**Supplemental Table 1**

Analytical imprecision of the PON3 assay

| | Intra-assay | | | Inter-assay | | |
|---|---|---|---|---|---|---|
| **Control material** | **Mean; mg/L** | **SD; mg/L** | **CV; %** | **Mean; mg/L** | **SD; mg/L** | **CV; %** |
| Pool A | 2.65 | 0.26 | 9.8 | 2.64 | 0.35 | 13.2 |
| Pool B | 1.36 | 0.09 | 6.6 | 1.37 | 0.18 | 13.1 |
| Pool C | 0.90 | 0.05 | 5.6 | 0.89 | 0.09 | 10.1 |

**Supplemental Table 2**

Selected biochemical and demographical variables

| **Variable** | **Value (*n* = 356)** |
|---|---|
| Age, years | 47.4 (15.1) |
| Female gender, % | 43.8 |
| Body mass index, kg/m$^2$ | 27.2 (5.0) |
| Smokers, % | 33.7 |
| Cholesterol, mmol/L | 5.3 (0.9) |
| Triglycerides, mmol/L | 1.27 (0.88) |
| HDL-cholesterol, mmol/L | 1.5 (0.4) |
| Apo A-I, g/L | 1.69 (0.28) |
| PON1 lactonase, U/L | 1.25 (0.73 – 2.01) |
| PON1 paraoxonase, U/L | 278.1 (161.19 – 580.4) |
| PON1 concentration, mg/L | 96.46 (43.57 – 291.09) |
| PON3 concentration, mg/L | 1.78 (1.00 – 2.47) |

Quantitative variables are expressed as means (SD) or as medians (95% CI) as explained in Materials and Methods. Qualitative variables are expressed as % of the total participants.

**Supplemental Table 3**

Correlation coefficients of the regression lines between serum PON3 concentration and other selected variables

| **Variable** | **Correlation with PON3 ( *r* )** | ***P*** |
|---|---|---|
| Body mass index | – 0.084 | 0.140 |
| PON1 concentration | 0.046 | 0.385 |
| PON1 lactonase activity | 0.057 | 0.285 |
| PON1 paraoxonase activity | – 0.062 | 0.243 |
| Cholesterol | – 0.092 | 0.082 |
| Triglycerides | – 0.025 | 0.641 |
| HDL cholesterol | – 0.025 | 0.880 |
| Apolipoprotein A-I | – 0.009 | 0.867 |

There were no significant relationships between PON3 and the other studied variables.

**Supplemental Table 4**

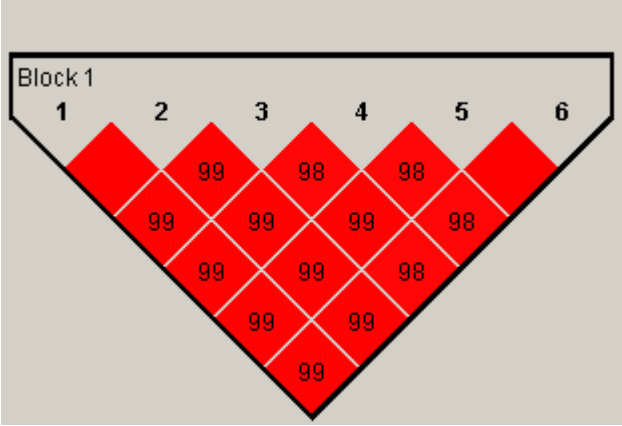
Distribution of PON3 genotypes in the studied population

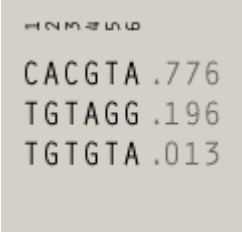
| **Polymorphism** | **dbSNP** | **Seattle SNP** | **Genotype frequency (*n* in parentheses)** | | | |
|---|---|---|---|---|---|---|
| $PON3_{-567}$ | rs11764079 | 5913 | CC/CT/TT | 59.8 (213) | 36.2 (129) | 3.9 (14) |
| $PON3_{-665}$ | rs11770903 | 5815 | AA/AG/GG | 59.8 (213) | 36.5 (130) | 3.7 (13) |
| $PON3_{-746}$ | rs17882539 | 5734 | CC/CT/TT | 59.7 (212) | 36.5 (130) | 3.9 (14) |
| $PON3_{-4105}$ | –– | 2375 | GG/GA/AA | 61.7 (220) | 35.1 (125) | 3.0 (11) |
| $PON3_{-4970}$ | –– | 1510 | TT/TG/GG | 62.7 (223) | 34.8 (124) | 2.5 (9) |
| $PON3_{-4984}$ | –– | 1496 | AA/AG/GG | 62.3 (222) | 34.8 (124) | 2.8 (10) |

**Supplemental Figure 1**

Haplotype block assignment was performed using the 'Solid Spine of Linkage Disequilibrium (LD)' implemented in the Haploview software (Barrett JC et al. Bioinformatics 2005;21:263-5). This method searches for a 'spine' of strong LD running from one marker to another along the legs of the triangle in the LD chart. This means that the first and the last markers in a block are in strong LD with all intermediate markers but that the intermediate markers are not necessarily in LD with each other.

One single LD block was defined:




| |
|---|
| 1: PON3$_{-567}$ |
| 2: PON3$_{-665}$ |
| 3: PON3$_{-746}$ |
| 4: PON3$_{-4105}$ |
| 5: PON3$_{-4970}$ |
| 6: PON3$_{-4984}$ |