**LETTER TO JMG**

Variation in dinucleotide (GT) repeat sequence in the first exon of the STAT6 gene is associated with atopic asthma and differentially regulates the promoter activity in vitro

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preparation of the IL-4/IL-13 mediated Th2 response is a characteristic of allergic diseases such as asthma, a common and often debilitating disease.1 STAT6 is a critical signalling molecule in the Th2 signalling pathway, and mice lacking STAT6 are protected from allergic pulmonary manifestations.2 The importance of STAT6 in asthma is also evident from studies showing that STAT6 gene expression is markedly upregulated in airway epithelial cells in asthma.3 STAT6 is important in the expression of VCAM-1 in endothelial cells and of chemokines, such as eotaxin, in epithelial cells following stimulation with IL-4 and IL-13.4 As a consequence, STAT6 has been considered a strong candidate for predisposition to atopic asthma. Indeed, the human STAT6 gene is mapped to chromosome 12q13.3 for predisposition to atopic asthma.5

Because of their close proximity to the transcription start site, they play a role in the transcriptional control of genes. Located near transcription sites, which makes it possible that variation in the length of repeat variants differentially regulates the promoter activity in vitro.

**MATERIALS AND METHODS**

**Study population and genotyping**

Fifteen randomly selected white American and 214 white British subjects were studied. Details of the British subject selection have been previously described.6 All the asthmatic subjects had physician diagnosed asthma with (a) recurrent breathlessness and chest tightness requiring ongoing treatment, (b) documented wheeze, and (c) documented labile airflow obstruction with variability in serial peak expiratory flow rates of >30%. Atopy was defined as a positive skin prick test of >5 mm and specific IgE (>3.5 kU/l) against either of the aeroallergens house dust mite or grass pollen. Measurement of total serum IgE was carried out by the CAP ELISA system (Pharmacia, Uppsala, Sweden). DNA samples were extracted using a commercial kit ( IsoQuick, Microprobe Corp, Garden Grove, USA), and subjected to PCR amplification of base pairs ~72 to ~115 (relative to the transcription start site; GenBank AF067575) of the STAT6 gene. Primers pairs 5’-TCTTCTCTGGCTCAGAG and 5’-CAACACCACCCACCGGA were used to amplify the fragment, which was then genotyped by a laser based 377 automated sequencer and GeneScan software (Applied Biosystems).

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Key points

- STAT6 is critical in Th2 cytokine signalling. Multiple sequence variants of the STAT6 gene have been identified, some of which are associated with atopic phenotypes in diverse populations.

- Seven dinucleotide GT repeat variants were identified in the noncoding exon 1 of STAT6. Case–control association analysis of 214 white British subjects demonstrated significant association with asthma of an allele with a 13GT repeat sequence (GT13) (OR 1.52, 95% confidence interval 1.02 to 2.28, p = 0.027), whereas the GT16 allele showed an inverse association with asthma (p = 0.018). Furthermore, individuals with the GT13 allele had a higher mean (SD) level of geometric mean IgE compared with individuals with the GT16 allele (480.04 (90.46) kU/l, n = 119 v 106.14 (46.12) kU/l, n = 22; p = 0.004).

- Transient transfection assays of different alleles revealed significantly higher transcriptional activity with the GT13 allele compared with the GT16 allele in Jurkat, HMC-1, and BEAS-2B cell lines.

- Gel shift assays demonstrated a binding complex when six GT alleles were used as a probe. The GT13 allele had significantly decreased binding stability compared with the GT16 allele in a reciprocal competitive assay.

- These findings suggest that the GT repeat polymorphism of the STAT6 gene contributes to susceptibility to atopic asthma and total serum IgE levels, and that variation in the length of the GT repeat sequence influences the regulation of promoter activity.
Reporter gene constructs, transient transfection, and luciferase assay

A genomic DNA fragment (nucleotides −702 to +169; relative to the transcriptional initiation site) containing the GT repeat region in exon 1 of the human STAT6 gene was amplified and cloned into a TA vector (Invitrogen, San Diego, CA, USA). The reporter constructs used were generated by subcloning the sequences containing GT repeats into the HindIII site of the pGL2 basic vector with luciferase (Promega, Madison, WI, USA), and the single copy sequence orientation and orientation of each reporter constructs were confirmed by sequencing analysis. Three different human cell lines were used in this study: HMC-1 (a mast cell line), Jurkat (a T cell line) and BEAS-2B (a bronchial epithelial cell line). Cells were transfected with 2 µg of reporter gene constructs or pGL2 basic vector without insertion using SuperFect (Qiagen, Santa Clarita, CA, USA) for HMC-1 and Jurkat cells, and FuGENE 6 for BEAS-2B cells (Qiagen) according to the manufacturer’s instructions. Transfections were always performed in duplicate. The luciferase assay used has been described previously.14

Electrophoretic mobility shift assay

Preparations of nuclear extracts and DNA binding conditions used for gel mobility shift assays were performed as described previously.14 The oligonucleotide sequences were: sense 5′-GAGAGGA(GT)nATGTA, antisense 5′-ATACAT(AC)nTCTCTC, where n ranged from 12 to 17. The complementary oligonucleotides were annealed, and the double stranded oligonucleotides were labelled with [γ-32P]-dATP. Total protein content was determined with Bradford protein assays (Bio-Rad, Hercules, CA, USA). In the absence or presence of varying amounts of unlabelled oligonucleotides (competitor), 20 µg of nuclear proteins were incubated for 20 minutes. Reactions were then incubated with 0.2 ng of GT repeat probes end labelled with [γ-32P] ATP. The complexes were resolved on a nondenaturing 5% polyacrylamide gel (acrylamide:bis-acrylamide 30:1), dried, and subjected to autoradiography. Densitometric scanning of the autoradiographs was also carried out. Each binding assay was performed in duplicate. The luciferase assay used has been described previously.14

Statistical analysis

Allele frequency, odds ratios, 95% confidence intervals, and significance values were estimated using SPSS (version 10; SPSS Inc, Chicago, IL, USA). Luciferase activities are expressed as mean (SEM). Differences in the mean luciferase activity for different dinucleotide repeat constructs were compared by using one way analysis of variance. A p value <0.05 was considered significant.

RESULTS

Association of the GT repeats with atopic phenotypes in a British population

GT repeats in exon 1 of STAT6 were genotyped in 15 unrelated white American and 214 white British individuals using a GeneScan assay. Seven distinct alleles were identified in these 229 subjects, ranging in size from GT12 to GT17 in the American, and GT13 to GT18 in the British subjects. Neither GT12 nor GT14 alleles have been previously found in studies of Japanese15 and German16 populations. GT13 and GT15 appeared to be more frequent in this population than other variants, consistent with the previous reports of Dutesch et al, who demonstrated 40.1% GT13 and 43.5% GT15 in a white population in Germany.17

The results of genotyping for the subjects with different phenotypes are presented in table 1. Among all the alleles, the GT13 repeat allelic frequency was significantly increased in the atopic asthmatic subjects compared with healthy controls (43% v 33%, p = 0.027, OR 1.52, 95% confidence interval (CI) 1.02 to 2.28). In contrast, the GT16 allelic frequency was significantly decreased in cases compared with controls (4% v 11%, p = 0.018, OR 0.39, 95% CI 0.17 to 0.92). No significant association with these alleles was found when atopy was analysed. A significant association of the GT13 allele with the IgE level was demonstrated by comparing the difference in the geometric mean level of total IgE between GT13 and GT16 alleles (fig 1). Individuals with the GT13 allele had a higher level of IgE compared with individuals with the GT16 allele (geometric mean (SD) IgE 480.04 (90.46) kU/l, n = 119 v 106.14 (61.2) kU/l, n = 22; p = 0.004). A 10 fold difference in geometric mean level of total serum IgE was noted between subjects with homozygous GT13 and GT16, but no statistical comparison could be made because of the small number (n = 3) of homozygous GT16 available in this population.

Dinucleotide repeat (GT) modulates the promoter activity

To examine the relationship between the length of the dinucleotide repeat and promoter activity, reporter gene assays were performed using luciferase constructs containing two short GT repeats (GT12 and GT13) and two long alleles (GT16 and GT17). A GT18 variant of reporter was not constructed because the frequency of the GT18 allele was low (<0.005) in the study populations. The results showed that while the relative transcriptional activity varied in BEAS-2B, Jurkat, and HMC-1 cells, the GT13 allele resulted in significantly higher transcriptional activity compared with the other three alleles in all three cell lines tested (fig 2). Most impressively, a mean fivefold greater transcriptional activity was observed in BEAS-2B cells (fig 2A) using the

Table 1 Association of GT repeat alleles with atopy and atopic asthma in the British population

<table>
<thead>
<tr>
<th>Allele</th>
<th>Non-atopic</th>
<th>Atopic</th>
<th>OR (95% CI)</th>
<th>P value</th>
<th>Non-atopic</th>
<th>Atopic asthma</th>
<th>OR (95% CI)</th>
<th>P value</th>
</tr>
</thead>
<tbody>
<tr>
<td>GT13</td>
<td>63 (35.2)</td>
<td>94 (37.9)</td>
<td>1.14 (0.76 to 1.69)</td>
<td>0.304</td>
<td>90 (33.2)</td>
<td>67 (43.0)</td>
<td>1.52 (1.02 to 2.28)</td>
<td>0.027</td>
</tr>
<tr>
<td>GT14</td>
<td>8 (4.5)</td>
<td>8 (3.2)</td>
<td>0.71 (0.27 to 1.96)</td>
<td>0.342</td>
<td>11 (4.0)</td>
<td>5 (3.2)</td>
<td>0.79 (0.23 to 2.33)</td>
<td>0.439</td>
</tr>
<tr>
<td>GT15</td>
<td>80 (44.7)</td>
<td>116 (46.8)</td>
<td>1.10 (0.75 to 1.61)</td>
<td>0.352</td>
<td>128 (47.2)</td>
<td>68 (43.6)</td>
<td>0.87 (0.38 to 1.30)</td>
<td>0.277</td>
</tr>
<tr>
<td>GT16</td>
<td>19 (10.6)</td>
<td>17 (6.9)</td>
<td>0.63 (0.31 to 1.23)</td>
<td>0.118</td>
<td>29 (10.7)</td>
<td>7 (4.4)</td>
<td>0.39 (0.17 to 0.92)</td>
<td>0.018*</td>
</tr>
<tr>
<td>GT17</td>
<td>9 (5.0)</td>
<td>13 (5.2)</td>
<td>1.05 (0.44 to 2.50)</td>
<td>0.548</td>
<td>13 (4.8)</td>
<td>9 (5.8)</td>
<td>1.22 (0.51 to 2.94)</td>
<td>0.407</td>
</tr>
</tbody>
</table>

Five common alleles in this study population are shown. P value for frequency differences of each allele v overall, *p<0.05 was considered significant. OR (95% CI), odds ratio and 95% confidence interval.
Numbers reflect mean (SE) of five independent experiments. Results are expressed as relative luciferase activity, the average value obtained from pGL2 basic transfected cells being taken as 1.

GT13 allele compared with the GT16 allele. The shortest allele, GT12, showed consistently lower activity compared with the other three alleles in all three cell lines, demonstrating that the transcriptional activity was not proportional to the size of the repeat sequence. The two long repeats, GT16 and GT17, demonstrated intermediate levels of transcriptional activity when all four alleles were compared. In HMC-1 cells, the GT17 allele showed significantly higher activity compared with GT12 and GT16, while the level of transcriptional activity was still lower than that seen for GT13 allele (fig 2B). No significant change in transcriptional activity was observed in any of the cell lines following activation with ionomycin (data not shown).

Dinucleotide repeats bind to nuclear protein(s)

To determine whether the differential promoter activity is due to the difference in transcription factor binding, gel shift assays were performed to investigate the binding patterns of nuclear proteins derived from different cell lines to the GT repeat. A protein–DNA complex formation was observed when all the GT repeat probes (GT12, GT13, GT14, GT15, GT16, and GT17) were examined (fig 3A). For instance, the GT12–protein complex was efficiently inhibited in a concentration-dependent manner by the presence of excess unlabelled GT12, but not by a non-specific probe, RANTES (fig 3B). To investigate the difference in DNA–protein binding between GT13 and GT16, a reciprocal gel shift competitive assay was performed, and the relative amounts of GT16 and GT13 binding complex formation in the presence of reciprocal GT13 and GT16 competitors were assessed (fig 4A). The results showed that IC50 for GT13 is 10 fold higher than that for GT16 (fig 4B), suggesting a relatively more stable binding of GT16 to the putative nuclear factor(s). Additional reciprocal gel shift competitive assays were also conducted for the shorter GT repeat allele, GT12, and the longer one, GT17 (fig 4C), which gave similar results; IC50 for GT12 is 12 fold higher than that for GT17 (fig 4D). These results imply that the longer GT repeat allele may have a relatively more stable binding to the putative nuclear factor(s) compared with the shorter repeat. Similar results were obtained from assays of nuclear extracts from Jurkat cells (data not shown). Together, the results suggested that the stability of the binding between the GT repeat sequences and protein(s) required for the transcriptional regulation may partially contribute to the functional alteration of STAT6 transcription.

DISCUSSION

Polymorphic dinucleotide repeats are common throughout the genome and widely used as genetic markers. Some polymorphic dinucleotide repeats have been shown to be functional in the regulation of gene transcription. A total of seven alleles of the GT repeats in various populations were detected in the first exon of STAT6, ranging in size from 12 to 17 repeat units in white American, and 13 to 18 in white British subjects. The result is somewhat at variance with two previous reports, implying that there are clear ethnic differences in allelic frequency of different GT repeats in diverse populations.

In this study, we provide evidence for a significant association of GT13 allele with atopic asthma in British whites. In addition, although the GT16 allele was not common, a significant association was found, which suggests a lower risk for atopic asthma. Consistent with this result, total serum IgE level, a major phenotypic marker of atopic asthma, was significantly higher for individuals with the GT13 allele compared with those with the GT16 allele. Of interest is the finding that a 10 fold difference in the geometric mean level of total serum IgE was seen between individuals with homozygous GT13 and GT16, but because of the small number of subjects with homozygous GT16 in this population, no statistical comparison could be made. Taken together, the GT13 allele or homozygous genotype suggests an increased production of total serum IgE, and subsequently contributes to the development of atopic asthma.

As a corollary, the allele frequency of GT13 has been reported to be higher in Japanese children with allergic asthma compared with healthy controls. Furthermore, the GT13 allele was found to be in significant linkage disequilibrium with a 3′-UTR SNP, G4291A, which has recently been reported to be associated with atopic asthma in another Japanese population. However, in a study of German whites, the GT16 allele was determined to be significantly associated with an increased eosinophil cell count, although the significance of this finding is unclear. Taken together, our results and previous reports suggest that the GT13 allele may be a strong predictor for atopic asthma. Further studies including more subjects and independent population are required to verify this genetic association.

Using reporter systems, the results from our present studies demonstrated that GT repeat alleles differentially regulate the constitutive promoter activity of the STAT6 gene.
In agreement with the data from the association analysis, the luciferase activity assays consistently showed that the GT13 allele has significantly increased promoter activity compared with the GT16 allele in the HMC-1, BEAS-2B, and Jurkat cells. These data are consistent with previously described findings showing allele size dependent modulation of transcriptional activity in vitro in several human genes encoding, for instance, human type 1 collagen, human growth hormone receptor, and the matrix metalloproteinase-9 enzyme.

The effect of these repeats on promoter activity could be explained by the formation of non-B-form DNA conformations that are involved in transcription, such as Z-, H- and cruciform DNA. Moreover, these repeat sequences capable of forming non-B-form DNA are known to occur with high frequency in eukaryotic genomes, particularly around promoter regions, and have been shown to be involved in many biological events, such as DNA replication, site specific recombination, and transcription. It has been shown by helical conformation analysis that the dinucleotide repeat is highly flexible, and that the longer the dinucleotide repeat, the longer the highly bendable section becomes. Because the GT repeat in exon 1 of STAT6 is in close proximity to the transcription start site, it is tempting to speculate that these GT repeat sequences may favour a DNA secondary structure, Z-DNA, which modulates the binding of transcription factors to the neighbouring transcriptional element. It is noted, however, that like other repeat sequences in a few genes, the influence on the transcriptional activity is not proportional to the size of the repeat sequences (fig 2). In addition, the level of transcriptional activity varies in different cell types, suggesting a cell type specific regulation and a complex modulatory mechanism.

Of interest, our experiments showed a DNA–protein binding complex with a similar binding pattern of nuclear proteins to different GT repeat alleles using gel shift assay. However, reciprocal gel shift competitive assays demonstrated that GT16 competes with the formation of the binding complex more efficiently than GT13, indicating that the GT13 allele has reduced stability compared with GT16. Consistently, a longer repeat allele, GT17, competes better than a shorter one, GT12. It is postulated that these GT repeats may either bind to transcriptional inactivator(s) (silencers), thus modifying the gene expression, or form non-B-form DNA conformations that differentially modulate the binding of transcription factors to the neighbouring transcriptional element. Moreover, the GT13 allele showed a reduced binding stability but with a decreased transcriptional activity, which is distinct from that seen for the GT16 allele. We therefore hypothesised that the effects of these GT repeat alleles are more likely due to the combination of binding to suppressive element(s) with various non-B-form DNA conformations. In fact, it is probably far more complex than this. At present, the nature of the putative binding factor(s) to double stranded simple repetitive DNA remains to be defined. Therefore, better understanding of the regulatory mechanism of the GT repeat sequence in transcription and, perhaps, in RNA stability and translation, awaits the identification of the GT repeat binding protein.

In summary, the data in this report illustrate that GT13 and GT16 repeat alleles in exon 1 of the human STAT6 gene may be crucial factors in the pathogenesis of atopic asthma and in the regulation of total serum IgE. We demonstrate that
variation in the length of the GT repeat sequence contributes to the regulation of gene transcriptional activity. The greater promoter activity of reporter constructs containing the GT13 variant is in agreement with the association of this variant with both high IgE levels and allergic asthma, and suggests that the associations with IgE and disease may result from higher transcriptional activity of promoters containing the GT13 variant. Further experiments are needed to provide a more detailed view on the mechanisms of transcriptional activation exerted by the GT repeat. These results provide a basis for continued investigation of the association of inherited polymorphisms of STAT6 with the pathogenesis of STAT6 mediated allergic diseases such as asthma.

ACKNOWLEDGEMENTS

The study was supported, in part, by NIH grants AI52468, HL68546, and AI50530, and by Philips Morris USA Inc.

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Conflict of interest: none declared

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Revised version received 16 December 2003

Accepted for publication 27 December 2003

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J Med Genet 2004 41: 535-539
doi: 10.1136/jmg.2003.015842

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