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Lp(a) mass levels increase significantly according to APOE genotype: An analysis of 431,239 patients

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Abstract

Objective—Lipoprotein(a) [Lp(a)] levels are genetically determined by hepatocyte apolipoprotein(a) synthesis, but catabolic pathways also influence circulating levels. APOE genotypes have different affinities for the LDL receptor (LDLR) and LDL related protein-1 (LRP-1), with ε 2 having the weakest binding to LDLR at <2% relative to ε 3 and ε 4.

Approach and Results—APOE genotypes (ε2/ε2, ε2/ε3, ε2/ε4, ε3/ε3, ε3/ε4 and ε4/ε4), $Lp(a)$ mass, directly-measured $Lp(a)$ cholesterol $(Lp(a)-C)$ levels and a variety of apoB-related lipoproteins were measured in 431,239 patients. The prevalence of APOE traits were: ε2:7.35%, ε3:77.56%, and ε4:15.09%. Mean (SD) Lp(a) levels were 65% higher in ε4/ε4 compared to ε2/ε2 genotypes and increased significantly according to *APOE* genotype: ϵ 2/ε2: 23.4(29.2), ϵ 2/ε3: 31.3(38.0), ε2/ε4: 32.8(38.5), ε3/ε3: 33.2(39.1), ε3/ε4: 35.5(41.6), and ε4/ε4: 38.5(44.1) mg/dL (P<0.0001). LDL-C, apoB, Lp(a)-C, LDL-C corrected for Lp(a)-C content, LDL particle number and small dense LDL also had similar patterns. Patients with LDL-C ≥250mg/dL, who are more likely to have LDLR mutations and reduced affinity for apoB, had higher Lp(a) levels across all apoE isoforms, but particularly in patients with ε2 alleles, compared to LDL <250mg/dL. The lowest Lp(a) mass levels were present in patients with ε2 isoforms and lowest LDL-C.

Conclusions—*APOE* genotypes strongly influence Lp(a) and apoB-related lipoprotein levels. This suggests that differences in affinity of apoE proteins for lipoprotein clearance receptors may

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affect $Lp(a)$ catabolism, suggesting a competition between $Lp(a)$ and apoE protein for similar receptors.

Keywords

Lp(a); apoE; genotype; cardiovascular disease; prevalence; populations; guidelines

Introduction

Lipoprotein(a) $[Lp(a)]$ is an independent and likely causal risk factor for cardiovascular disease (CVD) and calcific aortic valve stenosis (CAVS).¹⁻³ Lp(a) plasma levels are primarily (\sim 90%) determined by variations in the LPA gene locus,⁴ including the number of kringle IV₂ repeats and *LPA* single nucleotide polymorphisms. In addition, apolipoprotein(a) gene expression can be modulated by interlukin-6 that increases hepatocyte apolipoprotein(a) production, and by estrogen and bile acids that decrease production.^{5, 6} Clearance mechanisms are not well defined but the major possibilities include the LDL receptor (LDLR), scavenger receptor B1,⁷ plasminogen receptors and renal mechanisms.⁸

Apolipoprotein E (apoE) is polymorphic glycoprotein synthesized and secreted primarily by liver, brain, skin and macrophages.⁹ ApoE is present on very low density lipoproteins (VLDL), remnant lipoproteins and HDL and facilitates their clearance via the LDL receptor (LDLR) and the LDL related protein-1 (LRP1) and syndecan-1 (SDC1).^{10, 11} The 3 isoforms of APOE, ε2, ε3 and ε4, differ by single amino acid substitutions at two non-synonymous sites, which affect binding affinity for LDLR, LRP1 and SDC1. These variations are associated with differences in circulating VLDL-C, IDL-C and LDL-C levels, risk of CVD and the propensity to Alzheimer's disease.¹²

Although APOE genotypes have been associated with differences in lipoprotein levels, less is known about their role in influencing plasma $Lp(a)$ levels.^{13, 14} Previous studies reporting a relationship between Lp(a) and the apoE genotype are difficult to interpret as they suffer from low patient numbers in the less prevalent apoE genotypes. In particular controversy persists on whether the LDLR plays any significant role in Lp(a) clearance, and therefore if it influences plasma $Lp(a)$ levels under physiological conditions.^{8, 15} Furthermore, the relationship of *APOE* genotypes with Lp(a)-cholesterol [Lp(a)-C] and advanced measures of lipoproteins, such as plasma levels of apolipoprotein B-100, LDL particle number, small dense LDL and high-sensitivity C-reactive protein (hsCRP) has not been previously evaluated. In this study, we describe the relationship of $APOE$ genotypes with $Lp(a)$ levels and apoB-related lipoprotein measurements in a very large database from a referral laboratory.

Materials and Methods

Materials and Methods are available in the online-only Data Supplement Materials and Methods

Results

Baseline characteristics

The data is presented by APOE isoform genotype in Table 1. The prevalence of *APOE* traits were: ε 2: 7.35%, ε 3: 77.56%, and ε 4: 15.09%. The prevalence of *APOE* genotypes were: ε2/ε2: 0.61%, ε2/ε3: 11.17%, ε2/ε4: 2.3%, ε3/ε3: 60.41%, ε3/ε4: 23.14% and ε4/ε4: 2.38%.. The mean age range was approximately 54-56, ∼53% of patients were female and BMI was ∼30.

Lipid and lipoprotein variables

Corresponding mean(SD) $Lp(a)$ levels increased significantly according to $APOE$ genotype ranging from 23.4 mg/dL for ε 2/ ε 2 to 38.5(44.1) mg/dL for ε 4/ ε 4 (P<0.0001 ANOVA) (Table 1 and Figure 1). Median Lp(a) levels also increased by genotype, from 11 mg/dL for ε 2/ε2 to 20 mg/dL for ε 4/ε4. Along with Lp(a) mass, Lp(a)-C also increased according to APOE genotype. Mean LDL-C also increased by APOE genotype ranging from 49.6 mg/dL for ε2/ε2 to 114.3 mg/dL for ε4/ε4 (P<0.0001 ANOVA). Corresponding mean apoB levels ranged from 56.6 for ϵ 2/ ϵ 2 to 101.1 mg/dL for ϵ 4/ ϵ 4 (p<0.0001 ANOVA). Striking increases in LDL particle number and small dense LDL were also noted according to genotype, with lowest values in $\varepsilon 2/\varepsilon 2$ to highest values in $\varepsilon 4/\varepsilon 4$.

In contrast, median triglyceride levels were inversely associated with APOE genotype from 140 mg/dL to 109 mg/dL for ε4/ε4 (p<0.0001 ANOVA). A similar but modest inverse association was noted with HDL-C (P<0.0001 ANOVA). Finally, hsCRP was also inversely associated with APOE genotype, with highest values in highest values in ϵ 2/ ϵ 2 to lowest values in ε4/ε4 (Table 1).

For the patients with ϵ 2/ ϵ 2 phenotype, a portion of which can have elevated triglycerides when a secondary stimulus accelerates VLDL production, additional analyses were performed. Out of 2445 patients with ε2/ε2 phenotype, there were 1205, 782 and 93 patients with triglyceride levels 150 mg/dL, 200 mg/dL and 500 mg/dL, respectively. Patients with triglycerides < vs. 150 mg/dL (Lp(a) mean (SD) 23.1 (28.5 vs. 23.7 (30.0), p=0.54), <200 vs. 200 mg/dL (Lp(a) mean (SD) 23.6 (29.5 vs. 22.8 (9.2), p=0.53), or <500 vs. 500 mg/dL (Lp(a) mean (SD) 23.4 (29.1 vs. 23.5 (30.9), p=0.98), did not have significantly different levels. Figure 1 shows a graphical representation of some of the key relationships.

Correlations among variables

Using a validated Lp(a)-C assay, ¹⁶ the Spearman correlation between Lp(a) mass and Lp(a)-C was $r^2=0.79$ (p<0.001) and between Lp(a) mass and LDL-C $r^2=0.008$ (p<0.001) (Figure 2). All other correlations of $Lp(a)$ mass with variables in Table 1 had $r < 0.10$, but due to the large numbers all were statistically significant with $p<0.001$ (data not shown). Lp(a)-C also had a weak correlation with LDL-C (r^2 =0.012, p<0.001), total cholesterol (r^2 =0.018, p<0.001), HDL-C r^2 =0.0.38, p<0.001), and triglycerides (r^2 =-0.016, p<0.001). All other correlations of $Lp(a)$ -C with variables in table 1 had $r \le 0.10$, but due to the large numbers all were statistically significant with $p<0.001$ (data not shown).

Relationship Of Apoe Isoforms To Ldl-C ≥190 Mg/Dl And Ldl-C ≥250 Mg/Dl

Because LDLR mutation status was not available, we used LDL-C 190 mg/dL and LDL-C ≥250 mg/dL as potential surrogates for LDLR deficiency to derive insights into the potential role of the LDLR vis-à-vis APOE genotypes and Lp(a) catabolism. The analysis showed that compared to patients with LDL-C <190 mg/dL or <250 mg/dL, respectively, patients with LDL-C ≥190 mg/dL (mean (SD) Lp(a) 33.4 (39.4) mg/dL vs. 47.2 (50.9) mg/dL, p<0.001) and LDL ≥250 (mean (SD) Lp(a) 33.6 (39.6) mg/dL vs. 49.4 (53.1) mg/dL, p<0.001) had significantly higher Lp(a) levels.

When analyzed by $APOE$ isoform status and LDL-C cutoffs, the lowest $Lp(a)$ levels were present in ε2 genotypes with concomitant low LDL-C (Table 2). In contrast, ε2 genotypes with concomitant high LDL-C had the highest $Lp(a)$ levels. The differences in $Lp(a)$ levels according to *APOE* genotypes and normal or elevated LDL-C were greatest in ϵ 2 genotypes and smallest in ε 4 genotypes. For example, in individuals with ε 2/ ε 3 genotype (there was only one ϵ 2/ ϵ 2 individual with LDL 190, so this genotype could not be examined), Lp(a) levels were 31.2 (37.9) for LDL-C <190 mg/dL and 63.3 (57.5) for LDL $\,$ 190 mg/dL (p<0.001). In contrast, for ε4/ε4 Lp(a) levels were 38.1 (43.8) mg/dL for LDL-C <190 mg/dL and 50.2 (52.1) for LDL 190 mg/dL (p<0.001).

Discussion

The current data document that $APOE$ isoforms strongly influence $Lp(a)$ mass levels, with a 65% increase in $\varepsilon 4$ / $\varepsilon 4$ compared to $\varepsilon 2/\varepsilon 2$ genotypes. Consistent with this, Lp(a)-C levels, determined with an assay that strongly reflects $Lp(a)$ mass,¹⁶ also increased according to APOE genotypes. In addition, a variety of measures of lipoprotein particle number, including apoB levels, LDL particle number and small dense LDL had similar statistically significant associations. Finally, it was documented that concomitantly highly elevated LDL-C, a surrogate for LDLR deficiency, also influenced Lp(a) levels overall with higher levels in subjects with elevated LDL, as shown previously with a gene-dose relationship in subjects with homozygous and heterozygous familial hypercholesterolemia.^{17, 18} This relationship was particularly accentuated in patients with ϵ 2/ ϵ 2 genotypes that have the lowest affinity for the LDLR and LRP1. Because apoE proteins are not thought to directly affect hepatocyte synthesis of apolipoprotein(a) or impact $Lp(a)$ assembly or secretion, it suggests that $Lp(a)$ catabolism is influenced by apoE affinities for lipoprotein receptor clearance pathways such as LDLR and LRP1. These data further suggest a competition for such receptors by apoE and $Lp(a)$ that affect circulating $Lp(a)$ levels. It may also explain the weak to modest inverse correlation noted with Lp(a) and triglycerides in this study and several other studies, with higher $Lp(a)$ levels being associated with lower triglyceride levels.^{19, 20} Figure 3 represents a hypothetical construct of these relationships.

ApoE isoforms at the protein level are characterized by differences in 1 or 2 amino acids: ε3 has Cys-112 and Arg-158, ε4 has Arg-112 and Arg-158 and ε2 has Cys-112 and Cys-158. The LDLR binding activity for ε_3 and ε_4 is reported to be normal but ε_2 has $< 2\%$ of normal LDLR binding activity and is associated with recessive inheritance and low penetrance (10%) .^{12, 21, 22} The binding of apoE proteins to LRP1 has not been well-studies, but ligand blotting experiments suggest that lipid-bound apoE2 has 30-50% of normal LRP1 binding

activity.23 The defective binding of apoE2 to the LDLR results in clinical expression of type III hyperlipoproteinemia in the presence of another factor (diabetes, obesity, hypothyroidism or estrogen deficiency) that overwhelms the capacity of apoE2 to mediate remnant lipoprotein clearance due to increases in VLDL production or reduced LDLR expression. These amino acid differences also result in different affinities for triglyceride-rich lipoproteins that lead to different effects on remodeling of VLDL to LDL and in receptormediated remnant clearance.^{12, 24-30} The apoE4 protein is reported to prefer large, triglyceride-rich lipoproteins (VLDL and chylomicrons, while apoE3 and apoE2 proteins preferentially bind to small spherical HDL particles.^{31, 32} In that regard, the apoE4 isoform is associated with the lowest triglyceride levels but higher LDL-C. It is presumed that enrichment of apoE4 on VLDL accelerates its clearance from the circulation by liver LDLR, LRP1 and SDC1 consequently downregulating hepatic LDLR expression. In addition, the enrichment of apoE4 on VLDL can outcompete LDL binding to LDLR due to the 20-fold greater affinity of apoE3 and apoE4 for LDLR compared to apoB100, further increasing circulating LDL-C.9, 33

Controversy exists whether the LDLR is involved in clearance of Lp(a) and data from cell culture, animal and human studies have given conflicting results. Initial studies revealed that the clearance rate of $Lp(a)$ was similar when radiolabeled $Lp(a)$ is injected in very small numbers of human with homozygous or heterozygous familial hypercholesterolemia or mice with or without intact LDLR receptors.^{15, 34} Additionally, statins increase LDLR density but a seemingly paradoxical effect of statin-treatment on Lp(a) levels occurs and statins do not lower plasma Lp(a) levels. In fact, a recent analysis of 3896 patients on multiple statins as well as different doses of statins modestly raised mean Lp(a) levels by a mean of 11% and up to 50% in some studies.³⁵ These studies argue against a major role of the LDLR in $Lp(a)$ clearance.

However, Lp(a) was shown to compete for LDL for binding to human LDLR in intact fibroblasts and that overexpression of the human LDLR in mice led to faster clearance of $Lp(a)$ ³⁶ Additionally, patients with familial hypercholesterolemia with abnormalities in the LDLR not only have higher LDL-C but also 1.5-2 times higher Lp(a) in a gene-dose relationship compared to their unaffected siblings.^{17, 18} These studies argue for a role of the LDLR in clearance of Lp(a). More recent cell culture studies have also had conflicting results, with one study showing that Lp(a) catabolism in human hepatoma cell lines and primary fibroblasts is inhibited by PCSK9 via the LDLR, which mediated the effects of PCSK9 on Lp(a) internalization.⁸ However, another study suggests the LDLR plays no role, but that PCSK9 may potentiate $Lp(a)$ secretion, a pathway inhibited by PCSK9 antibodies.³⁷ The current data also favor that the LDLR is involved in clearing Lp(a), but that this is also influenced by the underlying *APOE* genotype that also competes for the same receptor. However, it is not possible to quantitate this effect, or the effect of non-LDLR pathways, such as plasminogen and SRB1 receptors.^{7, 8}

The apolipoprotein(a) molecule is large with molecular mass ∼200-900 KD and often larger than apolipoprotein B-100. It is covalently linked by a disulfide bond at cysteine number 4326 on apoB which is near the apoB docking site that binds to the LDLR. Thus, the apolipoprotein(a) of $Lp(a)$ may cause the apoB of $Lp(a)$ to be sterically hindered in its

interaction with the LDLR and thus slow Lp(a)'s clearance. This is supported by the fact that $Lp(a)$ has slower clearance rate than LDL, approximately a day longer with a fractional catabolic rate (FCR) of 0.22 pools/day versus FCR of 0.37 pools/day for LDL, 38 , 39 and that when apolipoprotein(a) synthesis is inhibited by antisense oligonucleotides (ASO), LDL-C is significantly reduced. The effect of the apolipoprotein(a) ASO on LDL is independent of effects on apoB synthesis and LDL- production, $40, 41$ which is in agreement with the different metabolic production routes for $Lp(a)$ and LDL production.⁴²

This study also demonstrates that LDL-C levels and apolipoprotein B-100 variables distribute in the same direction as $Lp(a)$ mass and $Lp(a)$ -C. Despite this, there is almost negligible correlation between Lp(a) and LDL-C or apoB due to different genetic influences in production of each. Despite the fact that Lp(a), unlike LDL, is not derived from a VLDL precursor the mechanisms associated with elevation of each may be similar. One may postulate that when apoE is present on larger chylomicron remnants and VLDL particles, it competes for binding to LDLR and LRP1, thereby slowing their clearance and leading to higher LDL-C and Lp(a) levels. When there is relatively high affinity for these receptors, such as apoE4(and apoE3, it leads to higher LDL-C, apoB and $Lp(a)$. In contrast, when there is lower affinity, such as with apoE2, LDL and Lp(a) particles can clear faster. In addition, the slower conversion of VLDL to LDL with ε2 genotype, leads to lower LDL levels, which further enhances Lp(a) clearance due to less LDL competition. The additional increment in circulating Lp(a) levels in $\varepsilon 4/\varepsilon 4$ patients is likely explained by the fact the $\varepsilon 4$ partitions preferentially on triglyceride-rich lipoproteins and thus generates a bigger mass of lipoproteins to outcompete Lp(a) binding.

It is also possible that LRP1 can be responsible for the observed apoE-Lp(a) correlation. The apoE2 isoform has negligible binding to LDLR $(< 2\%$ compared to ϵ 3). If LDLR was responsible for our observed association one could expect to see a reduction in plasma Lp(a) and Lp(a)-cholesterol levels between ε 3/ ε 3 and ε 2/ ε 2 patients greater than the observed 27% and 14%. In contrast LDL-C, LDL-P and apoB levels, both cleared by LDLR, are 50-55% lower in ϵ 2/ ϵ 2 patients. Binding of the ϵ 2 isoform to LRP1 is only reduced by 50-70% and can possibly explain the less drastic reduction in Lp(a) levels in ε 2/ ε 2 patients compared to LDL and apoB. The underlying mechanisms of elevation of Lp(a) in different APOE isoforms are evidently more complex and whether LDLR and LRP1 receptors pay a role in this relationship needs to be determined in experimental studies.

Limitations of this study are the lack of data on race and lipid-modifying therapies. This study provides a rationale to study the role of apoE in explaining differences in $Lp(a)$ and in therapeutic interventions such as with PCSK9 inhibitors and antisense oligonucleotides to Lp(a) lowering. $40, 43$

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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Abbreviations

Highlights

• Lp(a) levels were 65% higher in ε4/ε4 compared to ε2/ε2 genotypes.

- **•** LDL-C, apoB, directly measured Lp(a)-C, LDL-C corrected for Lp(a)-C content, LDL particle number and small dense LDL also had similar patterns.
- **•** Triglyceride and hsCRP levels were highest in ε2/ε2 and lowest in ε4/ε4 genotype.
- These data suggest that circulating Lp(a) levels are not only genetically determined by hepatocyte apolipoprotein(a) synthesis, but can also be influenced by the APOE genotype possibly due to apoE isoform differences in lipoprotein clearance pathways.

Figure 1.

Relationship of $APOE$ genotypes (prevalence shown in panel A) to $Lp(a)$ mass (B), $Lp(a)$ -C (C), LDL-C (D), LDL-C corr (E), apoB (F), LDL-particle number (LDL-P) (G), triglycerides (H) and small dense LDL (J).

Relationship of Lp(a) mass to Lp(a)-C and LDL-C.

Figure 3.

Conceptual rendition of the potential role of apoE, LDLR, LRP1 in the catabolsim of Lp(a). ApoE on triglyceride-rich lipoproteins (TRLs) compete with Lp(a) for binding to LDLR and LRP1 on hepatocytes. (A) ApoE2 is the lower affinity isoform for LDLR and LRP1, which allow LDL and Lp(a) particles to clear faster. (B-C) Relatively high affinity isoforms, such as apoE4 and apoE3 favor hepatic clearance of TRLs via LDLR and LRP1 over LDL and Lp(a). This results in elevated LDL-C, apoB and Lp(a) levels. (C) ApoE4 partitions preferentially on TRLs and thus generates a bigger mass of lipoproteins to outcompete Lp(a) binding.

Table 1

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The data is presented as mean (SD) or median (IQR).

11te caat is prosumed as incan (2017) of incoming to the second of the control of S6,853 in e3/e3, 34,995 in e3/e4, and 142 in e4/e4 groups.
For Lp(a)-C there were 667 patients in e2/e2, 84 in e2/e3, 62 in e2/e4, 86,853 in For Lp(a)-C there were 667 patients in e2/e2, 84 in e2/e3, 62 in e2/e4, 86,853 in e3/e3, 34,995 in e3/e4, and 142 in e4/e4 groups.

J.