

Abstract

234th American Chemical Society Meeting Proceedings, 2007 Aug; Boston, MA

When good cholesterol goes bad: Mass spectrometric approaches for the analysis of dysfunctional HDL

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BACKGROUND: Posttranslational oxidative modifications of lipoproteins are implicated in the pathogenesis of atherosclerotic vascular disease. Electrospray ionization tandem mass spectrometry (ESI-MS/MS) coupled with liquid chromatography is rapidly emerging as a powerful technique for pinpointing sites of amino acid oxidation within apolipoproteins. Oxidants generated by myeloperoxidase lead to the site specific oxidation apolipoprotein A-I – the major protein in HDL, and these posttranslational modifications are associated with major impacts on the biological function.

METHODS: We have recently used 2-dimensional liquid chromatography ESI-MS/MS to test the hypothesis that proteins implicated in inflammation might be enriched in the HDL of subjects with coronary artery disease (CAD).

CONCLUSION: Our observations suggest that HDL carries a unique cargo of proteins in CAD subjects and that certain of these proteins might make previously unsuspected contributions to the anti-inflammatory properties of HDL