Class I-restricted T-cell responses to a polymorphic peptide in a gene therapy clinical trial for alpha-1-antitrypsin deficiency

Roberto Calcedo
University of Pennsylvania

Let us know how access to this document benefits you.
Follow this and additional works at: https://escholarship.umassmed.edu/peds_pp

Part of the Congenital, Hereditary, and Neonatal Diseases and Abnormalities Commons, Digestive System Diseases Commons, Genetics and Genomics Commons, Medical Genetics Commons, Respiratory Tract Diseases Commons, and the Therapeutics Commons

Repository Citation

This material is brought to you by eScholarship@UMMS. It has been accepted for inclusion in Pediatric Publications and Presentations by an authorized administrator of eScholarship@UMMS. For more information, please contact Lisa.Palmer@umassmed.edu.
Class I-restricted T-cell responses to a polymorphic peptide in a gene therapy clinical trial for α-1-antitrypsin deficiency

Roberto Calcedo1,2, Suryanarayan Somanathan1,1, Qiuyue Qin3, Michael R. Betts4, Andrew J. Rech2, Robert H. Vonderheide5, Christian Mueller6, Terence R. Flotte7, and James M. Wilson8,9

1Gene Therapy Program, Department of Medicine, Perelman School of Medicine, University of Pennsylvania, Philadelphia, PA 19104; 2Department of Microbiology, Perelman School of Medicine, University of Pennsylvania, Philadelphia, PA 19104; 3Abramson Family Cancer Research Institute, Perelman School of Medicine, University of Pennsylvania, Philadelphia, PA 19104; and 4Department of Pediatrics, University of Massachusetts Medical School, Worcester, MA 01655

Adeno-associated virus (AAV)-mediated gene therapy is currently being pursued as a treatment for the monogenic disorder α-1-antitrypsin (AAT) deficiency. Results from phase I and II studies have shown relatively stable and dose-dependent increases in transgene-derived wild-type AAT after local intramuscular vector administration. In this report we describe the appearance of transgene-specific T-cell responses in two subjects that were part of the phase II trial. The patient with the more robust T-cell response, which was associated with a reduction in transgene expression, was characterized more thoroughly in this study. We learned that the AAT-specific T cells in this patient were cytolytic in phenotype, mapped to a peptide in the endogenous mutant AAT protein that contained a common polymorphism not incorporated into the transgene, and were restricted by a rare HLA class I C alleles present only in this patient. These human studies illustrate the genetic influence of the endogenous gene and HLA haplotype on the outcome of gene therapy.

Recombinant adeno-associated virus (AAV)-mediated gene therapy holds great promise for the treatment of multiple diseases (1–8). Preclinical mouse studies have demonstrated sustained correction with a relative paucity of transgene-specific immunity. Even when present, a potent cytotoxic T-cell (CTL) response was, by itself, insufficient to eliminate transgene expression without an accompanying inflammatory response (9, 10). However, successful transgene expression in small animal models does not always translate to nonhuman primate models and humans. For example, nonhuman primates injected i.v. with an AAV vector expressing GFP elicited a transgene-specific T-cell response that extinguished transgene expression and caused transient transaminitis, which was not seen in mice injected with a similar vector (11). In a hemophilia B trial, an increase in hepatic transaminases with a concomitant decrease in transgene expression was observed in four patients systemically administered with an AAV vector (12, 13). These and other observations have led to the hypothesis that capsid and transgene immunity may compromise the outcomes of AAV gene therapy clinical trials.

AAV gene therapy is currently being pursued as a treatment for the monogenic disorder α-1-antitrypsin (AAT) deficiency. Results from phase I and II studies have shown a dose-dependent increase in wild-type AAT (m-AAT) after local i.m. administration of AAV1 vectors (14–18). In these studies, AAV capsid-specific CD4+ and CD8+ T cells with a cytolytic phenotype were detected in blood following AAV administration. Interestingly, m-AAT transgene expression was stable in most patients and was associated with a regulatory T-cell response characterized by increased CD4+ CD25+FOXP3+ cells at the site of vector administration (18). However, T-cell responses to the AAT transgene were observed in a more limited number of patients who participated in the phase II clinical trial (17).

Here, we describe and characterize the AAT-specific immune responses found in two trial subjects. Our findings demonstrate the previously underappreciated role of coding sequence polymorphisms and HLA genotypes that in one patient triggered a class I-restricted immune response to the AAT transgene following gene transfer.

Results

The T-Cell Response to AAT Is Multifunctional and Is Mediated by CD8+ T Cells. The phase II clinical trial consisted of nine subjects stratified into three dose cohorts, 6e11, 1.9e12, and 6e12 viral genomes/kg, who were administered AAV1-AAT i.m. Analysis of AAV1 capsid and AAT transgene immunity by IFN-γ enzyme-linked immunospot (ELISPOT) assays indicated that all nine subjects developed AAV1 capsid-specific T cells (17), but only two subjects (305 and 401) developed AAT transgene-specific T cells (Fig. 1A and B). None of the subjects had detectable AAV1- or AAT-specific T cells in blood before vector administration,

Significance

The use of adeno-associated virus (AAV)-mediated gene therapy to treat monogenic disorders is currently being tested in phase I, II, and III clinical trials. An immune response to the newly introduced gene product remains a potential problem because of the patient’s lack of central and peripheral tolerance to foreign epitopes. In this study, we show the induction of a T-cell response to the therapeutic product in a α-1-antitrypsin (AAT)-deficient subject receiving AAV1-AAT treatment. The response was directed against an AAT epitope upstream of the mutation and was associated with a polymorphism present in the subject but not in the wild-type AAT therapeutic product. Our study highlights the importance of considering polymorphisms in the targeted population when designing a transgene.
suggesting that these were primary responses. Nonetheless, we cannot rule out the presence of AAV1- or AAT-specific memory T cells in lymphoid organs before vector administration and the induction of an anamnestic response. Of the two subjects with anti-AAT immunity, subject 305 had a delayed T-cell response to AAT peptide pool B 3 mo after vector administration. However, the low magnitude of the response precluded further analysis of this subject.

In contrast, subject 401, who is homozygous for the z-AAT mutation (Glu342Lys), had a sustained and persistent T-cell response to peptide pool B of AAT. The CEF peptide pool was used at each time point as a positive stimulation control. M, month; SFU, spot-forming units; Y, year. Asterisks indicate a positive response; the hashtag indicates that no sample analysis was available. (C) Full amino acid sequence of the AAT transgene indicating peptides included in pool A (black) and B (purple), the location of immunodominant epitopes (brown), the location of polymorphisms and z-AAT mutations (blue), and C-terminal cleavage sites for human proteasome (red). Superscript numbers indicate the amino acid position of the mature AAT protein.
expected to carry the Val213Ala polymorphism (20), suggests a possible HLA allele restriction. To identify the allele(s) most likely responsible for presenting the immunodominant epitope, we HLA-typed all trial subjects and compared the haplotype of subject 401 with that of the subjects who did not activate T cells (Table 1). We were looking for a rare HLA allele that segregated with the development of AAT-specific T cells. In this analysis, any HLA allele that was found in a subject who did not mount an AAT-specific T-cell response would be precluded from being responsible for presenting the immunodominant epitope in subject 401. Of the HLA alleles present in subject 401 (HLA-A*02/03, HLA-B*35/44, and HLA-C*04/05), HLA-C*04/05 uniquely segregated with the T-cell response in subject 401 (Table 1). Furthermore, we performed a computational HLA class I affinity prediction for 8- to 12-mer peptides spanning the polymorphic site for patient 401’s HLA genotype. This analysis revealed a single 8-mer peptide (HVDQVTTV) predicted to bind with high affinity to HLA-C*05:01; however, no peptides were predicted to bind with high affinity to HLA-A or -B alleles (Tables S2 and S3). This result suggests that the polymorphic site generates a high-affinity neoepitope in patients carrying the HLA-C*05:01 allele.

Fig. 2. Functional and phenotypic analysis of the AAT transgene-specific T-cell response in PBMCs from subject 401. (A and C) Functional profile of cytokine (IFN-γ, TNF, and IL-2), chemokine (MIP-1α), and surface expression of a degranulation factor (CD107a) by CD8+ (A) and CD4+ (C) T cells from PBMCs obtained at the 2.5-mo time point following stimulation with AAT peptide library, AAT pool B, or AAT immunodominant peptide 46 DTEEEDFHVDQVT. (B and D) Memory phenotype characterization of AAT-specific CD8+ (B) and CD4+ (D) T cells. Naive cells were defined as CD27– CD45RO–, Tcm cells were defined as CD27+CD45RO+, Tem cells were defined as CD27–CD45RO+, and Teff cells were defined as CD27–CD45RO+. Pie charts represent the total AAT-specific T-cell response. Each slice indicates the proportion of cells that produce one to five cytokines as indicated by different colors.

Table 1. HLA haplotyping of the subjects enrolled in the clinical trial

<table>
<thead>
<tr>
<th>Subject</th>
<th>A</th>
<th>B</th>
<th>C</th>
</tr>
</thead>
<tbody>
<tr>
<td>301</td>
<td>02, 29</td>
<td>18, 44</td>
<td>07, 16</td>
</tr>
<tr>
<td>302</td>
<td>01, 31</td>
<td>18, 57</td>
<td>06, 07</td>
</tr>
<tr>
<td>303</td>
<td>11, 30</td>
<td>13, 13</td>
<td>06, 06</td>
</tr>
<tr>
<td>304</td>
<td>03, 29</td>
<td>44, 51</td>
<td>15, 16</td>
</tr>
<tr>
<td>305</td>
<td>02, 02</td>
<td>35, 50</td>
<td>06, 15</td>
</tr>
<tr>
<td>401</td>
<td>02, 03</td>
<td>35, 44</td>
<td>04, 05</td>
</tr>
<tr>
<td>306</td>
<td>01, 02</td>
<td>07, 07</td>
<td>07, 07</td>
</tr>
<tr>
<td>307</td>
<td>02, 03</td>
<td>08, 45</td>
<td>06, 07</td>
</tr>
<tr>
<td>308</td>
<td>NA</td>
<td>NA</td>
<td>NA</td>
</tr>
</tbody>
</table>

NA, sample not available for HLA typing. Numbers indicate the two alleles for A, B, and C loci.
Discussion

The number of AAV clinical trials is increasing significantly, with vectors being administered for the treatment of a variety of disorders. Although T-cell responses to AAV capsid have been described previously (1, 13–15, 21, 22), the activation of cellular immune responses to the transgene products following AAV gene therapy has been less of a problem. It is hypothesized that patients carrying null mutations are at higher risks of mounting an immune response to the wild-type therapeutic gene product, because they should lack central and peripheral tolerance to all T-cell epitopes. Based on this consideration, patients with null genotypes have been excluded from participating in some ongoing AAV clinical trials. A corollary of this hypothesis is that patients with missense mutations are at a lower risk of mounting T-cell responses to the transgene-derived protein product because they should be tolerant to all epitopes except those involving the mutation.

A detailed analysis of the immune responses elicited in the AAV1-AAT clinical trial clearly demonstrates the development of T cells to the wild-type m-AAT transgene product in a subset of subjects. The subject with the most robust m-AAT T-cell response had lower transgene expression than the other two subjects in the same dose-level group, suggesting that the immune response may have compromised the outcome of the therapy (17). In addition, the strong AAV-specific T-cell response detected in this subject may have played a role in lowering transgene expression, although similar AAV-specific T-cell responses in the high-dose group did not compromise transgene expression (17). Interestingly, the immunodominant epitope in AAT was located outside the z-mutation and occurred in a previously identified polymorphic site.

Why was a T-cell response generated to an epitope spanning a polymorphic residue but not to the site of the z-mutation? Furthermore, why was this T-cell response present only in one subject? We believe that the answers to both questions relate to class I restrictions and HLA genotypes. In this regard, the z-AAT mutation occurred in a region not flanked by proteasome cleavage sites, suggesting that it may not be processed efficiently for class I presentation. Furthermore, based on in silico analyses, none of the HLA class I alleles present in the research subjects bound effectively to peptides spanning the z-AAT allele. A similar analysis of the AAT immunodominant epitope revealed proximity to proteasome cleavage sites and high-affinity binding to a rare HLA-C allele found only in subject 401. In vitro binding and T-cell activation studies confirmed HLA-C*05 class I restriction of this peptide to the T cells of subject 401.

Several mechanisms could explain the generation of T cells against m-AAT in subject 401. One possibility is that the polymorphism could have diminished class I binding relative to the same peptide from the m-AAT transgene; alternatively, the polymorphism could affect the actual processing of the peptide for class I presentation. Either scenario could result in incomplete deletion of T cells in the thymus to the polymorphic peptide ending with activation and targeting of T cells to transduced cells in the periphery. However, in silico analysis failed to reveal differential binding of HLA-C*05 to the polymorphic and wild-type immunodominant peptides, and the Val213Ala change does not appear to affect proteasome cleavage sites. Thus the in silico analysis argues against these hypotheses; however, this evidence is not definitive because nonanchor residues in class I presented peptides, although not influencing peptide binding, have been shown to have substantial effects on T-cell responses (23). Another possibility is that i.m. injection of AAV1/m-AAT broke peripheral tolerance to self-reactive T cells by activating local inflammation at the site of m-AAT expression; this possibility is consistent with the presence of persistent inflammation at the injection site (17). In this case the polymorphism is incidental. It is possible that both mechanisms contributed to the final result.

Gene therapy with AAV vectors could potentially activate an immune response to both the transgene and the viral capsid. The interplay of these immune responses may further influence the outcome of the treatment (24). It is interesting that other subjects in this trial developed CD8+ and CD4+ T-cell responses to capsid with a concomitant increase in FoxP3-expressing regulatory T-cell responses in both peripheral and locally infiltrating T cells (18). These subjects also demonstrated an exhausted CD8+ T-cell phenotype in situ, with expression of both PD-1 and PDL-1.
We conclude that the apparent reduction in transgene expression that developed in subject 401 in this trial was the result of a class I-restricted T-cell response to a peptide in AAT. This T-cell response and its consequence were limited to a single patient who happened to have a rare HLA-C allele that efficiently presented a peptide from the transgene-derived protein. We suspect that a polymorphism in the immunodominant peptide of both z-AAT alleles of subject 401 resulted in a lack of central tolerance that, combined with vector-induced inflammation, resulted in a robust T-cell response to vector-transduced cells. This study shows that HLA genotype and polymorphism play a substantial role in gene therapy and should be considered in the investigation of transgene expression in clinical trials. We speculate that class I restriction may influence the substantial patient-to-patient variability that has been seen in some of the AAV gene therapy hemophilia trials.

Methods

Clinical Trial. This study was conducted under the Food and Drug Administration’s Investigational New Drug program with approval from the institutional review boards and biosafety committees of the University of Massachusetts Medical School and Cincinnati Children’s Hospital. All procedures and protocols were in accordance with the tenets of the declaration of Helsinki. This study is registered with ClinicalTrials.gov (NCT01054339). All subjects provided informed consent.

IFN-γ ELISPOT. We analyzed IFN-γ released in PBMCs using previously described methods (1). PBMCs were stimulated in duplicate with medium alone, AAV1 virions or AAT peptide libraries. The CEF peptide pool (containing 32 MHC class I-restricted T-cell epitopes (8–12 amino acids in length) that contain sequences derived from the human cytomegalovirus, Epstein–Barr virus, and influenza virus) (Mabtech) served as a positive control, as previously described (25). Positive ELISPOT counts were defined as >55 spot-forming units per million lymphocytes, i.e., values three times over background (25).

Peptide Libraries. We synthesized a peptide library tailored for the full lengths of the AAT and the AAV1 capsid as 15-mer with 10-aa overlap (Mimotopes). The AAT peptide library was divided into two pools, A and B, and the AAV virion peptide 1 (VP1) peptide library was divided into three pools, A, B, and C, as previously described (14).

Intracellular Cytokine Staining. PBMCs were stimulated with the AAVID and AAT peptide libraries or with individual immunodominant AAT peptide 46 (DTEEEDFHVDQVTTV). Reactive T cells were analyzed functionally and phenotypically using previously described techniques (1). T-cell polyfunctionality was assessed by simultaneous detection of secreted TNF, CD107a, IL-2, MIP-1α, and IFN-γ. Cellular phenotypes were evaluated by the expression of the surface markers (CD3, CD4, CD8, CD27, and CD45RO). Naïve T cells were defined as CD27+CD45RO−, Tcm cells were defined as CD27+CD45RO+, Tem cells were defined as CD27−CD45RO+, and Teff cells were defined as CD27−CD45RO−.

T-Cell Receptor β Chain Deep-sequencing Analysis. Deep-sequencing analysis of the T-cell receptor β (TCR-β) chain was performed using patient PBMCs to detect all possible rearranged genomic sequences and to determine T-cell receptor variable region β (TCR-βv) use for each done (Adaptive Biotechnologies) as described earlier (18).

HLA haplotypes analysis. HLA analysis was performed by LabCorp in eight of nine subjects enrolled in the trial. Samples for HLA typing were not available from subject 308.

AAT Polymorphism Analysis. DNA was extracted from eight 10-μm paraffin-embedded muscle tissue sections using a QiAamp DNA formalin-fixed, paraffin-embedded tissue kit per the manufacturer’s instructions (Qiagen). A 545-bp product was amplified and sequenced (GeneWiz) using primers (forward: ttgatgtgagttcgacga and reverse: aagggctgaggaggtgaa) flanking exon 3 (26).

Cell Lines and Transfection. K562 cells were a gift from Carl June, University of Pennsylvania, Philadelphia, PA. Cells were transiently transduced using Lipofectamine reagent (Invitrogen). We used indirect immunofluorescence to image transiently transduced K562 cells expressing individual human HLA using an anti-human MHC class I antibody. Images were collected using a Nikon inverted microscope.

Computational HLA Class I Affinity Analysis. To identify peptides predicted to bind MHC class I with high affinity, a sliding window of 8- to 12-mer peptides centered on the amino acid of interest were generated and ranked for binding using the Immune Epitope Database and Analysis Resource (27). Peptides with an IC50 corresponding to a percentile rank of less than one against a standardized database were classified as high affinity.

Acknowledgments. We thank Dr. Bruce Trapnell and the staff at Cincinnati Children’s Hospital for providing samples from subject 401. This work was supported by National Heart, Lung, and Blood Institute Grant P01 HL059407-16A1 (to J.M.W.). The clinical trial was supported in part by Grant R01FD003896 from the Office of Orphan Products Development, US Food and Drug Administration.

Supporting Information

Calcedo et al. 10.1073/pnas.1617726114

Changes in T-Cell Repertoire Following Vector Administration

The functional analysis of T cells, which is limited to measurements of cytokine secretion or activation, does not reveal the complexity of the host immune response following vector administration. To understand the breadth of the T-cell response, we longitudinally probed the repertoire of T-cell receptor (TCR) diversity in subject 401. High-throughput sequencing of the TCR β-chain complementary determining region 3 was performed on PBMCs isolated before and 9 mo following vector administration. Briefly, we characterized TCR diversity from DNA isolated from the equivalent number of cells using next-generation sequencing (Adaptive Biotechnologies). We analyzed a total of 663,609 productive sequences from PBMCs isolated before vector administration and 998,208 productive sequences from PBMCs isolated 9 mo after vector administration. At both time points roughly 3.8% of the total sequences were unique clones (Table S1). However, we identified an increased number of productive sequences and unique clones from postinjection samples. This finding indicates an expansion in peripheral blood T-cell clones. For instance, the number of unique clones in peripheral blood increased by 36%, from 25,026 preinjection to 39,207 at 9 mo following vector administration (Table S1). This difference may reflect normal temporal variations in the peripheral blood TCR repertoire or may suggest cellular immune responses to persistent transgene expression. In support of an ongoing adaptive immune response, a VB7-9 bias was observed in samples collected at 9 mo.

Among the clonotypes, we found the unique sequence CASSWDSYEQYF at a frequency of 0.63% (Fig. S1), representing a substantial expansion of this particular clone in peripheral blood following vector administration. Similar analysis performed at the site of vector administration might demonstrate T-cell trafficking to the source of antigen expression. However, muscle biopsy was not available from subject 401. Interestingly, a similar analysis of the T-cell repertoire in another subject enrolled in the trial (subject 301) demonstrated the presence of unique high-frequency clones in both blood and muscle following vector administration (17). Based on this finding, we expected clone CASSWDSYEQYF identified in the blood from subject 401 to be present in muscle also.

The T-Cell Response to AAV1 is Multifunctional and Diverse

We compared the intracellular staining analyses of AAV1 capsid-specific T-cell responses from subject 401 and from two other trial subjects (302 and 306) (17) and found that AAV1-specific responses, although varied in magnitude, had a similar cytokine profile among subjects. In subject 401, CD8+ T cells predominantly expressed IFN-γ, TNF, IL-2, and MIP-1α (Fig. S3A) with 14% of AAV1-specific CD8+ T cells coexpressing at least three factors (Fig. S3B, pie chart). Although the CD8+ T-cell response to AAV1 was similar among the three subjects, there were differences in the functional profile. The main differences in subjects 306 and 302 were the increased numbers of CD8+ T cells coexpressing three factors (80% and 52%, respectively) and the activation of CD107a (Fig. S3A). Interestingly, we could not detect the expression of CD107a among the AAV1-specific T cells from subject 401. Despite these functional differences, the phenotypic profile of the T cells was similar across subjects with an abundance of Tcm and Teff cells (Fig. S3B).

CD4+ T-cell responses were similar between subjects 401 and 306, with up-regulation of IFN-γ, IL-2, and TNF (Fig. S3C). Fifty-nine percent and 80% of CD4+ T cells from subjects 401 and 306, respectively, coexpressed at least two factors (Fig. S3D, pie charts). The phenotypes of activated CD4+ Tem and Teff cells were similar in these subjects (Fig. S3D). AAV1-specific CD4+ T cells were not activated in subject 302 (Fig. S3C).

![Fig. S1] TCRB-chain deep-sequencing analysis of the number of T-cell clones in blood before (y axis) and after (x axis) gene transfer in subject 401. Green triangles indicate T-cell clones present before injection. Blue triangles indicate T-cell clones present after injection. Red circles indicate T-cell clones present both before and after injection.
Fig. S2. AAT polymorphism. DNA (A) and amino acid (B) sequence alignment from the AAT transgene and from the AAT region of subject 401 in which the polymorphism was detected. The amino acid sequence of immunodominant epitope peptide 46 is aligned to transgene and subject 401 AAT sequences. The enlarged letters indicate the specific base and amino acid responsible for the polymorphism and the z-mutation.

Fig. S3. Functional and phenotypic analysis of the AAV1 capsid-specific T-cell response in PBMCs from subjects 401, 302, and 306. (A and C) Functional profile of cytokine (IFN-γ, TNF, IL-2), chemokine (MIP-1α), and surface expression of degranulation factor (CD107a) by CD8+ (A) and CD4+ (C) T cells from PBMCs obtained 2.5 mo following stimulation with the AAV1 peptide library. (B and D) Memory phenotype characterization of AAV1-specific CD8+ (B) and CD4+ (D) T cells. Naive cells were defined as CD27+CD45RO−, Tcm cells as CD27+CD45RO+, Tem cells as CD27−CD45RO+, and Teff cells as CD27−CD45RO−. Pie charts represent the total AAV-specific T-cell response; each slice indicates the proportion of cells that produce one to five cytokines, as indicated by different colors.

Other Supporting Information Files

Table S1 (DOCX)
Table S2 (DOCX)
Table S3 (DOCX)