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Results from a family and DNA based active identification programme for familial hypercholesterolaemia

A H A ten Asbroek, P J Marang-van de Mheen, J C Defesche, J J P Kastelein, L J Gunning-Schepers

Heterozygous familial hypercholesterolaemia (FH) is a common inborn error of lipoprotein metabolism, which strongly predisposes for coronary artery disease and premature cardiac death. In 1994, a family based active identification programme for FH was implemented in the Netherlands. It is based on DNA diagnosis of the LDL-receptor gene mutation, which enables us to search selectively for patients in a high risk population. The programme initially targets first and second degree relatives of FH probands (diagnosed at Lipid Research Clinics throughout the country) and extends further into the family only when new patients are identified. The programme aims to identify mutation carriers and to refer them to Lipid Research Clinics for extensive individual risk assessment and, if necessary, treatment. As no carefully collected data are available for cholesterol levels among the general population of LDL-receptor gene mutation carriers, the large majority of whom are asymptomatic, we studied the prevalence of hypercholesterolaemia among screenees with a proved LDL-receptor gene mutation.

Methods and Results

Between 1994 and 1998 2814 adults were screened. The estimated response rate was constant over the years at 90%. For reasons of comparison with available population data for total serum cholesterol levels, we selected those who were between 20 and 60 years of age (1856 screenees). Depending on the available funds in the screening programme, which were lacking in certain periods, single cholesterol measurements were taken at the time of screening. Therefore, we analysed the data of all 1005 persons who had DNA test results as well as cholesterol measurements. These were a non-selective sample of the 1856 screenees. Depending on the proportion of people who were not screened for cholesterol determinations, this non-selective sample was larger than the sample of screenees with a DNA test result. Hence, in the analysis of the results, we only included screenees who had DNA test results.

Methods

DNA was isolated from the leucocyte fraction of 10 ml of freshly collected blood, followed by polymerase chain reaction and restriction enzyme analysis. From the perspective of the screening programme, the screenees that are already treated cannot be considered as new cases and they do not benefit from the screening programme in the same manner as newly identified cases. Therefore, we present the prevalence of hypercholesterolaemia among all screenees as well as the prevalence of hypercholesterolaemia among those not yet treated with HMG-CoA reductase inhibitors.

Table 1 shows the results for the screened population. It is evident that each age category contains LDL-receptor gene mutation carriers who do not have hypercholesterolaemia: 19.8% in all men, 32.3% in untreated men and 16.7% in untreated women. Furthermore, it is shown that the prevalence of mutation carriers among all screenees tends to be lower in the older age groups. This is probably the result of selective mortality. However, the prevalence of mutation carriers among untreated screenees is also lower in the older age groups. This is not purely the result of selective mortality but it is mainly attributable to the fact that an increasing proportion of those screened in the older age groups is already treated with cholesterol lowering drugs, and more in mutation carriers than in those without a mutation as they have generally higher cholesterol levels. This might also explain why the prevalence of hypercholesterolaemia in untreated female mutation carriers is lower in the older age groups.

Table 2 shows the results for the screened population. From the perspective of the screening programme, the screenees that are already treated cannot be considered as new cases and they do not benefit from the screening programme in the same manner as newly identified cases. Therefore, we present the prevalence of hypercholesterolaemia among all screenees as well as the prevalence of hypercholesterolaemia among those not yet treated with HMG-CoA reductase inhibitors.

Hypercholesterolaemia was defined as either an untreated total cholesterol (TC) level above the 95th centile for age and sex in the Dutch population (table 1), or as receiving HMG-CoA reductase inhibitors. We also show the total cholesterol distribution for the untreated screenees using conventional cut off points (<6.5, 6.5–7.9, 8 mmol/l). All LDL-receptor gene mutation carriers were heterozygotes. None of the screenees had been tested for a LDL-receptor gene mutation before.

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Table 2: Prevalence of hypercholesterolaemia* (HC) by sex, age group and DNA test result in all screenees and prevalence of hypercholesterolaemia, mean total serum cholesterol (TC), standard deviation (SD) and total serum cholesterol distribution, using conventional cut off values (6.5 and 8.0 mmol/l) as well as the 95th centile (C95)† in untreated screenees.

<table>
<thead>
<tr>
<th>Age</th>
<th>All‡</th>
<th>All FH+</th>
<th>All FH−</th>
<th>All FH+</th>
<th>All FH−</th>
<th>All FH+</th>
<th>All FH−</th>
<th>All FH+</th>
<th>All FH−</th>
<th>All FH+</th>
<th>All FH−</th>
<th>All FH+</th>
<th>All FH−</th>
<th>All FH+</th>
<th>All FH−</th>
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</thead>
<tbody>
<tr>
<td>20–29 years</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Number (%)</td>
<td>105</td>
<td>35 (33.3)</td>
<td>70 (66.7)</td>
<td>141</td>
<td>38 (28.5)</td>
<td>104</td>
<td>66 (54.0)</td>
<td>134</td>
<td>38 (28.5)</td>
<td>96 (71.6)</td>
<td>98 (100)</td>
<td>26 (26.5)</td>
<td>72 (73.5)</td>
<td>478</td>
<td>162 (33.9)</td>
</tr>
<tr>
<td>% HC</td>
<td>39.0</td>
<td>82.9</td>
<td>17.1</td>
<td>46.1</td>
<td>76.2</td>
<td>21.8</td>
<td>35.8</td>
<td>76.3</td>
<td>19.8</td>
<td>32.7</td>
<td>92.3</td>
<td>11.1</td>
<td>38.9</td>
<td>80.2</td>
<td>17.7</td>
</tr>
<tr>
<td>Untreated Number (%)</td>
<td>101</td>
<td>31 (30.7)</td>
<td>70 (69.3)</td>
<td>116</td>
<td>68 (58.5)</td>
<td>75 (64.7)</td>
<td>109</td>
<td>82 (75.2)</td>
<td>79 (87.3)</td>
<td>79 (87.3)</td>
<td>40 (12.7)</td>
<td>69 (87.3)</td>
<td>305</td>
<td>99 (24.4)</td>
<td></td>
</tr>
<tr>
<td>Mean TC (SD)</td>
<td>5.5 (1.4)</td>
<td>6.9 (1.3)</td>
<td>4.9 (0.9)</td>
<td>6.3 (1.5)</td>
<td>7.5 (1.4)</td>
<td>5.7 (1.1)</td>
<td>6.2 (1.2)</td>
<td>7.4 (1.0)</td>
<td>6.0 (1.1)</td>
<td>6.3 (1.0)</td>
<td>7.7 (0.7)</td>
<td>6.1 (0.9)</td>
<td>6.1 (1.3)</td>
<td>7.3 (1.3)</td>
<td>5.7 (1.1)</td>
</tr>
<tr>
<td>TC &lt; 6.5 (%)</td>
<td>81 (80.2)</td>
<td>13 (41.9)</td>
<td>68 (97.1)</td>
<td>68 (58.5)</td>
<td>10 (24.4)</td>
<td>58 (77.3)</td>
<td>71 (66.0)</td>
<td>4 (23.5)</td>
<td>67 (72.8)</td>
<td>52 (65.8)</td>
<td>0 (0)</td>
<td>52 (75.4)</td>
<td>272 (67.2)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>TC &gt; 8.0 (%)</td>
<td>9 (8.9)</td>
<td>9 (29.0)</td>
<td>0</td>
<td>14 (12.1)</td>
<td>12 (29.3)</td>
<td>2 (2.7)</td>
<td>8 (7.3)</td>
<td>5 (29.4)</td>
<td>3 (3.3)</td>
<td>8 (10.1)</td>
<td>4 (40.0)</td>
<td>3 (3.9)</td>
<td>39 (9.6)</td>
<td>30 (30.3)</td>
<td>9 (2.9)</td>
</tr>
</tbody>
</table>
formulated the research questions, assisted in writing, analyses and interpreting results. J C Defesche participated in data screening and cleaning, assisted in the analyses as well as in the interpretation of the data and assisted in writing the report. J P Kastelein assisted in writing and interpreting results. L J Gunning-Schepers was principal investigator, formulated the research questions, assisted in writing the report and is head of the study group.

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Conflicts of interest: none.


