

## EPR EVIDENCE FOR THE OXIDATION-INDUCED FORMATION OF NEGATIVELY CHARGED SPECIES ON THE LOW-DENSITY LIPOPROTEIN SURFACE

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Oxidation-induced increase of the net negative charge on low-density lipoprotein was studied by electrophoretic mobility and by electron paramagnetic resonance. The negative-charge increase is associated not only with neutralization of the lysine residues of apoprotein B, but also with the exposition of the excessive negatively charged residues on the lipoprotein surface. The accumulation of the negatively charged residues is believed to be brought about by the conformational change of apoprotein B, triggered by neutralization of lysines and cleavage of peptide bonds. Alternatively, reactive oxygen species could also convert histidine to aspartic acid and proline to glutamic acid.

**KEY WORDS:** EPR, low-density lipoprotein, ion binding, lipoprotein oxidation, electrophoretic mobility.

### INTRODUCTION

It has been demonstrated that oxidation induces changes of a number of physical, chemical and biological properties of low-density lipoprotein (LDL).<sup>1,2</sup> One of the easily noticeable oxidation-induced change is the increase of electrophoretic mobility.<sup>3-5</sup> In that respect, oxidation induces the same type of change on LDL as does acetylation. More important, both oxidation and acetylation modify LDL in the way that it is recognized by scavenger receptors on macrophages.<sup>3,5-11</sup> In the process of acetylation, positively charged lysine residues of apoprotein B are neutralized, and consequently the total negative charge of the LDL particle is increased. Neutralization and derivatization of lysines also take place upon oxidation.<sup>12</sup> In the present study we demonstrate that the oxidation-induced increase of the LDL net negative charge cannot be explained simply by neutralization of lysine positive charges. It will be shown that oxidation induces new negatively charged sites on the LDL surface, probably associated with the conformational change and cleavage of apolipoprotein B or with the generation of negatively charged amino acids by the direct attack of reactive oxygen on certain amino acids.<sup>3</sup>

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## MATERIALS AND METHODS

LDL was isolated from the fresh-drawn blood by ultracentrifugation, carefully avoiding lipid peroxidation,<sup>13</sup> and dialysed against the Tris-HCl buffer containing EDTA, pH 7.4. Prior to the oxidation EDTA was removed by extensive dialysis against the Tris-HCl buffer of selected ionic strength. Oxidation was performed by bubbling oxygen through the buffer outside the dialysis bag containing LDL.<sup>14</sup> After a selected time of such a mild oxidation the electrophoretic mobility of the sample was checked on agarose gel plates (Lipidophor system, Immuno A.G., Vienna). The path of the LDL band traversed in 80 min was determined densitometrically.

The samples with oxidation-induced mobility were examined for their capacity to bind divalent cations, Mn(II) ions, by EPR spectroscopy.<sup>15,16</sup> The Mn(II) ions were used as a structural probe to characterize changes induced by oxidation on the LDL surface. As previously described,<sup>15</sup> the binding of Mn(II) ions to LDL was determined from the difference in the observed amplitudes of the characteristic Mn(II) free EPR spectra in the presence and absence of native and oxidatively modified LDL in the solution (Figure 1). Further oxidation was prevented prior to the EPR measurements by dialysis of oxidized LDL against appropriate buffer containing butylated hydroxytoluene. The EPR spectra were recorded with a Varian E-109 spectrometer at a temperature of 37°C, keeping the temperature constant within 0.1°C to avoid misleading results caused by the strong temperature dependence of the Mn(II) ion EPR spectra.

## RESULTS

The manganese binding to native (unmodified) LDL has been thoroughly studied and

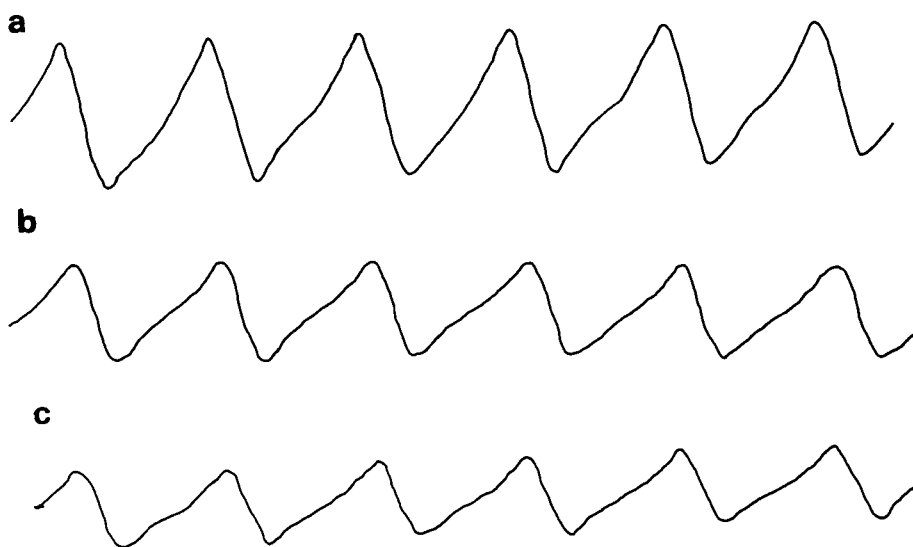


FIGURE 1 EPR spectra of 0.5 mM MnCl<sub>2</sub> in 0.02 M Tris-HCl, pH 7.4. A) without LDL; B) with 10.3 μmole native LDL/liter C) with 10.3 μmole oxidized LDL/liter.

the binding parameters rather precisely determined as a function of ionic strength.<sup>16</sup> Two types of independent binding sites have been found:  $n_1$ , "strong" binding sites characterized by a binding constant  $K_1$ , and  $n_2$ , "weak" binding sites with an association constant  $K_2$ . The "weak" sites are more pronounced in the buffer of high ionic strength, while the "strong" binding gives the main contribution to the LDL-ion binding when the LDL particles are in the low ionic buffer. The parameters of the manganese binding to native LDL have been determined by fitting the experimental data to the theoretical relation:

$$[\text{Mn}]_T = [\text{Mn}]_F \left[ 1 + \frac{K_1[n_1\text{LDL}]_T}{1 + K_1[\text{Mn}]_F} + \frac{K_2[n_2\text{LDL}]_T}{1 + K_2[\text{Mn}]_F} \right] \quad (1)$$

Expression (1) is derived from the simple binding scheme (2) and the definition of the association constants (3):



$$[\text{Mn}]_T = [\text{Mn}]_F + [n_1\text{LDL}]_B + [n_2\text{LDL}]_B$$

$$[n_1\text{LDL}]_T = [n_1\text{LDL}]_F + [n_1\text{LDL}]_B \quad (2)$$

$$[n_2\text{LDL}]_T = [n_2\text{LDL}]_F + [n_2\text{LDL}]_B$$

$$K_1 = \frac{[n_1\text{LDL}]_B}{[\text{Mn}]_F [n_1\text{LDL}]_F} \quad (3)$$

$$K_2 = \frac{[n_2\text{LDL}]_B}{[\text{Mn}]_F [n_2\text{LDL}]_F}$$

where prefixes  $T$ ,  $F$  and  $B$  to  $[\text{Mn}]$  denotes total, free and bound Mn(II) ion concentration, and to  $[n\text{LDL}]$  total, free and bound concentration of binding sites on LDL surface, respectively.

These two types of binding sites in the native LDL surface are characterized by  $n_1 = 8 \pm 3$  and  $n_2 = 170 \pm 30$ , with corresponding ionic-strength-dependent association constants.

Figure 2 shows the relative manganese binding  $[\text{Mn}]_B/[\text{Mn}]_T$ , to the oxidized LDL, in 0.02 M Tris-HCl buffer (experimental points). The figure also shows the binding curve (dashed line) of the native LDL under the same conditions (concentration, ionic strength and temperature). The curve has been calculated with the parameters. ( $n_1 = 8$ ,  $n_2 = 170$ ,  $K_1 = 4843 \text{ M}^{-1}$  and  $K_2 = 111 \text{ M}^{-1}$ ) determined in R.<sup>16</sup> It is obvious that the binding capacity of oxidized LDL is much higher than that of native LDL, particularly at low total Mn(II) concentration. To fit the experimental data for oxidized LDL to the theory, one or more of the four binding parameters (two binding constants,  $K_1$  and  $K_2$  and two numbers of binding sites,  $n_1$  and  $n_2$ ) has to be altered. The contribution of the abundant "weak" binding sites has been checked by Mn(II) binding to oxidized LDL in the buffer of higher ionic strength. At higher ionic strength (0.1 M Tris-HCl) alterations of the binding parameters  $n_2$  and  $K_2$  are expected to be observed. From the measurements presented in Figure 3 it follows that these sites are not significantly affected by oxidation. In contrast to that, less abundant "strong" binding sites, represented by  $n_1$  and  $K_1$ , expressed in the buffer of low ionic strength (Figure 2), manifest pronounced changes upon oxidation. The best fit of experimental points in Figure 2 has been achieved when only the value of  $n_1$  has been

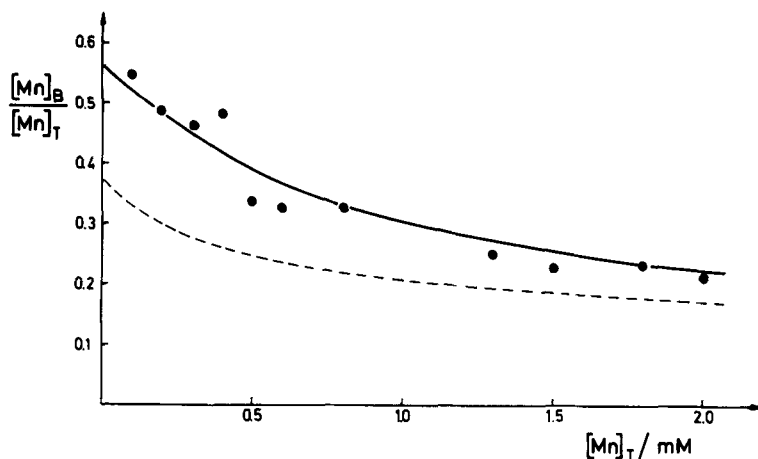


FIGURE 2 Binding of Mn(II) ions to LDL in 0.02 M Tris-HCl buffer. Relative binding of Mn(II) ions to LDL ( $10.3 \mu\text{mole/liter}$ , pH 7.4 at  $37^\circ\text{C}$ , in a 0.02 M Tris-HCl buffer) oxidized for 50 hours at room temperature. The dots are the experimental measurements and the solid line is the best fit to the relation (1), with the parameters  $n_1 = 20$ ,  $K_1 = 4843 \text{ M}^{-1}$ ,  $n_2 = 170$ ,  $K_2 = 111 \text{ M}^{-1}$ . The dashed line represents the expected binding to native LDL.

changed. The measurements presented in Figures 2 and 3 undoubtedly indicate the increase in number of "strong" binding sites. The best fit to the experimental points in both figures to the theoretical predictions (1) is obtained for the following set of binding parameters:  $n_1 = 20 \pm 3$ ,  $K_1 = 4843 \text{ M}^{-1}$  for "strong" and  $n_2 = 170 \pm 30$ ,  $K_2 = 111 \text{ M}^{-1}$  for "weak" binding sites. These values differ only in  $n_1$  (20 instead of 8) from those for native LDL under same conditions. There is no evidence for the oxidation-induced change of the remaining three parameters.

A qualitatively very similar situation has been found in LDL samples oxidized for

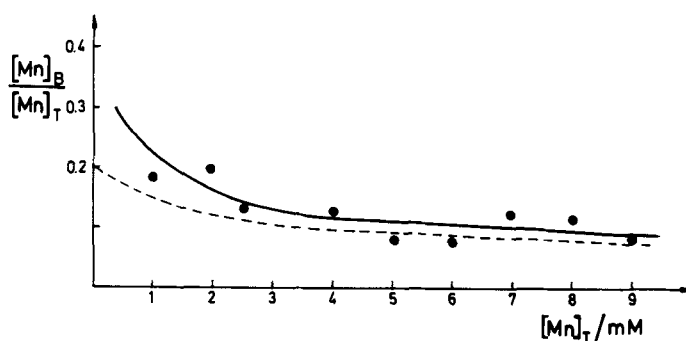


FIGURE 3 Mn(II) binding to LDL in 0.1 M Tris-HCl buffer. Relative binding of Mn(II) ions to LDL ( $10 \mu\text{mole/liter}$ , in a 0.1 M Tris-HCl buffer). The binding constants used for reconstruction of the binding curves (solid line and dashed line) are as those in Figure 2, corrected for the different electrolyte ionic strength ( $K_1 = 746 \text{ M}^{-1}$ ,  $K_2 = 64 \text{ M}^{-1}$ ). Other conditions are as in Figure 2.

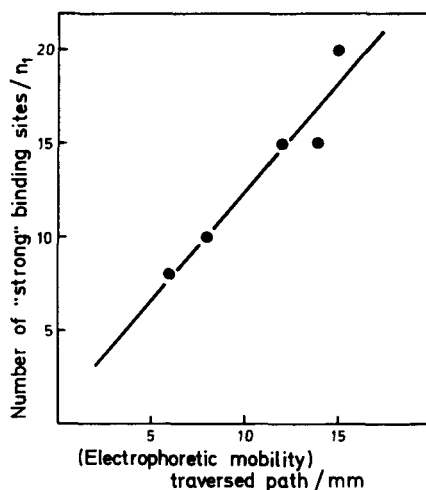


FIGURE 4 Number of Mn(II) binding sites vs. electrophoretic mobility. Correlation of electrophoretic mobility (measured as the total path traversed in 80 min.) and the number of "strong" binding sites,  $n_1$ , on the LDL surface.

shorter or longer times or in samples from five different preparations. To detect the increase in electrophoretic mobility the time of oxidation process depended on the *LDL* concentration and on the source of *LDL*. The increased electrophoretic mobility is associated with the increased number of "strong" binding sites,  $n_1$ , as shown in Figure 4 and is independent on *LDL* concentration or source of *LDL*. The increase from 8 (for unmodified *LDL*) to about 20 (for oxidized *LDL*) can be easily reached simply by mild oxygenation of the buffer. Stronger oxidation conditions (with 5–10  $\mu\text{M}$   $\text{CuCl}_2$ ) lead to  $n_1$  as large as 30.

## DISCUSSION

Oxidation induces neutralization and derivatization of lysine residues in apoprotein B in *LDL*,<sup>12</sup> leading to an increase of the net negative charge and hence to an increase of the electrophoretic mobility of the *LDL* particle. In the present study, in addition to electrophoresis we have used the method (EPR) sensitive only to negatively charged species exposed on the lipoprotein surface which are responsible for the binding of paramagnetic Mn(II) ions. Comparison of the results obtained by the two methods demonstrates that the neutralization of lysine residues is accompanied by the appearance of additional binding sites with strong affinity for divalent cations on the *LDL* surface. Although the chemical nature of the binding sites is unknown, it is safely concluded that the protein residues bearing a net negative charge must be "strong", while it is speculated that the phospholipid head group on the *LDL* surface is "weak".<sup>15</sup>

The appearance of the oxidation-induced new negatively charged species associated with "neutralization" of lysine could be explained in terms of the conformational change of apoprotein B. It has already been shown that the breakdown products generated during the peroxidation of unsaturated fatty acids, such as malondial-

dehyde and 4-hydroxynonenal, are able to modify reactive amino groups of the protein moiety of *LDL*.<sup>17-19</sup> The neutralization of lysine might be a trigger for the conformational change if, for instance, positively charged lysine residues in native *LDL* are coupled with negatively charged residues, such as aspartic acid, glutamic acid or sialic acid. Alternatively, it has been reported that oxidation of *LDL* is accompanied by degradation of the apoprotein.<sup>3</sup> Such a degradation may lead to a completely new arrangement and embedding of shorter polypeptides on the *LDL* surface. However, the attack of reactive oxygen species could also directly generate new negatively charged amino acid residues. Thus, histidine could be converted to aspartic acid and proline to glutamic acid.<sup>20</sup>

The studies with monoclonal antibodies<sup>21</sup> support our findings and suggestions that newly created negative sites play a role in the interaction of oxidized *LDL* and its receptors.

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