Susceptibility of low-density lipoprotein particles to aggregate depends on particle lipidome, is modifiable, and associates with future cardiovascular deaths

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Aims

Low-density lipoprotein (LDL) particles cause atherosclerotic cardiovascular disease (ASCVD) through their retention, modification, and accumulation within the arterial intima. High plasma concentrations of LDL drive this disease, but LDL quality may also contribute. Here, we focused on the intrinsic propensity of LDL to aggregate upon modification. We examined whether inter-individual differences in this quality are linked with LDL lipid composition and coronary artery disease (CAD) death, and basic mechanisms for plaque growth and destabilization.

See page 2574 for the editorial comment on this article (doi: 10.1093/eurheartj/ehy387)
We developed a novel, reproducible method to assess the susceptibility of LDL particles to aggregate during lipolysis induced ex vivo by human recombinant secretory sphingomyelinase. Among patients with an established CAD, we found that the presence of aggregation-prone LDL was predictive of future cardiovascular deaths, independent of conventional risk factors. Aggregation-prone LDL contained more sphingolipids and less phosphatidylcholines than did aggregation-resistant LDL. Three interventions in animal models to rationally alter LDL composition lowered its susceptibility to aggregate and slowed atherosclerosis. Similar compositional changes induced in humans by PCSK9 inhibition or healthy diet also lowered LDL aggregation susceptibility. Aggregated LDL in vitro activated macrophages and T cells, two key cell types involved in plaque progression and rupture.

Conclusion

Our results identify the susceptibility of LDL to aggregate as a novel measurable and modifiable factor in the progression of human ASCVD.

Keywords

Low-density lipoprotein • Atherosclerosis • Cardiovascular death • Sphingomyelin • Lipidomics

Translational perspective

Accumulation of low-density lipoprotein (LDL)-derived cholesterol in the arterial wall causes atherosclerotic cardiovascular disease (ASCVD). High plasma concentrations of LDL drive this disease, but LDL quality may also contribute. Here, inter-individual differences in LDL lipidome were found to determine the susceptibility of LDL to aggregate during lipolysis by human recombinant secretory sphingomyelinase. The presence of aggregation-prone LDL in plasma predicted future cardiovascular death in coronary artery disease patients. Interventions in pre-clinical models to rationally alter LDL composition lowered its susceptibility to aggregate and slowed atherosclerosis development. Our results identify the susceptibility of LDL to aggregate as a novel measurable and modifiable factor in the progression of human ASCVD.

Introduction

An elevated plasma concentration of low-density lipoprotein cholesterol (LDL-C) is a primary causal factor in the development of atherosclerotic cardiovascular disease (ASCVD) and significantly contributes to the total cardiovascular risk. However, even after efficient LDL-C-lowering, a substantial residual risk for ASCVD events remains. Atherosclerosis arises from subendothelial retention, or trapping, of LDL within the arterial intima, and several steps are required for plasma LDL-C to provoke normal arteries to become diseased. The retained lipoproteins become modified by arterial-wall enzymes and oxidants, tend to aggregate, and aggregated lipoprotein-derived particles are found both in human and in experimentally induced atherosclerotic lesions in animal models. The initial processes triggering aggregation of LDL particles have been proposed to include lipid peroxidation and proteolytic and lipolytic digestion of LDL by local enzymes, such as the mast cell chymase having chymotrypsin-like activity, the group V secretory phospholipase A2 (PLA2), which is produced by macrophages, as well as the secretory sphingomyelinase (SMase), which is released by macrophages and endothelial cells. Aggregation enhances the binding of lipoproteins to the arterial extracellular matrix, and their large size makes egress back across the endothelium nearly impossible. Moreover, aggregated LDL induces the formation of foam cells, a hallmark of lesions at all stages of atherogenesis. Indeed, the development of an atherosclerotic lesion involves a series of maladaptive responses of innate and adaptive immune cells to the retained, modified, and aggregated lipoprotein-derived material.

In this study, we focused on the intrinsic susceptibility of circulating LDL particles to aggregate upon modification, and, for the first time, examined inter-individual differences in this quality. This study aimed to determine whether the degree of aggregation susceptibility of LDL can predict future cardiovascular deaths and whether it can be modified by nutritional or medical treatment.

Materials and methods

Human plasma

Human blood plasma samples were obtained from healthy volunteers (Finnish Red Cross Blood Service, Helsinki, Finland), 100 samples derived from subjects participating in the Health 2000 Health Examination Survey, 48 samples from Corogene survey, 57 samples from SYSIDIET (Systems biology in controlled dietary interventions and cohort studies) survey, 29 samples from the 18-week diet group and 28 samples from the 24-week diet group, and 40 samples from the EQUATOR study.

The use of human material conformed to the principles outlined in the Declaration of Helsinki, and the studies were approved by the local ethics committees. Written informed consent was obtained from all participants.

Isolation of LDL and lipid and lipoprotein measurements

Lipid measurements

Fasting plasma total cholesterol and triglycerides were enzymatically measured (Roche Diagnostics, GmbH, Mannheim, Germany). ApoB-100 content was measured with ELISA-kit (MABTECH, Nacka, Sweden).

LDL isolation

LDL (d = 1.019 to 1.063 g/mL) was isolated from plasma by KBr-based sequential ultracen trifugation. LDL concentrations are expressed as their protein concentrations, which were determined by the BCA protein assay (Pierce, Rockford, USA) using bovine serum albumin as a standard, or as apoB-100 concentration determined by ELISA.
Measurement of LDL aggregation

Development of a method to quantify person-to-person variability in LDL aggregation-susceptibility is available in Supplementary material online, Methods and Figures S1–S3. In the assay we developed, LDL isolated from human plasma was extensively dialysed against 20 mM MES buffer, pH 5.5, containing 150 mM NaCl, 2 mM MgCl₂, 2 mM CaCl₂, and 50 μM ZnCl₂. The sample was diluted with the same buffer to give a final concentration of 0.2 mg of apoB-100/mL, then human recombinant secretory sphingomyelinase (hrSMase) was added to give a final enzyme concentration of 75 μg/mL, and the mixture was incubated at +37°C. The size of LDL was determined immediately and the hourly up to 6 h. An aliquot was taken at the same time points for phosphorylcholine measurement.

The degree of sphingomyelins (SM) hydrolysis was determined by measuring the phosphorylcholine content from the samples with Amplex Red reagent (Invitrogen).

SM- PC-, and LPC-enrichment of LDL ex vivo

LDL was enriched ex vivo with SM, PC, or LPC using phospholipid vesicles, as described in detail in Supplementary material online, Methods.

Mice

Large 'empty' vesicle-treated mice

Human APOB transgenic, Ldrl-/- mice on a chow diet, with food and water received ad libitum (13–19 weeks old for control with phosphate-buffered saline (PBS) and 19 weeks old for large 'empty' vesicle (LEV), weight 30–33 g; n = 16 per group) were injected once with PBS or with LEVs (also known as large unilamellar vesicles, 100-nm in diameter; dosed at 1000 mg PC/kg body weight). One hour after PBS or LEVs injection, plasma was collected, and the d < 1.063 g/mL KBr fraction was isolated using ultracentrifugation. Because LEVs can appear in the LDL density range, we collected the supernatant fraction after ultracentrifugation, loaded it onto a Superose 6 HR column (size-exclusion FPLC), and eluted with 150 mM NaCl, 1 mM EDTA pH 7.4. LDL fractions, which came out after the peak for LEVs and VLDL, were pooled and re-loaded onto the Superose 6 HR column, eluted with 150 mM NaCl, 1 mM EDTA pH 7.4, at which point no peak for LEVs or VLDL was detectable. LDL fractions were pooled in pairs (sample size, n = 16) and protein concentration was measured. The animal procedures were approved by the Animal Ethical Committee at the Gothenburg University.

Myriocin-treated mice

Male Ldrl-/-, Apob transgenic, Ldrl-/- mice on the C57BL/6 genetic background were obtained from Jackson Laboratory (Bar Harbor, ME, USA) and housed in the National Laboratory Animal Center of the University of Eastern Finland. Mice were divided into control (n = 11) and myriocin (n = 11) groups. The mice were fed on an high-fat atherogenic diet (21% milk fat, 0.2% cholesterol; Harlan Teklad; TD98137; colloquially called the ‘Western’ diet) from 14 to 22 weeks of age onwards, with food and water received ad libitum. Myriocin (0.3 mg/kg) (Biomol Research Laboratories Inc.) or PBS as control was injected intraperitoneally (i.p.) three times per week for 10 weeks. After 10 weeks on high-fat diet with myriocin/PBS treatment, mice were fasted for 4 h and terminal anaesthetised with isoflurane inhalation (Vetflurane 1000 mg/g, Virbab animal health). Blood was collected by heart puncture. These animal procedures were approved by the National Animal Experiment Board of Finland and carried out in accordance with the guidelines of The Finnish Act on Animal Experimentation.

Soat2-/-mice

Human APOB transgenic, Ldrl-/-, Soat2-/-, and human APOB transgenic, Ldrl-/- expressing sterol O-acyltransferase 2 (SOAT2) mice were fed on a diet rich in co-mono-saturated fat26 for 8 months, after which plasma was collected and LDL particles were isolated by ultracentrifugation. These animal procedures were approved by the Institutional Animal Care and Use Committee at Wake Forest University Health Sciences.

Assessment of atherosclerotic lesions

The degree of atherosclerosis was assessed by Sudan IV staining of the aortas as described in Supplementary material online.

Lipid mass spectrometry analyses

LDL lipids were analysed by mass spectrometry as described in Supplementary material online.

Circular dichroism analyses

The secondary structure of apoB-100 in LDL particles was determined by circular dichroism as described previously27 and in Supplementary material online.

Cell culture

Cell culture material and methods are available in Supplementary material online.

Mathematical modelling and statistical analyses

Mathematical modelling and statistical analyses are available in Supplementary material online.

Results

Measurement of the susceptibility of LDL to aggregate ex vivo

We developed a novel, reproducible method to quantify donor-to-donor variation in the susceptibility of LDL particles to aggregate (see Supplementary material online, Methods and Figures S1–S3). LDL was isolated from plasma samples by ultracentrifugation, aggregation of each LDL preparation was induced ex vivo by incubation with hrSMase, and the kinetics of aggregation were followed in real time by measuring the growth of the aggregates by dynamic light scattering (Figure 1A). Other agents to modify LDL ex vivo produced far smaller aggregates with negligible discrimination between individuals (see Supplementary material online, Figure S1a–e). In the absence of any modifying agent, LDL particles show no sign of aggregation (Supplementary material online, Methods).

We used our hrSMase-based assay to screen LDL aggregation susceptibility in samples derived from the Finnish Health 2000 Health Examination Survey30 which comprised largely healthy individuals (n = 100, Table 1, Figure 1B). To quantify the inter-individual variation in the aggregation susceptibility of LDL, we first developed a population-based generalized mixed-effect model (see Supplementary material online, Figure S3a). As described in the Supplementary material online, Methods, these data revealed that the inflection points in the curves of aggregate size vs. incubation time readily distinguished the aggregation susceptibility of the different LDL samples. Further, we found that LDL aggregate size at the 2-h time point correlated tightly and significantly with the inflection point (see Supplementary material...
Aggregation-prone LDL predicts CAD death

online, Figure S3b, rho = -0.961, P < 0.001). Importantly, the extent of aggregation at 2 h clearly identified subjects having extremely aggregation-prone LDL particles (Figure 1C, Quartile 1). Therefore, in further assays, aggregate size at this time point was used as a measure of LDL aggregation susceptibility.

**The susceptibility of LDL to aggregate predicts future cardiovascular deaths**

We next measured the aggregation susceptibility of LDL isolated from plasma samples derived from patients with clinically diagnosed coronary artery disease (CAD). The samples were from a nested case–control study that had been designed using samples from the Finnish Corogene study. The cases in that study included all patients who had experienced coronary death within an average follow-up of 2.5 years. Control patients were selected from the group who had no cardiovascular events during the follow-up period (Stable CAD group), and they were pairwise matched based on conventional CAD risk factors, statin use, and coronary stenosis index. The plasma samples selected for this study (n = 48) were from non-diabetic males, all of whom had ≥50% coronary stenosis (Table 2).

We again observed substantial inter-individual differences in the aggregation susceptibility of the isolated LDL particles. Importantly, in the CAD Death group, LDL particles aggregated significantly faster than in the Stable CAD group, the median sizes of the aggregates after incubation for 2 h being 1500 nm (range 150–3200 nm) and 940 nm (range 90–1990 nm), respectively (Figure 1D). Moreover, the 2-h aggregate sizes of LDL samples in both CAD groups were significantly higher than in the 100 LDL samples obtained from the Health 2000 study; median 90–1990 nm, respectively (Figure 1D). LDL aggregation at 2 h was not associated with the initial sizes of LDL particles, nor did it associate significantly with plasma concentrations of LDL-C, apoB-100, C-reactive protein (hsCRP), or lipoprotein (a), nor with statin use, age or smoking, but showed a negative correlation with plasma triglyceride levels (see Supplementary material online, Tables S1 and S2).
The susceptibility of LDL particles to aggregate strongly associates with the particle lipid composition

The surface monolayer of LDL particles comprises phospholipids, free cholesterol, ceramides (Cer), and a single copy of apoB-100 as the principal structural apolipoprotein of the particle (Figure 2A). Phosphatidylcholines (PC) are the major phospholipid class, followed by sphingomyelins (SM), and lysophosphatidylcholines (LPC). The surface also contains small amounts of other classes of phospholipids and ceramides. The particle core contains mainly cholesteryl esters (CE) and triacylglycerols (TAG). The compositions of isolated LDL preparations from the Health 2000 and Corogene studies described above were determined by quantitative mass spectrometry-based lipidomics. Volcano plots show the significant (P < 0.05) correlations between LDL aggregation and the molar percentages of specific lipids of the LDL surface (Figure 2B, C) and core (Figure 3A, B). Several sphingolipids (SMs and various forms of Cer) correlated positively (red) and various phosphatidylcholine (PC) species correlated negatively (blue) with LDL aggregation. Regarding the core lipids of LDL, the degree of LDL aggregation correlated negatively particularly with several 48–52 carbon TAGs in both cohorts (Figure 3A, B). Of note, of the lipids that significantly associate with LDL aggregation, the ceramides and TAG 50:4 differed significantly between the Stable CAD and CAD Death groups, ceramides being higher and TAG 50:4 lower in the case group.

**Direct enrichment LDL with different phospholipids changes aggregation susceptibility of LDL and conformation of apoB-100**

To determine causal effects of lipid composition on LDL aggregation, we next isolated LDL from four healthy volunteers and enriched the LDL with SM 18:1/16:0, PC 16:0/18:1, or LPC 16:0. Changes in the relative proportions of phospholipids in these lipid-enriched LDL particles were small (see Supplementary material online, Figure 5A and the final compositions were well within ranges we observed in other human LDL samples. Although the aggregability of control LDL from the four donors varied considerably (see Supplementary material online, Figure 5B, black lines), in each case the LDL preparations enriched with SM became more susceptible to aggregation during incubation with hrSMase, while LDL preparations enriched with PC or LPC became less susceptible. We know from previous studies that SMase-treatment of LDL induces conformational changes in apoB-100 that expose otherwise hidden segments of apoB-100 that mediate particle aggregation. In human subjects, decreases in LDL-SM by dietary change, or by PCSK9 inhibition decreased LDL aggregation susceptibility

To determine if a change in LDL lipid composition changes the aggregation susceptibility of LDL, we analysed samples from two different interventions: (i) SYSDIET, a dietary intervention, in which healthy volunteers with features of the metabolic syndrome were randomly assigned to either a Healthy Nordic diet (n = 33) or to a Control diet (n = 24) for 18 or 24 weeks and (ii) EQUATOR, a randomised placebo-controlled phase II trial of a fully human monoclonal antibody RG7652 that inhibits the function of proprotein convertase subtilisin/kexin type 9 (PCSK9, n = 25; placebo, n = 15). Fasting plasma samples were obtained at baseline and 29 days after treatment.

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First, we analysed the aggregation of LDL from plasma samples that had been collected from the Finnish participants in the SYSDIET study. Supplementary material online, Table S3 shows the clinical characteristics of these subjects at baseline and the end of the study, and Supplementary material online, Figure S5 shows the changes in
the macro- and micro-nutrient compositions of what each subject consumed based on food diaries at the beginning and at the end of the study.\textsuperscript{22, 23} In the Healthy Nordic diet group, LDL aggregation size at 2 h vs. LDL surface lipids in (B) Health 2000 samples and (C) in Corogene samples. Red circles indicate positive correlations, and blue circles indicate negative correlations. The identities of only those lipids with significance correlation values ($P < 0.05$) are indicated. Cer, ceramide; LPC, lysoosphatidylcholine; PC, phosphatidylcholine; SM, sphingomyelin.

The susceptibility of low-density lipoprotein (LDL) to aggregate strongly correlates with the surface lipid composition of the particles. (A) LDL was isolated from plasma and LDL lipidome was analysed using mass spectrometry. Volcano plots showing Spearman correlation coefficients of LDL aggregate size at 2 h vs. LDL surface lipids in (B) Health 2000 samples and (C) in Corogene samples. Red circles indicate positive correlations, and blue circles indicate negative correlations. The identities of only those lipids with significance correlation values ($P < 0.05$) are indicated. Cer, ceramide; LPC, lysophosphatidylcholine; PC, phosphatidylcholine; SM, sphingomyelin.

**Figure 2** The susceptibility of low-density lipoprotein (LDL) to aggregate strongly correlates with the surface lipid composition of the particles. (A) LDL was isolated from plasma and LDL lipidome was analysed using mass spectrometry. Volcano plots showing Spearman correlation coefficients of LDL aggregate size at 2 h vs. LDL surface lipids in (B) Health 2000 samples and (C) in Corogene samples. Red circles indicate positive correlations, and blue circles indicate negative correlations. The identities of only those lipids with significance correlation values ($P < 0.05$) are indicated. Cer, ceramide; LPC, lysoosphatidylcholine; PC, phosphatidylcholine; SM, sphingomyelin.

Pharmacological and genetic interventions in vivo to render LDL resistant to aggregation

To further examine our model linking changes in LDL lipids with changes in the susceptibility of LDL to aggregate, we carried out three interventions that had previously been shown to induce changes in LDL lipid composition and to decrease atherosclerosis in hypercholesterolaemic animals, but, remarkably, without changing the plasma lipoprotein phospholipid composition.\textsuperscript{29} The clinical characteristics of EQUATOR trial subjects at baseline and the end of the study are described in Supplementary material online, Table 4. In the treatment group of the EQUATOR trial, LDL aggregation susceptibility decreased in two-thirds of the subjects, whereas in the placebo group, only small changes in LDL aggregation occurred during the trial (Figure 4D, E). In addition, the overall change in aggregation susceptibility between the groups was significantly different between the two treatment groups ($P = 0.035$). The decrease in LDL aggregation in the treatment group correlated with an increase in several PC species and a decrease in several SM species (Figure 4F). In the control group, only PC 16:0/18:2 correlated significantly with decreased LDL aggregation susceptibility (see Supplementary material online, Figure S6b).
concentrations of LDL-C.\textsuperscript{30–32} In the first intervention, we administer-
ted a single intravenous bolus injection of large 100-nm ‘empty’ vesicles (LEVs, also known as large unilamellar vesicles) composed of a single lipid, PC 16:0/18:1, into human APOB100 transgenic/Ldlr\textsuperscript{-/-} mice (n = 16) fed on a regular chow diet. Control APOB100 transgenic/Ldlr\textsuperscript{-/-} littermates (n = 16) received an intravenous injection of an equivalent volume of PBS. Plasma was collected 1 h after the injection, and LDL was purified sequentially by ultracentrifugation and size-exclusion chromatography. Treatment with LEVs substantially altered LDL lipid composition in vivo (see Supplementary material online, Figure S7) and rendered LDL nearly completely resistant to aggregation ex vivo, even after 24 h of incubation with hrSMase (Figure SA and inset).

In the second intervention, we suppressed SM biosynthesis in Ldlr\textsuperscript{-/-}/ApoA\textsuperscript{100/100} mice using myriocin, an inhibitor of serine-palmitoyl transferase, the rate-limiting enzyme in SM biosynthesis. Inhibition of this enzyme in mice leads to the generation of SM-palmitoyl transferase, the rate-limiting enzyme in SM biosynthesis. In the third intervention, we investigated the effect of the composition of the lipid core of LDL particles on their susceptibility to aggregate by using mice deficient in SOAT2, and enzyme also known as acyl-CoA: cholesterol acyltransferase-2 or ACAT2. LDL was isolated from the plasma of APOB100 transgenic/Ldlr\textsuperscript{-/-}/Soat2\textsuperscript{-/-} mice (n = 5) and APOB100 transgenic/Ldlr\textsuperscript{-/-}/Soat2\textsuperscript{+/+} littermates (n = 3). LDL particles from SOAT2-deficient mice are characterized by enrichment in polyunsaturated CEs and TAGs, when compared with LDL from control mice.\textsuperscript{26} Here, we found that LDL particles from Soat2\textsuperscript{-/-} mice were particularly aggregation-resistant (Figure SD), consistent with our data from human LDL (Figure 3).

Aggregated LDL induces MMP-7 secretion from macrophage foam cells and activates T-cells in vitro

To study maladaptive cellular responses relevant to atherosclerosis, we examined the effects of hrSMase-aggregated LDL vs. native LDL on cultured human primary monocyte-derived macrophages and murine T-cell hybridomas that had been raised against oxidized LDL.\textsuperscript{33} Aggregated LDL induced accumulation of cholesteryl ester-rich lipid droplets in the human primary monocyte-derived macrophages (Figure 6A, B), consistent with prior literature.\textsuperscript{16} We also analysed the concentrations of several matrix metalloproteinases (MMPs) in the culture media and found that foam cells induced with hrSMase-treated LDL, but not with acetylated LDL, secrete increased amounts of MMP-7 (Figure 6C), a protease considered to be an
Figure 4 A dietary intervention and PCSK9 inhibition in human subjects improves their low-density lipoprotein (LDL) composition and renders their particles less susceptible to aggregate. Plasma samples were obtained from the SYSDIET-study, where participants were placed on either an iso-caloric healthy Nordic diet (n = 33) or a control diet (n = 25) for 18 or 24 weeks and from the EQUATOR study, a randomized placebo-controlled phase II trial of a monoclonal antibody inhibiting the function of PCSK9, RG7652, (n = 25), or placebo (n = 15) for 29 days. LDL was isolated, and aggregation analysed from samples before and after the diet/treatment period. (A and B) LDL aggregate sizes at the 2-h time point are shown in the diet group and control group before and after the diet period. Each line represents one subject and blue lines show a decrease and red lines an increase in aggregate size. (D and E) LDL aggregate sizes at the 2-h time point are shown in the PSCK9 inhibitor group and placebo group before and after the treatment period. Each line represents one subject and blue lines show a decrease and red lines an increase in aggregate size. (C and F) Volcano plot showing the Spearman correlation coefficients of LDL aggregate size at 2 h vs. LDL surface lipids in the SYSDIET study and in the EQUATOR study. PC, phosphatidylcholine; PE, phosphatidylethanolamine; SM, sphingomyelin.

Table 3  Multiple regression explaining the effect of dietary changes on changes in the 2 h aggregate size in the SYSDIET group

<table>
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<th>Predictors</th>
<th>b</th>
<th>SE b</th>
<th>β</th>
<th>t</th>
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<th>R²</th>
<th>Adjusted R²</th>
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<td>4.23</td>
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<td>0.494</td>
<td>0.456</td>
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<td>Δ Dietary Vitamin E</td>
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<td>362.3</td>
<td>-0.746</td>
<td>-5.05</td>
<td>&lt;0.001</td>
<td></td>
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<tr>
<td>Δ Dietary sucrose</td>
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<td>208.3</td>
<td>0.398</td>
<td>2.70</td>
<td>0.012</td>
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n = 31.
important contributor to weakening, and ensuing rupture of atherosclerotic plaques.\textsuperscript{34}

In parallel with macrophages, T cells are also recruited to atherosclerotic lesions. Triggered by LDL that is taken up and presented by antigen-presenting cells, T cells can accelerate atherosclerosis in hypercholesterolaemic animals and promote features associated with plaque instability.\textsuperscript{18} Paradoxically, T-cell hybridomas raised against oxidized LDL do not react to oxidized LDL.\textsuperscript{33} Nonetheless, T cells with a similar set of clonotypic T-cell receptors in hypercholesterolaemic mice have been shown to participate in the growth of their atherosclerotic plaques.\textsuperscript{18} Here, we found that the degree of LDL aggregation induced by SMase associated positively with the degree of T-cell activation, as measured by the secretion of interleukin-2 (Figure 6D, left panel). In contrast, consistent with earlier data,\textsuperscript{33} oxidized LDL inhibited the T-cell response (Figure 6D, right panel).

**Discussion**

In this study, we show that the susceptibility of LDL particles to aggregate in the presence of hrSMase varies significantly amongst human subjects and depends on the lipid composition of their LDL particles. The presence of aggregation-prone LDL was associated with future CAD deaths independently of conventional CAD risk factors including plasma LDL-C concentration, smoking, and hypertension. Importantly, we show that the susceptibility of LDL particles to aggregate can be favourably modified in humans by nutritional and
medical interventions and in vivo in animals by altering LDL lipid composition.

Aggregated LDL has been suggested to promote atherogenesis by inducing lipid accumulation in the arterial wall both extra- and intracellularly. A major trigger for aggregation of LDL particles within the arterial wall is their digestion by the secretory SMase, and genetic deletion of this enzyme in hypercholesterolaemic animals dramatically retards atherosclerotic plaque development. The importance of SMase in human atherogenesis is reflected by the observation that large LDL aggregates isolated from human atherosclerotic lesions are enriched in ceramides, the lipolytic products of SMase action. Aggregated lipoprotein particles accumulating in human atherosclerotic lesions also show signs of other modifications, such as proteolysis, lipolysis of both the core and the surface lipids, and oxidation. Interestingly, studies in vitro have shown that these modifications promote sphingomyelinase-induced LDL modification. In this study, we extend these earlier findings and show that foam cells generated by incubating macrophages in the presence of SMase-aggregated LDL secreted MMP-7, a proteinase with a potential role in the rupture of human atherosclerotic plaques. Moreover, we show that LDL aggregated by SMase can trigger a potent T-cell response against apoB-100. This maladaptive immunological mechanism may accelerate the progression of atherosclerosis and the development of plaque instability. In fact, SMase-induced modification and aggregation of LDL represents the first pathophysiologically plausible modification of LDL ex vivo that enhances the ability of LDL to activate T-cell hybridomas linked with atherosclerosis.

The present data indicate that aggregation-prone human LDL particles are enriched in SM and ceramides, and that they contain less choline phospholipids (PC and LPC) and TAGs than aggregation-resistant LDL particles. Causality of these lipids in LDL aggregation susceptibility was established by altering their contents in isolated LDL in vitro, in humans by diet and by PCSK9 inhibition, and in three atherosclerotic mouse models in vivo. Thus, increase in vitamin E consumption was associated with decreased LDL aggregation, and, when the aggregation data were normalized for changes in the consumption of vitamin E, increased intake of sucrose was found to associate with accelerated aggregation. Interestingly, plasma levels of SM have been strongly influenced by genetic effects. Such influence could partly explain our observation that the aggregation susceptibility decreased in only two-thirds of the subjects in the healthy diet group. Similarly, inhibition of PCSK9 decreased LDL aggregation in two-thirds of the subjects.
SM-rich LDL from apoE−/− mice has previously been shown to be prone to the formation of large aggregates. Here, we used three atherosclerotic mouse models, in which we modified the composition of LDL particles in vivo. We demonstrate here that an increase in LDL-PC by intravenous injection of PC-containing LEVs, a pharmacologically induced decrease in LDL-SM with myriocin, an inhibitor of SM biosynthesis, and a genetically induced increase in polyunsaturated CEs and TAGs in LDL, each decreased the susceptibility of LDL particles to aggregate. Importantly, each of these treatments has been shown to reduce atherosclerosis in hypercholesterolaemic animals, notably without influencing plasma concentrations of cholesterol.26, 30–32, 42

In most studies examining the relationship between lipid markers and ASCVD risk, the lipid composition of whole plasma, rather than that of circulating LDL particles, has been determined. Importantly, prior and current data indicate that aggregated LDL has the potential to promote multiple steps along the path to atherosclerosis.

In summary, aggregation-prone LDL was found to predict death from cardiovascular causes independent of conventional atherosclerosis risk factors. Importantly, prior and current data indicate that aggregated LDL has the potential to promote multiple steps along the path to atherosclerosis.
the atherogenic pathway from LDL retention to maladaptive responses that include initiation and growth of atherosclerotic lesions, plaque destabilization, and plaque rupture. Any treatment that induces a favourable change in LDL lipid composition offers a means to attenuate LDL aggregation within the arterial wall and its deleterious consequences. These results emphasize the importance of LDL quality in human aSCVD. Moreover, measurement of the susceptibility of LDL to aggregate may serve as a predictive biomarker for the identification of patients at significant residual or unrecognized risk of cardiovascular morbidity and mortality and who might benefit from personalised, targeted interventions.

**Supplementary material**

**Supplementary material** is available at *European Heart Journal* online.

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**Conflict of interest:** T.V., M.H., and R.L. are employed by Zora Biosciences and A.B. by Roche. K.J.W. has ownership interests in Gemphire Therapeutics, Inc., which is developing an orally administered lipoprotein-lowering agent, and in Hygiae, Inc., which provides insulin management services in Northern Ireland and in Michigan, USA. K.J.W. is also the inventor of a number of patents on the use of large empty vesicles (LEV) in atherosclerotic cardiovascular disease. M.R., P.T.K., and K.O. have applied for a patent on analysis of LDL aggregation susceptibility using hSRMase. All other authors declared no conflict of interest.

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