Evidence for an Antigen-driven Humoral Immune Response in Medullary Ductal Breast Cancer


Biotherapeutics Development Lab, Harvard Institute of Human Genetics, Harvard Medical School, and Division of Hematology-Oncology, Beth Israel Deaconess Medical Center, Boston, Massachusetts 02215

ABSTRACT

A minority of breast cancers is characterized by lymphoplasmacytic infiltrates that have been correlated with improved patient survivals. The association of improved prognosis with plasmacytic infiltrates has been classically linked with the rare medullary carcinoma subtype but is also evident in the smaller infiltrated fraction of the more abundant nonmedullary (not otherwise specified) tumors. It is our hypothesis that these plasma cell (PC) infiltrates represent a host humoral response driven by one or more tumor-derived neoantigens. As the index study group, two primary medullary carcinoma tumors were examined. Immunophenotyping confirmed a large number of IgG PCs in contradistinction to normal breast, which typically contains a lesser number of mainly IgA isotypes. IgG heavy and light chains were expressed as combinatorial phage Fab libraries. VH and VL sequences showed a preponderance of clonal groups in both patients, as identified by germ-line gene usage and junctional mutation patterns. Panning of phage Fab libraries against purified antigens excluded Her2/neu and p53 as the eliciting antigen, and failure of clonal enrichment by cell panning suggested that the neoantigen was not membrane expressed or was expressed at low levels. Cognate, original VH+VL pairs were obtained by single cell PCR of tumor PCs, which showed overlap with the pooled IgG libraries. Tumor-derived IgG V genes exhibited mutational patterns that were consistent with antigenic selection and affinity maturation. Where examined, IgG1 was the predominant isotype, consistent with a T-dependent (i.e., protein) antigen. From these data, we infer that the breast tumor PC infiltrates of the medullary carcinoma subtype are compatible with an autogenic tumor neoantigen-driven humoral immune response.

INTRODUCTION

In the search for new approaches in the understanding and treatment of malignancies, it has been proposed by Lippman (1) that “the most appropriate protein targets may emerge from a consideration of prognostic variables . . . shown to be of value in clinical practice.” The present study was undertaken to build on this premise, to explore the molecular basis for the apparently improved survival in PC*-infiltrated breast carcinomas. Breast cancer is remarkable among human malignancies in the incidence of lymphoplasmacytic infiltrates in a minority of tumors that suggest an ongoing humoral immune response. This finding has been considered characteristic of the medullary ductal carcinoma (MC) subtype, but PC-infiltrates are also present in a fraction of nonmedullary (NOS) infiltrating ductal carcinomas that may reflect similar etiologies.

MCs are relatively rare breast tumors, diagnosed in up to 5% of cases (2). Grossly, they are circumscribed without encapsulation and are infrequently bilateral. MC is also circumscribed microscopically, but its appearance is otherwise highly ominous, with large cells, abundant cytoplasm, large bizarre nuclei, and frequent mitoses. Virtually all are histologic nuclear grade III, usually the worst prognostically, and they display a high degree of aneuploidy and typically lack hormone receptors. Yet patients with MC often do better than predicted for size, grade, and lymph node status after surgery-only therapy (3–8). [For understanding the natural history of PC-infiltrated breast carcinomas, we prefer the mainly older literature on “surgery-only” treatment, because chemotherapies may have more impact on an immune response than on a resistant tumor, complicating for our purpose the otherwise excellent studies that include chemotherapies (e.g., Ref. 9.)] The tumor is infiltrated and surrounded with lymphocytes and plasma cells; in its most exuberant expression, it was classically designated “medullary carcinoma with lymphoid stroma.” Similarly, the presence of a PC infiltrate in NOS tumors is also favorable prognostically, suggesting that the PC reaction is the basis for the improved survival rather than the tumor histologic type. Ridolfi et al. (4) specifically examined the role of PCs in 192 cases of patients with MC in comparison with those with NOS and showed a correlation of increased PC infiltration with better survival in MC and NOS tumors alike, prompting the oft-stated impression that these tumors may be regulated by a host immune response. Finally, MC patients who failed primary therapy died the fastest of all of the groups (5), seemingly reflecting the aggressive histology of MC and the high proliferative index when the immune reaction was ineffective, again reinforcing the role of the immune response rather than the histology as determining the favorable prognosis.

As to the origin of the immune response, the infiltrates have been noted to be confined to the tumor bed itself without extending into the adjacent normal breast tissue, suggesting “some maladjustment between tumor and host” (3). The PCs in MC and infiltrated NOS were disproportionately of the IgG type, whereas uninvolved or contralateral breast tissue contained far fewer PCs, which were of the IgA type, as is typically associated with normal secretory epithelium (Refs. 10–12; a fourth reported IgG bias for a subset of MC; Ref. 13), leading to the speculation, “the stronger the stimulation by tumor-associated antigens, the higher the proportion of IgG” plasma cells (9). The antigenic phenotypes of the inflammatory infiltrates have been called “essentially similar” between MC and NOS (11, 14, 15), emphasizing again the centrality of the immune reaction rather than the tumor histologic type. The prominence of IgG versus the usual IgA plasma cells in MC and infiltrated NOS tumors alike, and the confinement of reactions to the tumor beds, suggest a specific response to one or more tumor-derived neoantigens in the tissues.

It is the primary hypothesis of this study that the diagnostic lymphoplasmacytic infiltrate typically observed in MC and less frequently in NOS tumors represents a matured, tumor-specific autogenic humoral immune response. The distinction between NOS-infiltrating...
ductal and MC histologically may be somewhat artificial in that the tumors likely represent a continuum, as evidenced by the interobserver variability and controversies in pathologic diagnosis (16–18), with the more important feature for our purpose being the presence of the PC infiltrates that is more common in MC as part of its diagnostic criteria. With this caveat in mind, as our index effort to address this question we selected two tumors of the MC subtype for initial examination by histological and molecular criteria for indicators of an antigen-driven humoral response.

Hallmarks of B-cell activation, differentiation, and proliferation were tracked by analysis of IgG sequences from both pooled sequences in combinatorial libraries and from single tumor-infiltrating PCs. Our data demonstrate clonal groups of immunoglobulin genes and confirm features consistent with the hypothesized antigen-driven tumor-derived B-cell immune response. These data suggesting an eliciting tumor neoantigen, with the clinical observation of improved prognosis in PC-infiltrated tumors, may, in turn, suggest that the antibodies secreted by these PCs may have an autoimmunetherapeutic antitumor benefit in these patients.

MATERIALS AND METHODS

Proteins

Purified Her2/neu was obtained from Dr. B. Fendlly (Genentech, South San Francisco, CA). p53 was obtained as a glutathione S-transferase-fusion protein from Dr. Dutta (Children’s Hospital, Boston, MA). Murine anti-Tac antibody was obtained from Dr. T. Waldmann (National Cancer Institute/NIH, Bethesda, MD).

Tumors and Cells

MC tumors were obtained as surgical discard samples under approval of the Institutional Review Board of the Beth Israel Deaconess Medical Center. A fresh, uninfused tumor was manually disaggregated and purified by Ficoll gradient centrifugation (Histopaque 1077; Sigma). Few viable tumor cells survived the procedure; the purification yielded mainly mononuclear cells (plasma cells and lymphocytes), which retained good viability. Cells (5 × 10⁷) were placed in solution D [6 M guanidinium isothiocyanate (Life Technologies, Inc.)] and human renal cell carcinoma line 293 (American Type Culture Collection, Bethesda, MD) and MC cell line HTB-24 (American Type Culture Collection) were maintained in RPMI 1640 supplemented with 10% FCS.

MC tumors likely represent a continuum, as evidenced by the interobserver variability and controversies in pathologic diagnosis (16–18), with the more important feature for our purpose being the presence of the PC infiltrates that is more common in MC as part of its diagnostic criteria. With this caveat in mind, as our index effort to address this question we selected two tumors of the MC subtype for initial examination by histological and molecular criteria for indicators of an antigen-driven humoral response.

Hallmarks of B-cell activation, differentiation, and proliferation were tracked by analysis of IgG sequences from both pooled sequences in combinatorial libraries and from single tumor-infiltrating PCs. Our data demonstrate clonal groups of immunoglobulin genes and confirm features consistent with the hypothesized antigen-driven tumor-derived B-cell immune response. These data suggesting an eliciting tumor neoantigen, with the clinical observation of improved prognosis in PC-infiltrated tumors, may, in turn, suggest that the antibodies secreted by these PCs may have an autoimmunetherapeutic antitumor benefit in these patients.

DNA Sequencing

Sequencing was done both by diodeoxy termination using Sequenase 2.0 from USB and by automated sequencing of PCR-amplified Hc and Lc inserts (ABI Prism dye termination system; Perkin Elmer). IgV genes was amplified for direct sequencing using PCR Ready-To-Go beads (Pharmacia) in a Perkin Elmer Thermocycler in a cycle of 94°C for 1 min, 55°C for 2 min, and 72°C for 3 min. NPC3-specific primers for the amplification of inserts from the combinatorial library were used for sequencing (20).

Germ-line gene usage was determined by comparison to the IMGT database of Ig sequences using the DNA-PLOT alignment tool (24) and by visual examination of sequences. Numbering and gene designations are as described for IMGT. Clonality was assessed on the basis of shared germ-line gene usage between sequences, mutated characters, and junctional mutation pattern, as determined by CLUSTALV alignment and examination of V(D)J junctions. Comparisons with germ-line genes for percentage of mutation were done for FR1, CDR1, FR2, CDR2, and FR3 regions only, and excluded the CDR3 portion of the V gene because of the high incidence of deletions in this region. Deletions were not scored as mutations for the purposes of total percentage of identity.

Library Construction

Combinatorial. Phage Fab display libraries were constructed from MCs from two patients designated patient 1 (GK library) and patient 2 (PT library) as described by Burton and Barbas (19). RNA was isolated from 5 × 10⁷ lymphoplasmacytoma cells frozen in solution D (above) by phenol-chloroform extraction and isopropanol precipitation. RNA was reverse transcribed using Superscript reverse transcriptase (Life Technologies, Inc.) and oligodeoxynucleotidylate (Perkin Elmer). Ig heavy and light chains were amplified by PCR as described (20). Three reactions were run for each sample, with one each for λ Lc, κ Lc, and γ1 Hc. Lc primers were used as described, with sets of 5’ Ig V consensus primers specific to κ Lc V gene families or λ Lc V gene families.

Patient 1 (GK) Hcs were amplified using a consensus 5’ primer (VHKG) with the sequence: AGGGTCAA/GTCGAG/CGACTCTGG and a VH4 primer with the sequence: CGG/CTCGAG/CAGGTCGA/CAGGAGTCCSG with the restriction cloning site marked. Patient 2 (PT) heavy chains were amplified with a mixture of 5’ Ig V consensus primers specific to Hc V gene families as described in Burton and Barbas (15). Constant region primers (3’) were specific to IgG1 Hc (CG1Z), and λ (CL2) or κ (CK1Z) Lcs.

PCR products were prepared and cloned into a Fab phage display vector as described in Kingsbury et al. (20) using the NPC3 M13 surface display system (gift of Dr. Carlos Barbas, Scripps Research Institute, La Jolla, CA) and VCSM13 helper phage (Stratagene). Phagmid isolates containing randomly paired Hcs and Lcs (1 Hc and 1 Lc per isolate) were selected for double inserts as described previously (21). Fifteen clones containing A Lc and γ1 Hc, and 15 clones containing κ Lc and γ1 Hc were selected randomly and sequenced from each patient for a total of 30 phagemid clones/patient.

Single Cell. An SC library was prepared from the PCs of patient 1. Stored lymphoplasmacytoma cells were thawed and stained with FITC-conjugated mouse antihuman CD38 (Caltag). CD38hi PCs (22) were sorted as SC into wells of 96-well PCR plate and amplified by RT-PCR with two rounds of nesting (PCR1 and PCR2), as described previously (23). Three sets of PCR1 reactions were run per cell: one for λ Lc, one for κ Lc, and one for γ (γ1) Hc. PCR1 employed pooled 5’ V family primers and a constant domain primer. PCR2 employed a nested constant primer and single V family primers. Single primer products from PCR2 were purified (Qiaguk; Qiagen) and directly sequenced. Multiple PCR products were sequenced from most single PCs.

DNA Sequencing

Sequencing was done both by diodeoxy termination using Sequenase 2.0 from USB and by automated sequencing of PCR-amplified Hc and Lc inserts (ABI Prism dye termination system; Perkin Elmer). IgV genes was amplified for direct sequencing using PCR Ready-To-Go beads (Pharmacia) in a Perkin Elmer Thermocycler in a cycle of 94°C for 1 min, 55°C for 2 min, and 72°C for 3 min. NPC3-specific primers for the amplification of inserts from the combinatorial library were used for sequencing (20).

Germ-line gene usage was determined by comparison to the IMGT database of Ig sequences using the DNA-PLOT alignment tool (24) and by visual examination of sequences. Numbering and gene designations are as described for IMGT. Clonality was assessed on the basis of shared germ-line gene usage between sequences, mutated characters, and junctional mutation pattern, as determined by CLUSTALV alignment and examination of V(D)J junctions. Comparisons with germ-line genes for percentage of mutation were done for FR1, CDR1, FR2, CDR2, and FR3 regions only, and excluded the CDR3 portion of the V gene because of the high incidence of deletions in this region. Deletions were not scored as mutations for the purposes of total percentage of identity.

PCR Error Rate

IgG1 CH1 sequence from randomly selected SC and combinatorial library clones were compared to the germ-line IgG CH1 sequence to determine the PCR error rate for combinatorial (0.4% after 35 cycles) and SC (0.18% after 70 cycles) library sequences. This would result in 1.1 mutations on average per Ig V gene in the combinatorial library but with no effect on the SC final sequences, which were resolved from multiple sequences and, thus, were error free (25, 26). All of the PCR errors were A > G or G > A transitions, as noted previously (27).

Internet address: http://imgt.cnusc.fr:8104.

7890
Panning

Purified Antigen-based Panning. EIA/RIA plates (Costar) were coated with 50 μl-well of a solution of 5 μg/ml antigen in 0.1 M NaHCO₃ (pH 8.5) overnight at 4°C, and blocked as described previously (20). Antigens were Her2/neu, p53, and MAT antibody (“Proteins,” above). Phage Fab suspensions containing 10¹² pfu in 25 μl were added to each well in quadruplicate and incubated for 2 hrs at 37°C. Phage were libraries or single clones of MC tumor-derived phage Fab, human anti-Id phage Fab clone (reactive with MAT) as positive control (20), or human anti-tetanus toxoid phage Fab as negative control. After incubation, phage were aspirated, the wells were washed, and bound phage was eluted, titered, and replicated as described previously (28).

Cell-based Panning. HTB24 medullary breast carcinoma cells and 293 embryonal kidney cells (negative control) were used in cell-based panning experiments as live or fixed cells as described earlier (29). Fixed cells were incubated with phage in PBS/10% horse serum. Live cells were incubated with phage in the appropriate growth medium, i.e. RPMI/10% FCS. Phage were eluted from the cells and replicated as described previously (28, 29). Eluted phage were compared with input phage by Alu “fingerprint” analysis for evidence of repertoire shift after cell panning (29).

Flow Cytometry. HTB24 and 293 cells were incubated with phage Fab with 10¹² phage in 0.1 ml of binding buffer (RPMI 1640 + 10% horse serum) for 30 min on ice, washed, and stained with anti-M13-FITC, then examined by cytofluorometry on a Coulter Epics II flow cytometer.

RESULTS

The aim of the present study was to evaluate whether the infiltration of lymphocytes and plasma cells, characteristic of MC, is attributable to an antigen-driven tumor-specific immune response. Two primary medullary breast tumor specimens were examined. Both samples had classic features with abundant infiltration of lymphocytes and PCs. Tissues were immunophenotyped and prepared as SC suspensions and immediately processed for M13 phagemid cloning or stored for later SC analysis. Hallmarks of an antigen-driven, tumor-specific immune response would be: (a) IgG versus IgA dominated; (b) a focused immune repertoire; (c) abundant somatic mutations concentrated in the antibody CDRs; and, ultimately, (d) antigen reactivity. These features were examined.

IgG Is the Dominant Isotype of Infiltrating PC Ig

Paraffin-embedded primary medullary carcinoma from patient 1 was sectioned, H & E stained, and immunohistochemically stained for IgA, IgG, and IgM (Fig. 1). Infiltrating cells were predominantly IgG with some IgA and few IgM. In separate, approximately matching fields, positively-staining cells were tallied as 207 IgG, 56 IgA, and 27...
IgM. Furthermore, whereas the IgA and IgM staining cells were predominantly mature plasma cells, the IgG+ cells included lymphoblasts, lymphoplasmablasts, and plasma cells, representing all stages of differentiation of the IgG B cell lineage, compatible with ongoing recruitment and B-cell differentiation in response to a locally produced antigen. A similar phenotype was evident for the tumor of patient 2. These results are consistent with observations published on April 13, 2017. © 2001 American Association for Cancer Research. Cancer Res. Downloaded from cancerres.aacrjournals.org on April 13, 2017.

Antibody Repertoire Focus

The sources of Ig mRNA for this analysis were mononuclear cell fractions from disaggregated primary tumors that contained a mixture of lymphocytes and PCs. Because of the vastly larger amount of Ig mRNA per cell in PCs versus B cells (up to ∼1000-fold greater), this mRNA-based cloning method effectively samples the most mature, PC-component of these infiltrates and is referred to as such in this presentation.

Libraries were initially prepared in a vector in which the VH and VL are displayed as Fab molecules on the tail proteins of M13 phage (phage Fab). This cloning method provided a sample of IgG VH heavy chains that are randomly paired with Vκ or Vλ light chains, as a so-called combinatorial library (30); both LC libraries are paired independently against the same IgG HC library. No single IgG primer captures the four subtypes and preserves the interchain disulfide configurations as needed for proper Fab assembly for phage display. Instead, IgG1 has come to be the default choice, because it typically dominates other subtypes in vivo and is the subtype of IgG that is most associated with T-dependent (i.e., protein) antigens (31).

The phage display format permitted analysis of the antibody repertoire focus by direct sequencing but also had potential advantages in antigen identification. Phage Fab enables screening for reactivity by “panning” against antigens as purified proteins (19, 20) and on cells (29, 32–34), and also permits antigen isolation by immunoprecipitation (28). Because this format randomizes the association of VH and VL, reactivity serves to define VH-VL pairs that are “antigen-competent” if not actually recreating the original plasma cell/B-cell pairing (35).

If the PC infiltrate is the result of an eliciting antigen within the tumor, this would be reflected by a restricted (focused) repertoire. Clonality was evaluated by sequencing of the library immunoglobulin V genes. Phagendom clones (∼15) with λ Lcs, and ∼15 phagendom clones with κ Lcs were randomly selected and sequenced from the separate combinatorial libraries for a total of 30 Hcs and 30 Lcs from each patient (Tables 1–4).

Definitive identification of clonal relatives was by comparison of V(D)J rearrangements and junctional mutation patterns. In general, unique specification of VDJ for Hc was enough to indicate clonality in this sample, whereas specification of VJ alone for Lc was frequently insufficient to specify clonality. The lower combinatorial possibilities and biases in J chain selection make the VL combinations more likely to be repeated on a random basis than the VHs. In this case, when VJ genes were the same, distinct clonal origins were nonetheless evident by the junctional mutation differences (Fig. 2). On the other hand, the possibility of phage clone duplications (“sibling clones”) was ruled out in these samples by the presence of different VH or VL partners in each different phage Fab (not shown) and by the different somatic mutations (below) that were present in the different isolates. Therefore, clonality in these samples is an authentic reflection of the tumor specimen and not an artifact of the cloning method.

Table 1 Germline Hc V gene usage and clonal groups of patient 1

<table>
<thead>
<tr>
<th>Clonal group</th>
<th>Clone</th>
<th>V gene</th>
<th>D gene</th>
<th>J gene</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>GKL3 HC</td>
<td>IGHV5-51*01</td>
<td>IGHD4-23*01</td>
<td>IGJH3*02</td>
</tr>
<tr>
<td></td>
<td>GKL20 HC</td>
<td>IGHV5-51*01</td>
<td>IGHD4-23*01</td>
<td>IGJH3*02</td>
</tr>
<tr>
<td></td>
<td>GKK14 HC</td>
<td>IGHV5-51*01</td>
<td>IGHD4-23*01</td>
<td>IGJH3*02</td>
</tr>
<tr>
<td></td>
<td>GKK139 HC</td>
<td>IGHV5-51*01</td>
<td>IGHD4-23*01</td>
<td>IGJH3*02</td>
</tr>
<tr>
<td></td>
<td>GKK55 HC</td>
<td>IGHV5-51*01</td>
<td>IGHD4-23*01</td>
<td>IGJH3*02</td>
</tr>
<tr>
<td></td>
<td>GKK15 HC</td>
<td>IGHV5-51*01</td>
<td>IGHD4-23*01</td>
<td>IGJH3*02</td>
</tr>
<tr>
<td></td>
<td>GKK69 HC</td>
<td>IGHV5-51*01</td>
<td>IGHD5-18*01</td>
<td>IGJH3*02</td>
</tr>
<tr>
<td></td>
<td>GKK41 HC</td>
<td>IGHV5-51*01</td>
<td>IGHD3*3-01</td>
<td>IGJH4*02</td>
</tr>
<tr>
<td></td>
<td>GKK137 HC</td>
<td>IGHV5-51*01</td>
<td>IGHD18*01</td>
<td>IGJH4*02</td>
</tr>
<tr>
<td></td>
<td>GKK61 HC</td>
<td>IGHV5-51*01</td>
<td>IGHD6*19</td>
<td>IGJH4*02</td>
</tr>
<tr>
<td>2</td>
<td>GKL27 HC</td>
<td>IGHV5-51*03</td>
<td>IGHD2*15</td>
<td>IGJH4*02</td>
</tr>
<tr>
<td></td>
<td>GKK129 HC</td>
<td>IGHV5-51*03</td>
<td>IGHD15*2-02</td>
<td>IGJH4*02</td>
</tr>
<tr>
<td></td>
<td>GKK22 HC</td>
<td>IGHV5-51*03</td>
<td>IGHD3*3-02</td>
<td>IGJH4*02</td>
</tr>
<tr>
<td></td>
<td>GKK26 HC</td>
<td>IGHV5-51*03</td>
<td>IGHD1-10*01</td>
<td>IGJH6*02</td>
</tr>
<tr>
<td>3</td>
<td>GKK61 HC</td>
<td>IGHV1-18*01</td>
<td>IGHD6*19</td>
<td>IGJH4*02</td>
</tr>
<tr>
<td></td>
<td>GKK16 HC</td>
<td>IGHV1-18*01</td>
<td>IGHD6*19</td>
<td>IGJH4*02</td>
</tr>
<tr>
<td></td>
<td>GKK34 HC</td>
<td>IGHV1-18*01</td>
<td>IGHD16*20</td>
<td>IGJH4*02</td>
</tr>
<tr>
<td></td>
<td>GKK11 HC</td>
<td>IGHV5-a*01</td>
<td>IGHD5-24*01</td>
<td>IGJH4*02</td>
</tr>
<tr>
<td></td>
<td>GKK118 HC</td>
<td>IGHV5-a*01</td>
<td>IGHD5-24*02</td>
<td>IGJH4*02</td>
</tr>
<tr>
<td></td>
<td>GKK18 HC</td>
<td>IGHV5-a*01</td>
<td>IGHD4-24*01</td>
<td>IGJH4*02</td>
</tr>
<tr>
<td></td>
<td>GKK35 HC</td>
<td>IGHV5-a*01</td>
<td>IGHD4-24*02</td>
<td>IGJH4*02</td>
</tr>
<tr>
<td></td>
<td>GKK38 HC</td>
<td>IGHV5-a*01</td>
<td>IGHD6*25</td>
<td>IGJH4*02</td>
</tr>
<tr>
<td>6</td>
<td>GKK88 HC</td>
<td>IGHV1-2*02</td>
<td>IGHD16*30</td>
<td>IGJH4*02</td>
</tr>
<tr>
<td></td>
<td>GKK4 HC</td>
<td>IGHV1-2*02</td>
<td>IGHD16*30</td>
<td>IGJH4*02</td>
</tr>
<tr>
<td></td>
<td>GKL11 HC</td>
<td>IGHV6<em>4-61</em>02</td>
<td>IGHD8<em>25</em>01</td>
<td>IGJH4*02</td>
</tr>
<tr>
<td></td>
<td>GKK64 HC</td>
<td>IGHV3<em>30-1/4-31</em>02</td>
<td>IGHD12*01</td>
<td>IGJH4*02</td>
</tr>
<tr>
<td></td>
<td>GKK86 HC</td>
<td>IGHV1<em>1</em>01</td>
<td>IGHD2*02</td>
<td>IGJH3*02</td>
</tr>
<tr>
<td></td>
<td>GKK10 HC</td>
<td>IGHV3<em>1-11</em>01</td>
<td>IGHD1<em>26</em>01</td>
<td>IGJH6*02</td>
</tr>
</tbody>
</table>

* Members of clonal groups with SC library members.

Table 2 Germline Lc V gene usage and clonal groups of patient 1

<table>
<thead>
<tr>
<th>Clonal group</th>
<th>Clone</th>
<th>V gene</th>
<th>I gene</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>GKK 15 LC</td>
<td>IGKV3-20*01</td>
<td>IGKJ1*01</td>
</tr>
<tr>
<td></td>
<td>GKK 69 LC</td>
<td>IGKV3*20-01</td>
<td>IGKJ1*01</td>
</tr>
<tr>
<td></td>
<td>GKK 1 LC</td>
<td>IGKV3*20-01</td>
<td>IGKJ1*01</td>
</tr>
<tr>
<td></td>
<td>GKK253 LC</td>
<td>IGKV3*20-01</td>
<td>IGKJ1*01</td>
</tr>
<tr>
<td></td>
<td>GKK 61 LC</td>
<td>IGKV3*20-01</td>
<td>IGKJ5*01</td>
</tr>
<tr>
<td></td>
<td>GKK 144 LC</td>
<td>IGKV1D-39*01</td>
<td>IGKJ1*01</td>
</tr>
<tr>
<td></td>
<td>GKK 88 LC</td>
<td>IGKV1D-39*01</td>
<td>IGKJ1*01</td>
</tr>
<tr>
<td>2</td>
<td>GKK 156 LC</td>
<td>IGKV2D*28+01</td>
<td>IGKJ1*01</td>
</tr>
<tr>
<td></td>
<td>GKK125 LC</td>
<td>IGKV2D*28+01</td>
<td>IGKJ1*01</td>
</tr>
<tr>
<td></td>
<td>GKK137 LC</td>
<td>IGKV4-1*01</td>
<td>IGKJ3*01</td>
</tr>
<tr>
<td></td>
<td>GKK 86LC</td>
<td>IGKV2*30-01</td>
<td>IGKJ1*01</td>
</tr>
<tr>
<td></td>
<td>GKK118 LC</td>
<td>IGKV3*11-01</td>
<td>IGKJ1*01</td>
</tr>
<tr>
<td></td>
<td>GKK139 LC</td>
<td>IGKV3*11-01</td>
<td>IGKJ4*01</td>
</tr>
<tr>
<td></td>
<td>GKK 22 LC</td>
<td>IGKV1*16-01</td>
<td>IGKJ1*01</td>
</tr>
</tbody>
</table>

* Members of clonal groups with SC library members.
For patient 1 (GK), a striking degree of clonality was revealed in Hc and Lc libraries. Among the VH sequences, there were six clonal groups, ranging in size from two to six members, accounting for 17/30 (57%) sequences examined (Table 1). Reuse of the same V and J with different D regions was evident with VH groups 1, 2, and 3 with nonreiterated clones and between groups 4 and 5 reiterated clones, in which the different D regions (and junctional mutations) signal independent, nonisoclonal B-cell origins. Among the κ sequences, there were two clonal groups consisting of 2 and 3 members, accounting for 5/15 (33%) κ Lcs examined (Table 2). Among the λ sequences, there were two clonal groups, consisting of 2 and 8 members, accounting for 10/15 (67%) total λ sequences analyzed.

A marked clonality was also evident in the libraries from patient 2 (PT). Within the 29 usable VH sequences, four clonal groups accounted for 21 (69%) sequences examined (Table 3). Clonal groups consisted of 2–9 members. As seen in patient 1, there was a similar reuse of specific VH genes with different D and/or J by different progenitor B cells, with groups 1 and 4 sharing VH with nonreiterated clones and groups 2 and 3 sharing with each other. Among the PT κ sequences, there were three clonal groups consisting of 2–4 members each, accounting for 6/14 (42%) of the sample (Table 4). Among the λ sequences, there were three clonal groups consisting of 2–5 members, accounting for 9/16 (56%) total λ sequences analyzed.

Table 5 summarizes these findings. In comparing the immune reactions of the two patients, one VL is shared (Vλ V2.1), but the response is otherwise distinct between them. The use of different fractions of the immune repertoire by different individuals with the same immunogen is typical (e.g., Ref. 36). The oligoclonality is very similar between the patients, with 6 clones (patient 1) and 4 clones (patient #2) dominating the γ1 response by the VH analyses. Together, these analyses show a remarkable degree of repertoire focusing in MC tumor tissue, with 30–70% of the isolates being repeated within these small samples, suggesting that a relatively few original B-cell clones (4–6) account for ≥50% of the total repertoire in the tumors.

Finally, the meaning of these statistics warrants clarification. The range of 30–70% pertains only to the fraction of the library that is comprised by these specific 4–6 clones and says nothing about those sample members that are represented only once. It is quite plausible that most or all of those IgV regions present singly (n = 1) in the sample are also elicited by the same neointagon(s) as the more abundant clones, but the single clones are present merely in the tumor at an average lower frequency that represents them only once in these specific samples. Thus, this estimate of a focused repertoire may be viewed as a minimum estimate that would be likely to be fractionally increased with a larger sample size.

### Table 3 Germ-line Hc V gene usage and clonal groups of patient 2

<table>
<thead>
<tr>
<th>Clonal group</th>
<th>Clone</th>
<th>V gene</th>
<th>D gene</th>
<th>J gene</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>PTL 36 HC</td>
<td>IGHV1-69-01</td>
<td>IGHD1-20-01</td>
<td>IGHD5-02</td>
</tr>
<tr>
<td>2</td>
<td>PTL 116 HC</td>
<td>IGHV1-69-01</td>
<td>IGHD1-20-01</td>
<td>IGHD5-02</td>
</tr>
<tr>
<td>3</td>
<td>PTL 118 HC</td>
<td>IGHV1-69-01</td>
<td>IGHD1-20-01</td>
<td>IGHD5-02</td>
</tr>
</tbody>
</table>

### Table 4 Germ-line Lc V gene usage and clonal groups of patient 2

<table>
<thead>
<tr>
<th>Clonal group</th>
<th>Clone</th>
<th>V gene</th>
<th>J gene</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>PTL 103 LC</td>
<td>IGKV1-39-01</td>
<td>IGKJ1-01</td>
</tr>
<tr>
<td>2</td>
<td>PTL 118 LC</td>
<td>IGKV1-39-01</td>
<td>IGKJ1-01</td>
</tr>
</tbody>
</table>

### Table 5 Repertoire focus in MC

<table>
<thead>
<tr>
<th>Patient #</th>
<th>VH</th>
<th>Va</th>
<th>Vκ</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>V5-51+01 (6)</td>
<td>V2-20+01 (2)</td>
<td>V1-51+01 (8)</td>
</tr>
<tr>
<td>2</td>
<td>V1-69+01 (9)</td>
<td>V1-39+01 (4)</td>
<td>V6-57+01 (5)</td>
</tr>
</tbody>
</table>

For patient 1 (GK), a striking degree of clonality was revealed in Hc and Lc libraries. Among the VH sequences, there were six clonal groups, ranging in size from two to six members, accounting for 17/30 (57%) sequences examined (Table 1). Reuse of the same V and J with different D regions was evident with VH groups 1, 2, and 3 with nonreiterated clones and between groups 4 and 5 reiterated clones, in which the different D regions (and junctional mutations) signal independent, nonisoclonal B-cell origins. Among the κ sequences, there were two clonal groups consisting of 2 and 3 members, accounting for 5/15 (33%) κ Lcs examined (Table 2). Among the λ sequences, there were two clonal groups, consisting of 2 and 8 members, accounting for 10/15 (67%) total λ sequences analyzed.

A marked clonality was also evident in the libraries from patient 2 (PT). Within the 29 usable VH sequences, four clonal groups accounted for 21 (69%) sequences examined (Table 3). Clonal groups consisted of 2–9 members. As seen in patient 1, there was a similar reuse of specific VH genes with different D and/or J by different progenitor B cells, with groups 1 and 4 sharing VH with nonreiterated clones and groups 2 and 3 sharing with each other. Among the PT κ sequences, there were three clonal groups consisting of 2–4 members each, accounting for 6/14 (42%) of the sample (Table 4). Among the λ sequences, there were three clonal groups consisting of 2–5 members, accounting for 9/16 (56%) total λ sequences analyzed.

Table 5 summarizes these findings. In comparing the immune reactions of the two patients, one VL is shared (Vλ V2.1), but the response is otherwise distinct between them. The use of different fractions of the immune repertoire by different individuals with the same immunogen is typical (e.g., Ref. 36). The oligoclonality is very similar between the patients, with 6 clones (patient 1) and 4 clones (patient #2) dominating the γ1 response by the VH analyses. Together, these analyses show a remarkable degree of repertoire focusing in MC tumor tissue, with 30–70% of the isolates being repeated within these small samples, suggesting that a relatively few original B-cell clones (4–6) account for ≥50% of the total repertoire in the tumors.

Finally, the meaning of these statistics warrants clarification. The range of 30–70% pertains only to the fraction of the library that is comprised by these specific 4–6 clones and says nothing about those sample members that are represented only once. It is quite plausible that most or all of those IgV regions present singly (n = 1) in the sample are also elicited by the same neointagon(s) as the more abundant clones, but the single clones are present merely in the tumor at an average lower frequency that represents them only once in these specific samples. Thus, this estimate of a focused repertoire may be viewed as a minimum estimate that would be likely to be fractionally increased with a larger sample size.
protein, we devised a cell-based panning method to select reactive phage Fab (29). Our positive control tests against a moderately expressed cell-bound antigen (~5–10,000/cell) showed enrichment of specific phage Fab by this technique at ~25-fold per round of panning (29), which would have yielded an ~100% pure population after 6 rounds with 1:10^6 specific-to-nonspecific phage. Similarly, cloned specific phage Fab were effective in staining procedures and in detecting cellular antigen by flow cytometry (29). For the present tests, an MC cell line (HTB-24) and a negative-control cell line (293) were used in 6 rounds of panning, but no repertoire shift or titer enrichment was detected with the unselected libraries of either patient (not shown). Results were also negative by flow cytometry in direct binding assays of the 60 phage-Fab clones against tumor cells (not shown). These negative cell-panning results forced a conclusion that the antigen: (a) was not surface-expressed; (b) was surface-expressed at too low a level for panning enrichment or for flow cytometry detection against background; or (c) was lost from the tumor cell line. No adequate source of MC tumor was available to employ primary tissue for panning, and viability after disaggregation was poor.

Thus, we were unable to identify either cognate VH-VL pairs or the eliciting antigen(s), or even to confirm the localization of eliciting antigen to the membrane or within the cell. Additional efforts to identify the antigen were deferred until native VH-VL pairs could be definitively established, thus enabling traditional molecular and biochemical methods for retrieving the antigen.

“Native” VH+VL Pairing: SC RT-PCR

Having failed to select for cognate VH+VL pairs independent of knowledge of the immunizing antigen, it proved necessary to identify the pairs within individual PCs. Accordingly, in parallel with the above panning efforts, we undertook development of methods for

---

5 M. Press, personal communication.
isolation of single PCs and recovery of VH+VL sequences by SC RT-PCR, which had not been standardized previously for human Ig genes (23). (An equivalent method has since appeared in the literature; Ref. 43.) This method was applied to prepare a SC IgG library with authentic VH-VL pairings.

PCs were isolated from disaggregated tumor from patient 1 and amplified by RT-PCR. Of 90 wells, one Lc (κ or λ, but not both) amplified from 28 and IgG1 Hc amplified from 20. One well of the 90 had both κ and λ products, implying two cells in a well, and was excluded from the analysis. All 20 of the IgG1 Hc amplifications had successful Lc amplifications, of which 18 were κ and 2 were λ, indicating a preponderance of κ-positive plasma cells. Useable sequence was obtained from 18. Of the 18, 1 (MCPC85) had useable sequence for Lc only.

Of the total PCs identified by Lc amplification, 71% (20/28) were IgG1. The remaining 29% of PCs (8/28) with Lc and no Hc amplification indicate an isotype other than IgG1, meaning that the total of IgA, IgM, and IgG2-4 PCs account for <30% of this tumor PC sample. No cells showed amplification of Hc without Lcs, whereas positive controls for Hcs did amplify, indicating that lack of Hc amplification in Lc-only wells is almost certainly attributable to a non-IgG1 Hc rather than PCR failure. Because the SC library is an unbiased sampling of the tumor, this 71% fraction (52–86%; 95% confidence interval) estimates the proportion of the total antibody response that is IgG1 and implies that this isotype is a fair sample of the total response that is present. This fraction may be compared with the combinatorial LC library from patient 1 in which ~70% of cells were IgG+ (207/290) versus ~30% for IgA+ and IgM+ combined.

The marked κ predominance in vivo (16/18; 91%) among the IgG1+ samples was unexpected and significantly different from the normal fraction of 60:40 κ:λ (P < 0.01 by χ²; Ref. 44), whereas only 3/8 (38%) of the non-IgG1 PCs in the sample were κ. In contrast, a control sample of 13 random tonsil PCs selected and analyzed identically consisted of 8 κ (62%) and 5 λ sequences (38%), reflecting typical in vivo ratios (23). Immunohistochemistry of patient tumor tissue indicated a slightly higher level of λ+ than κ+ PCs (not shown). Because the SC RT-PCR procedure samples the entire disaggregated tumor section but the immunohistochemical analysis samples only a single location, the divergent κ:λ tissue staining results may reflect heterogeneity within the tumor. We are unaware of a particular significance of a κ-dominated immune response.

Table 6 provides a clonal analysis of the individual Hc and Lc sequences in the SC library. Only two PCs (MCPC9 and MCPC15) were clonally related within this sample. However, when considered together with the combinatorial library sample (Table 7), an additional 7 members of the SC library were in clonal groups (total 9/20; 45%), 5 derived from comparison with the VS clones (Table 2) and 2 with the VH clones (Table 1). Similarly, the SC library revealed that 1 additional VH member and 4 additional VS members of the combinatorial library were clonal. Neither of the λ+ SC clones overlapped with any VH or VL of the combinatorial library sample.

Considered together, the combinatorial and SC library from patient 1 indicate a total of 8 VH clonal groups, accounting for 22/45 or 49%
of Hc sequences, 7 Vκ clonal groups, accounting for 16/30 or 53% of κ Lcs, and 2 Vλ clonal groups, accounting for 10/17 or 59% of the λ Lcs. These results are compatible with ~8 progenitor B-cell clones accounting for 50% of the response in the tumor of this patient.

Interestingly, none of the VH+VL of the IgG,κ or the IgG,λ members represented in the GK SC library was appropriately paired by chance in the GK combinatorial library, confirming our estimation (above) of a low probability of finding an original pairing in this small combinatorial sample. Similarly, although ~50% of the SC library was reiterative when compared with the phage Fab library, only one sequence was reiterated (n = 2) within the sample of 19 single PCs, and this clone was not present among either the VH or VL libraries of the phage Fab. The combined κ samples have reiteration in 16/30 clones or 53% with a mean frequency for all of the reiterated clones of 0.08 ± 0.02 (SD). With 7 clones of 0.08 frequency, the most probable number of reiterated clones in a sample of 16 single (κ) PCs is just 1, consistent with our observations (Table 6; calculation not shown). These observations emphasize the importance of adequate sample sizes to demonstrate reiteration when the frequencies of individual clones are in the range of ±10% in which a larger SC library would have been required to demonstrate focus if it were the sole source of representation.

Statistical analysis showed good concordance between the Vκ of the combinatorial and SC libraries (χ²; P = 0.49) in which the SC library was γ1 Hc derived. This is a particularly important point, because it indicates that the commitment to use the γ1 specific Hc primer in the combinatorial library was appropriate even if the cogenate VH+VL pairing was unknown, in effect confirming by a separate measure the IgG1 dominance of the immune response in the tumor of this patient. Although clonality is evident in the λ repertoire from the combinatorial library, it is a minor part of the total intratumoral response, and the small sample size of the SC library does not allow a suitably powered comparison (P = 0.20). Comparison of the VH, however, showed a significantly divergent representation between the two library formats (P = 0.04). The most abundant clonal group in the combinatorial library (1; Table 1) was absent in the SC library. This could suggest an amplification bias favoring the V5 family in preparing the phage Fab library in comparison with the SC library, which cannot be biased. The absence of repeated V5 family clones in the phage Fab library of tumor 2 (Table 3) might have been cited to counter the suggestion of a V5 bias in the PCR, but the PT combinatorial library (like the GK SC library) was prepared with a mixture of VH family primers rather than the single VH consensus primer applied in the GK library, and is, thus, uninformative to this point. The Lc GK libraries were prepared with mixtures of family-homologous primers and showed excellent concordance between the combinatorial and SC libraries. Finally, it is possible that the discrepancy between the GK SC and combinatorial VH libraries is attributable to small numbers and that a larger SC library would have revealed greater convergence with the combinatorial library.

The overlap between SC and combinatorial library sequences additionally confirm the existence of a focused intratumoral antibody repertoire.

Somatic Mutation of IgG V Genes

Somatic mutations of Ig V(D)J genes occur in B cells after antigen contact and are typically concentrated in the antigen-contacting CDR regions in affinity-matured Ig. Levels and patterns of mutation within the IgV regions (FR1-CDR1-FR2-CDR2-FR3) of MC-infiltrating PCs were analyzed. CDR3 was excluded because of the high incidence of deletions and D gene inversions in this region that complicate the analysis. The somatic mutation pattern versus germ line is shown in Fig. 4A for the largest VH clonal group. In this instance, it was possible to trace a common progenitor B cell and branching order through at least four rounds of division and differentiation, leading to three “clades” within this clonal group (Fig. 4B).

**Fig. 4.** Somatic mutation diversification in clonal group of tumor-infiltrating PCs. VH clonal group 1 of patient 2 was derived from a common progenitor B cell that used the IGHV1-69*01 gene (Table 3). A, alignment of VH sequences of clonal group. Alignment begins at base 23 of FR1 to exclude the primer annealing regions. Only codons containing mutations from germ line are shown. Clones 2 and 21 have the same sequence but are nonidentical clones, having been amplified with different primers (VH1a and VH6a, respectively (15)). B, clade analysis with genetic tree. Branching order of B and/or PC clones. Solid line circles (○) indicate germ line and actual sequenced PC clones. Dotted circles indicate deduced intermediates. Numbers within circles indicate designation of cloned gene. Numbers next to arrows indicate number of V gene mutations at each step.
Within the CDR regions of all of the patient 1 IgV regions compared, mutation levels ranged as high as 10% in individual sequences. Cognate germline V(D)J Ig genes are between 1 and 6%, total mutation levels of mutation in comparison to the basis of belonging or not belonging to a clonal group, as defined in Tables 1–4 and 6. Average values were determined for each group. Whereas overall group average levels of mutation in comparison to cognate germline V(D)J Ig genes are between 1 and 6%, total mutation levels ranged as high as 10% in individual sequences.

**Patient 1.** As seen in Fig. 5A, there is a higher level of mutation within the CDR regions of all of the patient 1 IgV regions compared to framework regions (FR), with the exception of λ light chains. For example, the average percentage of mutation of patient 1 clonal κ light chains across the Ig V region is:

<table>
<thead>
<tr>
<th>V Region</th>
<th>FR1</th>
<th>CDR1</th>
<th>FR2</th>
<th>CDR2</th>
<th>FR3</th>
</tr>
</thead>
<tbody>
<tr>
<td>klc clonal</td>
<td>1.0</td>
<td>9.6</td>
<td>3.3</td>
<td>6.3</td>
<td>2.1</td>
</tr>
</tbody>
</table>

Therefore, although the overall level of mutation for this group is only 2.8%, higher concentrations of mutations are clustered within the CDRs.

In contrast, clonal λ Lcs are almost completely unmutated, with overall mutation levels of 0.9%, including the two λ+ single PCs from the pool of 20 analyzed (MCPC54 and 57), with only 4 mutations (0.9%) each in the entire Ig V region. Nonclonal λ Lcs have overall levels of mutation only slightly lower than in the other non-λ groups at 2.5%, but mutations are not clustered within the CDRs.

**Patient 2.** As seen for patient 1, there is similarly a marked clustering of mutations within the CDRs in patient 2 in all of the sequences except clonal λ Lcs (Fig. 5B), which are, again, nearly unmutated. Unlike patient 1, however, patient 2 nonclonal λ chains have increased somatic mutation within the CDR regions.

In summary, mutations cluster within the CDR regions, a finding that is consistent with somatic mutation and affinity maturation of these sequences, and mutation frequencies do not differ appreciably between the “clonal” and “nonclonal” groups. This is not surprising in that the nonclonal groups are probably, in fact, mostly clonal but reiterated in the unselected libraries at a lower average frequency than those clones that are represented more than once. As stated above, the estimation of clonal fraction in the tumors is a lower estimate. Overall mutation levels and patterns are consistent with published values for other protein antigen-selected human antibodies.

**DISCUSSION**

Plasmacytic infiltration is a diagnostic feature of MC of the breast and is present in an equal number but smaller proportion of the more abundant NOS infiltrating ductal carcinomas. The objective of this study was to determine if these PC infiltrates represent a tumor-specific humoral immune response as opposed to a nonspecific cytokine-driven recruitment. Characteristics of a local antigen-driven B-cell response include a highly restricted Ig repertoire, IgG isotype, somatic mutation of Ig, and PC differentiation. Local secretion of chemotactic agents such as interleukin-6 could attract peripheral blood B cells in an antigen-independent manner that are largely unrestricted, IgM+, and unmutated (47, 48).

For the present study, we examined the IgV sequences of MC tumor-infiltrating PCs for similar germ-line gene usage to determine proliferation (clonality) and for evidence of antigen dependence such as somatic mutation within the CDRs and IgG isotype. In a recent evaluation, Kolan et al. (49) performed RT-PCR amplification of total VL and IgG VH from one MC tumor and sequenced several random isolates: 9 VH, 5 VL, and 10 VA. They offered a tentative conclusion of an oligoclonal Ig amplification based on an apparent reiteration of clones even within this limited sample. By the more extensive examination of the present study, we have made a definitive conclusion of local B proliferation compatible with local antigen exposure as determined by a high degree of clonality, IgG isotype, and somatic mutation in intratumoral PCs. In the absence of a defined tumor antigen, it was not possible to specify appropriately reactive VH+VL pairs from our combinatorial libraries. Similarly, the failure to enrich for phage-Fab clones on tumor cell panning suggested that the antigen is on the surface at too low a level to allow selection by this method, is not a membrane protein, or has been lost from the MC cell line we used. The development and application of single PC RT-PCR techniques in our study validated the repertoire focus of our initial combinatorial cloning effort and, furthermore, yielded appropriately paired VH+VL antibody fragments that will be important to future antigen identification efforts.

**Isotype Restriction of MC-infiltrating PCs.** As determined by both immunohistochemistry and SC RT-PCR, we confirmed that the infiltrating PCs of MC are predominantly (~70%) IgG+ rather than IgM or IgA. IgM is generally seen in primary tissue immune responses, whereas IgA predominates in all of the normal secretary
epithelium. The IgG-positive response observed in this and other studies of MC and in other PC-infiltrated NOS breast tumors (11) is consistent with early inferences of an intratumoral protein antigen and a matured immune response (10, 11). That the eliciting antigen is tumor-specific rather than broadly expressed is reinforced by the observation that the PC infiltrates in these tumors do not extend into the adjacent normal breast tissue (3-5, 8). Approximately 71% (20/28) of single PCs were IgG1+ in the tumor of the one patient in whom it was directly tested. IgG1 is the predominant antibody response in T-dependent antigens (47), supporting a presumption of a protein origin for the antigen.

**Restricted Immunoglobulin Repertoire of MC-infiltrating PCs.**

It has been estimated that a specific B-cell clone occurs in the peripheral blood at a frequency of no more than 1/20,000 (50). Even in hyperimmunized individuals, antitetanus antibodies were present in a total B-cell library in only 1:1000 to 1:5000 clones, and only 2/8 reactive clones that were sequenced showed the same V gene usage (39, 51). Similarly, in a limited sample of 13 single-tonsil PCs examined by RT-PCR, no reiteration was observed (23), consistent with a typically diverse representation in tonsil (26).

Clonal groups in the present study were defined by shared germ-line gene usage and shared junctional diversity patterns, because these recombination events occur in the bone marrow before circulation into the periphery. As determined by analysis of IgG sequences from both the combinatorial and SC libraries, the IgV gene repertoire used by tumor-infiltrating PCs was highly restricted in both patients, with 4–8 progenitor B cells accounting for 40–80% of the total response. The focused representation within the combinatorial library from patient 1 and by implication patient 2 was validated by the overlap of sequences from the SC library. Sequencing from single tumor-infiltrating PCs provides a sampling method that is not subject to either cloning-transformation because of other causes will have to await its definitive hypotheses that are the subject of our ongoing investigations. Finally, antigens of the host immune environment. On the other hand, MC is intriguing biology of MC and, plausibly, of NOS tumors as well, in which the response where it was directly examined, reinforcing the inference of a protein origin for the neoantigen.

These results add evidence to the long-held inference that there is a tumor-derived antigen that elicits the characteristic B cell/PC immune response in MC and PC-infiltrated NOS tumors. Identification of the antigen (or antigens) may provide clues as to the etiology and/or biology of MC and, plausibly, of NOS tumors as well, in which the response may be less prominent because of ancillary features of the host immune environment. On the other hand, MC is intriguing in its histological resemblance to murine mammary tumors, which are caused by a retrovirus (56). A human mammary tumor virus, either exogenously transmitted or endogenously activated, could provide a unifying synthesis of data on etiology both of the tumor and of the host immune response. Whether this repertoire focus and the eliciting antigen extend to PC-infiltrated, NOS breast tumors are additional hypotheses that are the subject of our ongoing investigations. Finally, conclusions as to whether the neoantigen is etiologic in these breast tumors or is merely expressed as a consequence of the malignant transformation because of other causes will have to await its definitive identification.

**ACKNOWLEDGMENTS**

We thank Dr. Steven Tahan, Department of Pathology, Beth Israel Deaconess Medical Center, for his key assistance in sample procurement. We thank Frank Rotonta and Marchon Davis for assistance in sequencing of the PT and GK libraries, and Andrew Jones for data analyses.

**REFERENCES**

7. Rosen, P. P., Groshen, S., Sargo, P. E., Kinne, D. W., and Hellman, S. Pathological prognostic factors in stage I (T1N0M0) and stage II (T1N1M0) breast carcinoma: a study of 644 patients with median follow-up of 18 years. J. Clin. Oncol., 7: 1239–
1251, 1989.


Evidence for an Antigen-driven Humoral Immune Response in Medullary Ductal Breast Cancer


Updated version
Access the most recent version of this article at:
http://cancerres.aacrjournals.org/content/61/21/7889

Cited articles
This article cites 48 articles, 21 of which you can access for free at:
http://cancerres.aacrjournals.org/content/61/21/7889.full.html#ref-list-1

Citing articles
This article has been cited by 16 HighWire-hosted articles. Access the articles at:
/content/61/21/7889.full.html#related-urls

E-mail alerts
Sign up to receive free email-alerts related to this article or journal.

Reprints and Subscriptions
To order reprints of this article or to subscribe to the journal, contact the AACR Publications Department at pubs@aacr.org.

Permissions
To request permission to re-use all or part of this article, contact the AACR Publications Department at permissions@aacr.org.