Dysfunctional HDL as a Diagnostic and Therapeutic Target

Jonathan D. Smith

Abstract—The atheroprotective effects of HDL are mediated by several mechanisms, including its role in reverse cholesterol transport and via its antiinflammatory properties. However, not all HDL is functionally similar. HDL and apolipoprotein A-I may become dysfunctional or even proinflammatory and thus promote atherosclerosis. ApoAI posttranslational modification can have a large impact on its function. Myeloperoxidase modification of apoAI impairs its function as a cholesterol acceptor, and the molecular changes induced by myeloperoxidase have been studied in detail. These studies provide the basis for the development of an oxidant-resistant form of apoAI and clinical measures of HDL modification and dysfunction, which may be useful as a treatment criterion. (Arterioscler Thromb Vasc Biol. 2009;29:00-00.)

Key Words: HDL ■ apolipoprotein A-I ■ reverse cholesterol transport ■ myeloperoxidase ■ antiinflammatory

High-density lipoprotein cholesterol (HDL-C) is an independent protective factor for coronary artery disease (CAD), as demonstrated by numerous epidemiological studies, such as the Framingham Heart Study. In interventional settings, niacin, which effectively raises HDL levels, given as a monotherapy or combined with other drugs has been shown to reduce CAD and cerebrovascular events. There are many proposed pathways by which HDL may protect against CAD. HDL and its major protein constituent apolipoprotein A-I (apoAI) play prime roles in mediating reverse cholesterol transport (RCT), the transfer of cholesterol from peripheral tissues, such as arterial wall cells, to the liver for excretion, and this likely plays a central role in the mechanism of the atheroprotective effect of HDL. RCT involves many steps, including the removal of cholesterol from cells (through ABCA1, which is responsible for the formation of nascent HDL, along with ABCG1, and SR-BI), the maturation of HDL through lecithin cholesterol acyltransferase (LCAT)-mediated free cholesterol esterification, and the uptake and excretion of HDL cholesterol by the liver. HDL cholesterol esters can also be transferred to apoB containing lipoproteins through the action of cholesterol ester transfer protein (CETP), and this cholesterol pool can participate in RCT by delivery to the liver through LDL receptor mediated uptake. Although CETP inhibition raises HDL-C levels, the recent failure of torcetrapib, a CETP inhibitor in a clinical outcomes trial raised the specter that CETP inhibition does not lead to dysfunctional HDL. HDL has many other activities aside from its role in RCT that can also contribute to its protective mechanism. These include the removal or detoxification of oxidized sterols and phospholipids, antiinflammatory activity, antioxidant activity, antithrombotic activity, and its protective and healing activities on endothelial cells. So, HDL-cholesterol is the “good cholesterol,” but there are many unresolved questions: are all HDL particles equally good, does HDL from different subjects perform the same; can HDL become dysfunctional; and, can “good cholesterol” be made into “better cholesterol”? This review describes the evidence for dysfunctional HDL and its underpinnings, as well as the potential use of HDL functionality as a diagnostic tool and therapeutic target.

Evidence for and Causes of Dysfunctional HDL

Fogelman and colleagues developed an assay to measure the antiinflammatory activity of HDL by determining the extent to which HDL inhibits monocyte chemotaxis induced by LDL using an in vitro reconstituted artery wall model by the coculture of smooth muscle cells and endothelial cells. Other assays for HDL function include cell free antioxidant activity, inhibition of endothelial cell adhesion molecule expression, and the ability of HDL to act as an acceptor of cellular cholesterol. Navab, Fogelman, and colleagues using this artery wall model system have demonstrated several conditions in which HDL can lose its antiinflammatory properties, including during the acute phase response when serum...
amyloid A partially replaces apoAI in HDL, during influenza A infection, and in apolipoprotein AII transgenic mice.\textsuperscript{12,13,14} In a seminal study, Ansell et al discovered that HDL from CAD subjects who had high levels of HDL had less antiinflammatory activity, in this coculture assay, than HDL derived from healthy control subjects, thus indicating that HDL from CAD subjects is dysfunctional.\textsuperscript{10} In fact, HDL from many CAD patients was actually proinflammatory, thus increasing monocyte chemotaxis in response to LDL, unlike the HDL from healthy controls that reduced monocyte chemotaxis.\textsuperscript{10} There are many possible alterations between this dysfunctional HDL and normal functional HDL.

One possibility is a change in the protein composition of HDL. Human HDL particles are quite heterogeneous, encompassing a range of sizes and densities. Each HDL particle carries apoAI and may also carry other apolipoproteins, such as apoAII, apoAIV, apoE, apoCs. In addition, HDL is associated with a panoply of accessory proteins, including LCAT, phospholipid transfer protein (PLTP), paraoxonase 1 (PON1), myeloperoxidase (MPO), serum amyloid A1, (SAA1), and platelet-activating factor acetylhydrolase (PAAF-AH). The HDL proteome is quite large,\textsuperscript{15} and each HDL particle cannot accommodate all of the accessory proteins; thus, a minority of the HDL particles must be associated with each accessory protein. Changes in HDL protein composition attributable to infection, inflammation, or diabetes have been shown to be associated with decreased function.\textsuperscript{12,14,16} An HDL proteomic study of HDL\textsubscript{3} from different subjects found that the levels of PON1, PON3, and apoAI correlate with HDLs antioxidant activity.\textsuperscript{17} Also, mouse models have been used to determine the effects of HDL protein composition changes, for example, HDL isolated from transgenic mice over expressing apoAI or PLPT show reduced function compared to control HDL.\textsuperscript{18,19}

Many studies have been performed to investigate the changes in HDL associated with inflammation. de Beer and colleagues have shown extensive HDL remodeling after treatment of mice with endotoxin, or in humans after surgery, leading to the so-called acute phase HDL, in which SAA and group Iia secretory phospholipase A2 (sPLA\textsubscript{2}-IIa) are increased and apoAI levels (and CETP levels in humans) are decreased.\textsuperscript{19} Because SAA itself can act as an acceptor for cellular cholesterol via ABCA1, SR-BI, and other pathways,\textsuperscript{20–22} the consequences of acute phase HDL on HDL function and RCT must be determined experimentally. Post-surgical human serum containing acute phase HDL maintains most of its ABCA1 and ABCG1 dependent cholesterol acceptor activity despite decreased HDL-C and apoAI levels.\textsuperscript{23} The in vitro incubation of HDL with SAA, sPLA\textsubscript{2}-IIa, and CETP leads to the marked displacement of apoAI from HDL generating lipid-free or lipid-poor apoAI, expected to undergo more rapid catabolism, but also expected to be a good ABCA1-mediated acceptor of cellular lipids.\textsuperscript{23} The overexpression of SAA and SR-BI in mice via adenoviral vectors also leads to the production of small lipid poor apoAI particles which are more rapidly cleared.\textsuperscript{24} Recently, Reilly’s laboratory demonstrated that LPS treatment in mice decreases RCT, although this was mediated primarily through the inhibition of liver sterol excretion associated with decreased expression of hepatic ABCG5, ABCG8, and ABCB11.\textsuperscript{25}

Another factor that might make HDL dysfunctional is a change in the HDL-associated lipids. HDL may acquire oxidized lipids from cells and by exchange with other particles, or HDL lipids may be oxidized in situ. Lipid peroxides may interfere with HDL antioxidant, antiinflammatory, and cholesterol acceptor activities. For example, treatment of HDL with 15-lipoxygenase, an enzyme forming lipid peroxides, reduces HDL cholesterol acceptor and antiinflammatory activities.\textsuperscript{26,27} HDL carries the bulk of lipid hydroperoxides in plasma.\textsuperscript{28} These lipid hydroperoxides can be converted into less reactive lipid hydroxides through specific methionine residues of apoAI and apoAII, with the concomitant formation of methionine sulfoxide.\textsuperscript{29} Fully functional HDL may promote lipid hydroperoxide metabolism and its uptake and clearance by the liver, which would be protective.\textsuperscript{29} In contrast, dysfunctional HDL might promote the transfer of lipid hydroperoxides to apoB-containing lipoproteins and promote VLDL and LDL oxidation.\textsuperscript{30}

A prominent factor that can lead to HDL dysfunction is the posttranslational modification of apoAI. Copper-mediated oxidation of HDL leads to altered HDL migration on an agarose gel, apoAI proteolysis, and decreased ability of HDL to unload cholesterol esters from cholesterol-loaded macrophages.\textsuperscript{31} Malondialdehyde modification of HDL leads to similar changes in regard to HDL structure and function and is associated with the loss of lysine and tryptophan residues and apoAI polymerization.\textsuperscript{32} HDL from diabetic subjects has evidence of glycate apoAI and apoAII, and this glycated apoAI has altered structure and lipid binding activity.\textsuperscript{33,34} Similarly, HDL incubated with high glucose results in a reduction in paraoxonase activity and decreased antiinflammatory activity.\textsuperscript{35} Lipid peroxides added to human plasma can covalently modify apoAI.\textsuperscript{36} Also, incubation of HDL with activated neutrophils was shown to render apoAI more negatively charged and decrease its cellular cholesterol acceptor activity.\textsuperscript{37,38}

**Myeloperoxidase Modification of ApoAI**

Myeloperoxidase (MPO) is an enzyme found in neutrophils, monocytes, and some macrophages that uses hydrogen peroxide to generate chlorinating and nitrating oxidants, which play an important role in killing microorganisms. However, these same reactive species can also modify host proteins and lipids. MPO is enriched in human atheroma,\textsuperscript{39} and its presence may promote lesion progression, by increasing LDL oxidation, and block plaque regression, by modifications of apoAI/HDL that impair RCT. Bergt et al demonstrated that incubation of HDL with MPO, in a chlorinating reaction (MPO/H\textsubscript{2}O\textsubscript{2}/Cl\textsuperscript{–}) that produces HOCl (chlorine bleach), or with reagent HOCl (at a very high 100:1 ratio of HOCl:apoAI) leads to a loss of unsaturated fatty acids in phospholipids and cholesterol esters, and the loss of cholesterol acceptor activity.\textsuperscript{40} Bergt et al also showed that modification of lipid-free apoAI at an HOCl:apoAI ratio of 25:1 led to the loss of apoAI methionine residues,\textsuperscript{40} consistent with the high sensitivity of methionine to MPO/H\textsubscript{2}O\textsubscript{2}/Cl\textsuperscript{–}.\textsuperscript{41} Subsequently, it was shown that selective apoAI methionine oxidation does not disrupt its
structure, and actually leads to an increase in lipid binding and cellular lipid acceptor activities, although apoAI Met-148 modification by MPO is associated with loss of LCAT activation. Berg et al also used mass spectroscopy to identify specific alterations caused by reagent or MPO generated HOCl, and they confirmed the disappearance of the methionine-containing tryptic peptides with concomitant production of methionine sulfoxide-containing peptides. The cholesterol acceptor activity of recombinant HDL (rHDL) made by cholate dialysis using apoAI and phosphatidylcholine is much more sensitive to the HOCl treatment, with loss of activity starting at an HOCl:apoAI ratio of 5:1. In addition to decreased lipid acceptor activity, treatment, with loss of activity starting at an HOCl:apoAI ratio of 5:1.40 In addition to decreased lipid acceptor activity, Panzenboeck et al also showed that MPO- or HOCl-modified HDL was more susceptible to uptake and degradation by macrophages, thus turning HDL from a lipid-accepting lipoprotein to a lipid-loading lipoprotein. Although methionine and cysteine residues (apoAI has no Cys residues) are the most sensitive to MPO generated oxidants, tyrosine, lysine, tryptophan, and other residues are also targets, with 3-chlorotyrosine being used as a fingerprint for MPO oxidants, as HOCl uniquely forms this adduct.46,47

Since 2004, the combined Smith, Hazen, and Kinter labs at the Cleveland Clinic and the combined Heineke and Oram labs at the University of Washington have each examined the MPO-induced molecular alterations in apoAI and their functional significances. Both teams fundamentally agree that MPO modification of apoAI is physiologically relevant by demonstrating that: (1) apoAI in plasma and more so in arterial lesions is a selective target of MPO modification that leads to the nitration and chlorination of specific apoAI tyrosine residues; (2) plasma apoAI nitro- and chloro-tyrosine levels are higher in coronary artery disease patients than in control subjects; and (3) apoAI tyrosine chlorination, whether in endogenous plasma or after in vitro MPO-mediated modification, is associated with the selective loss of ABCA1-mediated cholesterol acceptor activity, such that apoAI cholesterol acceptor activity was inversely correlated with apoAI nitro- and chloro-tyrosine levels. Wu et al demonstrated LCAT binding to apoAI at residues 159 to 180 in rHDL and that Tyr166 is required for LCAT activation, such that MPO-induced loss of LCAT activation correlates with loss of the Tyr166-containing parent peptide. Additionally, Zheng et al demonstrated direct binding of MPO with apoAI and identified residues 190 to 203 in apoAI helix 8 as the region that bind to MPO, thus providing a mechanism for the selective modification of apoAI in plasma. However, the precise mechanism by which MPO modification renders apoAI dysfunctional remains controversial.

Both groups using mass spectroscopy studies identified apoAI Tyr192, within helix 8, as the most sensitive site to MPO mediated chlorination. Furthermore, Berg et al demonstrated, using short synthetic peptides, that tyrosine chlorination is maximally stimulated when the tyrosine is 3 residues away from a lysine residue, which is the case for the sensitive Tyr192. The University of Washington group claimed that MPO impairment of the ABCA1-mediated cholesterol acceptor activity of apoAI is through methionine oxidation and site-specific chlorination of Tyr192, as treatment of MPO modified apoAI with the enzyme methionine sulfide reductase could partially restore the cholesterol acceptor activity of apoAI, particularly in a recombinant apoAI (r-apoAI) isoform with Try192 replaced by Phe. On the other hand, the Cleveland Clinic group made r-apoAI with all 7 Tyr residues replaced by Phe (7YF isoform), and found that it is equally susceptible to MPO or HOCl loss of cholesterol acceptor activity as the wild-type isoform. Furthermore, replacement of the 3 Met residues in apoAI with Val residues actually increased susceptibility to low doses of H2O2 in the complete MPO chlorination system, showing that apoAI Met residues can absorb HOCl oxidation without loss of function, hence protecting the other residues, and in agreement with the prior finding. Thus, the site-directed substitution and cholesterol efflux data indicate that neither methionine nor tyrosine serve as the oxidant sensitive residue involved in MPO-induced apoAI inactivation. Thus, the levels of plasma apoAI nitro- and chloro-tyrosine may serve as physiological useful and specific markers of MPO activity in vivo, even though tyrosine modification does not appear to be responsible for turning the “good” HDL-cholesterol “bad.”

**Discovery of MPO-Resistant ApoAI**

The Cleveland group extended and confirmed several prior observations on the effects of MPO or HOCl on apoAI structure, specifically the loss of alpha helix content, and the loss of tryptophan and lysine residues. MPO treatment of apoAI leads to the transient conversion of apoAI lysine residues to lysine e-chloramine that spontaneously decompose to α-amino acid, a product that is enriched in apoAI recovered from atheroma versus plasma. However, apoAI with lysine residues modified and rendered less reactive by reductive methylation is not protected from MPO induced loss of function. Thus, lysine modification by MPO is not likely to be the initiating event in formation of dysfunctional HDL. The Cleveland group used mass spectrometry to identify mono- and di-hydroxytryptophan at all 4 Trp positions in apoAI isolated from human atheroma. Thus, Peng et al created r-apoAI with all 4 Trp residues replaced. The replacement by 4 Leu residues leads to an inactive 4WL isoform, whereas the replacement by 4 Phe residues creates an active 4WF isoform. Thus, apoAI activity appears to require both hydrophobic and aromatic residues in the Trp positions. When the 4WF and wild-type apoAI isoforms were treated with increasing oxidant stress from MPO or HOCl, the 4WF isoform is markedly resistant to loss of cholesterol acceptor activity. Thus, the 4WF apoAI isoform is MPO resistant and may be a better therapeutic reagent to promote the regression of atherosclerotic plaques, an environment where MPO and MPO-derived oxidants are abundant. If this strategy is successful, then “good” cholesterol can be made “better.”

**Diagnostic Use of Dysfunctional HDL**

The Figure summarizes the central role that inflammation plays in creating dysfunctional HDL and reduced RCT. Biomarkers associated with dysfunctional HDL may be useful for identifying subjects at most risk for a coronary event. Hazen and colleagues reported that plasma MPO levels

Sources of Funding

A portion of the work described in this review was supported by the NIH (HL066082).

Disclosures

None.

References


Sources of Funding

A portion of the work described in this review was supported by the NIH (HL066082).

Disclosures

None.

References

by guest on August 29, 2017 http://atvb.ahajournals.org/ Downloaded from

31. Nagano Y, Arai H, Kita T. High density lipoprotein loses its effect to
30. McPherson PA, Young IS, McKibben B, McEneny J. High density
28. Bowry VW, Stanley KK, Stocker R. High density lipoprotein is the major
22. Abe-Dohmae S, Kato KH, Kumon Y, Hu W, Ishigami H, Iwamoto N,
25. McGillicuddy FC, de la Llera MM, Hinkle CC, Joshi MR, Chiquoine EH,
22. Abe-Dohmae S, Kato KH, Kumon Y, Hu W, Ishigami H, Iwamoto N,
25. McGillicuddy FC, de la Llera MM, Hinkle CC, Joshi MR, Chiquoine EH,
40. Bergt C, Reicher H, Malle E, Sattler W. Hypochlorite modification of
43. Shao B, Cavigiolio G, Brot N, Oda MN, Heinecke JW. Methionine oxidation
43. Shao B, Cavigiolio G, Brot N, Oda MN, Heinecke JW. Methionine oxidation
38. Zhang R, Brennan ML, Fu X, Byun J, O’brien K, McDonald TO, Singh P,
37. Brubaker G, Peng DQ, Somerlot B, Abdollahian DJ, Smith JD. Apo-
27. Kircher G, Ponsin G, Berthozene F. Characterization of the non enzymatic
glycation of high density lipoprotein in diabetic patients. Diabetes Metab.

22. Abe-Dohmae S, Kato KH, Kumon Y, Hu W, Ishigami H, Iwamoto N,
25. McGillicuddy FC, de la Llera MM, Hinkle CC, Joshi MR, Chiquoine EH,
25. McGillicuddy FC, de la Llera MM, Hinkle CC, Joshi MR, Chiquoine EH,
40. Bergt C, Reicher H, Malle E, Sattler W. Hypochlorite modification of
43. Shao B, Cavigiolio G, Brot N, Oda MN, Heinecke JW. Methionine oxidation
43. Shao B, Cavigiolio G, Brot N, Oda MN, Heinecke JW. Methionine oxidation
38. Zhang R, Brennan ML, Fu X, Byun J, O’brien K, McDonald TO, Singh P,
37. Brubaker G, Peng DQ, Somerlot B, Abdollahian DJ, Smith JD. Apo-
27. Kircher G, Ponsin G, Berthozene F. Characterization of the non enzymatic
glycation of high density lipoprotein in diabetic patients. Diabetes Metab.

22. Abe-Dohmae S, Kato KH, Kumon Y, Hu W, Ishigami H, Iwamoto N,
25. McGillicuddy FC, de la Llera MM, Hinkle CC, Joshi MR, Chiquoine EH,
25. McGillicuddy FC, de la Llera MM, Hinkle CC, Joshi MR, Chiquoine EH,
40. Bergt C, Reicher H, Malle E, Sattler W. Hypochlorite modification of
43. Shao B, Cavigiolio G, Brot N, Oda MN, Heinecke JW. Methionine oxidation
43. Shao B, Cavigiolio G, Brot N, Oda MN, Heinecke JW. Methionine oxidation
38. Zhang R, Brennan ML, Fu X, Byun J, O’brien K, McDonald TO, Singh P,
37. Brubaker G, Peng DQ, Somerlot B, Abdollahian DJ, Smith JD. Apo-
27. Kircher G, Ponsin G, Berthozene F. Characterization of the non enzymatic
glycation of high density lipoprotein in diabetic patients. Diabetes Metab.

22. Abe-Dohmae S, Kato KH, Kumon Y, Hu W, Ishigami H, Iwamoto N,
25. McGillicuddy FC, de la Llera MM, Hinkle CC, Joshi MR, Chiquoine EH,
25. McGillicuddy FC, de la Llera MM, Hinkle CC, Joshi MR, Chiquoine EH,
40. Bergt C, Reicher H, Malle E, Sattler W. Hypochlorite modification of
43. Shao B, Cavigiolio G, Brot N, Oda MN, Heinecke JW. Methionine oxidation
43. Shao B, Cavigiolio G, Brot N, Oda MN, Heinecke JW. Methionine oxidation
38. Zhang R, Brennan ML, Fu X, Byun J, O’brien K, McDonald TO, Singh P,
37. Brubaker G, Peng DQ, Somerlot B, Abdollahian DJ, Smith JD. Apo-
27. Kircher G, Ponsin G, Berthozene F. Characterization of the non enzymatic
glycation of high density lipoprotein in diabetic patients. Diabetes Metab.

22. Abe-Dohmae S, Kato KH, Kumon Y, Hu W, Ishigami H, Iwamoto N,
25. McGillicuddy FC, de la Llera MM, Hinkle CC, Joshi MR, Chiquoine EH,
25. McGillicuddy FC, de la Llera MM, Hinkle CC, Joshi MR, Chiquoine EH,
40. Bergt C, Reicher H, Malle E, Sattler W. Hypochlorite modification of
43. Shao B, Cavigiolio G, Brot N, Oda MN, Heinecke JW. Methionine oxidation
43. Shao B, Cavigiolio G, Brot N, Oda MN, Heinecke JW. Methionine oxidation
38. Zhang R, Brennan ML, Fu X, Byun J, O’brien K, McDonald TO, Singh P,
37. Brubaker G, Peng DQ, Somerlot B, Abdollahian DJ, Smith JD. Apo-
27. Kircher G, Ponsin G, Berthozene F. Characterization of the non enzymatic
glycation of high density lipoprotein in diabetic patients. Diabetes Metab.

22. Abe-Dohmae S, Kato KH, Kumon Y, Hu W, Ishigami H, Iwamoto N,
25. McGillicuddy FC, de la Llera MM, Hinkle CC, Joshi MR, Chiquoine EH,
25. McGillicuddy FC, de la Llera MM, Hinkle CC, Joshi MR, Chiquoine EH,
40. Bergt C, Reicher H, Malle E, Sattler W. Hypochlorite modification of
43. Shao B, Cavigiolio G, Brot N, Oda MN, Heinecke JW. Methionine oxidation
43. Shao B, Cavigiolio G, Brot N, Oda MN, Heinecke JW. Methionine oxidation
38. Zhang R, Brennan ML, Fu X, Byun J, O’brien K, McDonald TO, Singh P,
37. Brubaker G, Peng DQ, Somerlot B, Abdollahian DJ, Smith JD. Apo-
27. Kircher G, Ponsin G, Berthozene F. Characterization of the non enzymatic
glycation of high density lipoprotein in diabetic patients. Diabetes Metab.
Dysfunctional HDL as a Diagnostic and Therapeutic Target
Jonathan D. Smith

Arterioscler Thromb Vasc Biol. published online August 13, 2009;
Arteriosclerosis, Thrombosis, and Vascular Biology is published by the American Heart Association, 7272 Greenville Avenue, Dallas, TX 75231
Copyright © 2009 American Heart Association, Inc. All rights reserved.
Print ISSN: 1079-5642. Online ISSN: 1524-4636

The online version of this article, along with updated information and services, is located on the World Wide Web at:
http://atvb.ahajournals.org/content/early/2009/08/13/ATVBAHA.108.179226.citation

Permissions: Requests for permissions to reproduce figures, tables, or portions of articles originally published in Arteriosclerosis, Thrombosis, and Vascular Biology can be obtained via RightsLink, a service of the Copyright Clearance Center, not the Editorial Office. Once the online version of the published article for which permission is being requested is located, click Request Permissions in the middle column of the Web page under Services. Further information about this process is available in the Permissions and Rights Question and Answer document.

Reprints: Information about reprints can be found online at:
http://www.lww.com/reprints

Subscriptions: Information about subscribing to Arteriosclerosis, Thrombosis, and Vascular Biology is online at:
http://atvb.ahajournals.org//subscriptions/