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# Repertoire Shift in the Humoral Response to Phosphocholine-Keyhole Limpet Hemocyanin: V<sub>H</sub> Somatic Mutation in Germinal Center B Cells Impairs T15 Ig Function<sup>1</sup>

Gregory D. Wiens,<sup>2</sup> McKay Brown, and Marvin B. Rittenberg

Phosphocholine (PC) is a naturally occurring Ag common to many pathogenic microorganisms. Early in the primary response to PC conjugated to keyhole limpet hemocyanin (KLH), T15 Id<sup>+</sup> Abs constitute >90% of the serum Ig in BALB/c mice. During the late primary and memory response to PC-protein, a shift in the repertoire occurs and T15 Id<sup>+</sup> Abs lose dominance. In this study, we use immunohistochemistry and single germinal center microdissection to locate T15 Id<sup>+</sup> cells in the spleen in a primary response to PC-KLH. We demonstrate T15 Id<sup>+</sup> B cells and V<sub>H</sub>1-DFL16.1-JH1 and V<sub>K</sub>22-J<sub>K</sub>5 rearrangements in germinal centers early in the immune response; thus loss of T15 dominance is not due to lack of T15 cells within germinal centers. One-hundred thirty one V<sub>H</sub>1 and 57 V<sub>K</sub>22 rearrangements were cloned and sequenced. Thirty four percent of the V<sub>H</sub>1 clones and 37% of the V<sub>K</sub>22 clones contained somatic mutations indicating participation in the germinal center response. Six variant T15 H clones were expressed with wild-type T15 L chain in vitro. Two of these Abs were defective in secretion providing the first evidence that mutation occurring in vivo can disrupt Ig assembly and secretion. Of the four secretion-competent Abs, two failed to display binding to PC-protein, while the other two displayed altered carrier recognition. These results indicate that somatic mutation of T15 in vivo can result in the loss of binding and secretion, potentially leading to B cell wastage. The failure of T15 to gain affinity enhancing mutations in the face of these detrimental changes may contribute to repertoire shift. *The Journal of Immunology*, 2003, 170: 5095–5102.

Phosphocholine (PC)<sup>3</sup> is an epitope present on *Streptococcus pneumoniae* and a number of other pathogenic microorganisms (reviewed in Ref. 1). In the primary Ab response to PC conjugated to PC-keyhole limpet hemocyanin (PC-KLH), BALB/c mice produce large amounts of T15 idiotype Ab, which is highly protective against pneumococcal infection (2, 3). These Abs bind to free PC and are classified as group I Abs (4, 5). During the late primary and early secondary responses to PC-KLH, a shift in the Ab repertoire from group I to group II Abs occurs. Group II Abs possess a different fine specificity and use a diverse set of V gene combinations that differ from group I (reviewed in Ref. 6). Group II Abs bind *p*-nitrophenyl PC (NPPC) (4) or aminophenyl PC (7) but bind weakly or not at all to phosphocholine itself, (4, 8) and are not protective against pneumococcal challenge (9–11). Understanding the fate and location of T15<sup>+</sup> B cells provides an important model for dissecting the molecular basis of repertoire shift and the maintenance of protective immunity.

T15 Id<sup>+</sup> cells are derived from CD5<sup>+</sup> lineage B cells (7, 12–16) with precursors distinct from group II Abs (17–19). Reconstitution experiments have suggested that CD5<sup>+</sup> cells cannot form germinal centers (20), which might preclude T15 from accumulating mutations. The ability to participate in germinal center reactions remains unclear since Miller et al. (21) have reported T15 Id<sup>+</sup> germinal centers from which they could amplify the canonical V<sub>H</sub>1-DFL16.1-JH1 rearrangement of T15; however, the presence of the T15 V<sub>K</sub>22-J<sub>K</sub>5 rearrangement was not formally demonstrated.

Because of its importance in protective immunity, and lack of evidence for somatic mutations that enhance Ag binding, it has been suggested that the T15 Ab may be unable to tolerate substantial somatic mutation in the H chain (22, 23) or L chain (24). This would limit affinity maturation and lead to loss of T15 dominance due to the appearance of other Abs more tolerant of somatic mutations. Previously, we introduced random mutations into the T15 H chain CDR2 region in vitro and expressed the mutant H chains with the germline T15 L chain. Of 46 T15 mutants, none displayed significantly increased binding for PC-containing compounds while ~50% of the multisite mutants had significantly impaired Ag binding and 10% of the mutants were not secreted from the transfected cells (25–27). These results support the notion that T15 may not be able to tolerate mutations. Our in vitro studies did not indicate whether similar deleterious somatic mutations would occur normally in vivo or whether they might contribute to repertoire shift. These issues are examined herein.

We confirm that T15 Id<sup>+</sup> germinal centers can be found during a primary response to PC-KLH and that these germinal centers contain rearranged V<sub>H</sub>1-DFL16.1-JH1 as reported by Miller et al. (21). We extend their findings to demonstrate rearranged V<sub>K</sub>22-J<sub>K</sub>5 genes in the same pool of cells from single microdissected T15<sup>+</sup> germinal centers. The repertoire shift occurred by the late primary response as group II Abs increased to predominate in the serum. To assess the effects of somatic mutation on V<sub>H</sub>1 genes

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<sup>3</sup> Abbreviations used in this paper: PC, phosphocholine; KLH, keyhole limpet hemocyanin; NPPC, *p*-nitrophenyl PC; PNA, peanut agglutinin; EPC, 6-(*O*-phosphocholine) hydroxyhexanoate; WT, wild type; CDR, complementarity determining region; V<sub>H</sub>, V region of Ig H chain; V<sub>L</sub>, V region of Ig L chain; WT, wild type.

obtained from primary response germinal centers, six variant H chains were coexpressed with the unmutated T15 L chain. Four of the tested mutants containing one to four amino acid substitutions either lost binding to PC-protein or failed to pair with the T15 L chain. These results highlight the harmful effects of mutation on Ig function and are the first evidence that mutation occurring in germinal centers can affect Ig assembly and secretion. We discuss the molecular mechanisms of how somatic mutations alter binding and secretion of Ig in the context of a T15 structural model and how these findings contribute to understanding of repertoire shift.

## Materials and Methods

### Animals and immunization

PC-KLH was prepared as described (28) and had a hapten to protein molar ratio of 40 per 100,000 m.w. KLH. Female BALB/c mice were purchased from The Jackson Laboratory (Bar Harbor, ME) and housed under specific pathogen-free conditions. For primary responses, 8-wk-old mice were immunized once i.p. with 60  $\mu\text{g}$  of PC-KLH precipitated in alum. For secondary responses, mice were immunized i.p. with 100  $\mu\text{g}$  of PC-KLH in saline. Serum and spleens were obtained from euthanized mice on days 3, 5, 7, and 13 after primary immunization or on days 47 and 55 (7 and 13 days after secondary immunization). Spleen samples were processed for immunohistochemistry as described (29).

### T15 and anti-PC ELISA

Anti-PC serum Ab was quantified by ELISA using dilutions of purified T15 Id<sup>+</sup> hybridoma Ab PCM11 (6) as a standard. Dilutions of serum in PBS containing 1% BSA and 0.04% sodium azide were incubated in ELISA wells coated with PC<sub>19</sub>BSA (1  $\mu\text{g ml}^{-1}$ ). Inhibition by PC or NPPC was determined by incubating a 1/1000 dilution of serum with 0.01 M free hapten. After washing, wells were incubated with a mixture of purified goat anti-mouse  $\kappa$  and goat anti-mouse  $\lambda$  coupled to alkaline phosphatase (Southern Biotechnology Associates, Birmingham, AL). The concentration of anti-PC Ab was determined by comparison of the A410 values to the PCM11 standard curve.

The amount of T15 Id<sup>+</sup> IgM Ab present in serum samples was quantified by ELISA using PCM11 hybridoma Ab as a standard. Dilutions of serum were incubated in wells coated with purified anti-T15 Ab AB1-2 (30) at 1  $\mu\text{g ml}^{-1}$ , followed by incubation with purified goat anti-mouse IgM coupled to alkaline phosphatase (Zymed Laboratories, South San Francisco, CA). The amount of T15 Id<sup>+</sup> IgG in serum was determined in an ELISA by comparison to a pool of Abs containing T15 IgG2b (25) and T15 Id<sup>+</sup> IgG3 hybridoma Abs PCG1-7 (IgG1), PCG2a-2 (IgG2a), and PCG3-1 (IgG3) derived from spleen cells of BALB/c mice immunized with PC-KLH (6). Serum dilutions were incubated in wells coated with purified TC54 (31) at 0.5  $\mu\text{g ml}^{-1}$ , followed by incubation with rat anti-mouse IgG coupled to alkaline phosphatase (Zymed Laboratories).

### Immunohistochemistry

Goat anti-T15 serum was obtained from Dr. J. Kenny (National Institutes of Health, Bethesda, MD). The Ab was affinity purified on a T15-Sepharose 4B column and adsorbed on mouse IgM $\kappa$  and mouse IgG1 $\kappa$  coupled to Sepharose 4B. The goat anti-T15 Id strongly recognized T15 Ab but also had minor reactivity with the group I myeloma Abs M511 (16-fold lower), M603 (196-fold lower), and M167 (66-fold lower). No reactivity was observed with the group II hybridomas D16 ( $\gamma$ 2b, $\kappa$ ) (26), M3C65 ( $\gamma$ 2b,  $\lambda$ ) (32), PCG1-1 ( $\gamma$ 1,  $\kappa$ ) (6), or with IgA $\lambda$  of unrelated specificity (Zymed Laboratories). Confirmation of T15 Id staining in germinal centers was performed using biotinylated anti-T15 Ab AB1-2 which requires the T15 H and L chains for binding (30). Germinal centers were identified by staining with peanut agglutinin (PNA)-HRP (EY Laboratories, San Mateo, CA). For staining, spleen sections were rehydrated in PBS, pH 7.4, and blocked with PBS containing 1% BSA. HRP reactivity was visualized using 0.4 mg ml<sup>-1</sup> 3-amino-9-ethyl-carbazole, and alkaline-phosphatase-labeled Abs were detected with naphthol-AS-MX phosphate and Fast Blue BB salt (Sigma-Aldrich, St. Louis, MO) as described (29).

### Microdissection of cells, DNA amplification, and sequencing

Cells from T15 Id<sup>+</sup>, PNA<sup>+</sup> germinal centers were microdissected from spleen sections using a micromanipulator (Narishige MHW-103, Tokyo, Japan) controlled micropipette as described (29). Microdissected tissue, containing groups of 10–50 cells, was digested in proteinase K containing buffer (33) and the DNA was subjected to two rounds of PCR in a 9700

GeneAmp PCR System (Applied Biosystems, Foster City, CA). Each round of PCR consisted of 38 cycles (94°C for 1 min, 58°C for 40 s, 72°C for 1 min) with the last incubation at 72°C for 7 min. PCRs were conducted in a 50- $\mu\text{l}$  volume containing 200  $\mu\text{M}$  dNTP, 0.01% gelatin (Sigma-Aldrich), and 2.5 U PfuTurbo DNA polymerase, and 1 $\times$  cloned Pfu DNA polymerase reaction buffer (Stratagene, La Jolla, CA). The first round of amplification contained primers (10 pM of each) to amplify V<sub>H</sub>1-JH1 and V $\kappa$ 22-J $\kappa$ 5 rearrangements. Primers were also included for the RAG-1 gene to determine the PCR error frequencies. All primers included in the first round tube were: V<sub>H</sub>1For no. 3, 5'-GTG TGT GCA TAT GTG TGT AAC AGG G-3'; V<sub>H</sub>1Rev no. 3, 5'-GGG AGA TCT GAG AAT ATC TTT TCC CG-3'; V $\kappa$ 22 5' no. 1, 5'-AAA CTG AGC AGT GTC AAA CAG CAG G-3'; J $\kappa$ 5Int no. 1, 5'-CGT CAA CTG ATA ATG AGC CCT CTC C-3'; RAG-1For no. 1, 5'-ATT CTA AGC CCC CTC ATT GC-3'; RAG-1Rev no. 1, 5'-TCC GAA ACC GTC TAA ACA GC-3'. V<sub>H</sub>1, V $\kappa$ 22, and RAG-1 were amplified in separate tubes in the second round using internal primers (20 pM each): V<sub>H</sub>1For no. 4, 5'-TGC AGG TAT CCA GTG TGA GG-3' and JH1Rev no. 4, 5'-CCA GCT TAC CTG AGG AGA CG-3', or V $\kappa$ 22 For no. 2, 5'-AGC AAA TTT TAA CTG CTG CTA TAT TCC G-3' and J $\kappa$ 5Int no. 2, 5'-TAA CTC CAA CAT GAA AAC TGT G-3', or RAG-1For no. 2, 5'-TCA TCG AGA CAG TCC CTT CC-3' and RAG-1Rev no. 2, 5'-TTT AGC GGG ACA TGA AGA GC-3'. DNA from PCRs was purified from agarose using the QIAquick Gel Extraction kit (Qiagen, Valencia, CA). PCR products were cloned into the pSTBlue-1 vector and transformed into Nova Blue competent cells using the Perfectly Blunt Cloning kit (Novagen, Madison, WI). DNA was purified and subjected to automated, fluorescent DNA sequencing (ABI 377; Applied Biosystems) in both directions. As a positive control, 10 T15 Id<sup>+</sup> PCM-11 hybridoma cells were placed in lysis buffer and VDJ and VJ rearrangements amplified, cloned, and sequenced as described above. As a negative control, microdissection pipette tips were dipped in buffer surrounding tissue sections and subjected to PCR amplification in each experiment. No VDJ, VJ, or RAG1 PCR products were observed.

### Nucleotide sequence accession numbers

Sequences of the cloned V<sub>H</sub> and V<sub>L</sub> genes have been deposited in the GenBank database under accession numbers AY194179-AY194222.

### Expression of mutant V<sub>H</sub>I genes

Wild-type (WT) and mutant VDJ rearrangements were reamplified by PCR with primers *Xho*I/V<sub>H</sub>1, 5'-ATC TTA TCT CGA GCA GGT ATC CAG TGT GAG GTG AAG C-3' and *JH1/Nco*I, 5'-ATG AAA CCA CCA TGG TTA CCT GAG GAG ACG GTG ACC GTG-3' to introduce the *Xho*I and *Nco*I restriction sites. PCR products were digested and ligated into the pSV2-S107 expression vector containing the BALB/c  $\gamma$ 2b C region gene and the unmutated T15 L chain gene (34). The vector was engineered to contain *Xho*I and *Nco*I restriction sites flanking the T15 VDJ region, called pSV2-S107(X/N). Transfectants of the WT and mutant Abs were obtained by transfecting SP2/0 cells as described (25). Stable transfectants secreting Ab or producing intracellular H and L chains as determined by ELISA were saved for further analysis.

### Ag-binding assays

Secreted Ab was purified from cell culture supernatants using protein A-Sepharose (Amersham Biosciences, Uppsala, Sweden), then dialyzed against PBS-containing 0.04% sodium azide. Binding of T15 mutant Abs relative to WT was determined by ELISA as described (35). Abs were tested for binding to PC-histone, 6-(*O*-phosphocholine) hydroxyhexanoate (EPC)-BSA, *S. pneumoniae* strain R36A, *Trichinella spiralis*, and *Ascaris suum* as described (35).

### Secretion assays

Stable transfectants were plated in triplicate at  $1 \times 10^6$  cells ml<sup>-1</sup> of tissue culture medium in a 12-well plate. After a 4-h incubation, culture supernatants and cell lysates were collected as described (26). The concentration of Ig proteins in supernatants and cell lysates was determined by sandwich ELISA as described (26). Briefly, to determine H + L in the supernatant or lysate, ELISA plates were coated with rabbit anti-mouse IgG2b (Zymed Laboratories) and the amount of bound Ig from the lysate or supernatant was determined by a secondary alkaline phosphatase-conjugated, goat anti-mouse  $\kappa$  Ab (Southern Biotechnology Associates). All antisera were used at a 1/1000 dilution. Standard curves were generated using affinity purified Ab from transfected SP2/0 cells producing WT T15 Ab.

## Results

### Repertoire shift in serum Abs occurs in the late primary Ig response of BALB/c mice immunized with PC-KLH

Mice were immunized with PC-KLH and serum was collected on the days indicated (Fig. 1A). The concentration and specificity of serum Ab is shown. The anti-PC Ab level averaged  $175 \pm 87 \mu\text{g ml}^{-1}$  by day 7, a 44-fold increase over preimmune levels, while T15 Id<sup>+</sup> Ab averaged  $122 \pm 29 \mu\text{g ml}^{-1}$ , a 23-fold increase above preimmune levels. Consistent with previous findings, the majority of PC-BSA binding, as determined by hapten inhibition ELISA, was inhibited by  $10^{-2}$  M free PC (92% at day 7 and 98% at day 13) indicating that most Ab produced early in the primary response has a group I binding phenotype (Fig. 1B). However, by day 42 of the immune response only 17% of anti-PC Abs could be inhibited by free PC. Those anti-PC Abs that were not inhibited by free PC were inhibited by NPPC and thus are characteristic of group II Abs that develop during repertoire shift in BALB/c mice after PC-KLH immunization (Fig. 1C).

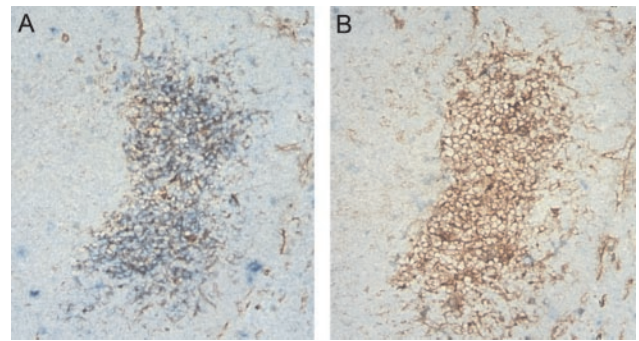
### Day 7 germinal centers stain with anti-T15 Id<sup>+</sup> Abs and contain rearranged *V<sub>H</sub>1-DFL16.1-JH1* genes and *V $\kappa$ 22-J $\kappa$ 5* genes

To follow the location of T15 Id<sup>+</sup> B cells in vivo, spleen sections were stained with a polyclonal anti-T15 serum or with biotinylated monoclonal AB1-2. The same or adjacent sections were also stained with PNA which is a marker of germinal center B cells. Germinal centers were not observed on days 3 and 5, but by day 7 after immunization, PNA<sup>+</sup> germinal centers were numerous and 77% were T15 Id<sup>+</sup>. A representative germinal center is shown (Fig. 2A). The anti-T15 staining was specific, as it was completely inhibited by preincubation of spleen sections with the T15 Id<sup>+</sup> mAb, PCM11 (Fig. 2B). In addition to the Id<sup>+</sup> germinal centers, numerous foci of T15 Id<sup>+</sup> cells were also present outside of germinal centers (data not shown).

To determine whether the T15 Id<sup>+</sup> cells contained canonical T15 VDJ and VJ rearrangements, groups of cells from Id<sup>+</sup> germinal centers were microdissected from spleen sections and rearranged H and L chain genes were amplified using nested primers. T15 VDJ and VJ rearrangements were readily amplified from germinal centers of the primary response. DNA from 19 microdissected germinal centers resulted in 19 positive T15 VDJ amplifications and 16 VJ amplifications.

### Low levels of somatic mutations are present in *V<sub>H</sub>1* and *V $\kappa$ 22*

To determine whether somatic mutations were introduced during the primary response to PC-KLH, 131 *V<sub>H</sub>1*, and 57 *V $\kappa$ 22* rearrangements were cloned and sequenced. Day 7 was chosen as this time point would capture B cells undergoing early events in mutation and selection within splenic germinal centers (36). Consistent

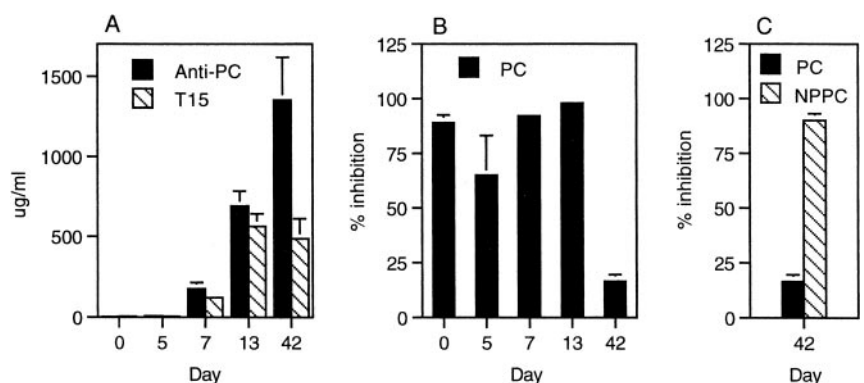


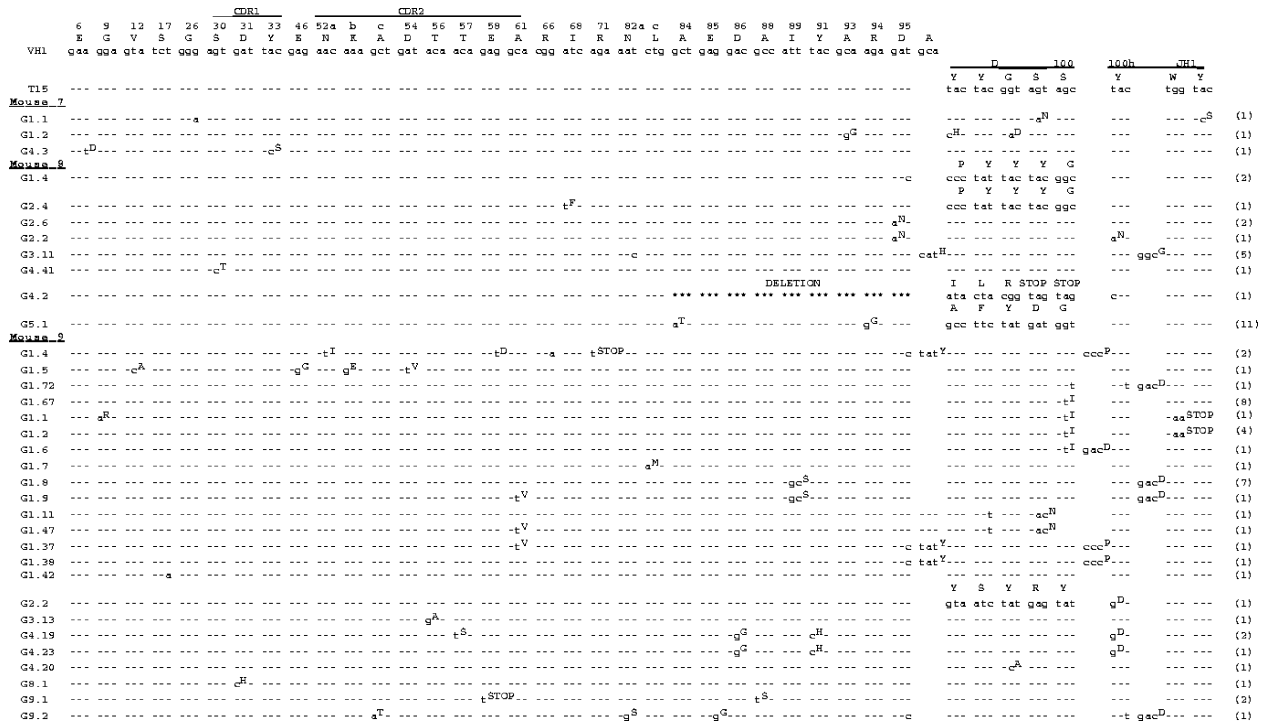
**FIGURE 2.** Representative immunostaining pattern of sequential sections from BALB/c spleen day 7 after immunization with PC-KLH. *A*, Germinal centers were double-stained with anti-T15 Id (blue) and PNA (brown). *B*, T15 Id<sup>+</sup> immunostaining (blue) is inhibited by preincubation with PCM11, a T15 Id<sup>+</sup> Ab, PNA (brown).

with this, many sequences were found to be unmutated; however, 34% of *V<sub>H</sub>1* clones and 37% of *V $\kappa$ 22* clones contained one to four mutations in the V region. Possible “N” additions at the V/D junctions were not scored as V region mutations but are shown in Fig. 3. The overall mutation frequency, calculated for amino acids 1–95, for *V<sub>H</sub>1* clones was 1/484 bp and for *V $\kappa$ 22* clones was 1/785 bp. The PCR error frequency was 1/10608 bp, estimated by sequencing of the RAG-1 gene amplified in the same PCRs indicating that nearly all (~95%) of the mutations are introduced by somatic hypermutation. Fig. 3 shows the unique T15 H chain V regions obtained from day 7 germinal centers. Most VDJ rearrangements use the T15 canonical *V<sub>H</sub>1-DFL16.1-JH1* gene segments typical of T15, but 4 of 34 unique sequences show alternative D region amino acids. Four groups of clones from mouse 9 appear to be related, as they were amplified from the same germinal center cell populations, share complementarity determining region (CDR)3 junctions, and have shared mutations (G1.1 and G1.2; G1.8 and G1.9; G1.37 and G1.38; G4.19 and G4.23). One clone (G4.2, mouse 8) has a deletion in the internal heptamer region (37) resulting in stop codons. Four other unique sequences from mouse 9 also included stop codons: one in CDR2 (G9.1), one in FW3 (G1.4), and two in JH1 (G1.1 and G1.2). The replacement to silent ratios (R:S) for the *V<sub>H</sub>* CDRs was 14:0 and was 3.8:1 for the FW regions.

The mutated T15 L chain V regions are shown in Fig. 4. Although these clones are also mutated by day 7, fewer unique L chain clones were found (17.5%) compared with the sequenced H chain clones (26%). One stop codon was generated in the CDR1 region (G2.48, mouse 9) in a clone that is probably related to clone

**FIGURE 1.** Anti-PC Ab response to PC-KLH-immunized BALB/c mice. *A*, Anti-PC levels, T15 Id, and (*B*) inhibition by free PC were determined by ELISA in serum collected on different days after immunization. *C*, Inhibition of PC-histone binding by free PC and NPPC was determined for serum collected 42 days following immunization. Ab concentrations or inhibition values from three to six mice were averaged  $\pm$  SEM.





**FIGURE 3.** Somatic mutations and CDR3 sequences in rearranged T15 V<sub>H</sub> genes recovered from microdissected T15 Id<sup>+</sup> germinal centers, 7 days after immunization with PC-KLH. Amplified sequences from three mice are compared with the germline V<sub>H</sub>1 gene and are aligned to the rearranged V<sub>H</sub>1 and JH1 from the T15 myeloma. “G” refers to the germinal center number and is followed by the clone designation. The number of identical clones analyzed is listed in parentheses at the end of each sequence. The deletion that occurred in mouse 8 G4.2 is indicated by a series of asterisks, and the sequence 3’ of the deletion is aligned to JH1. This sequence was obtained from a single germinal center cell. Sequences are numbered according to Kabat (72). Sequences G1.4 and G2.4 from mouse 8 use DFL16.1 with Pro<sup>96</sup> encoded by N nucleotide addition. This same junctional/DFL sequence has been observed in sequences amplified from adult bone marrow pre-B cells (73). Mouse 8 G5.1 uses DSP2.9 and mouse 9 G2.2 could use DSP2.2.

G2.43. The R:S ratio in the L chain was 4:1 in the CDRs and 4:1 in the FW regions.

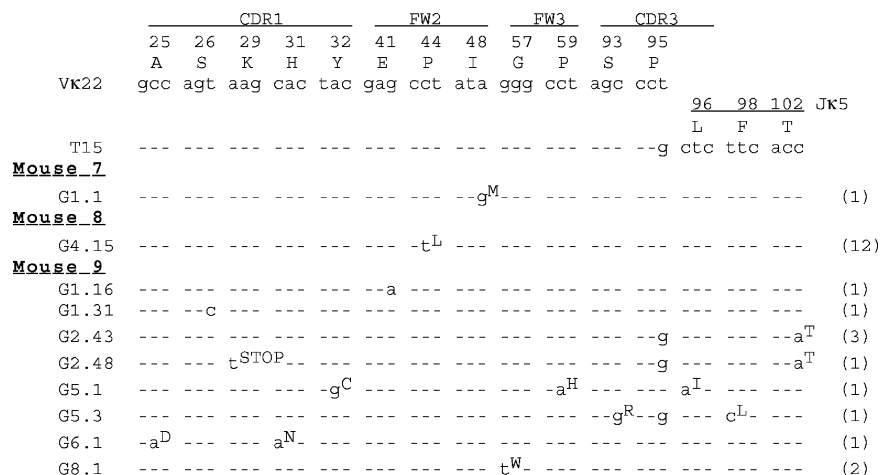
To determine whether T15 B cells with mutated sequences were also present in germinal centers after the secondary response, PCR analysis was conducted on germinal centers on days 7 and 13 after boosting with PC-KLH. At these time points, germinal centers were numerous and large in size (data not shown). Only two V<sub>H</sub>1 amplifications and no Vκ22 amplifications were obtained from 26 individual germinal centers in PC-KLH-boosted mice, even though RAG-1 was amplified in 23 of 23 PCRs. Of the two V<sub>H</sub>1 amplifications, all sequences were germline (*n* = 20). PCR conditions were appropriate for amplification as V<sub>H</sub>1 and Vκ22 rearrangements were amplified from 9 of 10 Id<sup>+</sup> foci. These data indicate

that B cells with V1-JH1 and Vκ22-Jκ5 rearranged V genes were infrequent in secondary response germinal centers but could be readily identified outside of germinal centers.

*Deleterious somatic mutations in T15 V<sub>H</sub> affect Ag binding*

To determine whether deleterious mutations other than stop codons were being generated in the primary response germinal centers, we identified a set of 7 V<sub>H</sub>1 clones including WT to put into the pSV2-S107 (*XhoI/NcoI*) expression vector, replacing the S107 WT V<sub>H</sub>1 with the cloned V<sub>H</sub>1 rearrangements and retaining the unmutated S107 WT Vκ22 (Fig. 5). The S107 WT Vκ22 gene was used, as to our knowledge, the canonical T15 H chain rearrangements that we chose for expression studies have not been

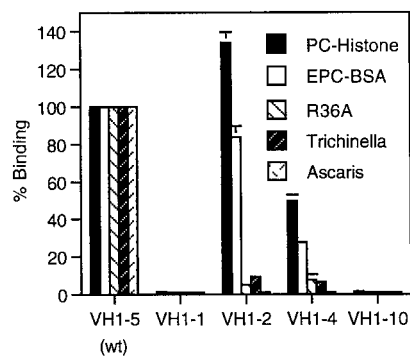
**FIGURE 4.** Sequences of amplified Vκ22 to Jκ5 rearrangements. The sequences are compared with germline Vκ22 and to the T15 myeloma L chain. The number of identical clones analyzed are listed in parentheses after each sequence.



Clone	CDR										D				JH1		Sec.	Bind.	
	1					CDR2													
	6	33	52c	56	57	82a	85	86	91	95	96	100	100h	100i	Y	W			
T15	E	Y	A	T	T	N	E	D	Y	D	Y	Y	G	S	S	Y	W		
VH1-5 (WT)	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	+
VH1-1 G4.3	D	S	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-
VH1-2 G1.4	-	-	-	-	-	-	-	-	-	-	P	Y	Y	Y	G	-	-	+	+
VH1-4 G3.13	-	-	-	A	-	-	-	-	-	-	-	-	-	-	-	-	-	+	+
VH1-6 G4.19	-	-	-	-	S	-	-	G	H	-	-	-	-	-	-	D	-	-	nd
VH1-8 G4.23	-	-	-	-	-	-	-	G	H	-	-	-	-	-	-	D	-	-	nd
VH1-10 G9.2	-	-	T	-	-	S	G	-	-	-	-	-	-	-	-	-	D	+	-

**FIGURE 5.** Amino acid sequence of cloned VDJ rearrangements expressed in *pSV2-S107(X/N)*. The expressed Ab name is listed (V<sub>H</sub>1-1, etc.) as well as the original clone name from Fig. 3 (G4.3, etc.). The ability of the Ab to be secreted from the cell (Sec.) and the binding to PC protein (Bind.) are indicated. V<sub>H</sub>1-6 and V<sub>H</sub>1-8 were not secreted and thus were not assayed for binding ability, indicated by nd.

reported to pair with other L chains. The specific V<sub>H</sub>1 clones were chosen because they might have deleterious mutations as determined by analysis of the mutation in the context of the T15 structural model and the amino acid substitution frequency within the Kabat database of Ig sequences (38, 39). After transfection into SP2/0 cells, transfectants were assayed for ability to be secreted and for ability to bind Ag. WT and four mutant transfectants secreted Ab and were assayed by ELISA for binding to a variety of PC-containing Ags (Fig. 6). PC is coupled to the histone protein via a nitrophenyl linker, as is PC in the PC-KLH used for immunization. EPC-BSA has a linear nine-carbon linker joining the PC hapten to the protein carrier (9). The three natural PC-containing pathogens, *S. pneumoniae* strain R36A, *T. spiralis*, and *A. suum*, were chosen because they differ from each other in the form of PC Ag displayed on the surface of the organism (40). Compared with WT, two of the Abs, V<sub>H</sub>1-1 and V<sub>H</sub>1-10, have lost the ability to bind to any of the PC-Ags present in the panel. Two other Abs, V<sub>H</sub>1-2 and V<sub>H</sub>1-4, retain binding ability but show differential recognition of the panel of PC Ags, exhibiting very poor binding to *S. pneumoniae* R36A, *T. spiralis*, and no detectable binding to *A. suum*. To verify that the V<sub>H</sub>1-2 and V<sub>H</sub>1-4 Abs can recognize the PC hapten, we inhibited the binding to PC-histone using different concentrations of free PC hapten. The I<sub>50</sub> (hapten concentration needed to inhibit Ab binding by 50%) values were 0.005 mM for WT, 0.02 mM for V<sub>H</sub>1-2, and 0.003 mM for V<sub>H</sub>1-4. The similar I<sub>50</sub> value of V<sub>H</sub>1-4 to WT indicates that V<sub>H</sub>1-4 can recognize PC as well as WT. However, the single CDR2 mutation T56A in V<sub>H</sub>1-4 modifies the Ab so that it no longer has a broad Ag recognition range, but has become more specific for PC in the form of the immunizing Ag. A similar restricted pattern of recognition of PC-containing Ags is seen with V<sub>H</sub>1-2 which has changes in CDR3 due to use of different D region amino acids.



**FIGURE 6.** Binding of mutants to PC-histone, EPC-BSA, *S. pneumoniae* strain R36A, *T. spiralis*, or *A. suum*. Purified Abs were tested by ELISA for binding to Ag-coated wells relative to WT T15. The results represent the average of three experiments done in triplicate and the error bars are the SD.

*Deleterious mutations in T15 V<sub>H</sub>1 affect Ab secretion*

Two transfectants (V<sub>H</sub>1-6 and V<sub>H</sub>1-8) consistently failed to secrete Ig upon primary screening. At least 50 antibiotic resistant clones of each mutant were screened from three separate transfections. Stable transfectants secreted <1% of WT amounts of Ig (Table I). The secretion defect was not due to a defect in H chain or L chain synthesis as intracellular levels were similar to or above WT as determined by ELISA. To confirm these results, metabolic labeling of stable transfectants was conducted for 4 h with [<sup>35</sup>S]Met/Cys. Abundant intracellular H and L chains were found for mutants V<sub>H</sub>1-6 and V<sub>H</sub>1-8 (data not shown). The presence of the mutations in the transfected cell mRNA was confirmed by RT-PCR and direct sequencing of the PCR products (data not shown). These results indicate that V<sub>H</sub>1 genes, harvested from germinal centers, can contain mutations that impair assembly and secretion with the V<sub>κ</sub>22 L chain.

**Discussion**

The molecular basis for loss of dominance of T15 Id<sup>+</sup> Abs during the late primary and early memory response to PC protein is not completely understood. We demonstrate in this study that T15 Id<sup>+</sup> cells are present within PNA<sup>+</sup> germinal centers during the primary immune response to PC-KLH. Both rearranged V<sub>H</sub>1-DFL16.1-JH1 genes as well as rearranged V<sub>κ</sub>22-J<sub>κ</sub>5 genes were readily amplified from microdissected single germinal centers before the repertoire shift in serum Ab. Although we have not formally demonstrated the presence of T15 V<sub>H</sub> and V<sub>L</sub> genes within a single cell, the V<sub>κ</sub>22-J<sub>κ</sub>5 L chains form functional PC binding sites only when paired with the T15 H chain (41). Taken together, the amplification of canonical T15 H and L rearrangements within cells of the same germinal centers supports our immunohistochemical identification of T15 Id<sup>+</sup> cells. These findings are consistent with other studies in which T15 Id<sup>+</sup> cells were observed in germinal centers 7 days after immunization with other types of PC-containing Ags, including EPC-KLH (21) and *S. pneumoniae* R36A (42). Our results

Table I. Impaired assembly and secretion due to V<sub>H</sub> somatic mutation

Transfected Construct <sup>a</sup>	Supernatant H+L <sup>b</sup> (%)	Intracellular H (%)	Intracellular L (%)
T15 WT	100	100	100
VH1-6 (H11)	<1	482	349
VH1-8 (D4)	<1	635	73

<sup>a</sup> T15 WT or mutant H chains constructs were transfected into SP2/0 cells. Triplicate cultures of stable transfectants were cultured for 4 h in fresh medium and the concentrations of secreted and intracellular Ig were determined as described in Materials and Methods. Data are representative of at least three separate experiments.

<sup>b</sup> T15 WT supernatant H+L = 68.0 ng/10<sup>6</sup> cells; intracellular H = 43.2 ng/10<sup>6</sup> cells; intracellular L = 153.8 ng/10<sup>6</sup> cells. SD were <15% of mean values.

extend these findings as the presence of V $\kappa$ 22-J $\kappa$ 5 rearrangements had not been formally demonstrated. The T15 Id<sup>+</sup> PNA<sup>+</sup> cells appear to be active participants in the germinal center reaction as somatic mutations were observed in the amplified VDJ genes and VJ genes at a frequency comparable to mutation seen in other T cell-dependent germinal center responses (36, 43) and is higher than that seen in T cell-independent germinal center responses (44). Collectively, our results argue that repertoire shift occurs even though mutated T15 Id<sup>+</sup> cells are present in the microenvironment of the germinal center early in the immune response.

*Why do T15 Id<sup>+</sup> B cells enter germinal centers during the primary response yet fail to maintain idiotype dominance?*

Ab affinity dependent competition among B cell clones in transgenic and Ig-targeted mice is an important factor limiting the persistence of low affinity cells within germinal centers (45, 46). In the absence of competition, both high and low affinity B cells are equally able to respond to Ag and form germinal centers; however, in adoptive transfer competition experiments only high affinity B cells selectively accumulate during the primary response. Our finding of T15<sup>+</sup> cells undergoing mutation within germinal centers early in the primary response suggests that competition between group I and group II precursors may be occurring within germinal centers. Group II precursors may be at an initial disadvantage as their precursor frequency is much lower than group I precursors (17–19). In addition, the affinity of germline and some mutated group II appear to be the same or lower than  $1.8 \times 10^5 \text{ M}^{-1}$ , the affinity of unmutated T15 for NPPC (8). This argues against initial affinity providing a competitive advantage for group II Ab precursors. However, the contribution of the carrier molecule to binding could be significant. For example, the affinity of the M3C65 group II Ab for NPPC conjugated to peptide is  $\sim 110$  times greater than the affinity for NPPC (32). Thus, the apparent similarity of affinity between group I and group II precursors for NPPC may not fully reflect the affinity of group II B cells for the carrier determinants present on the selecting ligand. In addition, the selective forces in vivo are likely to be complex as the B cell receptor is sensitive to binding kinetics ( $k_{\text{on}}$  and  $k_{\text{off}}$ ), avidity, and epitope density and organization (47–52). Clearly, group II Abs develop higher affinity binding for the PC carrier as recurrent mutations can increase the affinity for the PC-protein complex up to 1000-fold greater than T15 (32, 53). In the M3C65-NPPC cocrystal, somatic mutations in the L chain directly enhance contact with the nitrophenyl group linking PC to KLH (32). In addition, group II Abs exhibit a higher efficiency for clonal expansion (19) suggesting that the potential of mutated group II Ab precursors to be favorably selected and expanded may provide a critical selective advantage.

*Deleterious somatic mutation within germinal centers*

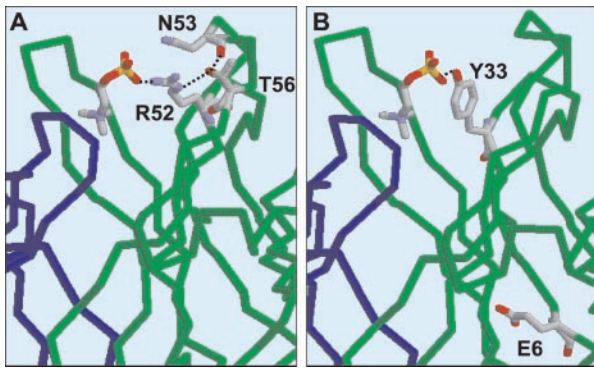
It has been previously proposed that T15 Abs are unable to form better combining sites in response to somatic mutation (22–25, 54). T15 Abs are reported to undergo little affinity maturation (23, 55) and in vitro studies have demonstrated that random mutations introduced into T15V<sub>H</sub> CDR2 and framework region 2 frequently resulted in loss of binding or failure to be secreted (25, 26, 56, 57). However, group II V regions appear to be equally susceptible to harmful mutations (54, 56, 58). A caveat of these studies was that only limited regions of T15 and group II Abs were mutated in vitro. As identification of somatic mutation altering Ig secretion was a novel observation, we wanted to determine whether some of the mutations generated during an immune response in vivo would also be deleterious to Ab function. All mutated V<sub>H</sub> genes chosen for expression with the germline T15 L chain were impacted by somatic mutation: two mutants exhibited impaired secretion and

two lost binding to PC protein. The fifth mutant and the clone that contained a novel D region displayed selective binding to PC protein-containing Ags with very little or no binding to PC displayed in the context of other carrier molecules. In addition to the secretion and binding loss mutants, four V<sub>H</sub> and one V<sub>L</sub> sequence contained stop codons. Two V<sub>H</sub> and the one V $\kappa$ , mutated within the V region genes, were likely introduced by somatic mutation in vivo. The two stop codons in the J gene of the clonally related sequences (G1.1 and G1.2, mouse 9) could have arisen via somatic mutation or during gene rearrangement. One clone (G4.2, mouse 8) had a deletion in the region of the internal heptamer resulting in stop codons, indicating perhaps an unsuccessful secondary rearrangement attempt. This sequence was obtained from a single T15 Id<sup>+</sup> TUNEL<sup>+</sup> cell (data not shown). These results suggest that somatic mutation in germinal centers and possibly secondary rearrangements may frequently lead to loss of binding, impaired Ig secretion, and potentially apoptosis. Overall, our minimum estimate of the magnitude of impairment of the in vivo-mutated Abs shown in Fig. 3 is 33% (9 of 27). If these cells die within germinal centers, such mutations may contribute to the high rate of apoptosis seen in germinal centers (59) and would be in agreement with models of B cell selection within germinal centers (60–64).

At present it is unclear whether B cells expressing nonfunctional Ig receptors can continue to proliferate before selection. Among our T15 H chain sequences, two sets of clonally related sequences are nonfunctional. Clonally related sequences G1.1 and G1.2 (mouse 9) both contain stop codons within the J region that would preclude Ab expression. In addition, clonally related sequences G4.19 and G4.23 (mouse 9) were secretion impaired when coexpressed with the germline T15 L chain. Although these data suggest that some proliferation may occur after deleterious mutation, alternative explanations are also possible. These V<sub>H</sub> genes may belong to the excluded allele or have undergone receptor editing and now express a second functional H chain. In addition, the mutational status of the L chain originally paired with the secretion-defective H chains is unknown and might have compensated for the secretion defect. In most cases, we could not address the L chain mutation status as PCR amplification of both rearranged H and L chains from microdissected single cells proved difficult. Thus, it is formally possible that compensatory mutations in the L chain may have existed. Studies are currently underway to examine directly the proliferative potential and in vivo fate of B cells harboring deleterious Ig mutations and to determine whether compensatory mechanisms may rescue Ab function during an immune response as we have demonstrated in our in vitro studies (65–67).

*Molecular basis of altered binding*

We examined the molecular contributions of in vivo-generated mutations to PC binding and carrier recognition in a computer-generated model of the T15 combining site (38). Mutant V<sub>H</sub>1-4 contains a single mutation located between the first and second loops of HCDR2. The Thr<sup>56</sup> to Ala replacement would disrupt both the Thr<sup>56</sup> H bond to Arg<sup>52</sup> and to Asn<sup>53</sup> (Fig. 7A). These disruptions may influence binding in two ways: first, by increasing the conformational flexibility of the Arg<sup>52</sup> side chain that directly contributes to PC binding via a critical salt bridge to PC (25, 38, 68); second, the substitution may alter carrier recognition (Fig. 6) either directly through the loss of the surface-exposed Thr<sup>56</sup> or indirectly by the disruption of the H bond formed with Asn<sup>53</sup> located in the first loop of HCDR2. These results underscore our previous observation that mutations in the first loop of CDR2 affect carrier recognition and discrimination among PC-containing Ags (35). The carrier discrimination of V<sub>H</sub>1-2 is even more pronounced as it binds PC protein better than WT yet displays poor binding to S.



**FIGURE 7.** Computer generated model of the T15 combining site (38) showing the location of mutations in  $V_H1-4$  (A) and  $V_H1-1$  (B). A side view of the T15 Fv is displayed as a  $C\alpha$  trace with selected side chains. The  $V_H$  domain (green) is on the *right* and  $V_L$  (blue) is on the *left*. PC is shown in the combining site as a stick image. A, The location of Thr<sup>56</sup> is shown as well as the PC contact residue Arg<sup>52</sup> and Asn<sup>53</sup>. Shown are Thr<sup>56</sup>  $\gamma$ -oxygen H-bond to the  $\epsilon$  nitrogen of Arg<sup>52</sup> and to the backbone carbonyl oxygen of Asn<sup>53</sup>. B, The Tyr<sup>33</sup> side chain hydroxyl forms a hydrogen bond with the O1 oxygen of PC. Atom colors: O is red; N is light blue, P is yellow, and C is white. The image was created with RasMac (version 2.6; MultiCHEM Facility, University of California, Berkeley, CA).

*pneumoniae*, *T. spiralis*, and *A. suum*. The binding profiles of mutants  $V_H1-4$  and  $V_H1-2$  emphasize the role of somatic mutation and selection in modification of the combining site toward specific recognition of the immunizing Ag.

Two mutants,  $V_H1-1$  and  $V_H1-10$ , bind poorly to all of the five PC-containing Ags.  $V_H1-1$  contains only two mutations. The Tyr<sup>33</sup> side chain hydroxyl forms a hydrogen bond with PC and thus mutation of this contact residue would directly alter binding (Fig. 7B). The Glu<sup>6</sup> to Asp change may also contribute to loss of binding as the residue at position 6 is a key amino acid in framework 1 confirmation, folding, and stability of single-chain Fvs (69, 70). Mutant  $V_H1-10$  is more difficult to analyze as it contains three amino acid replacements and a D region insertion. Both the Ala<sup>52c</sup> to Thr and Asn<sup>82a</sup> to Ser mutations have been observed in anti-PC Abs (39) while the Glu<sup>85</sup> to Gly has not been previously reported nor has the Asp<sup>100h</sup> D region insertion. The Asp insertion could affect the Trp<sup>100i</sup> contact with PC (38) or the Tyr<sup>100h</sup> interaction with L chain (65).

#### Molecular basis of altered secretion

Two clonally related  $V_H$  mutants containing either three ( $V_H1-8$ ) or four ( $V_H1-6$ ) amino acid substitutions failed to be secreted with the germline T15 L chain. This phenotype was consistent among multiple transfectants that each produced intracellular H and L chains but failed to readily form  $H_2L_2$  complexes (data not shown). In addition, mutant H chains displayed an association with molecular chaperones BiP and GRP94 implicating retention in the endoplasmic reticulum (data not shown), a result similar to our previous findings with Ab secretion mutants created by in vitro mutagenesis (27, 57). The molecular basis of secretion loss is difficult to dissect for mutants  $V_H1-6$  and  $V_H1-8$  because they contain multiple mutations. Both Abs contain an infrequent Tyr<sup>91</sup> to His mutation. Tyr<sup>91</sup> is part of a very conserved motif (YCARD) that is present in most Abs. Tyr<sup>91</sup> is buried in the core of the  $V_H$  and perhaps His<sup>91</sup> cannot be accommodated within this buried region next to Cys<sup>92</sup>. Possibly this substitution disrupts the  $V_H$  domain disulfide bond. It is also possible that the Tyr<sup>100h</sup> to Asp mutation may be critical as Tyr<sup>100h</sup> directly contacts L chain. The removal of 4 amino acids (Ser<sup>99</sup> to Trp<sup>100i</sup>) rescued secretion in four T15

low secretion mutants indicating that HCDR3 conformation can alter secretion of some Ab mutants (65).

In summary, our data indicate that the failure of T15 Id<sup>+</sup> Abs to maintain dominance in the late primary response to PC-KLH cannot solely be due to exclusion from the germinal center microenvironment or the somatic hypermutation process during the early primary response. When somatic mutations occurred, most of the T15 H chains tested by expression with a germline T15 L chain resulted in either impaired PC binding or nonsecretion. Mutations in HCDR2 and HCDR3 also significantly restricted Ab recognition to PC and PC protein and severely reduced or abrogated recognition of PC displayed in the context of different pathogenic microorganisms. In our model of repertoire shift, the high precursor frequency and B1 origin of T15<sup>+</sup> B cells result in rapid Ab production in response to primary PC protein immunization. Some T15 cells enter germinal centers and are capable of undergoing somatic hypermutation. However, these cells are not expanded due to deleterious somatic mutation and clonal competition with group II Abs having more diverse combining sites that can mutate to bind the PC protein carrier with high affinity. Affinity based competition within germinal centers (45, 46) and the bone marrow (71) then leads to repertoire shift during the late primary and memory response.

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#### References

- Harnett, W., and M. M. Harnett. 1999. Phosphorylcholine: friend or foe of the immune system? *Immunol. Today* 20:125.
- Briles, D. E., J. L. Claffin, K. Schroer, and C. Forman. 1981. Mouse IgG3 antibodies are highly protective against infection with *Streptococcus pneumoniae*. *Nature* 294:88.
- Briles, D. E., C. Forman, S. Hudak, and J. L. Claffin. 1982. Anti-phosphorylcholine antibodies of the T15 idotype are optimally protective against *Streptococcus pneumoniae*. *J. Exp. Med.* 156:1171.
- Chang, S. P., M. Brown, and M. B. Rittenberg. 1982. Immunologic memory to phosphorylcholine. II. PC-KLH induces two antibody population that dominate different isotypes. *J. Immunol.* 128:702.
- Chang, S. P., M. Brown, and M. B. Rittenberg. 1982. Immunologic memory to phosphorylcholine. III. IgM includes a fine specificity population distinct from TEPC 15. *J. Immunol.* 129:1559.
- Stenzel-Poore, M. P., U. Bruderer, and M. B. Rittenberg. 1988. The adaptive potential of the memory response: clonal recruitment and epitope recognition. *Immunol. Rev.* 105:114.
- Wicker, L. S., G. Guelde, I. Scher, and J. J. Kenny. 1982. Antibodies from the Lyb5-B cell subset predominate in the secondary IgG response to phosphocholine. *J. Immunol.* 129:950.
- Bruderer, U., M. P. Stenzel-Poore, H. P. Bachinger, J. H. Fellman, and M. B. Rittenberg. 1989. Antibody combining site heterogeneity within the response to phosphocholine-keyhole limpet hemocyanin. *Mol. Immunol.* 26:63.
- Kenny, J. J., G. Guelde, R. T. Fischer, and D. L. Longo. 1994. Induction of phosphocholine-specific antibodies in X-linked immune deficient mice: in vivo protection against a *Streptococcus pneumoniae* challenge. *Int. Immunol.* 6:561.
- Fischer, R. T., D. L. Longo, and J. J. Kenny. 1995. A novel phosphocholine antigen protects both normal and X-linked immune deficient mice against *Streptococcus pneumoniae*: comparison of the 6-O-phosphocholine hydroxyhexanoate-conjugate with other phosphocholine-containing vaccines. *J. Immunol.* 154:3373.
- Guo, W. X., A. M. Burger, R. T. Fischer, D. G. Sieckmann, D. L. Longo, and J. J. Kenny. 1997. Sequence changes at the V-D junction of the  $V_H1$  heavy chain of anti-phosphocholine antibodies alter binding to and protection against *Streptococcus pneumoniae*. *Int. Immunol.* 9:665.
- Wicker, L. S., G. Guelde, I. Scher, and J. J. Kenny. 1983. The asymmetry in idotype-isotype expression in the response to phosphocholine is due to divergence in the expressed repertoires of Lyb-5<sup>+</sup> and Lyb-5<sup>-</sup> B cells. *J. Immunol.* 131:2468.
- Masmoudi, H., T. Mota-Santos, F. Huetz, A. Coutinho, and P. A. Cazenave. 1990. All T15 Id-positive antibodies (but not the majority of  $V_H1T15^+$  antibodies) are produced by peritoneal CD5<sup>+</sup> B lymphocytes. *Int. Immunol.* 2:515.
- Taki, S., M. Schmitt, D. Tarlinton, I. Forster, and K. Rajewsky. 1992. T cell-dependent antibody production by Ly-1 B cells. *Ann. N.Y. Acad. Sci.* 651:328.



15. Martin, F., A. M. Oliver, and J. F. Kearney. 2001. Marginal zone and B1 B cells unite in the early response against T-independent blood-borne particulate antigens. *Immunity* 14:617.
16. Ansel, K. M., R. B. Harris, and J. G. Cyster. 2002. CXCL13 is required for B1 cell homing, natural antibody production, and body cavity immunity. *Immunity* 16:67.
17. Chen, C., U. Bruderer, and M. B. Rittenberg. 1992. The developmental patterns of B cell precursors distinguishing between environmental and nonenvironmental forms of phosphocholine. *Cell. Immunol.* 143:378.
18. Wu, P., and R. E. Ward. 1993. Ig repertoire expression of BALB/c primary and secondary B cell precursors specific for phosphorylcholine. *J. Immunol.* 150:3862.
19. Wu, P. Q., and R. E. Ward. 1994. The secondary B cell lineage for phosphorylcholine is conserved in CBA/CAHN-xid/J mice. *Cell. Immunol.* 155:345.
20. Linton, P. J., D. Lo, L. Lai, G. J. Thorbecke, and N. R. Klinman. 1992. Among naive precursor cell subpopulations only progenitors of memory B cells originate germinal centers. *Eur. J. Immunol.* 22:1293.
21. Miller, C., J. Stedra, G. Kelsø, and J. Cerny. 1995. Facultative role of germinal centers and T cells in the somatic diversification of IgV<sub>H</sub> genes. *J. Exp. Med.* 181:1319.
22. Feeney, A. J., S. L. Clarke, and D. E. Mosier. 1988. Specific H chain junctional diversity may be required for non-T15 antibodies to bind phosphorylcholine. *J. Immunol.* 141:1267.
23. Claffin, J. L., and J. Berry. 1988. Genetics of the phosphocholine-specific antibody response to *Streptococcus pneumoniae*: germ-line but not mutated T15 antibodies are dominantly selected. *J. Immunol.* 141:4012.
24. Spira, G., H. L. Aguila, and M. D. Scharff. 1988. T15 PC binding monoclonal antibodies retain specificity when they switch from IgM to IgG. *J. Immunol.* 140:2675.
25. Chen, C., V. A. Roberts, and M. B. Rittenberg. 1992. Generation and analysis of random point mutations in an antibody CDR2 sequence: many mutated antibodies lose their ability to bind antigen. *J. Exp. Med.* 176:855.
26. Chen, C., T. M. Martin, S. Stevens, and M. B. Rittenberg. 1994. Defective secretion of an immunoglobulin caused by mutations in the heavy chain complementarity determining region 2. *J. Exp. Med.* 180:577.
27. Martin, T. M., G. D. Wiens, and M. B. Rittenberg. 1998. Inefficient assembly and intracellular accumulation of antibodies with mutations in V<sub>H</sub> CDR2. *J. Immunol.* 160:5963.
28. Chesebro, B., and H. Metzger. 1972. Affinity labeling of a phosphorylcholine binding mouse myeloma protein. *Biochemistry* 11:766.
29. Jacob, J., R. Kassir, and G. Kelsø. 1991. In situ studies of the primary immune response to (4-hydroxy-3-nitrophenyl)acetyl. I. The architecture and dynamics of responding cell populations. *J. Exp. Med.* 173:1165.
30. Kearney, J. F., R. Barletta, Z. S. Quan, and J. Quintans. 1981. Monoclonal vs. heterogeneous anti-H-8 antibodies in the analysis of the anti-phosphorylcholine response in BALB/c mice. *Eur. J. Immunol.* 11:877.
31. Desaynard, C., A. M. Giusti, and M. D. Scharff. 1984. Rat anti-T15 monoclonal antibodies with specificity for V<sub>H1</sub> and V<sub>H1</sub>-V<sub>L</sub> epitopes. *Mol. Immunol.* 21:961.
32. Brown, M., M. A. Schumacher, G. D. Wiens, R. G. Brennan, and M. B. Rittenberg. 2000. The structural basis of repertoire shift in an immune response to phosphocholine. *J. Exp. Med.* 191:2101.
33. Jacob, J., and G. Kelsø. 1992. In situ studies of the primary immune response to (4-hydroxy-3-nitrophenyl)acetyl. II. A common clonal origin for periarteriolar lymphoid sheath-associated foci and germinal centers. *J. Exp. Med.* 176:679.
34. Jackson, D. Y., J. R. Prudent, E. P. Baldwin, and P. G. Schultz. 1991. A mutagenesis study of a catalytic antibody. *Proc. Natl. Acad. Sci. USA* 88:58.
35. Brown, M., G. D. Wiens, T. O'Hare, M. P. Stenzel-Poore, and M. B. Rittenberg. 1999. Replacements in the exposed loop of the T15 antibody V<sub>H</sub> CDR2 affect carrier recognition of PC-containing pathogens. *Mol. Immunol.* 36:205.
36. Jacob, J., J. Przylepa, C. Miller, and G. Kelsø. 1993. In situ studies of the primary immune response to (4-hydroxy-3-nitrophenyl)acetyl. III. The kinetics of V region mutation and selection in germinal center B cells. *J. Exp. Med.* 178:1293.
37. Taki, S., F. Schwenk, and K. Rajewsky. 1995. Rearrangement of upstream D<sub>H</sub> and V<sub>H</sub> genes to a rearranged immunoglobulin variable region gene inserted into the DQ52-JH region of the immunoglobulin heavy chain locus. *Eur. J. Immunol.* 25:1888.
38. Brown, M., M. B. Rittenberg, C. Chen, and V. A. Roberts. 1996. Tolerance to single, but not multiple, amino acid replacements in antibody V<sub>H</sub> CDR2: a means of minimizing B cell wastage from somatic hypermutation? *J. Immunol.* 156:3285.
39. Johnson, G., and T. T. Wu. 2000. Kabat database and its applications: 30 years after the first variability plot. *Nucleic Acids Res.* 28:214.
40. Choy, W. F., M. H. Ng, and P. L. Lim. 1991. *Trichinella spiralis*: light microscope monoclonal antibody localization and immunochemical characterization of phosphorylcholine and other antigens in the muscle larva. *Exp. Parasitol.* 73:172.
41. Kenny, J. J., C. M. Moratz, G. Guelde, C. D. O'Connell, J. George, C. Dell, S. J. Penner, J. S. Weber, J. Berry, J. L. Claffin, and D. L. Longo. 1992. Antigen binding and idiotype analysis of antibodies obtained after electroproportion of heavy and light chain genes encoding phosphocholine-specific antibodies: a model for T15 idiotype dominance. *J. Exp. Med.* 176:1637.
42. Razzeca, K. J., E. Pillemer, I. L. Weissman, and R. V. Rouse. 1986. In situ identification of idiotype-positive cells participating in the immune response to phosphorylcholine. *Eur. J. Immunol.* 16:393.
43. Jacob, J., G. Kelsø, K. Rajewsky, and U. Weiss. 1991. Intracloonal generation of antibody mutants in germinal centres. *Nature* 354:389.
44. Toellner, K. M., W. E. Jenkinson, D. R. Taylor, M. Khan, D. M. Sze, D. M. Sansom, C. G. Vinuesa, and I. C. MacLennan. 2002. Low-level hypermutation in T cell-independent germinal centers compared with high mutation rates associated with T cell-dependent germinal centers. *J. Exp. Med.* 195:383.
45. Dal Porto, J. M., A. M. Haberman, G. Kelsø, and M. J. Shlomchik. 2002. Very low affinity B cells form germinal centers, become memory B cells, and participate in secondary immune responses when higher affinity competition is reduced. *J. Exp. Med.* 195:1215.
46. Shih, T. A., E. Meffre, M. Roederer, and M. C. Nussenzweig. 2002. Role of BCR affinity in T cell dependent antibody responses in vivo. *Nat. Immunol.* 3:570.
47. Foote, J., and C. Milstein. 1991. Kinetic maturation of an immune response. *Nature* 352:530.
48. Foote, J., and H. N. Eisen. 1995. Kinetic and affinity limits on antibodies produced during immune responses. *Proc. Natl. Acad. Sci. USA* 92:1254.
49. Roost, H.-P., M. F. Bachmann, A. Haag, U. Kalinke, V. Pliska, H. Hengartner, and R. M. Zinkernagel. 1995. Early high-affinity neutralizing anti-viral IgG responses without further overall improvements of affinity. *Proc. Natl. Acad. Sci. USA* 92:1257.
50. Bachmann, M. F., U. Kalinke, A. Althage, G. Freer, C. Burkhardt, H. Roost, M. Aguet, H. Hengartner, and R. M. Zinkernagel. 1997. The role of antibody concentration and avidity in antiviral protection. *Science* 276:2024.
51. Kouskoff, V., S. Famiglietti, G. Lacaud, P. Lang, J. E. Rider, B. K. Kay, J. C. Cambier, and D. Nemazee. 1998. Antigens varying in affinity for the B cell receptor induce differential B lymphocyte responses. *J. Exp. Med.* 188:1453.
52. Batista, F. D., and M. S. Neuberger. 1998. Affinity dependence of the B cell response to antigen: a threshold, a ceiling, and the importance of off-rate. *Immunity* 8:751.
53. Brown, M., M. Stenzel-Poore, S. Stevens, S. K. Kondoleon, J. Ng, H. P. Bachinger, and M. B. Rittenberg. 1992. Immunologic memory to phosphocholine keyhole limpet hemocyanin: recurrent mutations in the  $\lambda$ 1 light chain increase affinity for antigen. *J. Immunol.* 148:339.
54. Chen, C., V. A. Roberts, S. Stevens, M. Brown, M. P. Stenzel-Poore, and M. B. Rittenberg. 1995. Enhancement and destruction of antibody function by somatic mutation: unequal occurrence is controlled by V gene combinatorial associations. *EMBO J.* 14:2784.
55. Gearhart, P. J., N. D. Johnson, R. Douglas, and L. Hood. 1981. IgG antibodies to phosphorylcholine exhibit more diversity than their IgM counterparts. *Nature* 291:29.
56. Wiens, G. D., K. A. Heldwein, M. P. Stenzel-Poore, and M. B. Rittenberg. 1997. Somatic mutation in V<sub>H</sub> complementarity-determining region 2 and framework region 2: differential effects on antigen binding and Ig secretion. *J. Immunol.* 159:1293.
57. Wiens, G. D., A. Lekkerkerker, I. Veltman, and M. B. Rittenberg. 2001. Mutation of a single conserved residue in V<sub>H</sub> complementarity-determining region 2 results in a severe Ig secretion defect. *J. Immunol.* 167:2179.
58. Wiens, G. D., V. A. Roberts, E. A. Whitcomb, T. O'Hare, M. P. Stenzel-Poore, and M. B. Rittenberg. 1998. Harmful somatic mutations: lessons from the dark side. *Immunol. Rev.* 162:197.
59. Odartchenko, N., M. Lewerenz, B. Sordat, B. Roos, and H. Cottier. 1967. Mechanism and significance of cell death within germinal centers. In *Germinal Centers in Immune Responses*. H. Cottier, N. Odartchenko, R. Schindler, and C. C. Congdon, eds. Springer-Verlag, Berlin, p. 212.
60. MacLennan, I. C., and D. Gray. 1986. Antigen-driven selection of virgin and memory B cells. *Immunol. Rev.* 91:61.
61. Hardie, D. L., G. D. Johnson, M. Khan, and I. C. MacLennan. 1993. Quantitative analysis of molecules which distinguish functional compartments within germinal centers. *Eur. J. Immunol.* 23:997.
62. MacLennan, I. C. M., A. Gulbranson-Judge, M. Casamayor-Palleja, E. Chan, D. M.-Y. Sze, S. A. Luther, and H. A. Orbea. 1997. The changing preference of T and B cells for partners as T-dependent antibody responses develop. *Immunol. Rev.* 156:53.
63. Kelsø, G. 1996. The germinal center: a crucible for lymphocyte selection. *Sem. Immunol.* 8:179.
64. Kelsø, G. 1996. Life and death in germinal centers (redux). *Immunity* 4:107.
65. Martin, T. M., C. Kowalczyk, S. Stevens, G. D. Wiens, M. P. Stenzel-Poore, and M. B. Rittenberg. 1996. Deletion in HCDR3 rescues T15 antibody mutants from a secretion defect caused by mutations in HCDR2. *J. Immunol.* 157:4341.
66. Wiens, G. D., T. O'Hare, and M. B. Rittenberg. 2001. Recovering antibody secretion using a hapten ligand as a chemical chaperone. *J. Biol. Chem.* 276:40933.
67. Whitcomb, E., T. Martin, and M. Rittenberg. 2003. Restoration of Ig secretion: mutation of germline-encoded residues in T15L chains leads to secretion of free light chains and assembled antibody complexes bearing secretion-impaired heavy chains. *J. Immunol.* 170:1903.
68. Glockshuber, R., J. Stadlmüller, and A. Pluckthun. 1991. Mapping and modification of an antibody hapten binding site: a site-directed mutagenesis study of McPC603. *Biochemistry* 30:3049.
69. Jung, S., S. Spinelli, B. Schimmele, A. Honegger, L. Pugliese, C. Cambillau, and A. Pluckthun. 2001. The importance of framework residues H6, H7 and H10 in antibody heavy chains: experimental evidence for a new structural subclassification of antibody V<sub>H</sub> domains. *J. Mol. Biol.* 309:701.
70. Honegger, A., and A. Pluckthun. 2001. The influence of the buried glutamine or glutamate residue in position 6 on the structure of immunoglobulin variable domains. *J. Mol. Biol.* 309:687.
71. Takahashi, Y., P. R. Dutta, D. M. Cerasoli, and G. Kelsø. 1998. In situ studies of the primary immune response to (4-hydroxy-3-nitrophenyl)acetyl. V. Affinity maturation develops in two stages of clonal selection. *J. Exp. Med.* 187:885.
72. Kabat, E. A., T. T. Wu, H. M. Perry, K. S. Gottesman, and C. Foeller. 1991. *Sequences of proteins of immunological interest*. 5th Ed. U.S. Department of Health and Human Services, Public Health Service, National Institutes of Health, Bethesda.
73. Feeney, A. J. 1991. Predominance of the prototypic T15 anti-phosphorylcholine junctional sequence in neonatal pre-B cells. *J. Immunol.* 147:4343.