	Homozygous rare allele c.239 C>A, ACG>AAG, Thr <sub>80</sub> >Lys	None
P2 (B.II-1)	25	21,6	299	14	1384	3820	7.5	9.5	Homozygous rare allele c.3 G>T, ATG>ATT, Met <sub>1</sub> >Ile	Homozygous rare allele rs3135506 ( <i>APOA5</i> )
P2 mother (B.I-2)	43	23,7	211	52	58		ND	ND	Heterozygous c.3 G>T, ATG>ATT, Met <sub>1</sub> >Ile	Heterozygous rs3135506 ( <i>APOA5</i> )
P2 brother (B.II-2)	24	23,9	154	45	59		ND	ND	Absent	Homozygous rare allele rs3135506 ( <i>APOA5</i> )
P2 sister (B.II-3)	17	25,1	183	47	86		ND	ND	Absent	None
P2 brother (B.II-4)	6	15,2	174	54	77		ND	ND	Heterozygous c.3 G>T, ATG>ATT, Met <sub>1</sub> >Ile	Heterozygous <i>APOA5</i> SNPs rs3135506 and rs662799

**Subject:** P: proband. The subject's code according to the pedigrees displayed in figure 1 is indicated in parentheses. **BMI:** body mass index. **TC:** total cholesterol. **TG:** triglycerides. **HDL-C:** cholesterol in high density lipoproteins. **Max. TG:** highest level of triglyceride reported. **ApoCII:** Apolipoprotein C2. **SNPs:** Single nucleotide polymorphisms. *APOE* (rs429358 and rs7412, alleles ε2, ε3 and ε4) and *APOA5* (rs662799 and rs3135506) common variants were screened.



**Table 2. Mutations found in the GPIHBP1 gene in severe hypertriglyceridemic patients**

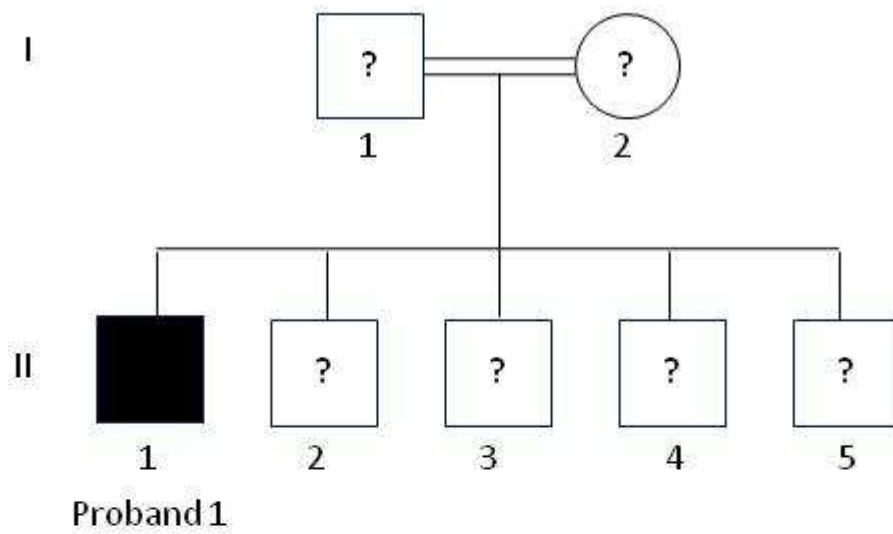
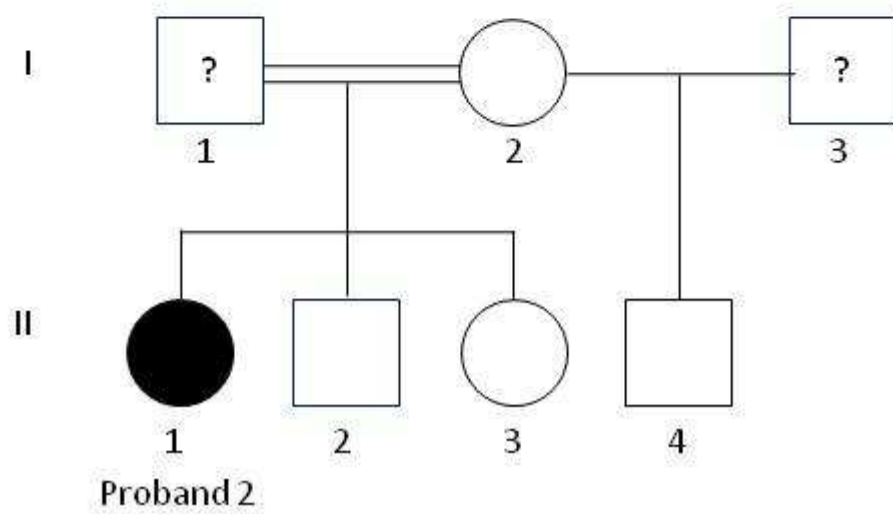
Report	Mutation (HO: homozygous; CHE; compound heterozygous)	Patient code	Gender, age	Origin	PC	Pancreatitis (age of onset)	Associated symptoms	Max. TG	Min. TG
Wang J. and Hegele R.A; 2007 <sup>24</sup>	c.166 G>C, p.G56R (HO)	II-3	F, 47 y	NA	No	RP (22 y)	NO	7120	≈886
	c.166 G>C, p.G56R (HO)	II-1	M, 52 y	NA	No	RP (25 y)	CHD	4272	≈886
Beigneux A.P. et al.; 2009 <sup>25</sup>	c.344 A>C, p.Q115P (HO)	P	M, 33 y	Columbian	NA	No	HSM	3366	774
Franssen R. et al.; 2010 <sup>26</sup>	c.194 G>A, p.C65Y (HO)	P	M, 3 y	Arabian	Yes	Yes (1 y)	LR	4005	1575
Olivecrona G. et al.; 2010 <sup>27</sup>	c.194 G>C, p.C65S + c.202 T>G, p.C68G (CHE)	II-3	M, 13 y	Swedish	No	No	SM	1727	638
	c.194 G>C, p.C65S + c.202 T>G, p.C68G (CHE)	II-2	F, 18 y	Swedish	No	Abdominal pain	LR	5049	NA
	c.194 G>C, p.C65S + c.202 T>G, p.C68G (CHE)	II-4	F, 2 y	Swedish	No	Yes (childhood)	HSM	4296	NA
Charriere S. et al.; 2011 <sup>16</sup>	c.266 G>T, p.C89F + c.1-?_2282+?del (gene del), p.0 (HO)	AII-1	M, 6 m	NA	No	Yes (6 m)	NO	1736	266
	c.523G>C, p.G175R (HO)	BII-2	M, 26 y	Algerian	No	RP	NO	5757	≈886
Coca-Prieto I. et al.; 2011 <sup>23</sup>	c.203G>A, p.C68Y (HO)	C	F, 30 y	Spanish	No	Yes (6 y)	NO	1398	≈886
Rios J.J. et al.; 2012 <sup>18</sup>	17499bp del, including GPIHBP1, p.0 (HO)	A.V-1	M, 2 m	Asian indian	No	No	LR	37248	905
	17499bp del, including GPIHBP1, p.0 (HO)	A.III-9	F, 44 y	Asian indian	No	Yes (29 y)	NA	981	NA
	c.203G>A, p.C68Y (HO)	B.II-7	F, 36 y	Salvadoran	No	Yes (24 y)	EX	6484	NA
Surendran R.P., et al.; 2012 <sup>14</sup>	c.194G>A, p.C65Y (HO)	P	NA	NA	NA	NA	NA	>886	NA
	c.323C>G, p.T108R (HO)	P	M, 1 y	NA	NI	Yes	NO	>886	381
	c.344 A>C, p.Q115P (HO)	P	NA	NA	NA	NA	NA	>886	NA
Yamamoto H. et al., 2013 <sup>13</sup>	c.202T>C, p.C68R (HO)	P	F, 54 y	Japanese	Yes	RP (27 y)	CAD	2640	790

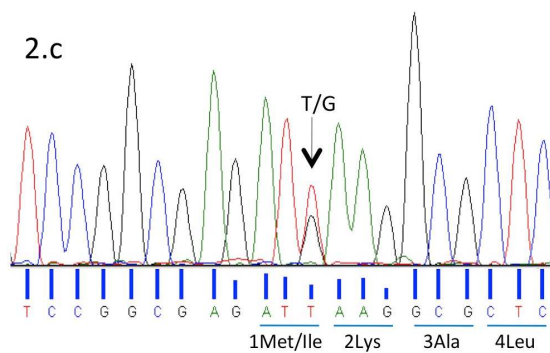
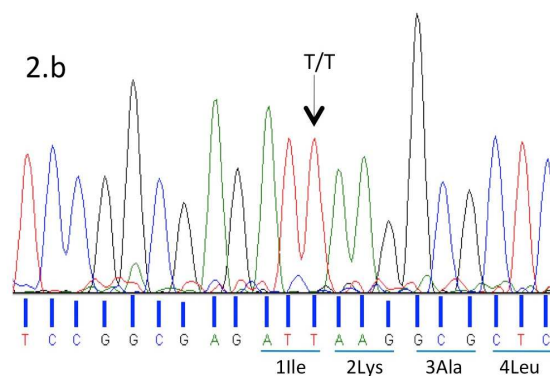
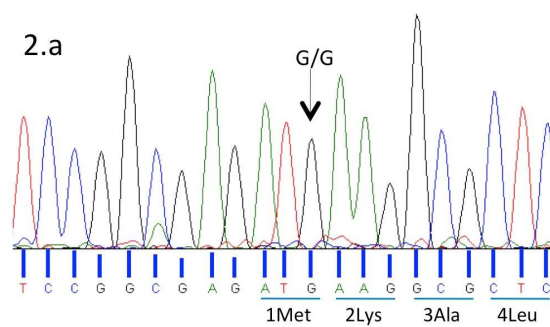
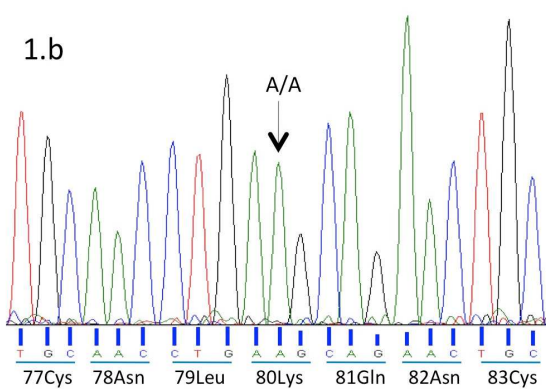
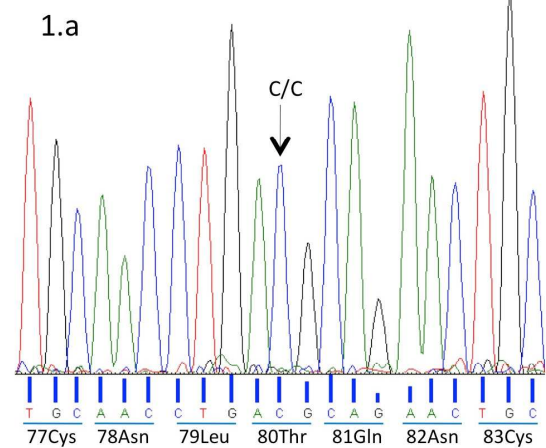


Table 2. Continued

Report	Mutation (HO: homozygous; CHE; compound heterozygous)	Patient code	Gender, age	Origin	PC	Pancreatitis (age of onset)	Associated symptoms	Max. TG	Min. TG
Berge K.E. et al.; 2014 <sup>17</sup>	c.182-?_555+?del (Ex3-4 del), p.0 (HO)	VI:2	F, 22 y	Pakistani	Yes	RP	NA	5314	NA
	c.182-?_555+?del (Ex3-4 del), p.0 (HO)	VI:1	M, 37 y	Pakistan	Yes	RP	NA	8857	NA
	c.182-?_555+?del (Ex3-4 del), p.0 (HO)	VI:3	M, 40 y	Pakistani	Yes	No	NA	>3543	NA
	c.182-?_555+?del (Ex3-4 del), p.0 (HO)	VI:4	F, 37 y	Pakistan	Yes	RP	NA	2391	NA
Gonzaga-Jauregui C. et al.; 2014 <sup>28</sup>	c.331A>C, p.T111P + c.413_429del, p.P140Sfs*161 (CHE)	P	F, 5 w	Hispanic	No	Yes (2 y)	EX	12031	626
Plengpanich W. et al., 2014 <sup>12</sup>	c.320C>G, p.S107C (HO)	II-8	F, 46 y	Thai	No	Abdominal pain	NO	6448	505
	c.320C>G, p.S107C (HO)	II-1	M, 64 y	Thai	No	NA	NA	842	NA
	c.320C>G, p.S107C (HO)	II-10	M, 43 y	Thai	No	NA	NA	673	NA
Ahmad Z. et al., 2014 <sup>29</sup>	c.267C>A, p.C89* + c.85-88GAGGdel, p.E29Tfs*50 (CHE)	P	F, 6 m	Caucasian	No	Yes	EX	2665	423
Buonuomo P.S. et al., 2015 <sup>19</sup>	c.154-162AACAGGCTdelTCTTins, p.N52Sfs*253 + c.319 T>C, p.S107P (CHE)	P	F, 3 d	Italian	No	No	NO	1667	235
This report	c.239 C>A, p.T80K (HO)	A.II-1	M, 37 y	Pakistani	Yes	RP (23 y)	NO	4489	≈1000
	c.3 G>T, p.M1I (HO)	B.II-1	F, 25 y	Ecuadorian	Yes	RP (15 y)	NO	3820	343

NA (throughout the table): data not available. **Patient code:** code given to each particular patient in the original reference. When there are more than one member of the same family the proband is listed the first. P: no code is given either because one single proband or unrelated patients are studied. **Gender and age:** M: male, F: female, y: years, m: months, w: weeks, d: days. **PC:** reported parent's consanguinity. In references 24 and 27 common ancestors are suspected. **Pancreatitis:** it is indicated whether the patient suffered or not from pancreatitis (Yes/ No) or just abdominal pain. RP: recurrent pancreatitis. The age of the first episode is indicated in parentheses when available. **Associated symptoms:** CHD: coronary heart disease, NO: not observed, HSM: hepatosplenomegaly, LR: lipemia retinalis, SM: splenomegaly. **Max. TG:** highest triglyceride level reported for each patient. **Min. TG:** lowest triglyceride level achieved for each patient under different treatments and formula diets. The common *GPIHBP1* variant p.C14F, rs11538389 is described in references 13 and 16 and the variant p.S144F, rs78367243 is found in reference 14. References 13, 16, 17, 23-28 and this report include information on LPL activity. ApoCII levels are given in references 13, 23, 25, 26 and in this report. *In vitro* functional analyses of the mutations are carried out in reports 12, 13, 16, 25-27.

**A****B**



- We studied two patients with recurrent pancreatitis and severe hypertriglyceridemia
- Patients exhibited low lipoprotein lipase activity but no rare variants in this gene
- We identified two novel missense mutations in the *GPIHBP1* gene
- One patient was homozygous for the mutation c.239 C>A, ACG>AAG, p.Thr<sub>80</sub>>Lys
- The other patient was homozygous for the mutation c.3 G>T, ATG>ATT, p.Met<sub>1</sub>>Ile

Supplementary Table S1

<i>LPL</i> sequencing			
	Variants	Region	State
Proband 1	No variants found	-	-
Proband 2	c.1164 C>A, ACC>ACA, Thr361>Thr	Exon 8	Heterozygosity

<i>APC2</i> sequencing			
	Variants	Region	State
Proband 1	IVS3+38_40 del 3bp (ACC)	IVS3	Homozygosity
Proband 2	UTR5' -109 G>C	UTR 5'	Heterozygosity
	UTR 5' -24 G>T	UTR 5'	Heterozygosity
	IVS1-67 G>T	IVS1	Homozygosity
	IVS3+38_40 del 3bp	IVS3	Homozygosity
	IVS3-151 C>G	IVS3	Heterozygosity
	IVS3-150_-148 del 3bp	IVS3	Heterozygosity
	IVS3-81 C>T	IVS3	Heterozygosity