Serum Antibodies to Blood Group A Predict Survival on PROSTVAC-VF

Christopher T. Campbell1, James L. Gulley2, Oyindasola Oyelaran1, James W. Hodge2, Jeffrey Schlom2, and Jeffrey C. Gildersleeve1

Abstract

Purpose: There is evidence that therapeutic cancer vaccines can lengthen survival for some patients with cancer, but responses vary widely from one person to another. Methods to predict clinical outcomes will advance the field and provide new insights into critical determinants of in vivo efficacy.

Experimental Design: This retrospective study included 141 subjects from phase II trials of PROST-VAC-VF, a poxvirus-based cancer vaccine currently in phase III clinical trials for advanced prostate cancer. A glycan microarray was used to profile prevaccination antiglycan antibody populations in sera as potential biomarkers for PROSTVAC-VF. The screen for predictive biomarkers identified antiglycan antibodies that consistently stratified subjects into groups with different Kaplan–Meier survival estimates. Because of the potential for overfitting, a permutation test was used to estimate the false discovery rate.

Results: Prevaccination antibody levels to blood group A trisaccharide (BG-Atri) were found to have a statistically significant correlation with survival. Long-term survival was approximately doubled in subjects with abundant anti-BG-Atri immunoglobulin M (IgM) relative to subjects with little or no preexisting IgM for BG-Atri. This survival correlation was specific to vaccine treatment, as no correlation was observed in control patients immunized with wild-type poxviruses lacking the key tumor antigen, prostate-specific antigen (PSA). Moreover, anti-BG-Atri IgM levels were not correlated with general measures of disease severity, such as PSA levels, Gleason score, or Halabi predicted survival.

Conclusion: In addition to reporting a new potentially predictive biomarker for PROSTVAC-VF, this study highlights the use of glycan microarray technology for improving our understanding of vaccine immunology. Clin Cancer Res; 19(5); 1290–9. ©2012 AACR.

Introduction

Personalized medicine bases treatment decisions on characteristics of individual patients and their diseases (1). One particular area set to benefit from personalized medicine is cancer vaccine therapy (2), which trains the immune system to recognize and eliminate malignant cells. While numerous clinical trials have been conducted and one therapeutic cancer vaccine has earned U.S. Food and Drug Administration (FDA) approval, clinical responses vary widely from one patient to another. Certain patients achieve long-lasting responses, whereas others seem to receive little or no benefit. A longstanding objective in the field is to devise methods to predict a patient’s benefit from cancer vaccine therapy. By targeting treatment to likely responders, a predictive method can significantly improve clinical efficacy while simultaneously reducing health care costs.

Methods to optimize treatment decisions generally fall into 2 categories: (i) assessing immune responses after vaccination, and (ii) predicting clinical outcomes before vaccination. A number of studies have identified survival associations with immune responses measured after vaccination. Potential biomarkers (reviewed in refs. 3–5) include T-cell responses, delayed type hypersensitivity, immunosuppressive regulatory T cells, cytokine profiles, humoral responses, antivector titers, and circulating tumor cells. While promising, none of these approaches have been fully validated. Moreover, these methods require treatment of patients for at least several months before assessing response. Methods to predict outcomes before treatment can avoid unnecessary side effects in patients unlikely to benefit from the vaccine as well as allow patients to pursue alternative treatments at an earlier time point in the course of their disease. At present,
Cancer vaccines can be very effective for treating patients, but clinical responses vary widely from one patient to another. Strategies to target treatment to likely responders could significantly improve clinical efficacy, minimize unnecessary side effects, and reduce health care costs. In this study, we show that overall postvaccination survival for patients treated with PROSTVAC-VF correlates with preexisting serum immunoglobulin M levels for the blood group A glycan. Antibody group A levels did not correlate with survival in control patients and were independent of various measures of disease severity. Therefore, measurement of serum antibody group A levels before vaccination could provide a simple method for preselecting patients that are likely to benefit from PROSTVAC-VF therapy. Finally, these studies emphasize the potential of serum antiglycan antibodies as a convenient, understudied reservoir of biomarkers to advance personalized medicine and suggest new avenues for improving poxvirus-based vaccines.
High-throughput profiling of serum antiglycan antibodies

Serum antiglycan antibodies (diluted 1:50 and 1:200) were profiled on a glycan microarray (204 array components listed in Supplementary Table S1), which previously has been validated with numerous monoclonal antibodies and lectins (26–28) and shown to have excellent reproducibility (29). Arrays were printed as previously described (30, 31) except SMP2 pins (TeleChem) replaced SMP3 pins, and the print buffer included Dylight 649 (0.7 μg/mL; Thermo Scientific) to assess print quality before being washed away before serum assays. Bound antiglycan antibodies were detected with fluorescent secondary antibodies (Jackson Immunoresearch) specific for IgM, immunoglobulin G (IgG), or total immunoglobulin.

Because more than 800 arrays were required, experiments were designed to minimize technical variations and help assess quality (32). Slides came from the fewest possible print batches, and consistency of print batches was checked using reference serum. Samples were analyzed in a random order to ensure intermixing of controls and vaccinated subjects with varied responses to PROSTVAC-VF. In addition, the same experimenter collected all array data, and samples were analyzed on replicate slides to identify technical faults.

The data discussed in this publication have been deposited in National Center for Biotechnology Information’s (NCBI) Gene Expression Omnibus (GEO; 33) and are accessible through GEO Series accession number GSE42184 (http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?token=hzafreaseemfa&acc=GSE42184).

Glycan profiling of viral vectors

Glycans on viral vectors were assayed by adapting the glycan microarray for a competitive binding assay. Serum [diluted 1:500 in 1% bovine serum albumin (BSA) and 0.3% human serum albumin] was preblocked for 1.5 hours at 37°C with vaccinia (9.1E9 pfu) and fowlpox (6.9E10 pfu) that had been propagated in chicken embryo dermal cells, purified with a sucrose gradient, and UV inactivated. Presence of particular glycans on viral vectors was detected as reduced binding of preblocked serum relative to binding of control serum.

Second, ELISA measured BG-A glycans on viral vectors. Viral vectors (diluted to 10 μg/mL in carbonate buffer, pH 9.6) were coated onto Maxisorp plates (Nunc) and incubated with monoclonal anti-BG-A antibody HE-195 (GeneTex; diluted 1:100 in PBS + 3% BSA). Next, bound monoclonal antibody was detected with alkaline phosphatase–conjugated secondary antibody (Jackson Immunoresearch; diluted 1:250) that catalyzed the conversion of methylumbelliferylphosphate (Sigma; 26 μg/mL in Tris pH 9.0) into a fluorescent indicator.

Measurements of overall titers to viral vectors

Assays of antivaccinia and anti-fowlpox IgG titers were previously reported (23, 24, 34).

Statistical analyses

Training set leads were identified as statistically significant survival differences between subjects with high versus low prevaccination antibody levels (nonparametric log rank P value less than 0.05 for Kaplan–Meier survival estimator). To avoid noise at low antibody signals, a minimum threshold (seven times the background signal) was set for stratifying subjects. In addition, all strata needed ≥7 subjects as disproportionate strata (e.g., 5 vs. 23 subjects) show chance survival differences more frequently than predicted by log-rank P values.

Because of the potential for overfitting of data, lead validation required consistent, statistically significant survival differences after accounting for multiple comparisons by permutation testing (34). Probability of type I error (α) was estimated as the frequency of random permutations (3,000 runs) with ≥1 lead showing survival differences, at thresholds determined by the training set, with equal or better significance than observed for the lead (e.g., for BG-A1 IgM, difference in median survival = 14.7 months and P = 0.005).

Correlations between antiglycan antibodies and clinical or other immunologic data were assessed by nonparametric Kendall correlations (τ) and their associated P values calculated using Partek Genomics Suite.

Results

Prevaccination antibodies to blood group A predict postvaccination survival

Serum antiglycan antibodies of PROSTVAC-VF recipients were profiled with glycan microarrays (Fig. 1) containing 171 structurally distinct glycans (Supplementary Table S1; refs. 26, 29, 30). We tested for survival correlations with antiglycan antibody levels in 2 stages (training and validation) to reduce false positives common when conducting multiple comparisons. The training stage used sera from 28 subjects enrolled in a single center, phase II study of PROSTVAC-VF for metastatic castration-resistant prostate cancer (24). Next, potential biomarkers from the initial training set were validated in an independent set of 76 patients from a separate, multicenter phase II study (23). As controls, samples were obtained from 37 prostate cancer subjects inoculated with wild-type vectors (vaccinia and fowlpox lacking the 4 transgenes) coadministered with saline injections instead of GM-CSF (23). In each case, all clinical data were blinded until after completion of antibody profiling.

Of 39 leads identified by the training set (Supplementary Table S2), only prevaccination levels of serum IgM antibodies to blood group A trisaccharide [BG-A1 = GalNAcα1-3(Fucα1-2)Galβ1] were statistically significant in both the training (P = 0.04; Fig. 2A) and validation sets (P = 0.005; Fig. 2B) after correcting for multiple comparisons (α = 0.036). That is, there was a 3.6% likelihood that chance would produce a survival correlation for any lead equivalent to or better than the survival correlation observed for anti-BG-A IgM. Median survival for subjects with abundant IgM for BG-A1 was significantly longer than for subjects with
little or no anti-BG-A<sub>Hi</sub> IgM. Upper quartiles for prevaccination anti-BG-A<sub>Hi</sub> IgM survived nearly twice as long as the lowest quartile [median survival of 13.9 vs. 33.7 months in training set (P = 0.05); 17.1 vs. 31.0 months in validation set (P = 0.01)]. In addition, median actual survival for the upper quartiles was 11.5 to 15.7 months longer than their median Halabli predicted survival (training = 18.0 months; validation = 19.5 months) and 14.4 to 17.1 months longer

Figure 1. Overview of glycommunomics. A comprehensive profile of an individual’s serum antiglycan antibodies was obtained using 5 μL of serum and a glycan microarray containing 220 features robotically spotted onto a glass slide. Analogous to protein antigen arrays, captured antibodies were labeled with fluorescent secondary antibodies, and scanning quantified the amount of IgM, IgG, or total immunoglobulin bound to each glycan.

Figure 2. Kaplan–Meier survival curves for subjects stratified by levels of preexisting anti-BG-A<sub>Hi</sub> IgM. A, training set. B, validation set. C, validation set using a lower threshold. D, control subjects. The same threshold was applied for stratifications in A, B, and D.
than the median survival of controls (16.6 months). There was no survival correlation with anti-BG-Atri IgG.

Our 2-stage analysis was designed to validate potential biomarkers at the same threshold in both training and validation sets to guard against overfitting. The small training set, however, was not adequately powered to evaluate extreme cutoff values as estimates based on strata containing few subjects are prone to small sample size effects (35). The larger number of subjects in the validation set allowed us to more accurately evaluate cutoff values for Kaplan–Meier analysis. At the optimal cutoff, where approximately 22% of the patients were below the threshold, the survival correlation was even stronger ($P = 3E-6$; Fig. 2C). Therefore, performance of anti-BG-Atri IgM as a biomarker may be improved as larger numbers of patients are evaluated and the cutoff is further refined.

**Anti-BG-Atri IgM are prognostic specifically for vaccinated subjects**

As a first step in investigating the biologic basis for improved survival in subjects with abundant serum levels of IgM for BG-Atri before vaccination, we assessed whether this correlation was specific for vaccinated subjects or whether anti-BG-Atri IgM are generally prognostic. We profiled serum antiglycan antibodies of control subjects inoculated with wild-type viral vectors. There was no correlation with survival for subjects treated with control vectors (Fig. 2D); therefore, levels of anti-BG-Atri IgM were specifically predictive of survival after treatment with PROSTVAC-VF. Also, we evaluated relationships between anti-BG-Atri IgM levels and measures of disease severity, such as PSA level and Gleason score. Third, we tested for associations with prognostic factors, such as Halabi predicted survival (36) and age. No correlation with these factors was observed (Fig. 3), indicating the link between survival and anti-BG-Atri IgM is unlikely to be an epiphenomenon.

**Array’s diversity helps refine structure of antigen associated with improved survival**

High-throughput glycoinmunomic profiling provided considerable information about the binding properties of the antibody populations associated with vaccine efficacy.
The blood group A determinant is defined as the trisaccharide, GalNAcα1-3(Fucα1-2)Gal; however, this trisaccharide can be found in nature attached to various oligosaccharide chains. Six distinct tetrasaccharide variants of the blood group A antigen have been described (referred to as blood groups A1 through A6). In addition, the blood group H and B antigens share considerable structural similarities with the blood group A antigen. The array contained many structurally related glycans (Fig. 4), but survival correlated with prevaccination levels of IgM to BG-Atri uniquely. Interestingly, all substitutions, eliminations, or truncations of BG-Atri weakened the survival correlation (Table 1). The low degree of correlation between antibody binding for structurally related glycans indicated that distinct antibody populations recognize each structural variant. Improved survival, in particular, was not associated with antibodies for a common blood group A variant in humans (BG-A1 = GalNAcα1-3(Fucα1-2)Galβ1-3GlcNAcβ1-3Galβ1), which are strongly associated with blood type (29) and previously have been found to be distinct from anti-BG-Atri IgM (37). Antibodies to blood groups B and H did not correlate with survival. There was no survival correlation for the terminal disaccharide of the Forssman antigen (Fsdi = GalNAcα1-3GalNAc). Reduction of antibody binding to BG-A and Forssman glycans was substantially larger than the nonspecific adsorption of other antibodies to the poxviruses. Notably, the glycan profile of purified poxviruses is consistent with the glycosylation of chicken embryos, which produce both blood group A–like glycans and Forssman antigen (42). ELISA confirmed the presence of BG-Atri on the viral vectors (Fig. 5B). Furthermore, we have previously observed antibody responses to BG-Atri in patients vaccinated with PROSTVAC-VF, providing additional evidence of BG-A–like glycans on the poxvirus surface (26). Interestingly, although PROSTVAC-VF’s vectors apparently contain BG-Atri, levels of antibodies to these glycans were unrelated to prevaccination overall antivaccinia IgG titers (Fig. 6). This indicates that antiglycan immunity provides distinct information from overall titers, which are poor predictors of postvaccination survival (23).

**Discussion**

Cancer vaccines can produce durable responses in some patients, but others receive little or no immediately observable benefit. Critical determinants of *in vivo* vaccine efficacy are poorly understood. In this study, we show that preexisting serum antibody levels to BG-Atri correlate positively with overall survival for patients treated with PROSTVAC-VF. The correlation was statistically significant in patients from 2 separate phase II clinical trials encompassing over 100 patients and remained statistically significant even after correcting for multiple comparisons. In addition, the survival correlation was specific to PROSTVAC-VF as antibody levels were: (i) independent of disease severity (PSA levels, Gleason score), (ii) independent of other prognostic factors (Halabi predicted disease severity).
survival and age), and (iii) not correlated with survival in control patients inoculated with wild-type viral vectors lacking PSA and costimulatory transgenes.

The survival correlation of anti-BG-Atri IgM in vaccinated subjects is intriguing. BG-Atri is the terminal trisaccharide portion of the blood group A antigen, which is expressed at high levels on red blood cells, epithelia, epidermis, and mucins of blood type A and AB individuals (43). Although the biologic roles of ABO blood group antigens are still not well understood, it is known that antibodies to nonself ABO blood group antigens develop early on in life and are maintained at relatively constant levels in healthy adults (29, 44). These antibodies have been proposed to provide a barrier to curb the spread of certain diseases across individuals of different blood types (45). Moreover, strong immune responses to "foreign" ABO blood group antigens limit incompatible blood transfusions and organ transplants.

In the case of PROSTVAC-VF, the anti-BG-Atri IgM bind a blood group A-like glycan on the surface of the poxvirus. The glycan is presumably carried over from chicken embryo dermal cells, the host cells used for production of PROSTVAC-VF. Antibody bound to viral vectors can influence immune responses in a variety of ways. For example, emerging evidence indicates that certain types of preexisting antibodies, referred to as "natural antibodies" or B-1 class antibodies, may augment vaccine responses by linking innate and adaptive immunity (46). These natural antibodies, which include many antiglycan antibodies, have been shown in murine models to enhance immune responses in a complement-dependent manner (47). Studies on the α-gal antigen (48, 49) provide additional precedent for carbohydrates as vaccine adjuvants. Binding of preexisting antibodies to the α-gal glycan on vaccines has been shown to enhance antigen uptake and presentation and induce stronger immune responses (50, 51). In fact, attachment of the α-gal glycan to antigens can significantly enhance their immunogenicity (50, 51). Anti-BG-Atri IgM binding to PROSTVAC-VF’s viral vectors may increase immunogenicity in a similar manner.

Although other preexisting serum antibodies may bind the poxvirus vectors, anti-BG-Atri IgM seem to be unique. Preexisting antibodies for a vaccine’s viral vectors have long been investigated as potentially influencing vaccine efficacy. For example, several studies have evaluated relationships between overall antibody titers to poxvirus vectors and survival (23, 24). These studies have primarily grown out of concerns that preexisting neutralizing antibodies to the vectors would render virus-based vaccines ineffective; however, these studies showed no correlation between overall titers to poxvirus vectors and survival.

Table 1. Structural specificity of antigen associated with improved overall survival

<table>
<thead>
<tr>
<th>Minimum P value</th>
<th>Stratifications with P &lt; 0.005</th>
<th>Correlation (r) with BG-Atri</th>
</tr>
</thead>
<tbody>
<tr>
<td>BG-Atri</td>
<td>1.39E-07</td>
<td>26</td>
</tr>
<tr>
<td>BG-Atri (4/BSA)</td>
<td>1.96E-05</td>
<td>5</td>
</tr>
<tr>
<td>GalNAc α (4/BSA)</td>
<td>5.02E-04</td>
<td>2</td>
</tr>
<tr>
<td>BG-Atri (17/BSA)</td>
<td>0.0015</td>
<td>0</td>
</tr>
<tr>
<td>Ac-A-Tr(Thr)-S-G (5/BSA)</td>
<td>0.0019</td>
<td>0</td>
</tr>
<tr>
<td>GalNAc α (22/BSA)</td>
<td>0.0031</td>
<td>0</td>
</tr>
<tr>
<td>GalNAc α (22/BSA)</td>
<td>0.0061</td>
<td>0</td>
</tr>
<tr>
<td>Ac-A-Tr(Thr)-S-G (23/BSA)</td>
<td>0.0067</td>
<td>0</td>
</tr>
<tr>
<td>Ac-A-Tr(Thr)-S-G (8/BSA)</td>
<td>0.0073</td>
<td>0</td>
</tr>
<tr>
<td>BG-A1</td>
<td>0.0083</td>
<td>0</td>
</tr>
<tr>
<td>BG-H2</td>
<td>0.014</td>
<td>0</td>
</tr>
<tr>
<td>Fxα (31/BSA)</td>
<td>0.019</td>
<td>0</td>
</tr>
<tr>
<td>BG-B1</td>
<td>0.029</td>
<td>0</td>
</tr>
<tr>
<td>Fxα (21/BSA)</td>
<td>0.048</td>
<td>0</td>
</tr>
<tr>
<td>BG-ADD Lewis B hexa</td>
<td>0.063</td>
<td>0</td>
</tr>
<tr>
<td>Fxα (4/BSA)</td>
<td>0.066</td>
<td>0</td>
</tr>
<tr>
<td>BG-H1</td>
<td>0.094</td>
<td>0</td>
</tr>
<tr>
<td>BG-B1 (3)</td>
<td>0.15</td>
<td>0</td>
</tr>
</tbody>
</table>

NOTE: For each glycan structurally similar to BG-Atri, the table contains the minimum log-rank P value of all possible Kaplan–Meier survival curves stratified by IgM antibody levels for that particular glycan. Also listed are the numbers of stratifications (65 possible containing 6–70 subjects) whose Kaplan–Meier survival curves have log-rank P values <0.005. The degree of cross-reactivity of anti-BG-Atri IgM for structurally similar glycans was estimated by Kendall correlations (r) between IgM antibodies levels for BG-Atri and related glycans.
Moreover, there are numerous other glycans on the poxvirus surface. Of the antiglycan antibody populations detectable on our array, however, only preexisting anti-BG-Atri IgM correlated with clinical outcome, possibly due to a higher level of expression of the corresponding antigen on the viral surface than other glycans, a unique location of the antigen, or more substantial variability in anti-BG-Atri IgM levels among patients. It is important to note that antibody-mediated immune enhancement could occur in patients receiving either PROSTVAC-VF or the wild-type control poxviruses; however, the correlation of anti-BG-Atri IgM with survival was only observed in patients treated with PROSTVAC-VF. Therefore, these antibodies correlate with clinical outcome only when coupled with immune stimulation toward a tumor antigen.

Our results have a number of important implications. They provide the first evidence that anticarbohydrate antibodies could be useful biomarkers for PROSTVAC-VF. In principle, potential patients may be prescreened for IgM antibodies to BG-Atri as one criterion for treatment with PROSTVAC-VF. Although our study comprised over 100 vaccinated patients, as well as controls to show the prognostic specificity of anti-BG-Atri IgM, additional prospective studies with larger numbers of patients and control subjects will be an important focus of future research. The ongoing phase III clinical trial on PROSTVAC-VF is anticipated to enroll 1,200 patients, and samples from this study could provide additional validation of anti-BG-Atri IgM as a predictor of clinical response (25).

Second, glycan composition and consistency may be critical features of vaccine potency. Factors that influence glycan expression, such as type of host cell and growth conditions, may significantly affect clinical outcomes for poxvirus-based vaccines and optimizing these factors may improve efficacy. Analysis of a viral vector’s glycans also may be an important quality control assessment. Third, anti-BG-Atri IgM may be relevant to other pox-based therapies, such as other cancer vaccines [e.g., PANVAC (52) and rV-NY-ESO-1 (53)], oncolytic poxviruses (54, 55), and HIV vaccines [e.g., ALVAC-HIV (56)]. Because these poxviruses are often produced in chicken-derived cells, they also could display blood group A–like glycans.
on their surfaces. Therefore, antibodies to BG-A,B could influence their clinical efficacy too. Analogously, antibodies to blood group B may be relevant for vaccines propagated in other cell lines that express blood group B. By addressing technical challenges in studying carbohydrate–protein interactions, glycan microarrays provide a powerful tool for exploring connections between antigenic antibodies and disease.

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

Authors’ Contributions

Conception and design: C.T. Campbell, J.L. Gulley, J.W. Hodge, J. Schlom, J.C. Gildersleeve

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Acquisition of data (prospective patients, provided facilities, etc.): C.T. Campbell, J.L. Gulley, J.W. Hodge

Analysis and interpretation of data (e.g., statistical analysis, bioinformatics, computational analysis): C.T. Campbell, J.L. Gulley, J. Schlom, J.C. Gildersleeve

Writing, review, and/or revision of the manuscript: C.T. Campbell, J.L. Gulley, J.W. Hodge, J.C. Gildersleeve

Administrative, technical, or material support (i.e., reporting or organizing data, constructing databases): C.T. Campbell

Study supervision: J.C. Gildersleeve

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References


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34. Good PI. Permutation, parametric and bootstrap tests of hypotheses.
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