Intrauterine death: an approach to the analysis of genetic heterogeneity

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SUMMARY A study of survival time of zygotes in utero and the relationship with parental phenotype of a series of genetic polymorphisms was carried out in 41 couples with habitual abortion. Variability of intrauterine survival time was found to be much higher between families than within families suggesting that several genetic entities contribute to the condition clinically defined as habitual abortion. Significant differences of survival time were found in relation to the length of the paternal Y chromosome and to the maternal phenotypes of PGM; and Ss. These observations are in line with previous data suggesting intrauterine selection in these polymorphisms. Further studies of the timing of intrauterine death in relation to 'normal' genetic polymorphisms may help to clarify the aetiology of spontaneous fetal loss.

Recent studies indicate that the overall death rate of zygotes ranges between 25 and 75%.1,2 Besides environmental agents, genetic factors are considered to be of paramount importance in this phenomenon.2-5 As in other phases of life, it is likely that both monogenic and polygenic heredity play an important part in intrauterine survival. Genetic factors may also play a role in predisposing to chromosomal aberration frequently observed in clinically recognisable spontaneous abortion.3 It is well known that genotypes expressing their deleterious effects after birth show a characteristic chronological pattern of manifestations. The timing of clinical manifestations and death is usually different between genotypes and very similar within families. By analogy, the study of survival time of zygotes in women with repeated abortion not resulting from anatomical or other known environmental causes, and the analysis of relationships with genetic factors statistically associated with fetal death, may improve the understanding of the aetiology of intrauterine death.

Material and methods

Forty-one couples who had had at least two consecutive abortions were examined. A total of 140 abortions was recorded.

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Table Gestational duration in habitual abortion. Relation with parental phenotype of some genetic polymorphisms.

<table>
<thead>
<tr>
<th>Variable</th>
<th>Category</th>
<th>All aborted fetuses</th>
<th>First aborted fetus</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>No of abortion</td>
<td>Mean gestation (weeks)</td>
<td>SD</td>
</tr>
<tr>
<td>Total population</td>
<td>140</td>
<td>11.42</td>
<td>4.26</td>
</tr>
<tr>
<td>Long Y chromosome in the father*</td>
<td>Present</td>
<td>23</td>
<td>14.1</td>
</tr>
<tr>
<td>Maternal PGM genotype</td>
<td>Absent</td>
<td>117</td>
<td>10.9</td>
</tr>
<tr>
<td></td>
<td>Homozygote</td>
<td>99</td>
<td>10.8</td>
</tr>
<tr>
<td>Maternal ADA genotype</td>
<td>Heterozygote</td>
<td>41</td>
<td>12.9</td>
</tr>
<tr>
<td>HLA-Bw35 antigen in the mother</td>
<td>Present</td>
<td>133</td>
<td>11.4</td>
</tr>
<tr>
<td></td>
<td>Absent</td>
<td>7</td>
<td>11.0</td>
</tr>
<tr>
<td>HLA-A antigens of the couple</td>
<td>Sharing the same antigen</td>
<td>52</td>
<td>10.9</td>
</tr>
<tr>
<td></td>
<td>Not sharing the same antigen</td>
<td>66</td>
<td>11.9</td>
</tr>
<tr>
<td>HLA-B antigens of the couple</td>
<td>Sharing the same antigen</td>
<td>34</td>
<td>12.3</td>
</tr>
<tr>
<td></td>
<td>Not sharing the same antigen</td>
<td>75</td>
<td>10.8</td>
</tr>
<tr>
<td>Maternal Ss genotype</td>
<td>SS</td>
<td>40</td>
<td>10.5</td>
</tr>
<tr>
<td></td>
<td>Others</td>
<td>115</td>
<td>11.0</td>
</tr>
<tr>
<td>Paternal Ss genotype</td>
<td>SS</td>
<td>25</td>
<td>13.4</td>
</tr>
<tr>
<td></td>
<td>Others</td>
<td>115</td>
<td>11.7</td>
</tr>
<tr>
<td>Maternal Secretor phenotype</td>
<td>Not Secretor</td>
<td>70</td>
<td>11.3</td>
</tr>
<tr>
<td></td>
<td>Secretor</td>
<td>70</td>
<td>11.6</td>
</tr>
<tr>
<td>Paternal Secretor phenotype</td>
<td>Not Secretor</td>
<td>77</td>
<td>11.0</td>
</tr>
<tr>
<td></td>
<td>Secretor</td>
<td>63</td>
<td>12.0</td>
</tr>
<tr>
<td>Wife-husband ABO incompatibility</td>
<td>Present</td>
<td>57</td>
<td>11.1</td>
</tr>
<tr>
<td></td>
<td>Absent</td>
<td>83</td>
<td>11.7</td>
</tr>
</tbody>
</table>

*Criterion adopted for defining a Y chromosome as long was a ratio Y/F ≥ 1.0.

determined in 35 couples. Preliminary data concerning the phenotype distribution of some of these systems have been published elsewhere.8–11

Variables included in the present analysis are reported in the table. Selection of variables and their subdivision into categories was based on statistical association with spontaneous abortion observed in our sample or reported by other investigators.8–14 Statistical analyses were carried out using the SPSS programme with a 370/158 IBM computer.15

Results

The distribution of the mean gestational duration calculated for each couple with habitual abortion is depicted in the figure. Couples were quite uniformly distributed over the range observed in our sample. Variability of intrauterine survival time was much higher between families than within families. Variance analysis showed significant heterogeneity among couples.

The relation between gestational duration and some parental genetic variables is analysed in the table. Significant differences in intrauterine survival time were observed in relation to the length of the paternal Y chromosome and maternal PGM, and Ss phenotypes. The same pattern of associations was observed after examination of only the first aborted fetus of the couples.

Variance analysis showed no interaction between maternal PGM, phenotype, maternal Ss phenotype, and length of Y chromosome in the father in their effects on gestational duration of aborted fetuses.

Discussion

The distribution of the mean gestational durations and the heterogeneity between families are compatible with the conjecture that several genetic entities contribute to the condition clinically defined

FIGURE Distribution of mean duration of gestation (weeks) in couples with habitual abortion.

Variance analysis. Total number of abortions = 140

Mean square  df
Between families  31.3363  40
Within families 12.8355  99
F = 2.4414, p<0.01.
as habitual abortion. ‘Normal’ genetic polymorphisms seem at present to be the most interesting candidates for the analysis of multifactorial variables influencing intrauterine development and survival.\textsuperscript{16}

Association with spontaneous abortion has been observed for ABO,\textsuperscript{12} HLA,\textsuperscript{8-13} PI,\textsuperscript{17} MNSs,\textsuperscript{9} PGM,\textsuperscript{10} Secretor (Bottini \textit{et al}, unpublished observations), ADA,\textsuperscript{11} and chromosomal variants.\textsuperscript{14} The observation of a relationship between gestational duration and a given polymorphism reinforces the statistical inference based on the increased proportion of a particular phenotype in spontaneous abortion. If a given genotype predisposes to fetal loss, a temporal pattern of recurrence could be associated with that genotype. The relevant phenomenon is the existence of a temporal distribution of fetal losses different from that observed among other genotypes. A decrease of intrauterine survival in comparison to other lethal conditions would not necessarily be expected.

The present analysis supports the view that PGM, Ss, and structural variation of the Y chromosome influence intrauterine selection and survival.

Our approach has not shown significant results for ADA, HLA, ABO, and Secretor. Several hypotheses for this can be put forward. (1) Statistical association previously reported was fortuitous, (2) the size of the present sample is not sufficient to reveal slight differences of gestational duration, and (3) these factors exert a protective action during the whole span of gestation and therefore lack a typical temporal pattern of manifestations.

The selection of couples with repeated abortions may have definite advantages for our study. While the correct assignment of a single episode of abortion as spontaneous or induced is generally difficult, our cases are certainly all spontaneous and it is likely that our sampling method selects families genetically predisposed.

The exact ascertainment of gestational duration is difficult; this, however, should not affect the results of our analysis since the error is likely to be independent of the genetic marker investigated. The fact that the pattern of relationships between the gestational durations and the polymorphisms was the same when considering only the first aborted fetuses (for which the exact ascertainment of gestational duration was more difficult) supports this view.

Although many more families should be studied in order to draw definite conclusions, our observations suggest that the analysis of genetic polymorphisms in relation to the timing of fetal death may give insight into the aetiology of habitual abortion and into the identification of the forces which maintain genetic variability.

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References


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