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DOI
10.1136/jech.55.7.500

Publication date
2001

Published in
Journal of Epidemiology and Community Health

Citation for published version (APA):

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*J. Epidemiol. Community Health* 2001;55;500-502
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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.1 In 1994, a family based active identification programme for FH was implemented in the Netherlands.2 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 screenes 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%.3 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 screenes). 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 screenes between 20 and 60 years of age. Cholesterol was measured using commercially available kits (Boehringer Mannheim, Mannheim, Germany). Genomic DNA was isolated from the leucocyte fraction of 10 ml of freshly collected blood, followed by polymerase chain reaction and restriction enzyme analysis.

Table 1: MORGEN Project data 1996–1997: mean (SD) total serum cholesterol (TC) as well as 95th centile (C95) in the general Dutch population by sex and age group

<table>
<thead>
<tr>
<th>Age group (y)</th>
<th>Men</th>
<th>Women</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Number</td>
<td>Mean TC (SD)</td>
</tr>
<tr>
<td>20–29</td>
<td>889</td>
<td>4.4 (0.9)</td>
</tr>
<tr>
<td>30–39</td>
<td>1210</td>
<td>5.5 (1.0)</td>
</tr>
<tr>
<td>40–49</td>
<td>1030</td>
<td>5.5 (1.0)</td>
</tr>
<tr>
<td>50–59</td>
<td>843</td>
<td>4.6 (0.8)</td>
</tr>
<tr>
<td>C95</td>
<td>5.8</td>
<td>6.7</td>
</tr>
</tbody>
</table>

From the perspective of the screening programme, the screenes 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 screenes 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, or as receiving HMG-CoA reductase inhibitors. We also show the total cholesterol distribution for the untreated screenes 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 screenes had been tested for a LDL-receptor gene mutation before.

Table 2 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 women, 28.7% in untreated women. Furthermore, it is shown that the prevalence of mutation carriers among all screenes 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 screenes 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 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 group</th>
<th>Sex</th>
<th>All‡</th>
<th>FH+</th>
<th>FH−</th>
<th>All‡</th>
<th>FH+</th>
<th>FH−</th>
<th>All‡</th>
<th>FH+</th>
<th>FH−</th>
<th>All‡</th>
<th>FH+</th>
<th>FH−</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>Number (%)</td>
<td>105 (100)</td>
<td>35 (33.3)</td>
<td>70 (66.7)</td>
<td>141 (100)</td>
<td>63 (44.7)</td>
<td>78 (55.3)</td>
<td>134 (100)</td>
<td>38 (28.4)</td>
<td>96 (71.6)</td>
<td>98 (100)</td>
<td>26 (26.5)</td>
</tr>
<tr>
<td></td>
<td></td>
<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>
</tr>
<tr>
<td></td>
<td></td>
<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>
</tr>
<tr>
<td></td>
<td></td>
<td>TC &lt; 8.0 (%)</td>
<td>11 (10.9)</td>
<td>9 (29.0)</td>
<td>2 (2.9)</td>
<td>34 (29.3)</td>
<td>19 (36.3)</td>
<td>15 (20.0)</td>
<td>30 (27.5)</td>
<td>8 (47.1)</td>
<td>22 (23.9)</td>
<td>19 (24.1)</td>
<td>6 (60.0)</td>
</tr>
<tr>
<td></td>
<td></td>
<td>% &gt; C95</td>
<td>36.6</td>
<td>80.6</td>
<td>17.1</td>
<td>34.5</td>
<td>63.4</td>
<td>18.7</td>
<td>21.1</td>
<td>47.1</td>
<td>16.5</td>
<td>67.7</td>
<td>15.0</td>
</tr>
</tbody>
</table>

A H A ten Asbroek was the main author and carried out the analyses and interpreted data. P J Marang-van de Mheen
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 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.

Funding: this study is funded by the Health Research and Development Council (grant number 28–2751).
Conflicts of interest: none.