Understanding anti-Rh(D) antibodies on a molecular level would facilitate the genetic analysis of the human immune response to Rh(D), lead to the design of therapeutically useful reagents that modulate antibody binding, and provide relevant information regarding the structural organization of Rh(D) epitopes. Previously, we described a Fab/phage display-based method for producing a large array of anti-Rh(D) antibodies from the peripheral blood lymphocytes of a single alloimmunized donor. In the current study, we present a detailed analysis of 83 randomly selected clones. Sequence analysis showed the presence of 28 unique \( \gamma_i \) heavy chain and 41 unique light chain gene segments. These paired to produce 53 unique Fabs that had specificity for at least half of the major Rh(D) epitopes. Surprisingly, despite this diversity, only 4 closely related heavy chain germline genes were used (V\(H\)3-30, V\(H\)3-30.3, V\(H\)3-33, and V\(H\)3-21). Similarly, nearly all \( V_l \) light chains (15/18) were derived from one germline gene (DPK9). Light chains showed a more diverse \( V_l \) gene usage, but all (23/23) used the identical J\( \lambda_2 \) gene. Several Fabs that differed in epitope specificity used identical heavy chains but different light chains. In particular, 2 such clones differed by only 3 residues, which resulted in a change from epD2 to epD3 specificity. These results suggest a model in which footprints of anti-Rh(D) antibodies are essentially identical to one another, and Rh(D) epitopes, as classically defined by panels of Rh(D) variant cells, are not discrete entities. Furthermore, these data imply that the epitope specificity of an anti-Rh(D) antibody can change during the course of somatic mutation. From a clinical perspective, this process, which we term epitope migration, has significance for the design of agents that modulate antibody production and for the creation of mimetics that block antibody binding in the settings of transfusion reactions and hemolytic disease of the newborn.

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MATeRIALS and MeTHODS

Production of Monoclonal Anti-Rh(D) Phage-Displayed and Soluble Fab Molecules

Methods for the isolation of human anti-Rh(D)—specific antibodies from γH and γλ Fab/phage display libraries using the pComb3H phagemid vector and a cell-surface panning protocol have been previously published.21 Soluble anti-Rh(D) Fab preparations for inhibition studies were produced from bacterial cultures transfected with plasmid DNA from which the M13 gene III coat protein sequence had been excised as described.21,26 Cultures were grown by shaking at 300 RPM at 37°C in superbroth (30 g/L tryptone, 20 g/L yeast, 10 g/L MOPS, pH 7.00) containing 20 mmol/L MgCl2 and 50 µg/mL carbencillin to an OD600 of 0.5. Isopropyl-β-D-thiogalactopyranoside (IPTG) was added to 1 mmol/L and cultures were shaken overnight at 30°C. Bacterial pellets were harvested and resuspended in 1/50th of the initial culture volume with osmotic shock buffer (500 mmol/L sucrose, 1 mmol/L EDTA, 100 mmol/L Tris, pH 8.00), incubated for 30 minutes at 4°C, and centrifuged at 16,000 g for 15 minutes at 4°C. Fab-containing supernatants were dialyzed against phosphate-buffered saline (PBS) and used in agglutination experiments without further purification.

Anti-Rh(D) Antibody Binding Assays

The binding of anti-Rh(D) Fab/phage or soluble Fab molecules to normal or partial Rh(D) antigens was assessed by indirect agglutination assays as described.21,22 Briefly, 100 µL aliquots of phage-displayed Fabs or soluble Fabs were incubated with 50 µL of a 3% suspension of RBCs. After 1 hour of incubation at 37°C, the RBCs were washed three times with 2 mL of cold PBS to remove unbound antibody. The resulting RBC pellets were resuspended in 100 µL of a 10 µg/mL solution of sheep anti-M13 antibody (5 Prime-3 Prime, Boulder, CO) and centrifuged at 16,000 g for 15 minutes at 4°C. Fab-containing supernatants were dialyzed against phosphate-buffered saline (PBS) and used in agglutination experiments without further purification.

Sequence Analysis of Anti-Rh(D) Heavy and Light Chains

Nucleotide Sequencing and Analysis

Plasmid DNA for sequencing was prepared using the Qiawell system (Qiagen, Chatsworth, CA). Double-stranded DNA was sequenced using light chain or heavy chain Ig constant region reverse primers or a set of unique pComb3H vector primers that anneal 5’ to the respective Ig chain26,27 and automated fluorescence sequencing (Applied Biosystems, Foster City, CA; DNA Sequencing Facility, University of Pennsylvania Department of Genetics and Cancer Center, Philadelphia, PA). Sequence analysis and variable region germline assignments were performed using DNAlign® and the V Base Directory of Human V Gene Sequences (March 1997 update).28 Germline assignments were corroborated with the MacVector (v. 6.0) software package (Oxford Molecular Group, Oxford, UK) against the same database. Multiple sequence alignments and predictions of isoelectric point were calculated using the Pileup and Isoelectric programs of the GCG software package (v. 8.0.1; GCG, Madison, WI). Statistical analysis was performed with Statview (Abacus Concepts, Berkeley, CA).

Because of the large number of heavy and light chain sequences (N = 69), only alignments of the predicted amino acid sequences are presented. Nucleotide sequences of all clones are available in Genbank.

RESULTS

Sequence Analysis of Anti-Rh(D) Heavy and Light Chains

We previously reported on the use of Fab/phage display and cell-surface panning to isolate a large array of anti-Rh(D) antibodies from the peripheral blood lymphocytes of a single hyperimmunized donor.22,29 Separate γH and γλ Fab/phage display libraries had been constructed and contained 7 × 10^7 and 3 × 10^9 independent transformants, respectively, based on electroporation efficiency. Each library was panned independently using a simultaneous positive/negative selection strategy with magnetically labeled Rh(D)-positive RBCs and unmodified Rh(D)-negative RBCs as described. After two rounds of panning, 32 of 36 γHλ and 15 of 15 γHκ randomly chosen clones were positive for anti-Rh(D) activity. After the third round of panning, 24 of 24 γHλ and 12 of 12 γHκ clones were positive. Nucleotide sequencing of the 83 positive clones showed a total of 28 unique heavy and 41 unique light chains. Because of combinatorial effects during phage display library construction, heavy and light chain gene segments paired to produce 53 unique Fab antibodies.22

Anti-Rh(D) heavy chains. All of the heavy chain sequences used VHIII family-encoded gene products (Figs 1 and 2).
Several sequences shared identical VDJ joining regions, and 12 unique VDJ rearrangements were identified and designated VDJ1 through VDJ12. Alignment of these sequences against the V Base Directory of Human V Gene Sequences\textsuperscript{29} showed that only four $V_{\text{H}}$III genes were used by these antibodies: VH3-21, VH3-30, VH3-33, and VH3-30.3. VH3-21 was used by 1 of the 12 VDJs and 2 of the 28 clones; VH3-30 by 1 VDJ and 6 clones; VH3-33 by 9 VDJs and 19 clones; and VH3-30.3 by 1 VDJ and 1 clone. Interestingly, VH3-30, VH3-33, and VH3-30.3 comprise a set of closely related genes (98\% homology; Fig 2B) and their next nearest neighbor, VH3-07, is only 90\% homologous (Fig 2C). Hereafter, these three genes are referred to as the VH3-33 superspecies. Heavy chain E1 differed from VH3-21 by 6 mutations and from VH3-48 by 10 mutations; hence, it was assigned to the former germline gene. Because there were no common mutations among the VH3-33 clones, it is highly probable that the donor possessed the VH3-33 germline gene. However, we could not formally rule out gene duplication with allelic variants of VH3-33 or the existence of variant alleles of the other germline genes in the donor. The isolation of clones sharing multiple VDJ joining regions argues that cloning artifacts cannot account for the $V_{\text{H}}$ gene restrictions observed.

Neither $J_{\text{H}}$ nor $D$ segments showed restriction. At least 9 different D segments were used and $I_{\text{H}}$ gene use comprised $I_{\text{H}}$6 (5 VDJs and 9 clones), $I_{\text{H}}$4 (4 VDJs and 10 clones), $I_{\text{H}}$3 (2 VDJs and 8 clones), and $I_{\text{H}}$5 (1 VDJ and 1 clone). All four $V_{\text{H}}$ genes were Chothia class 1-3,\textsuperscript{11} and the CDR3s showed a narrow range of length from 15 to 19 residues. Because rearranged heavy chain genes demonstrate extensive diversity, clones sharing identical VDJ rearrangements are generally considered to have arisen from the same clone. Based on nucleotide alignment with the germline genes (data not shown), an ontogeny tree was constructed for the 12 VDJs and 28 clones (Fig 3). By using the most parsimonious mutation scheme (ie, postulating the minimum number of mutations), putative intermediate antibodies were derived for several of the VDJs and were designated Ca, Cb, Da, Db, and Dc (Figs 2A and 3). Compared with the isolated heavy chain clones, which displayed between 6 and 23 nucleotide differences from their germline counterparts, these putative intermediates had between 3 and 12 mutations from germline. Based on the ontogeny tree, the number of independent mutations could be tabulated among the clones. The most commonly mutated residues were 52a and 58 (7 independent mutations), followed by residues 30, 31, and 50 (6 mutations) and residue 55 (5 mutations). In the VH3-33 superspecies, residues 52a and 58 in CDR2 are tyrosines and residue 52a was mutated to phenylalanine in 6 of the 11 VDJs derived from VH3-33 superspecies $V_{\text{H}}$ genes. Mutations at residue 58 comprised glutamate (3), aspartate (2), histidine (1), and asparagine (1). The AGY serines at residues 30, 31, and 55 were mutated to a number of different amino acids, although the AGY serine at 82b was conserved in all clones. The valine at residue 50 in the VH3-33 superspecies also had a diverse set of mutations. This distribution of hot spots is similar to that seen with nonproductive rearrangements as previously reported by Dörner et al.\textsuperscript{32}
Anti-Rh(D) light chains. Seventeen of the 18 κ light chains were from the VκI family and the remaining light chain originated from a VκII family member germline gene (Fig 4). Only 4 Vκ germline genes were used (15 clones were derived from DPK9 alone), and the κ light chain clones had between 1 and 49 mutations from their corresponding Vκ germline genes. All 5 of the known Jκ genes were used and were each joined to the DPK9 gene in one or more clones. Because the light chains showed considerably less diversity in their joining regions than the heavy chains, it was difficult to assign common clonal
Assessment of the Diversity of the Unpanned Libraries

To determine whether the apparent restriction in gene usage of the anti-Rh(D) antibodies could have been due to preselection factors (i.e., cloning artifacts), we assessed the diversity of the unpanned libraries. We sequenced 39 randomly picked clones, we determined that there were no duplicate heavy or light chain sequences and that there was significant heterogeneity in V gene family representation before selection (Fig 6). In fact, the variable region gene family distribution was not unlike that found by other investigators for IgG-secreting lymphocytes in adult peripheral blood. Furthermore, of the 14 VhIII-encoded negative clones, only one used a VH3-33 superspecies germline gene (VH3-30.3); the other 13 were encoded by VH3-07 (3), 3-09 (2), 3-15 (2), 3-48 (2), 3-72 (2), 3-23 (1), and DP-58 (1). Therefore, the restriction of the 83 anti-Rh(D) clones to the VH3-33, 3-30, 3-30.3, and 2-31 genes is significant and not a result of skewed representation of certain germline genes within the originally constructed γLκ and γLλ Fab/phage libraries.

**Heavy and Light Chain Contribution to Rh(D) Epitope Specificity**

Because of the conformational dependency of Rh(D) antigenicity, Rh(D) epitopes have been classically defined through the use of RBCs obtained from rare individuals whose cells appear to produce Rh(D) antigens lacking certain epitopes. Examining the pattern of agglutination of a particular anti-Rh(D) MoAb with such sets of partial Rh(D) RBCs enables one to categorize that antibody’s fine specificity.

Monoclonal Fab/phage preparations were prepared in triplicate for each of the 53 anti-Rh(D) clones and tested against a panel of Rh(D) category cells IIIa/c, IVa, IVb, Va, VI, and VII. This panel of cells can differentiate between the Rh(D) epitope specificities as described by Lomas et al (designated epitopes epD1, epD2, epD3, epD4, epD5, and epD6/7). Agglutination experiments with the Fab/phage clones showed five different patterns of reactivity, including a new pattern that had not been described in the original study by Lomas et al in the more recently described 9, 30, or 37 epitope systems (Figs 7 and 8). Although nearly all Fab/phage gave unequivocal agglutination reactions, a few antibodies gave repeatedly weak patterns of reactivity against one of the panel cells. For these reactions, monoclonal Fab/phage were prepared on at least four separate occasions to verify the patterns of reactivity.

The most commonly recognized epitope was epD6/7, against which 13 clones were directed. Interestingly, monoclonal anti-Rh(D) clones isolated using conventional tissue culture methods are most often specific for epD6/7, epD2, epD1, and epD3 were recognized by 10, 7, and 2 clones, respectively. Six clones agglutinated cells of categories IIIa/c, IVa, and VII, but not of categories IVb, Va, and VI, and were designated anti-epDX. This pattern is identical to epD1, except that the IVa cell is agglutinated. Three clones gave intermediate reactions with cell IVa, but otherwise showed patterns consistent with epDX or epD1. These clones were designated epDX′ or epD1X, depending on whether this reactivity against cell IVa was stronger or weaker, respectively (Fig 8). Similarly, reaction patterns for epD1 and epD2 differ by a positive reaction with the category Va cell; therefore, one clone was given epD21 specificity because it gave only moderate reactivity against that cell. Such variable reactions against one or more partial Rh(D) cells have been observed for anti-Rh(D) MoAbs produced through conventional tissue culture methods.

Because of the reassortment of heavy and light chain gene segments that occurs during the construction of a phage display library, a number of clones were isolated that shared either a heavy (eg, E1) or light (eg, M3) chain sequence (Fig 8). Some heavy chains were found to have paired with both κ and λ light chains (eg, C1, D20), and each demonstrated anti-Rh(D)
specificity. Interestingly, some heavy chains (eg, E1, D12) mapped to different epitopes depending on the light chains with which they were paired. In particular, the light chains of two such clones, E1/M2 and E1/M3, differed by only 3 amino acid residues (Fig 5) and these differences appear to confer specificity for epD2 versus epD3.

**Inhibition Studies**

To investigate the topological relationships among the Rh(D) epitopes, inhibition studies were performed. Previous work by Gorick et al37 using pairs of unlabeled and 125I-labeled anti-Rh(D) MoAbs demonstrated that antibodies to at least 3 different Rh(D) epitopes (subsequently identified as epD1, D6, and D7) could inhibit one another. We have confirmed and extended these findings using recombinant antibodies to 5 Rh(D) epitopes (Fig 9). In one series of experiments, we exploited the ability to express each antibody in both a soluble Fab as well as phage-displayed form to ask whether a soluble Fab against one epitope would inhibit the agglutination induced by an Fab/phage directed against a different epitope. Reciprocal pairs of soluble Fabs and Fab/phage specific for epD1, epD2, epD3, epD6/7, and epDX were tested. All 10 combinations showed mutual inhibition patterns (shown in Fig 9A for an anti-epD3/anti-epD6/7 combination). To show that this inhibition was not due to nonspecific factors, a control with an irrelevant RBC-binding recombinant antibody (an anti-blood group B antibody) was performed (Fig 9B). That sufficient inhibitory amounts of soluble Fab was present were first verified by demonstrating that each soluble Fab could inhibit its own Fab/phage (Fig 9A and B; samples on diagonal). Similar results were obtained using pairs of soluble Fabs which differed in their light chain isotype composition (Fig 9C).

**Isoelectric Point (pI) Analysis of Anti-Rh(D) Antibodies**

The restriction in V_H germline gene usage to only four V_H III family members was intriguing in light of their ability to confer specificity to a number of Rh(D) epitopes. As suggested by Boucher et al10 V_H germline gene segments used to encode anti-Rh(D) antibodies are among the most cationic segments available in the human V_H repertoire that may be used to account for the relatively high pI of polyclonal anti-Rh(D)–containing antisera.38,39 Although the cationic nature of the antibodies may be important for binding to Rh(D), it has also been suggested that a constitutive net positive charge may be necessary to permeate the highly negative RBC surface potential, thus permitting antibody to contact antigen.34 In either case, analysis of the predicted pI for the 28 heavy chains and 41 light chains isolated here showed an interesting phenomenon for the heavy versus light chains. Using the pI interval scale of Boucher et al,10 the average pI of the 4 germline V_H segments used to encode anti-Rh(D) antibodies is among the most cationic segments available in the human V_H repertoire that may be used to account for the relatively high pI of polyclonal anti-Rh(D)–containing antisera.38,39 Although the cationic nature of the antibodies may be important for binding to Rh(D), it has also been suggested that a constitutive net positive charge may be necessary to permeate the highly negative RBC surface potential, thus permitting antibody to contact antigen.34 In either case, analysis of the predicted pI for the 28 heavy chains and 41 light chains isolated here showed an interesting phenomenon for the heavy versus light chains. Using the pI interval scale of Boucher et al,10 the average pI of the 4 germline V_H segments used to encode the 28 heavy chains is high (9.87 ± 0.15) and significantly higher than that of 39 randomly picked, non-Rh(D) binding clones from the original unpanned libraries (9.24 ± 0.80, P < 10⁻⁵). Similar to the results of Boucher et al,10 the addition of D and J_H segments and the introduction of somatic mutation did not significantly change the pI of the average

---

**Table 1**

<table>
<thead>
<tr>
<th>V_H</th>
<th>J_H</th>
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<tr>
<td>D1</td>
<td>F1</td>
</tr>
<tr>
<td>D2</td>
<td>F2</td>
</tr>
<tr>
<td>D3</td>
<td>F3</td>
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<tr>
<td>D4</td>
<td>F4</td>
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</tbody>
</table>

**Fig 4.** (A) Alignment of anti-Rh(D) light chains to their nearest germline V and J genes shows predominance of DPK-9 usage from the V_k family. Nomenclature for clones is similar to that for heavy chains but uses the letters F through I. (B) Alignment of the four V_k genes used by anti-Rh(D) light chains. The key is the same as that used in Fig 2A. Genbank accession numbers for anti-Rh(D) light chains are listed in the Appendix.
anti-Rh(D) heavy chain (9.81 ± 0.33, P < .37). However, for the light chains, the average pI of their germline counterparts was not cationic, but the light chains became so through the addition of J_l segments and somatic mutation. Overall, for all 18 κ and 23 λ light chains, paired t-test analyses before and after somatic mutation showed a significant increase in net positive charge when comparing germline V_l (6.63 ± 1.47) with expressed V_l (7.28 ± 1.51, P < 10^−3) or germline V_lJ_l (7.43 ± 1.38) with expressed V_lJ_l (7.93 ± 1.70, P < 10^−3).

Fig 5. (A) Alignment of anti-Rh(D) light chains to their nearest germline V and J genes and (B) alignment of the 10 V_l germline genes used shows the use of a diverse set of variable region genes derived from multiple families. However, all of the clones use the identical J_l gene segment. Nomenclature for the clones is similar to that for heavy chains but uses the letters J through S. The key is the same as that used in Fig 2A. Genbank accession numbers for anti-Rh(D) light chains are listed in the Appendix.
permitted the identification of a new epitope designated epDX.

Inclusion of the category IVb cell (not available in our previous

chain gene. The only qualitative
discrepancy was in Vκ light chains demonstrated a slight preference for Vκ light chains were biased

towards Vκ1 family members and λ light chains demonstrated the preferential use of the Jκ2Vasicek gene. The only qualitative
discrepancy was in Vκ family usage, where Fab/phage clones demonstrated a slight preference for Vκ1 versus VκIII family members for conventional monoclonals. However, in both
cohorts, DPL16 was used more often than any other λ light

chain gene.

It has been suggested in the literature that the VH4-34

(VH4.21) germline gene, a gene used by many autoantibodies and cold agglutinins,40-42 may play an important role in the

immune response to RH(D). However, these conclusions arose from the analysis of IgM monoclonals and only 2 of the 21

published anti-RH(D) IgG sequences used VH4-34. In a related series of experiments, we pooled aliquots of the γκ and

γλκλ obtained after the second and third rounds of selection and then panned them against the VH4-34 specific rat

anti-idiotypic MoAb (9G44). Although we successfully enriched for VH4-34 encoded antibodies, the Fab/phage were not

specific for RH(D) and displayed serological characteristics similar to those of cold agglutinins (data not shown). We are
currently examining a µ phage display library from the same donor to compare gene usage.

Rh(D) Epitopes and Significance of Antibody Sequences

Since the initial report by Argall et al45 in 1953, it has been

recognized that rare individuals who type as RH(D)-positive can
produce allo-anti-RH(D) antibodies in response to RH(D) immu-
nization by transfusion or pregnancy. This phenomenon was
explained by hypothesizing that the RH(D) antigen is a mosaic structure and that these individuals were producing alloantibodies
to parts of the mosaic they lack. By systematically examin-
ing patterns of reactivity between their cells and sera, RBCs expressing partial RH(D) antigens were divided into categories,

each presumed to have a different abnormality in their RH(D) antigen. Through the subsequent use of index panels of

monoclonal anti-RH(D) antibodies, a series of epitopes were
defined of which the number and combination varied from one
RH(D) category to another. As new monoclonals were produced,
their reactivity profiles against these partial RH(D) RBCs
became the standard method for determining RH(D) antibody
epitope specificity. Molecular analyses of partial RH(D) pheno-
types have shown that the RH(D) genes in these individuals have
either undergone intergenic recombination with the highly

homologous RH(CE) gene or, less commonly, have sustained
point mutation(s).46

As noted earlier, to investigate the topological relationships
among RH(D) epitopes, Gorick et al37 performed competition
experiments with RH(D) MoAbs and observed varying degrees of
inhibition. These results, when combined with those of
Lomas et al,6 suggested a model for RH(D) in which epitopes are
spatially distinct yet demonstrate a certain degree of overlap, as
shown in Fig 10A. This model explained how antibodies to two
different RH(D) epitopes (in this case epD2 and epD3) could
inhibit each other’s binding to wild-type RH(D) and how a change in the structure of RH(D) in category VI RBCs (asterisk,
Fig 10A) would cause the loss of epD2. However, based on this
concept of RH(D) epitopes as distinct domains, we would expect
that antibodies against different epitopes of RH(D) would be
structurally and genetically distinct as well. Thus, it was
surprising that our anti-RH(D) clones demonstrated such marked
restriction in gene usage. For example, only two superspecies of
VH genes were used despite specificities for 4 of the original 6
RH(D) epitopes described by Lomas et al.6 Furthermore, multiple specificities could arise from a single heavy chain
depending on the light chain with which it was paired (eg, E1
with M2, M3, L3, or L4). In addition, other clones repeatedly
demonstrated variable weak reactivity against certain Rh(D) category RBCs that would affect the epitope specificities to which they were assigned (e.g., C1 with O1, M1, or J5).

Several hypotheses could account for these findings. The most simplistic interpretation is that the heavy chain does not directly interact with the antigen, but rather is responsible for bringing the antibody in close proximity with the antigen. The specific interactions between the light chain and the antigen would then determine the epitope specificity for that antibody. In this regard, our data are consistent with the observations of Boucher et al.\textsuperscript{10} on the relative cationic nature of anti-Rh(D) heavy chains. However, because we found that light chains become cationic during somatic mutation, the charge of the entire antibody may play a role in its ability to bind, resulting in the selection and expansion of particular B-cell clones.

A more compelling hypothesis is that Rh(D) epitopes do not differ spatially but differ only in the number and arrangement of contact residues presented (Fig 10B). In other words, the footprints of most, if not all, anti-Rh(D) antibodies are essentially identical to one another. The genetic events that produce partial Rh(D) molecules result in the loss of certain critical key points of contact necessary for some antibodies to bind; alternatively, they result in the formation of new structures that interfere with the binding of other anti-Rh(D) Igs. For example, the introduction of a ledge in Rh(D) category VI cells (asterisk, Fig 10B) does not interfere with the binding of an anti-epD3 antibody, but does prevent the binding of anti-epD2. Therefore, category VI RBCs are said to have epD3 but lack epD2.

This model is consistent with our inhibition experiments (Fig 9) and with those of Gorick et al.\textsuperscript{37} and offers an explanation for the marked restriction in heavy chain gene usage. It also reconciles a mechanism by which one heavy chain (e.g., E1) can confer binding to multiple epitopes and why some of our recombinant anti-Rh(D) antibodies, as well as some convention-
ally produced monoclonals, display variable reactivity against certain categories of partial Rh(D) RBCs. From the antigen’s perspective, this model explains how a single point mutation in Rh(D) can result in the loss of multiple Rh(D) epitopes (such as T283I in category HMi RBCs) and how the residues associated with the expression of some epitopes appear to be distributed among nearly all the extracellular loops of Rh(D). It also provides an understanding as to how epitopes can fit on the relatively small extracellularly exposed surface of the Rh(D) molecule.

This concept of coincident epitopes is best exemplified by comparing the E1/M2 and E1/M3 clones. The only difference between the reactivity of E1/M2 and E1/M3 is the ability of the latter antibody to agglutinate Rh(D) category VI cells (Fig 7). Hence, E1/M2 is classified as an anti-epD2 and E1/M3 as an anti-epD3 antibody. Light chains M2 and M3 differ by only 3 residues: D82A, G95A, and W96V (Fig 5). Therefore, some combination of these residues confers reactivity against category VI cells. In other words, epD2 and epD3, as seen by the E1/M2 and E1/M3 antibodies, differ by the binding constraints.

Fig 9. Inhibition studies with recombinant anti-Rh(D) antibodies. Panels show results of representative experiments demonstrating the mutual inhibition of antibodies directed at 2 different Rh(D) epitopes (in this example, epD3 and epD6/7; A and C), but not between an Rh(D) antibody and an unrelated recombinant anti-RBC antibody (an anti-blood group B antibody; B). In (A), Rh(D)-positive RBCs were incubated with soluble Fabs only, phage-displayed Fabs only, or combinations of the two, as indicated. In (B), Rh(D)-positive RBCs that were blood group B were used. After washing, RBCs were resuspended in anti-M13 antibody and assessed for agglutination induced by phage-displayed Fabs. Soluble Fabs were used full-strength, whereas Fab/phage preparations were present in limiting amounts to increase the sensitivity of the inhibition assay (see the Materials and Methods). In (C), mutual inhibition of epD3 and epD6/7 anti-Rh(D) antibodies was demonstrated with Rh(D)-positive RBCs, soluble Fab, and light chain isotype-specific antisera (see text for details). In these examples, the anti-epD3 and anti-epD6/7 antibodies were clones E1/M3 and D5/I3, respectively. The anti-blood group B antibody was isolated from an IgG phage display library made from the splenic B cells of a blood group O donor.

Table 1. Comparison of Current IgG Fab/Phage Library-Derived Anti-Rh(D) MoAbs With Those Previously Produced by Conventional Tissue Culture Methods

<table>
<thead>
<tr>
<th>Attribute</th>
<th>Previously Published*</th>
<th>Current Study</th>
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<tbody>
<tr>
<td>Heavy Chains</td>
<td></td>
<td></td>
</tr>
<tr>
<td>VH3 family derived</td>
<td>12/21 (57%)</td>
<td>28/28 (100%)</td>
</tr>
<tr>
<td>VH3-33 superspecies/VH3</td>
<td>10/12 (83%)</td>
<td>11/12 (92%)</td>
</tr>
<tr>
<td>VH3-33/VH3</td>
<td>9/12 (75%)</td>
<td>9/12 (75%)</td>
</tr>
<tr>
<td>VH3-21/VH3</td>
<td>1/12 (8%)</td>
<td>1/12 (8%)</td>
</tr>
<tr>
<td>VH4-34 derived</td>
<td>2/11 (10%)</td>
<td>1/12 (10%)</td>
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<tr>
<td>J H6 usage</td>
<td>15/21 (71%)</td>
<td>9/12 (32%)</td>
</tr>
<tr>
<td>CDR3 length</td>
<td>16-20 (28%)</td>
<td>15-19</td>
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| Light Chains              |                       |                        |
| k Light Chains            |                       |                        |
| Vκ1 family derived/total k | 8/12 (67%)           | 17/18 (94%)           |
| Jκ1 usage/total k         | 4/12 (33%)            | 6/12 (33%)            |
| Jκ2 usage/total k         | 4/12 (33%)            | 6/12 (33%)            |

| Light Chains              |                       |                        |
| l Light Chains            |                       |                        |
| Vλ1 family derived/total λ | 2/8 (25%)            | 12/23 (52%)           |
| Vλ3 family derived/total λ | 5/8 (63%)            | 5/23 (22%)            |
| DPL16 derived/Vκ3 family | 3/5 (60%)             | 4/5 (80%)             |
| J λ2Vasicek usage/total λ | 6/8 (75%)            | 23/23 (100%)          |

*Compiled from a total of 21 sequences of IgG anti-Rh(D) antibodies isolated from multiple subjects originally published by Bye et al., Hughes et al., Chouchane et al., and Boucher et al. and available from Genbank. One light chain (Oak-3) was not available in Genbank and was not included in the assessment.

†For heavy chains, the left column tabulates each clone separately and the right column tabulates clones on the basis of shared V-D-J joining regions.

‡VH3-33 superspecies defined as the group of VH3 family germline genes comprising VH3-33, VH3-30, and VH30.3.

§CDR3 length outlier.
imposed by at most three mutations. If the model depicted in Fig 10A were correct and the epitopes were independent, these mutations would have to cause enough structural alteration in the antibody combining site so that a completely separate epitope on the same antigen would be recognized. It would seem unlikely that these 3 mutations could cause such a change, especially given the lack of internal homology domains in Rh(D). Thus, we conclude that it is far more plausible that the footprints of these 2 antibodies are essentially identical and that one or more of these mutations (eg, the tryptophan in CDR3 of M2) prevent(s) the interaction of E1/M2 with category VI RBCs. Because other clones demonstrate that the light chain can confer specificity against epD1, epD2, or epD3 (with the E1 heavy chain); epD1 or epDX (with C5); and epD1, epD2, and epD6/7 (with D12), we suggest that all 5 of these epitopes have similar antibody combining sites.

Immunologic and Clinical Implications of Proposed Model

The model depicted in Fig 10B leads to additional predictions concerning the Rh(D) immune response beyond simply clarifying what is meant by an Rh(D) epitope. It is commonly stated in the transfusion medicine literature that individuals whose RBCs express partial Rh(D) antigens are free to make antibodies to the Rh(D) epitopes they lack. Therefore, an individual who produces category VI RBCs should be able to make anti-epD2 but not anti-epD3. If these epitopes were truly independent, then the immune repertoire of the anti-epD2 antibodies made by a category VI individual would be similar to those produced by an Rh(D)-negative person. However, to the immune system, epD2 and epD3 are not independent. We postulate that the somatic mutation of an anti-epD3 antibody can change its fine specificity to that of epD2 (or vice versa, Fig 10C). Suppose that the preferred way of making an anti-epD2 antibody is to go through an anti-epD3 intermediate. To an Rh(D)-negative individual, this process can take place unimpeded. However, in a category VI individual, this route would be unfavorable because an anti-epD3 antibody would be self-reactive. As a result, such an individual would have to make anti-epD2 antibodies by following alternative routes or by tolerating some degree of autoreactivity in the process. With respect to the latter point, it is of interest to note that a transient production of auto-anti-Rh(D) frequently precedes or accompanies the early production of allo-anti-Rh(D) in individuals who express partial Rh(D) antigens.49-54 We would predict, therefore, that the anti-epD2 antibodies from a category VI individual would be different in composition (ie, gene usage) and quite possibly quantitatively depressed as compared with an Rh(D)-negative individual. This may be analogous to the antibodies of the ABO blood group system in which it has been observed that anti-A and anti-B titers in blood group O individuals are significantly higher than in blood group B or A individuals, respectively.55 Blood group O individuals are unconstrained in creating their anti-A and anti-B immune repertoires, whereas individuals who produce A or B antigens (2 nearly identical structures) must do so in a manner that avoids self-reactivity.

In the case of antibodies E1/M2 and E1/M3, they appear to have arisen from a common precursor B cell rather than directly from each other (Fig 5). To test the framework of our hypothesis, ie, somatic mutation resulting in epitope migration of an antibody, we are constructing the precursors and potential intermediates between the M2 and M3 light chains and will then determine what Rh(D) epitope specificities (if any) they express. This concept of epitope migration has been previously reported for murine anti-cryptococcal56 and anti-type II collagen57 antibodies.

If the proposed model for Rh(D) epitopes is correct, then the
question of the number of epitopes may be obsolete. There may be as many epitopes as can be differentiated by the number of cell categories, ie, $2^n$ epitopes, where $n$ is the number of distinct partial Rh(D) RBCs. A more important question is the interrelationships between the various epitopes. For example, are some epitopes further away than others—not in the topological sense, but in terms of the number of mutational hits an antibody needs to receive to change its serologic reactivity. Furthermore, does the humoral immune response in a partial Rh(D) individual differ from that in an Rh(D)-negative individual in the manner predicted by this model? One may find that allo-anti-Rh(D) antibodies made by partial Rh(D) individuals are not as clinically significant, ie, capable of inducing hemolysis. This may explain why hemolytic disease of the newborn due to anti-Rh(D) produced by pregnant individuals with partial Rh(D) phenotypes is so rare even when taking into account the low prevalence of the partial Rh(D) phenotypes. A better understanding of the immune response to Rh(D) in these patients may alleviate concerns regarding the need to identify such individuals to ensure that they only receive Rh(D)-negative blood products for transfusion and Rh(D)-immune globulin during pregnancy. Furthermore, with respect to the design of recombinant Rh(D)-immune globulin for use in Rh(D)-negative patients, it may not be necessary to formulate cocktails of MoAbs containing multiple Rh(D) epitope specificities.

In summary, we have studied the genetic and immunological properties of a large array of anti-Rh(D) antibodies to elucidate this clinically significant human immune response on a molecular level. Our results show that anti-Rh(D) antibodies display a high degree of structural relatedness and the ability to inhibit each other’s binding despite differences in epitope specificity. These findings suggest that Rh(D) epitopes are not spatially distinct and that Rh(D) antibodies may undergo epitope migration as a result of somatic mutation. The end result is that the prevalence of certain anti-Rh(D) specificities in the immune repertoire may be a function not only of what epitopes an individual lacks, but of the number of accessible pathways that the individual’s immune system can use that avoid self-reactivity. This process may be a general feature of human immune responses to other clinically significant, closely related epitopes.

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APPENDIX

Genbank accession numbers for anti-Rh(D) heavy chains are as follows: B01, AF044419; C01, AF044420; C03, AF044421; C04, AF044422; C05, AF044423; C08, AF044424; C10, AF044425; D01, AF044426; D03, AF044427; D04, AF044428; D05, AF044429; D07, AF044430; D08, AF044431; D09, AF044432; D10, AF044433; D11, AF044434; D12, AF044435; D13, AF044436; D14, AF044437; D15, AF044438; D16, AF044439; D17, AF044440; D18, AF044441; D20, AF044442; D30, AF044443; D31, AF044444; E01, AF044445; E03, AF044446. Genbank accession numbers for anti-Rh(D) $\kappa$ light chains are as follows: F01, AF044447; G01, AF044448; H01, AF044449; I01, AF044450; I02, AF044451; I03, AF044452; I04, AF044453; I05, AF044454; I06, AF044455; I07, AF044456; I08, AF044457; I09, AF044458; I10, AF044459; I11, AF044460; I12, AF044461; I13, AF044462; I15, AF044463; I16, AF044464. Genbank accession numbers for anti-Rh(D) $\lambda$ light chains are as follows: J01, AF044465; J02, AF044466; J04, AF044467; J06, AF044468; K01, AF044469; K02, AF044470; K03, AF044471; L01, AF044472; L03, AF044473; L04, AF044474; L05, AF044475; M01, AF044476; M02, AF044477; M03, AF044478; N01, AF044479; N02, AF044480; O01, AF044481; O02, AF044482; O03, AF044483; P01, AF044484; Q01, AF044485; R01, AF044486; S01, AF044487.

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Genetic and Immunological Properties of Phage-Displayed Human Anti-Rh(D) Antibodies: Implications for Rh(D) Epitope Topology

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