

Roxana Mehran, MD

\*Gregg W. Stone, MD

\*Mount Sinai Medical Center

Cardiovascular Research Foundation

1700 Broadway, 9th Floor

New York, New York 10019

E-mail: [gregg.stone@mountsinai.org](mailto:gregg.stone@mountsinai.org)

Twitter: @GreggWStone

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## High-Density Lipoproteins Are the Main Carriers of PCSK9 in the Circulation

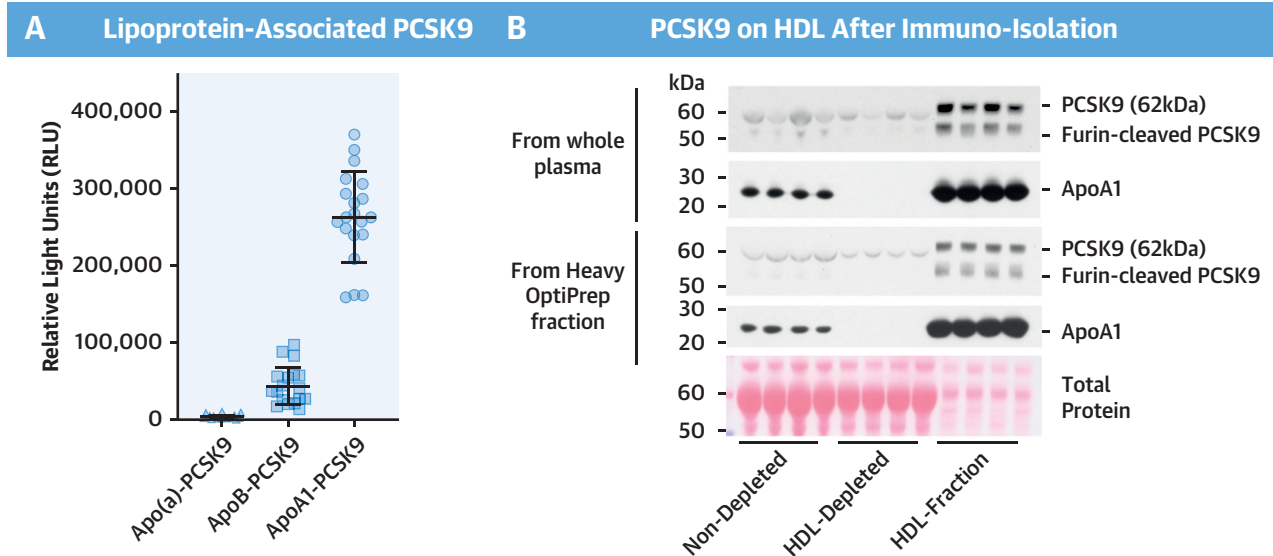


Proprotein convertase subtilisin/kexin type 9 (PCSK9), a secreted protein that regulates circulating low-density lipoprotein (LDL) through the hepatic LDL receptor degradation pathway, is the latest therapeutic target to further lower cholesterol in patients on maximal statin therapy (1). Circulating

PCSK9 has been shown to bind to LDL and lipoprotein(a) (Lp[a]). The latter is an LDL particle carrying apolipoprotein(a) as an additional protein component (2,3). Furthermore, the multimeric state of PCSK9 is thought to be influenced by lipoproteins, including high-density lipoprotein (HDL), regulating the LDL receptor-degrading capabilities of PCSK9 (4). However, the presence of PCSK9 on other lipoprotein particles is less well established, in particular in humans.

The potential associations of PCSK9 with different human lipoproteins was first determined by immunocapture, as previously described (5). Alirocumab, a human monoclonal antibody to PCSK9, was coated as a capture antibody to measure plasma PCSK9 in 20 healthy volunteers. Antibodies specific for apolipoprotein(a), apolipoprotein B (ApoB), and apolipoprotein A1 were then used to interrogate PCSK9-lipoprotein associations with Lp(a), ApoB-containing lipoproteins, and HDL, respectively. Measurement of lipoprotein-associated PCSK9 suggested a predominant association of PCSK9 with HDL (Figure 1A). For validation, plasma was subject to an anti-ApoB immunoprecipitation (Sun Diagnostics, New Gloucester, Maine). Successful removal of ApoB-carrying lipoproteins, including Lp(a), as confirmed by targeted mass spectrometry, led to only a <20% removal of PCSK9 as measured by enzyme-linked immunosorbent assay (DY3888, R&D Systems, Minneapolis, Minnesota; data not shown). In contrast, HDL removal using an HDL immunodepletion column (Genway Biotech, San Diego, California) resulted in a >90% removal of PCSK9 from fasting plasma (data not shown).

Next, nondepleted plasma, HDL-depleted plasma, and the HDL fraction were compared for apolipoprotein A1 (ab52945, Abcam, Cambridge, United Kingdom) by immunoblotting (Figure 1B). Notably, efficient HDL depletion resulted in a profound enrichment of both full-length and furin-cleaved PCSK9 (ab181142, Abcam) in the HDL fraction. Targeted mass spectrometry, however, also revealed a nonspecific removal of up to 50% of ApoB upon HDL depletion. OptiPrep density gradient centrifugation (Sigma Aldrich, St. Louis, Missouri) has been used previously in the determination of PCSK9 association with LDL (2). When pooled fasting plasma was separated using OptiPrep gradients, apolipoprotein A1 was observed in the “heavy” and “medium” fractions. Thus, the LDL-containing “medium” fraction is not devoid of HDL. Finally, to address the ApoB contamination upon HDL depletion, the HDL immune isolation was repeated from the ApoB-depleted, “heavy” OptiPrep fraction. This experiment

**FIGURE 1 PCSK9 Is Primarily Associated With HDL in Human Plasma**

**(A)** Proprotein convertase subtilisin/kexin type 9 (PCSK9) levels. Bound PCSK9 on different lipoproteins. **(B)** Immuno-isolated high-density lipoprotein (HDL). Non-depleted plasma, HDL-depleted plasma, and the HDL fraction were subjected to immunoblotting to assess for enrichment of PCSK9 and apolipoprotein A1 (ApoA1). The findings were replicated using fasting plasma separated by OptiPrep density gradient centrifugation, with HDL being immuno-isolated from the apolipoprotein B (ApoB)-depleted, "heavy" fraction. Apo(a) = apolipoprotein(a).

replicated the finding of PCSK9 enrichment in HDL as observed in whole plasma (Figure 1B).

Previous work has explored the associations of PCSK9 with LDL and Lp(a). Our experiments highlight for the first time that PCSK9 is predominantly associated with HDL in human plasma. We provide 5 lines of evidence to support our conclusion: immunocapture of PCSK9-associated lipoproteins, plasma PCSK9 concentrations after ApoB and after HDL depletion, and enrichment of PCSK9 on HDL after immune isolation from plasma and from an ApoB-depleted OptiPrep fraction. Our first experiment (Figure 1A) relies on immunocapture, raising the possibility that the relatively low signal for ApoB and apolipoprotein(a)-associated PCSK9 could be due to epitope masking, alongside the possibility that the different sizes of lipoprotein particles influence their efficiency to be detected. The subsequent experiments, however, provide unambiguous evidence that HDL removal is sufficient to capture the majority of PCSK9 from human plasma (Figure 1B). Unlike other methods for lipoprotein isolation (i.e., ultracentrifugation), immune isolation may reduce the loss of HDL-associated PCSK9. Further studies are now required to determine whether HDL is capable of altering PCSK9 functionality. For example, PCSK9

binding to LDL was shown to inhibit PCSK9-mediated degradation of the LDL receptor (2). The ability of PCSK9 to bind multiple lipoprotein classes raises the possibility that changes in PCSK9-lipoprotein compartmentalization could be an underappreciated regulator of its biological activity.

Sean A. Burnap, MSc  
Abhishek Joshi, BA(Hons), BMBCCh  
Sotirios Tsimikas, MD  
Carlos Fernández-Hernando, PhD  
Stefan Kiechl, MD  
Sarah E. Berry, PhD  
Wendy Hall, PhD  
Bodo Levkau, MD  
\*Manuel Mayr, MD, PhD

\*King's British Heart Foundation Centre  
King's College London  
125 Coldharbour Lane  
London, SE5 9NU  
United Kingdom  
E-mail: [manuel.mayr@kcl.ac.uk](mailto:manuel.mayr@kcl.ac.uk)  
Twitter: @Vascular\_Prot  
<https://doi.org/10.1016/j.jacc.2020.01.033>

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# Myocardial Edema and Remodeling



## A Link Between Acute Myocarditis and Septic Cardiomyopathy?

We read with great interest the paper by Aquaro et al. (1), reporting an association between cardiac magnetic resonance remodeling patterns at the 6-month follow-up and prognosis in acute myocarditis (AM). We recently reported the presence of subepicardial edema in patients with septic cardiomyopathy (SCM), which also evolved with persistent late gadolinium enhancement (LGE) and late T2 hypersignal resolution (2). Importantly, SCM is believed to be reversible, but little is known about long-term outcomes in survivors. Therefore, it is tempting to speculate that, although distinct in etiology, similar inflammation-driven

remodeling patterns might carry prognostic implications in both entities. This underscores the fact that, despite seemingly preserved cardiac function in survivors, SCM may also have long-term consequences, and this issue should be addressed in future studies.

Myocardial edema results from an imbalance between microvascular filtration and lymphatic fluid removal. Until now, attention has been mainly focused on microvascular endothelial barrier dysfunction, whereas factors governing myocardial lymphatic clearance remain poorly understood. Interestingly, although the observation of dilated lymphatics in myocardial segments with edema and LGE suggests lymphatic overload as cause of edema in chronic heart failure (3), in the context of acute SCM, we have observed collapsed subepicardial lymphatic pre-collectors (2), a previously unappreciated and potentially relevant mechanism of inflammation-induced lymphatic failure with possible implications in AM.

Notwithstanding the apparent protection associated with persistent edema at 6 months when compared with LGE without edema (definite fibrosis), care should be taken to interpret this as a benign pattern. Actually, it may identify myocardial areas at risk with persistent inflammation or dysfunctional lymphatic clearance, with which a milder remodeling process might be associated, but not without the risk of later progression to fibrosis and impact on prognosis (2). In fact, stimulation of lymphatic clearance has been shown to attenuate experimental myocardial remodeling (4), suggesting edema resolution mechanisms as currently unexplored therapeutic targets in AM.

In conclusion, cardiac magnetic resonance imaging suggests a link between AM and SCM pathophysiology, with edema and inflammation as common mechanisms of myocardial injury and remodeling.

Francisco Vasques-Nóvoa, MD  
António Angélico-Gonçalves, MD  
Nuno Bettencourt, MD, PhD  
Adelino F. Leite-Moreira, MD, PhD  
\*Roberto Roncon-Albuquerque Jr., MD, PhD

\*Cardiovascular R&D Center  
Department of Surgery and Physiology  
Faculty of Medicine of the University of Porto  
Al. Prof. Hernâni Monteiro  
4200-319, Porto  
Portugal

E-mail: [rra\\_jr@yahoo.com](mailto:rra_jr@yahoo.com)

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