STUDIES ON THE Gm AND InV FACTORS IN JAPANESE INDIVIDUALS AND FAMILIES

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Genetically determined difference in serum proteins like genetic variation in blood types, eye-color has become apparent in recent years. In conjunction with the study of serum globulin, different types of haptoglobin and transferrin have been discovered. Later, the existence of variant among certain alpha-globulin and beta-globulin has been reported. The discovery of human gamma-globulin groups was achieved as a by-product of the investigation of rheumatoid factor present in the serum of most patients with adult chronic rheumatoid arthritis.

In 1956, Grubb noted agglutination of the sensitized cells by certain selected rheumatoid sera. This reaction was inhibited by some normal sera but not by others. Ability to inhibit this agglutination system was shown to be hereditary and the active component responsible for this inhibitory action was discovered to present in gamma-globulin fraction. This inhibitor was named as Gm (a), an abbreviation for gamma-globulin, and person whose sera contained the inhibitor was described as Gm (a+) and that lacking the inhibitor as Gm (a−). Another factor, InV factor, was reported by Ropartz, Lenoir and Rivat. This factor is inherited independently of Gm (a), (b), (x) or (r).

These gamma-globulin factors were considered to be very useful aids for the study of polymorphisis of human gamma-globulin. Furthermore, it is interesting enough to note that some factors are made by different alleles in different races. This is the purpose of the paper to report Gm and InV factors among 258 unrelated Japanese individuals and analyze family studies.

MATERIALS AND METHODS

Blood specimens were collected from the central laboratory of Serum was separated as soon as possible and kept frozen at −20 °C until use. Gamma-globulin factors were determined with Gm (a), (b), (x), (c)
and InV (a). Reagents and their optimum dilution we used are tabulated in Table 1.

Table 1
Reagents for Typing

<table>
<thead>
<tr>
<th>Factor</th>
<th>Anti-factor</th>
<th>Dilution of anti-factor</th>
<th>Anti-D</th>
<th>Dilution of anti-D</th>
<th>Dilution of test serum</th>
</tr>
</thead>
<tbody>
<tr>
<td>Gm (a)</td>
<td>Wils.</td>
<td>1:8</td>
<td>251</td>
<td>1:5</td>
<td>1:8 or 1:16</td>
</tr>
<tr>
<td>Gm (b)</td>
<td>Draves</td>
<td>1:4</td>
<td>E.W</td>
<td>1:3</td>
<td>1:8 or 1:16</td>
</tr>
<tr>
<td>Gm (x)</td>
<td>Taylor</td>
<td>1:8</td>
<td>Ham</td>
<td>1:10</td>
<td>1:8 or 1:16</td>
</tr>
<tr>
<td>Gm (c)</td>
<td>Kellum</td>
<td>1:16</td>
<td>Warren</td>
<td>1:5</td>
<td>1:8 or 1:16</td>
</tr>
<tr>
<td>InV (a)</td>
<td>Mathew</td>
<td>1:8</td>
<td>Roehm</td>
<td>1:5</td>
<td>1:16 or 1:32</td>
</tr>
</tbody>
</table>

The test was performed by a drop methods. One drop of the diluted serum sample to be tested was mixed with one drop of diluted anti-factor (agglutinator) for 5 minutes. Then one drop of 1% anti-D sensitized cell suspension was added. The mixture was well shaken and left standing in a moist chamber at room temperature for 45 minutes.

Two series of controls were performed at the same time; One was to examine whether the agglutinator was suitable for the test, and the other was to confirm the test serum itself not to agglutinate the sensitized cells. If a test serum itself agglutinated the sensitized cells, it was omitted from this study.

Agglutination of this system was easily determined by naked eyes.

RESULTS AND DISCUSSION

A) Population study

The result of population study is shown in Table 2. As is clear in this table, Japanese individuals are all Gm (a+) and Gm (c-) so far tested. Our data was analyzed by the use of the maximum likelihood equation on the basis of

Table 2
Frequency of Gm and InV Factors

<table>
<thead>
<tr>
<th></th>
<th>No. of serum tested</th>
<th>No. of serum reacted positive</th>
</tr>
</thead>
<tbody>
<tr>
<td>Gm (a)</td>
<td>258</td>
<td>258 100%</td>
</tr>
<tr>
<td>Gm (b)</td>
<td>&quot;</td>
<td>49 18.98</td>
</tr>
<tr>
<td>Gm (x)</td>
<td>&quot;</td>
<td>83 32.16</td>
</tr>
<tr>
<td>Gm (c)</td>
<td>&quot;</td>
<td>0 0</td>
</tr>
<tr>
<td>InV (a)</td>
<td>&quot;</td>
<td>125 48.47</td>
</tr>
</tbody>
</table>
assumption of Gma, Gmax, Gmab alleles. Let the frequency of Gma=P, Gmax=Q and Gmab=R, then the maximum likelihood estimates were:

\[ P = 1 - q - r \]
\[ Q = 1 - \sqrt{1 - 0.287 - 0.035} \]
\[ R = 1 - \sqrt{1 - 0.156 - 0.035} \]

From Table 3,

\[ Q = 1 - \sqrt{1 - 0.287 - 0.035} \]
\[ = 1 - \sqrt{1 - 0.322} \]
\[ = 1 - \sqrt{0.678} \]
\[ R = 1 - \sqrt{1 - 0.156 - 0.035} \]
\[ = 1 - \sqrt{1 - 0.191} \]
\[ = 1 - \sqrt{0.809} \]

The estimates calculated from data of Kawasaki in the table are

\[ P = 0.724 \]
\[ Q = 0.176 \]
\[ R = 0.10 \]

As is shown in Table 4, observed number indicates the close agreement with

<table>
<thead>
<tr>
<th>Exp. frequency</th>
<th>Exp. No.</th>
<th>ob. No.</th>
<th>d</th>
<th>d^2</th>
<th>d^2/E</th>
</tr>
</thead>
<tbody>
<tr>
<td>Gm (b-x-) = P^2</td>
<td>0.524</td>
<td>135.19</td>
<td>135</td>
<td>0.19</td>
<td>0.0316</td>
</tr>
<tr>
<td>Gm (b-x+) = Q^2 + 2pq</td>
<td>0.285</td>
<td>73.53</td>
<td>74</td>
<td>0.47</td>
<td>0.221</td>
</tr>
<tr>
<td>Gm (b+x-) = R^2 + 2pr</td>
<td>0.155</td>
<td>39.99</td>
<td>40</td>
<td>0.01</td>
<td>0.0001</td>
</tr>
<tr>
<td>Gm (b+x+) = 2qr</td>
<td>0.035</td>
<td>9.03</td>
<td>9</td>
<td>0.03</td>
<td>0.0009</td>
</tr>
</tbody>
</table>

Note: All Japanese are Gm (a+c-), therefore these are not listed.
the calculated number. This fact is highly indicative of the evidence that the Japanese have a \( Gm^a, Gm^{ax}, \) and \( Gm^{ab} \) not like caucasians who possess \( Gm^a, Gm^b, \) and \( Gm^{ex} \).\(^{5(6)(7)}\)

\( \text{InV} \) factor is thought to sit on the locus different from that of \( \text{Gm} \). Calculation of \( \text{InV} \) \((a)\) factor based on our data from Kawasaki disclosed the expected gene frequency to be:

\[
\begin{align*}
\text{InV}^a &= P, \quad \text{InV}^b = Q \\
\text{InV}^a &= 1 - \sqrt{1-0.48} \\
&= 1 - \sqrt{0.52} \\
&= 1 - 0.721 \\
&= 0.279 \\
\text{InV}^b &= 1 - \text{InV}^a \\
&= 1 - 0.279 \\
&= 0.721
\end{align*}
\]

B) Family study

Data of family study for \( \text{Gm} \) phenotypes are shown in Table 5. The distribution of \( \text{Gm} \) phenotypes of offsprings again agreed with the assumption of three \( \text{Gm} \) alleles of \( Gm^a, Gm^{ab} \) and \( Gm^{ex} \). In short, all Japanese are \( Gm \ (a+), \) \( Gm \ (c-) \) and have three \( Gm \) alleles. The allele frequencies from our data showed a close resemblance with those reported previously by others.\(^{8}\)

\begin{table}
\centering
\caption{Gm Data for 12 Japanese}
\begin{tabular}{|c|c|c|c|c|c|}
\hline
\textbf{Mating} & \textbf{No. of families} & \textbf{Total} & \multicolumn{3}{c|}{\textbf{Offsprings}} \\
& & & \textbf{a} & \textbf{ab} & \textbf{ax} & \textbf{axb} \\
\hline
\textbf{a} \cdot \textbf{a} & 8 & 13 & 13 & - & - & - \\
\textbf{a} \cdot \textbf{ab} & 8 & 15 & 9 & 6 & - & - \\
\textbf{a} \cdot \textbf{ax} & 11 & 23 & 10 & - & 13 & - \\
\textbf{a} \cdot \textbf{axb} & 2 & 3 & - & 2 & 1 & - \\
\textbf{ax} \cdot \textbf{ax} & 4 & 6 & - & - & 6 & - \\
\textbf{ax} \cdot \textbf{ab} & 6 & 10 & 1 & 4 & 2 & 3 \\
\textbf{ax} \cdot \textbf{axb} & 1 & 2 & - & - & 2 & - \\
\textbf{ab} \cdot \textbf{ab} & 1 & 1 & - & 1 & - & - \\
\textbf{ab} \cdot \textbf{axb} & 1 & 2 & - & 2 & - & - \\
\hline
\textbf{Total} & 42 & 75 & 33 & 15 & 24 & 3 \\
\hline
\end{tabular}
\end{table}

SUMMARY

Population and family studies for \( \text{Gm} \) and \( \text{InV} \) systems were performed on Japanese individuals in Kawasaki City, near Tokyo.
Data obtained indicated a close resemblance with previous reports on the Japanese. The allele frequencies agreed with an expectation based on the assumption of alleles \( \text{Gm}^{a}, \text{Gm}^{ax} \) and \( \text{Gm}^{ab} \) in the Japanese.

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**REFERENCES**