

Supplementary Information

Apolipoprotein A-I structural organization in high density lipoproteins isolated from human plasma

Rong Huang¹, R. A. Gangani D. Silva¹, W. Gray Jerome², Anatol Kontush^{3,4,5}, M. John Chapman^{3,4,5}, Linda K. Curtiss⁶, Timothy J. Hodges⁷, and W. Sean Davidson¹

¹Department of Pathology and Laboratory Medicine, University of Cincinnati, Cincinnati, Ohio, USA. ²Department of Pathology, Vanderbilt University Medical Center, Nashville, Tennessee, USA. ³Université Pierre et Marie Curie - Paris 6, Paris, France. ⁴National Institute of Health and Medical Research (INSERM) Dyslipoproteinemia and Atherosclerosis Research Unit (UMR 939), Paris, France. ⁵Assistance Publique-Hopitaux de Paris, Groupe hospitalier Pitié - Salpêtrière, Paris, France. ⁶Department of Immunology and Vascular Biology, The Scripps Research Institute, La Jolla, California, USA. ⁷Department of Mathematical Sciences, University of Cincinnati, Cincinnati, Ohio, USA.

Corresponding author:

W. Sean Davidson, Department of Pathology and Laboratory Medicine, University of Cincinnati, 2120 E. Galbraith Rd., Cincinnati, Ohio 45237-0507 USA Telephone: (513) 558-3707; Fax: (513) 558-1312; E-mail: Sean.Davidson@UC.edu

Supplementary Figures

- 1: Particle size characterization.
- 2: Correlation of particle diameters calculated from composition vs. experimental measurement.
- 3: Cross-linking of various LpA-I particles as a function of increasing concentrations of BS³ cross-linker.
- 4: Correlation of particle diameters calculated from composition vs. experimental measurement.
- 5: Characterization of gel filtration isolated LpA-I_{2b} and LpA-I_{3b} and comparison of their cross-linking patterns.
- 6: Association constant of monoclonal antibody AI-115.1 to immobilized HDL subfractions by surface plasmon resonance.
- 7: Evaluation of the Double Super Helix (DSH) model in native LpA-I particles.

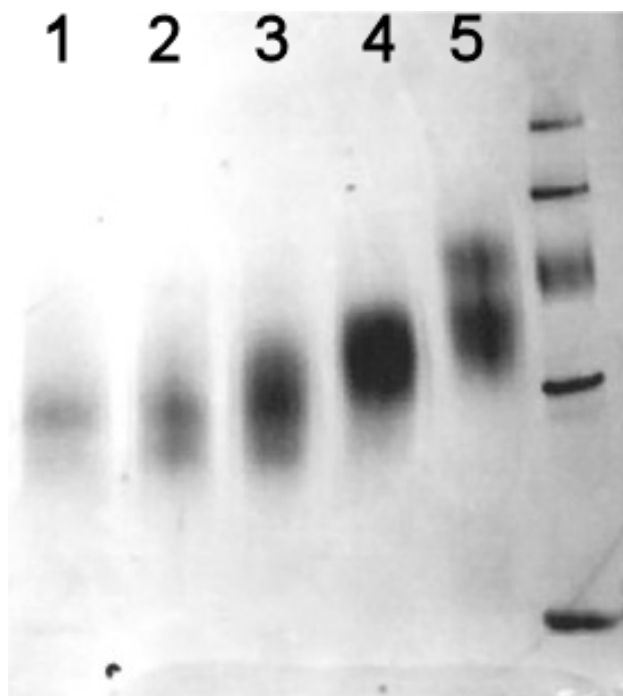
Supplementary Tables

- 1: Calculated number of molecules per particle for each of the major components of HDL.
- 2: Particle twist calculation parameters.

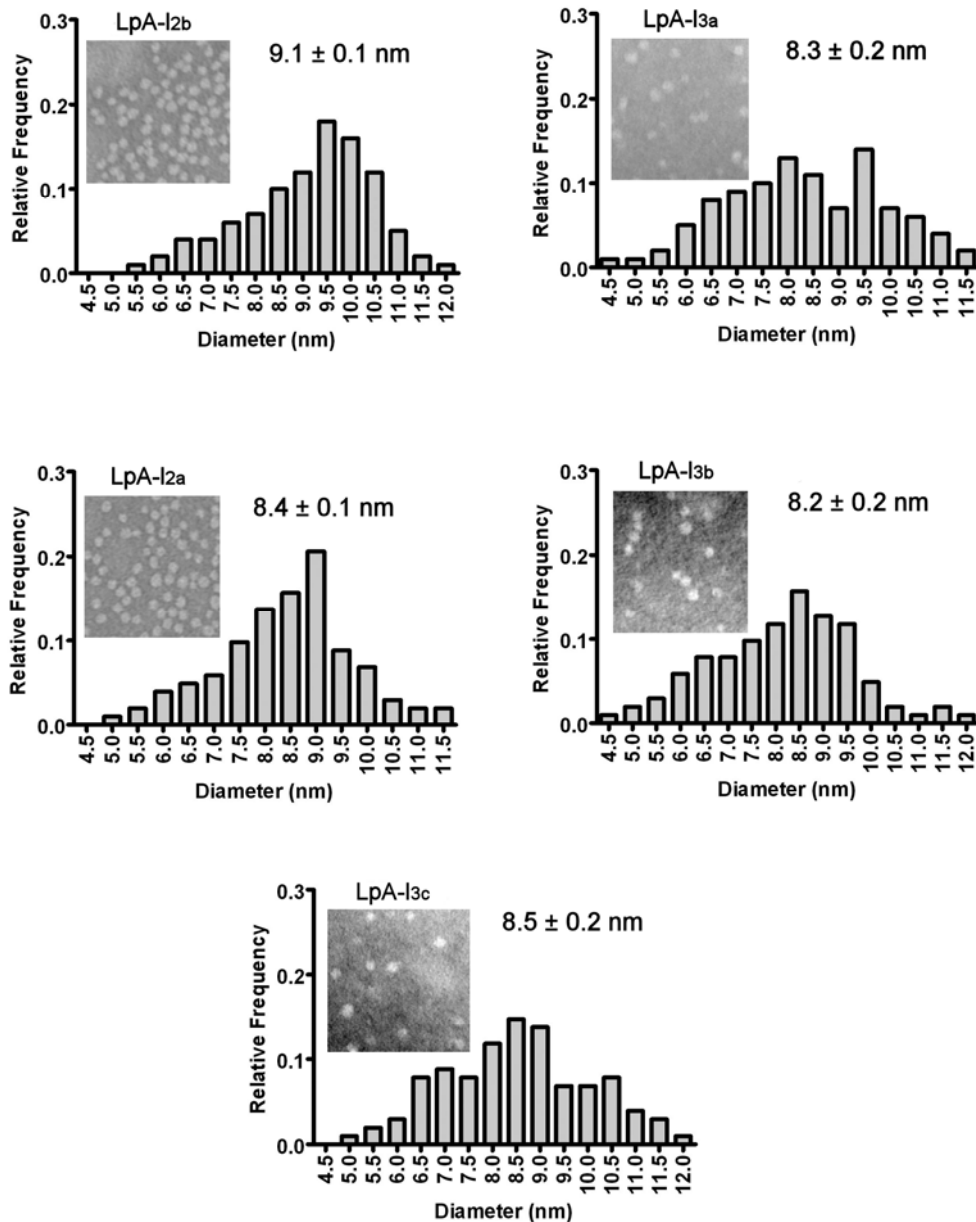
Supplementary Methods

Supplementary References

a



b



Supplementary Figure 1: Particle size characterization. (a) Representative native gel electrophoresis of five HDL subfractions (not LpA-I) obtained from a healthy normolipidemic control subject. Lane 1, HDL_{3c}; lane 2, HDL_{3b}; lane 3, HDL_{3a}; lane 4, HDL_{2a}; lane 5, HDL_{2b} and standards (thyroglobulin, ferritin, catalase, LDH and albumin corresponding to 669, 440, 232, 140 and 66 kDa in the descending order). The calculated mean hydrated diameters of HDL subfractions are: 8.7 ± 0.3 , 8.7 ± 0.2 , 9.0 ± 0.3 , 9.8 ± 0.5 and 11.3 ± 0.4 nm for HDL_{3c}, 3b, 3a, 2a and 2b, respectively (mean \pm standard deviation (S.D.) for 7 normolipidemic controls). (b) Negative stain electron microscopy of LpA-I samples from one healthy normolipidemic donor. Inset shows a negative stain image of the particles. Histograms were generated as described in **Supplementary Methods**. Average diameter as measured by image analysis is shown \pm 1 S.D.

