Analysis of the Structural Correlates for Antibody Polyreactivity by Multiple Reassortments of Chimeric Human Immunoglobulin Heavy and Light Chain V Segments

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Summary

Polyreactive antibodies (Abs) constitute a major proportion of the early Ab repertoire and are an important component of the natural defense mechanisms against infections. They are primarily immunoglobulin M (IgM) and bind a variety of structurally dissimilar self and exogenous antigens (Ags) with moderate affinity. We analyzed the contribution of Ig polyvalency and of heavy (H) and light (L) chain variable (V) regions to polyreactivity in recombinatorial experiments involving the Vn-D-Jn and Ve-Je gene segments of a human polyreactive IgM, monoclonal antibody 55 (mAb55), and those of a human monoreactive anti-insulin IgG, mAb13, in an in vitro Cyl and Cs human expression system. These mAbs are virtually identical in their V and VK gene segment sequences. First, we expressed the Vn-D-Jn and Ve-Je genes of the IgM mAb55 as V segments of an IgG molecule. The bivalent recombinant IgG Ab bound multiple Ags with an efficiency only slightly lower than that of the original decavalent IgM mAb55, suggesting that class switch to IgG does not affect the Ig polyreactivity. Second, we coexpressed the mAb55-derived H or K chain with the mAb13-derived K or H chain, respectively. The hybrid IgG Ab bearing the mAb55-derived H chain V segment paired with the mAb13-derived K chain V segment, but not that bearing the mAb13-derived H chain V segment paired with the mAb55-derived K chain V segment, bound multiple Ags, suggesting that the Ig H chain plays a major role in the Ig polyreactivity. Third, we shuffled the framework 1 (FR1)-FR3 and complementarity determining region 3 (CDR3) regions of the H and K chain V segments of the mAb55-derived IgG molecule with the corresponding regions of the monoreactive IgG mAb13. The mAb55-derived IgG molecule lost polyreactivity when the H chain CDR3, but not the FR1-FR3 region, was replaced by the corresponding region of mAb13, suggesting that within the H chain, the CDR3 provides the major structural correlate for multiple Ag-binding. This was formally proved by the multiple Ag-binding of the originally monoreactive mAb13-derived IgG molecule grafted with the mAb55-derived H chain CDR3. The polyreactivity of this chimeric IgG was maximized by grafting of the mAb55-derived k chain FR1-FR3, but not that of the k chain CDR3. The mAb55-derived k chain FR1-FR3 (an unmutated Vk 325 segment), however, failed to yield a polyreactive Ab when grafted onto an IgG that was in all other parts identical with mAb13. Rather, this chimeric molecule showed full specificity for insulin. Thus, the polyreactivity of the human mAb55 can be fully preserved after Ig class switch, and depends primarily on the contribution of structures that are generated through somatic rearrangement events (H chain CDR3), and structures that represent the expression of an unmutated gene (Vk 325 segment).

Sera of healthy humans and animals contain natural antibodies (Abs) that react with a variety of self and exogenous Ags. Most natural mAbs generated from humans and mice are polyreactive, i.e., they bind multiple, even very heterogeneous, Ags such as polysaccharides, nucleic acids, hapten, and proteins, including structural cellular and tissue components and soluble hormones, generally with moderate intrinsic affinity (for a review see reference 1). Because of their broad reactivity with exogenous Ags, natural Abs may play a major role both in defense against invading bacteria or viruses before specific Abs are generated, and in clearance of cellular debris and certain toxic substances. Because of their reactivity with various self Ags, including DNA, IgG Fc fragment, and phospholipids, natural Abs may serve as templates for
some of the high-affinity autoantibodies emerging in patients with autoimmune disease.

The multiple Ag-binding activity and primordial Ig class, mainly IgM, of natural Abs contrast with the exquisite specificity and mature Ig class, mainly IgG, of the Ag-induced Abs. Despite their moderate intrinsic affinity, polyreactive Abs generally display a high avidity for Ag due to the decavalency of the predominant IgM class. Consequently, their effectiveness in binding Ag would be expected to decrease dramatically, because of a decrease in overall avidity, after Ig class switch and substitution of a y for a H chain (2). The characteristic spectra of Ag-binding activities of polyreactive Abs presumably reflect fundamental differences in the structure of their Ag-binding sites, as compared to those of Ag-induced (monoreactive) specific Abs, although the limited molecular data available have failed to yield definitive clues to such differences (3–12). It has been suggested that polyreactive Abs rely on the utilization of selected Vn genes, possibly in unmutated configuration, for the recognition of multiple Ags (1, 11, 12). However, recent data have shown that these Abs use various arrays of different Vn and Vl gene segments, as well as different D H and/or Jl gene segments, suggesting that the somatically generated H chain CDR3 may provide the crucial structural correlate for multiple Ag-binding (6, 13, 14).

To analyze the contribution of different Ig V regions to polyreactivity and to assess the impact of class switch to IgG on the ability of an originally polyreactive IgM Ab to bind multiple Ags, we performed recombinatorial experiments involving a human polyreactive IgM, mAb55 (3) and a human monoreactive anti-insulin IgG, mAb13 (15). These two mAbs were chosen because they use the same Vn and Vl gene segments in a highly similar configuration and with highly conserved FR structures (7, 16). Analysis of the chimeric molecules generated by replacing different portions of the polyreactive mAb55 H and L chain V segments with the corresponding portions of the monoreactive mAb13 and by expressing the "wild-type" or recombinant H and L chain V gene segments juxtaposed with the same C fragments, respectively, demonstrating that Ab polyreactivity was not affected by class switch from IgM to IgG and was dependent on the structure of the H chain CDR3 and that of the unmaturated Vn 325 framework 1 (FR1) - FR3 segment.

Materials and Methods

Cloning and Sequencing of the Vn-D-Jn and Vl-Jl Genes of mAb55 and mAb13. The polyreactive IgM κ, mAb55, and the monoreactive anti-insulin IgG κ, mAb13, were generated by EBV transformation and somatic cell hybridization techniques using peripheral B cells from a healthy subject and a patient with insulin-dependent diabetes mellitus (IDDM), respectively (3, 15). IgM κ mAb55 was shown to be at least pentameric by size fractionation analysis on a Superose 12 column (Pharmacia LKB Biotechnology, Piscataway, NJ).

The sequences of the mAb55 Vn-D-Jn, Vl-D-Jl, and mAb13 Vn-D-Jn, Vl-D-Jl gene segments have been reported (7, 16); that of the mAb55 Vl-Jl gene segment was derived for the purpose of these studies using described procedures (7–10). These sequences are depicted in Fig. 1 A, and are summarized in Table I. The two mAb Vn gene sequences were 96.4% identical throughout the coding area, differing from that of the germline H11 gene (17) in five (mAb13) and nine (mAb55) nucleotides. Both mAbs utilized the DXP1 gene (18) but in different reading frames, and complemented by different unencoded nucleotides and different truncated Jl genes (19). The sequences of the mAb55 and mAb13 Vl-Jl genes were 93.8% identical throughout the coding area. The mAb55 Vl gene sequence was identical to that of the germline kv325 gene (20) except for a silent T → G change at position 288; that of the mAb13 Vl gene differed in six nucleotides from the sequence of the germline kv3g gene (21). Both mAbs used a J1 gene (22).

Expression Vectors. The pcDNA1 and pSRXRDIG plasmid vectors (23) were used for the in vitro expression of the human Ig Vn-D-Jn, and Vl-Jl gene segments, respectively. pcDNA1 is a mammalian expression vector derived from pcDNA1/Neo (Invitrogen Corp., San Diego, CA) (Fig. 2 A). It encodes a human CMV promoter, a murine leader sequence, a human IgGl H chain, and a Rous sarcoma virus (RSV) ITR-driven neomycin resistance gene. pSRXRDIG is a mammalian expression vector derived from pUC18 (Fig. 2 B). It contains a SV40 promoter, a murine leader sequence, a whole human Ig κ L chain, and a DHFR gene for selection by methotrexate.

Introduction of mAb55 and mAb13 Vn-D-Jn, Gene Segments into pcDNA1 Vector. The unique HindIII and Xhol sites, 5‘ and 3‘, respectively, of the leader-Vn-D-Jn gene segment in pcDNA1 were utilized for the introduction of the rearranged mAb55 or mAb13 Vn-D-Jn gene segment (Fig. 2 A). The mouse H chain leader sequence of pcDNA1 and the Vl-D-Jl gene segment of mAb55 (or mAb13) were amplified in separate PCRs (PCR 1 and PCR 2), and joined by “recombinant” PCR to yield the recombinant “leader-mAb55 (or mAb13) Vn-D-Jn” gene segment (Fig. 3 A), using the sense H leader (5’ gggaagcttctecaccatgggatgg 3’) and the antisense H-leader (5’ gggaagcttctecaccTGAGGAGACAGTGACCA 3’ for mAb13 Jl) or (5’ gggaagcttctecaccTGAGGAGACAGTGACCA 3’ for mAb55 Jl) and the antisense H-Ov2 (5’ cggctcagtcacatacgtcagtgac 3’) or the antisense H-Ov1 (5’ GCGTACCTGAGGAGACAGTGGTAACCG 3’ for mAb55 Jl) and the antisense H-Ov2 (5’ cggctcagtcacatacgtcagtgac 3’). These sequences of restriction sites are underlined. The sequences of the primers at the ends to be joined (H-Ov1 and H-Ov2) were complementary and allowed for partial annealing of the PCR 1 and PCR 2 products and performance of a recombinant PCR by addition of excess

Figure 1. Nucleotide (A) and deduced amino acid (B) sequences of the Vn, D-Jn, Vl, and Jl gene segments of mAb55 and mAb13. The top sequence in each cluster is that of the germline gene to which the remaining sequences of the cluster were compared. Dashes indicate identities. Solid lines on the top of each cluster depict CDRs. Dots represent deletions. Lowercase letters denote untranslated sequences. The sequences encompassed by the GIII-FR3 and xIII-FR3 primers are underlined. The present sequences are available from EMBL/GenBank/DDJB under accession numbers L08084, L32748, D16833, and D16834.
The recombinant pcDNAIG plasmids were amplified by transformation of competent MCI061/F3 cells (Invitrogen Corp.), and selection with ampicillin and tetracycline. Plasmid DNA was isolated using a plasmid kit (Qiagen Inc., Chatsworth, CA).

Introduction of mAb55 and mAb13 V(D)J Gene Segments into pSXRDIG Vector. The unique HindIII and XhoI sites, 5' and 3', respectively, of the leader-V(D)J gene segment in pSXRDIG, were utilized for the insertion of the mAb55 or mAb13 V(D)J gene segment (Fig. 2B). The murine κ-leader sequences of pCarH and the mAb55 (or mAb13) V(D)J gene segments were amplified in separate PCRs and joined by recombinant PCR (Fig. 3 A). The sequences of the primers used for these PCRs were as follows: sense κ-leader (5' gggaagcttatcaagatgaagtca 3'), antisense κ-Ov1 (5' CAAACAATTTCGATGCAACGATCAGA 3'); sense κ-Ov2 (5' gcaggttccagatgcGAAATTGTGTTGACGCAGTCT 3'), antisense κ-FR4 (5' ggcgtcgactacctggTTCATTCCTCACCCTTGG 3'). The recombinant fragment, leader-mAb55 V-(D)J or leader-mAb13 V-(D)J, was inserted into pSXRDIG after digestion with HindIII and XhoI. Recombinant pSXRDIG plasmids were amplified in competent DH5α cells by selection with ampicillin.

Construction of Recombinant (rec)V.13-55 and recV.55-13 Gene Segments. The method used to construct the recV.13-55 gene segment is schematized in Fig. 3 B. The sequence encoding the leader through FR3 area of mAb13 H chain V segment was PCR amplified using the sense H-leader and antisense GIII-FR3 B (5' CGGCCTCAGACGTGTCACTTC 3') primers (Fig. 1 A). The sequence encoding the FR3 through FR4 area of mAb55 H chain V segment was PCR amplified using the sense GIII-FR3 A (5' GCAATGAACAGTCTGAGAGCCG 3') (the reverse complement of GIII-FR3 B) and the antisense H-FR4 primers. The two amplified fragments were purified and joined by recombinant PCR. The same primers, except for the H-FR4 primer, and recombinant PCR were used for the construction of the recV.55-13 gene segment. The recV.13-55 and recV.55-13 gene segments were introduced into pcDNAIG as described above.

Construction of recV.13-55 and recV.55-13 Gene Segments. The

Figure 2. Structure of the pcDNAIG (A) and pSXRDIG (B) expression vectors. The segment between HindIII and XhoI sites, comprising the Ig H or κ chain gene is detailed. Boxes indicate exons: (Shaded boxes) mouse leader exons; (open boxes) human Ig V gene chain exons (hatched boxes) human Ig C gene chain exons. Solid lines indicate introns and non-coding sequences. (ColEl) ColEl origin bases; (DHRF) dihydrofolate reductase gene for methotrexate selection; (HBS pA) HBV surface antigen Poly(A) site; (La) mouse H chain leader sequence; (Lα) mouse κ leader sequence; (M3 ori) M3 origin bases; (P CMV) human CMV promoters; (P SV40) SV40 promoter; (RSV LTR) RSV LTR sequence; (supF) supF suppressor tRNA gene; (SV40 Polyoma ori) SV40 origin base and polyoma origin bases; (SV40 splice/poly A site; (Neomycin) neomycin resistance gene.

H-leader and H-FR4 primers (Fig. 3 A). The recombinant fragment was sequenced, to ensure that no unintended mutations were introduced during PCR amplification (8, 10, 16, 24), digested with HindIII and XhoI, ligated into pcDNAIG previously digested with HindIII and XhoI and freed of its original V-(D)-J gene segment. The unique HindIII and XhoI sites, 5' and 3" of the murine leader sequence were made complementary to one another by including nucleotides at the 5' end that are complementary to the 3' portion of the other primer (see Materials and Methods). Primers “leader” and “FR4” were designed to yield final recombinant products bearing HindIII and XhoI sites used for the introduction into the expression vectors.

(B) Construction of the chimeric V13-55 (recV.13-55 or recV.13-55) gene segment. Gene segments amplified from the recombinant leader-mAb 13-V(D)-J gene sequence by the leader and FR3 B primers (PCR 1), and amplified from the recombinant leader-mAb 35V(D)-J gene sequence by the FR3 A and FR4 primers (PCR 2) were joined by recombinant PCR. See Materials and Methods for the sequences of the sense FR3 A (GIIIFR3 A and κIII FR3 A) and the antisense FR3 B (GIIIFR3 B and κIII FR3 B) primers.

Figure 3. (A) Construction of the recombinant “mouse leader-human mAb55V(D)-J” gene segment (leader-mAb 55V(D)-J or leader-mAb 55 V(D)-J). Solid ( ), shaded ( ), and hatched ( ) lines depict the sequences of the expression vector (pcDNAIG or pSXRDIG), that of the V-(D)-J gene segment to be substituted, and that of the V(D)-J gene segment of mAb55, respectively. (Broken arrows) Nucleotide chain elongation by DNA polymerase. (Open boxes) Restriction sites. The mouse leader Ig V gene segment in the expression vector and the V-(D)-J or V(D)-J gene segment of mAb55 were amplified in separate PCR (PCR 1 and PCR 2), and joined by recombinant PCR. Primers used at the end to be joined (primers Ovl and Oro2) were made complementary to another by including nucleotides at the 5' end that are complementary to the 3' portion of the other primer (see Materials and Methods). Primers “leader” and “FR4” were designed to yield final recombinant products bearing HindIII and XhoI sites used for the introduction into the expression vectors.

(B) Construction of the chimeric V13-55 (recV.13-55 or recV.13-55) gene segment. Gene segments amplified from the recombinant leader-mAb 13-V(D)-J gene sequence by the leader and FR3 B primers (PCR 1), and amplified from the recombinant leader-mAb 35V(D)-J gene sequence by the FR3 A and FR4 primers (PCR 2) were joined by recombinant PCR. See Materials and Methods for the sequences of the sense FR3 A (GIIIFR3 A and κIII FR3 A) and the antisense FR3 B (GIIIFR3 B and κIII FR3 B) primers.
method used to construct the recV₁₃-55 and recV₁₅-55-13 gene segments was similar to that used for construction of the recV₁₅-55-13 gene segments (Fig. 3 B). The sequence encoding the leader though the FR3 area of mAh₁₃ and mAh₅₅ κ V segment was PCR amplified using the sense κ-leader and antisense κ-FR3 B (5' GCTGACAG-TAATCACCTGCAAATCCTTC 3') primers (Fig. 1 A). The sequence encoding the FR3 though FR4 area of mAh₅₅ or mAh₁₃ κ V segment was amplified using the sense κ-FR3 A (5' GAG-ATTTTGCACTGTAATCTGCACG 3') and antisense κ-FR4 primers. For each pair of segments, the two amplified DNAs were purified, joined by recombinant PCR, and introduced into pSXRDIG.

**Cell Culture and Transfection.** Mammalian F3B6 cells were used in all transfection experiments. F3B6 is the Ig nonsecretor human-mouse heterohybridoma used as fusion partner for the generation of mAh₁₃ and mAh₅₅ (3, 15). F3B6 cells were cultured in RPMI-1640 (BioWhittaker, Walkersville, MD) with 10% FCS, 1% L-glutamine, and antibiotics (FCS-RPMI), washed, and then resuspended in FCS-RPMI at 10⁷/ml. The cell suspension (75 μl) containing pcDNAIG (4 μg) and pSXRDIG (4 μg) vector DNA was transformed into an ice-cold electroporation cuvette with a 0.4-cm gap (Invitrogen Corp.). After application of an electric pulse of 750 V/cm with a capacitance of 1,000 μF using the Electroporator™ (Invitrogen Corp.) and a power supply (model 4000; Gibco BRL, Gaithersburg, MD), the cuvette was kept on ice for 10 min. Cells were then transferred to a flask containing 10 ml of prewarmed FCS-RPMI. After a 48-h culture, culture medium was changed to selective medium containing 0.4 mg/ml of G418 (Geneticin; Gibco BRL), and cells were distributed into 96-well flat-bottom plates. Neomycin only was used as selecting agent, because in transfectants expressing only pcDNAIG (H chain), the accumulation of unsecretable H chain molecules leads to cell death. Clumps of transformant cells were detected within 7–10 days. After 2 wk, culture fluids were tested by ELISAs using plates coated with goat F(ab')₂ fragment specific to human IgG + 7 + κ H chains. Double γ1 and κ chain producer cells were identified by developing separate ELISA plates with peroxidase-conjugated affinity-purified goat anti-human Ig κ chain probes (Cappel, Organon Teknika Corp., Durham, NC) (3–5). In each transfection, 5–12 clones secreting IgG κ were generated. The three most efficient secretors were expanded and frozen.

**Ab Purification, Binding Assays, and Measurement of Relative Avidity (Avᵣ).** IgG mAbs were purified from culture supernatant by 50% ammonium sulfate precipitation followed by absorption of the solubilized IgG onto a GammaBind G-Sepharose column (Pharmacia LKB Biotechnology), and elution with 100 mM glycine-HCl buffer (pH 2.7). Eluates were brought to pH 7.5 by addition of neutralizing buffer (pH 9.0), dialyzed against PBS, and stored in aliquots at 4°C. mAb binding to human recombinant insulin (Eli Lilly Research Laboratories, Indianapolis, IN), single stranded (ss)DNA, human recombinant IL-1α (BASF Biotech Corp., Worcester, MA), polyclonal human IgG Fc fragment, tetanus toxoid, and BSA were measured using appropriate ELISAs (3–5). IgG bound to solid-phase IgG Fc fragment were measured using a peroxidase-conjugated, affinity-purified goat anti-human Ig κ chain probe (Cappel, Organon Teknika Corp.). Binding of mAbs to soluble insulin was measured by competitive ELISA (3–10, 15, 16). Briefly, increasing amounts (0.25–100 μg) of soluble insulin were mixed with a constant amount of Ab in 100 μl of PBS containing 0.05% Tween 20 (PBS-Tween) and 1% BSA. After an 18-h incubation at room temperature, the mixtures were transferred into ELISA plates precoated with insulin. After a 1-h incubation and subsequent washing with PBS-Tween, the amount of Ab bound to the solid-
Figure 4. Binding of the original IgM mAb55 (A), recIgG55 (B), original IgG mAb13 (C), recIgG13 (D), recVH55-55/recVg55-13 (E), recVH55-13/recVg55-55 (F), recVH13-55/recVg13-13 (G), recVH13-13/recVg13-55 (H), and recVH13-13/recVg13-13 (L) antibodies to human recombinant insulin (●), ssDNA (Δ), tetanus toxoid (■), human recombinant IL-1β (▲), human IgG Fc fragment (○), and BSA (□). Bars below each panel schematize the composition of each original or recombinant antibody. (Open boxes) Human Cγ and Cx segments; and (shaded boxes) human Cμ segments. (Hatched boxes) The V segments derived from the polyreactive mAb55; (open boxes) those derived from the monoreactive anti-insulin IgG mAb13. The Ag-binding activity of each antibody is expressed as optical absorbance at 492 nm.
Table 1. Structure and Properties of Human mAb55 and mAb13

<table>
<thead>
<tr>
<th>Clone</th>
<th>Source</th>
<th>Chains</th>
<th>Reactivity</th>
<th>$A_{\text{vel}}$ for insulin</th>
<th>$V_{\text{H}}$ gene</th>
<th>$D$ gene</th>
<th>$J_{\text{H}}$ gene</th>
<th>$V_{\text{K}}$ gene</th>
<th>$J_{\text{K}}$ gene</th>
</tr>
</thead>
<tbody>
<tr>
<td>mAb55</td>
<td>Healthy subject</td>
<td>$\mu$</td>
<td>Polyreactive</td>
<td>$5.0 \times 10^{-7}$</td>
<td>H11$^*$</td>
<td>DXP'1$^*$</td>
<td>J$_6^6$</td>
<td>kv325$^1$</td>
<td>J1$^1$</td>
</tr>
<tr>
<td>mAb13</td>
<td>IDDM patient</td>
<td>$\gamma_1, \kappa$</td>
<td>Monoreactive (anti-insulin)</td>
<td>$4.9 \times 10^{-9}$</td>
<td>H11</td>
<td>DXP'1$^*$</td>
<td>J$_2^2$</td>
<td>kv3g$^*$</td>
<td>J$_1^1$</td>
</tr>
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</table>

* The sequence of the germline H11 gene has been reported by Rechavi et al. (17).
$^1$ D genes have been reported by Ichihara et al. (18).
$^2$ J$_6$ genes have been reported by Ravetch et al. (19).
$^3$ The sequence of germline kv325 gene has been reported by Kipps et al. (20).
$^4$ J$_1$ genes have been reported by Heiter et al. (22).
$^5$ The sequence of germline kv3g gene has been reported by Pech et al. (21).

bound in a dose-saturable fashion and with an efficiency only slightly lower than that of the original pentameric IgM mAb55 to the six self and exogenous Ags tested (Fig. 4, A and B). This slightly lower multiple Ag-binding efficiency was reflected in a slightly lower $A_{\text{vel}}$ for insulin of the reclgG55 when compared with its IgM counterpart ($8.5 \times 10^{-7}$ vs. $5.0 \times 10^{-7}$ g/μl). These experiments show that class switch from IgM to IgG does not significantly affect the ability of mAb55 to bind multiple Ags, and that polyreactivity is a function inherent to the V portion of the Ig molecule.

Contribution of the mAb55 $V_{\text{H}},D,J_{\text{H}}$ Segment to Polyreactivity. To evaluate the relative contribution of the whole $V_{\text{H}},D,J_{\text{H}}$ and $V_{\text{K}},J_{\text{K}}$ segments to the polyreactivity of the reclgG55 Ab, we first inserted the $V_{\text{H}},D,J_{\text{H}}$ and $V_{\text{K}},J_{\text{K}}$ gene segments derived from mAb13 into the C3,1 pcDNAIG and C3,3 pcXRDIG vectors, respectively, and simultaneously expressed the recombinant Ig chains by transfection of F3B6 cells. Pairing of the recombinant $H$ and $\kappa$ chains yielded a fully functional molecule, designated reclgG13, which bound insulin in a dose-saturable fashion and with an efficiency comparable to that of the original mAb13 ($A_{\text{vel}}$ for insulin was $7.5 \times 10^{-5}$ g/μl, compared with $4.9 \times 10^{-9}$ g/μl for mAb13) but none of the other Ags tested (Fig. 4, C and D).

Having shown that the expression of mAb55 and mAb13 V gene segments juxtaposed with the same Cγ1 and Cκ genes in a recombinant system did not essentially alter the distinct original Ag-binding features of the two mAbs, we constructed: (a) the hybrid IgG molecule recV$_{\text{H}},V_{\text{K}},55$-55/recV$_{\text{E}},13-13$ bearing the mAb55-derived H chain V segment and the mAb13-derived $\kappa$ chain V segment, and (b) the hybrid IgG molecule recV$_{\text{H}},V_{\text{K}},55$-55/recV$_{\text{E}},55-55$ bearing the mAb13-derived H chain V segment and the mAb55-derived $\kappa$ chain V segment. Although somewhat less efficiently ($A_{\text{vel}}$ for insulin, $1.2 \times 10^{-6}$ g/μl), the recV$_{\text{H}},V_{\text{K}},V_{\text{E}},13-13$ hybrid Ab bound multiple Ags in a fashion similar to that of the recIgG55 (recV$_{\text{H}},V_{\text{K}},55-55$/recV$_{\text{E}},55-55$) and the original polyreactive IgM mAb55 molecules (Fig. 4, E, B, and A). In contrast, the recV$_{\text{H}},V_{\text{K}},13-13$/recV$_{\text{E}},55-55$ hybrid Ab did not bind any of the Ags tested (Fig. 4 F). The failure of this Ab to bind insulin may have been due to a "damping" effect by the recV$_{\text{H}},55-55$ segment on the inherent insulin specificity of the recV$_{\text{H}},13-13$ segment, since the recV$_{\text{H}},13-13$ segment showed full expression of insulin specificity (Ichiyoshi, Y., M. Zhou, and P. Casali, manuscript submitted for publication) when paired with the $V_{\text{L}}$ segment of mAb10 (14) which is very different in sequence from the $V_{\text{L}}$ segment of mAb13 or mAb55. This phenomenon is reminiscent of the finding by Radic et al. (25) who showed that the H chain of murine anti-DNA 3H9 Ab contains most or all of the required determinants for double stranded (ds)DNA binding, but its pairing with certain L chains can result in abrogation of this binding. Thus, the mAb55 $V_{\text{H}},D,J_{\text{H}}$ segment is necessary and sufficient for multiple Ag-binding.

Role of the H Chain CDR3 in mAb55 Polyreactivity. To determine whether mAb55 polyreactivity rests in the $V_{\text{H}}$ segment itself (Fkl through FIL3 sequence) or the somatically generated H chain CDR3, we evaluated the functional role of the discrete $V_{\text{H}}$ segment and CDR3, using: (a) the recV$_{\text{E}},13-55$ gene segment, constructed by juxtaposing the mAb13-derived $V_{\text{H}}$ segment with the mAb55-derived D-J$_{\text{H}}$ segment; and (b) the recV$_{\text{E}},55-13$ gene segment, constructed by juxtaposing the mAb55-derived $V_{\text{H}}$ segment with the mAb13-derived D-J$_{\text{H}}$ segment. In these gene recombinations, the last residue of the $V_{\text{H}}$ segment, which is a Val in mAb55 and an Arg in mAb13, was regarded as part of the CDR3, because FR residues adjacent to CDR might contribute to the conformation of the CDR loop itself (26). The two chimeric gene segments were inserted into the Cyl pcDNAIG vectors, and separately expressed by transfection of F3B6 cells along with the $V_{\text{K}},J_{\text{K}}$ gene segment derived from the polyreactive mAb55 (recV$_{\text{H}},V_{\text{K}},55-55$/recV$_{\text{E}},55-55$) to yield the recV$_{\text{H}},13-13$/recV$_{\text{E}},55-55$ and recV$_{\text{H}},55-13$/recV$_{\text{E}},55-55$ Ab mol-
molecules. Consistent with the role of the H chain CDR3 in providing the structural correlate for polyreactivity, the recV13-55/recV~55-55, but not the recV55-13/recV~55-55, IgG Ab bound multiple Ags (Fig. 4, G and H). In fact, the extent to which the recV13-55/recV~55-55 molecule bound to the Ags tested was comparable (AV~L for insulin, 9.4 × 10^{-7} g/μl) to that of the reclgG55 and that of the original IgM mAb55 (Fig. 4, B and A). Thus, the CDR3, not the Vκ segment, is the crucial element providing the structural correlate for the polyreactivity displayed by the mAb55 H chain. This contention was further strengthened by the demonstration that grafting of the mAb55-derived H chain CDR3 onto a molecule which was in all other parts identical to mAb13 enabled the molecule to bind multiple Ags. The Ab resulting from the pairing of the recV13-55 gene segment with the recV13-13 gene segment bound to all Ags tested, although less efficiently, in a fashion similar to that of the recV55-55/recV~13-13 hybrid molecule, which was encoded by the whole arm mAb55-derived Vb-D-Jκ gene segment (Fig. 4, I and E).

Role of the Vκ Segment in mAb55 Polyreactivity. Analysis of the recV13-55/recV~13-13 gene molecule emphasized the role of the H chain CDR3 in Ag-binding. It also indicated that the mAb55 κ chain contributed to polyreactivity. This was initially suggested by the slightly suboptimal binding to multiple Ags displayed by the recV13-55 segment paired with the recV13-13 segment (Fig. 4 E). To determine which portion of the mAb55 Vκ chain was synergistic with the H chain in binding Ags, we substituted the Vκ FR1-FR3 or κ chain CDR3-FR4 sequence of the recV13-55/V~13-13 molecule with the respective corresponding sequences derived from mAb55. To this end, we constructed: (a) the recV13-55 gene segment, by juxtaposing the mAb13-derived Vκ sequence, encoding the FR1-FR3, with the CDR3-FR4; and (b) the recV13-55 gene segment, by juxtaposing the mAb55-derived Vκ sequence, encoding the FR1-FR3, with the mAb13-derived Vκ sequence, encoding the CDR3-FR4. The two chimeric gene segments were inserted into the Cκ pSXRDIG vectors, and separately expressed by transfection of F3B6 cells as paired with the recV13-55 gene segment, to yield recV13-55/reCV13-13 and recV13-55/recV13-13 molecules. Grafting of the mAb55-derived Vκ,FR1-FR3 sequence, but not the κ chain CDR3-FR4 sequence, onto the L chain of the recV13-55/reCV13-13 molecule significantly enhanced the multiple Ag-binding activity of this Ab (Fig. 4, K and J). In fact, the recV13-55/recV55-13 molecule bound multiple Ags with an efficiency (AV~L for insulin, 8.4 × 10^{-7} g/μl) comparable to that of the integral reclgG55 Ab (Fig. 4 B). The germline configuration of the mAb55-derived Vκ325 FR1-FR3 segment is crucial in Ag-binding by the autologous H chain CDR3, but may not be sufficient to independently provide a structural correlate for polyreactivity, as grafting of the mAb55-derived Vκ gene segment onto a molecule encoded in all other parts by mAb13-derived gene segments failed to generate a polyreactive Ab. Instead, this Ab, recV13-13/recV55-13, bound specifically to insulin but to none of the other Ags (Fig. 4 L). Its exquisite specificity for insulin (AV~L, 6.0 × 10^{-9} g/μl) was comparable to that measured for reclgG13 and that of the original mAb13 (Fig. 4, D and C).

Discussion

In the present studies, we investigated the contributions of valency and of primary structure of V segments to the multiple Ag-binding of a human polyreactive IgM Ab, mAb55. The recombinant Ig Vn and Vκ gene expression system we adopted was designed to produce a complete human IgG1 κ molecule. Accordingly, the IgM mAb55-derived Vn-D-Jκ and Vκ-Jκ gene segments were expressed and secreted as a recombinant bivalent monomer (designated reclgG55), effectively "switching" the polyreactive IgM to IgG. On a weight-to-weight basis, the multiple Ag-binding of the reclgG55 molecule closely mimicked that of the wild-type IgM mAb55, showing that IgM to IgG class switch does not necessarily affect the characteristic feature of a polyreactive Ab, and that recognition of multiple Ags is a function that is absolutely restricted to the Ig V domains. This finding suggests that the role of natural polyreactive IgM extends far beyond that of providing the structural elements of the idiotypic regulatory network in early ontogeny, and that of enhancing opsonization and/or complement activation after binding invading microorganisms in the early phases of infection. Natural polyreactive IgM-producing cells may include the precursors of cells producing high-affinity polyreactive IgG or IgA autoantibodies or Abs to exogenous microbial Ags, after undergoing an Ag-dependent process of clonal activation and expansion entailing class switch and, possibly, somatic mutation and Ag selection (8–10).

The experiments involving the hybrid IgG molecules generated by coexpressing the mAb55-derived H or κ chain V segment with the mAb13-derived κ or H chain V segment, respectively, clearly demonstrated that the H chain plays a major role in mAb55 polyreactivity. This is consistent with previous observations that the specificity of monoreactive-specific Abs and autoantibodies is mainly determined by the H chain V segment (26, 27), although in some cases the L chain seems to play a critical role in defining epitope specificity (28, 29). Individual Ig H chains can bind Ag independently of the contribution of any L chain, as originally shown by Utsumi and Karush (30) in an isolated rabbit H chain to p-azophenyl-β-lactoside, and by Jaton et al. (31) in an isolated rabbit H chain to the 2,4-dinitrophenyl group. These early findings have recently been extended by experiments showing efficient Ag-binding of cloned murein Vκ domains, "single domain antibodies," to lysozyme or KLH (32), and by the observation that a broad Ag-binding repertoire is provided by naturally occurring Ig H chain dimers in the camel (33). Finally, x-ray crystallography has demonstrated in at least three Ag-Ab systems that the number of Ag-contacting residues in the H chain far exceeds that in the L chain (34, 35).

The experiments, in which the presence or absence of the mAb55-derived H chain CDR3 sequence resulted in acquisi-
tion or abolition, respectively, of polyreactivity, whether in a mAb55 or mAb13-like structural context, indicated that the CDR3 provides a critical structural correlate for the multiple Ag-binding activity of mAb55. The generated chimeric molecules satisfied the criteria set by Chothia and Lesk (26), i.e., they were identical in those canonical FR sequences that are adjacent to the CDRs, and are critical for the full preservation of the CDR loop structure. Thus, our choice of Abs and experimental design for shuffling the FR and CDR sequences should have prevented the structural deleterious effects which might be observed when CDR sequences are grafted onto FR contexts different from those of the original Ab molecule (37, 38). The H chain CDR3 of mAb55 is exceptionally long (31 amino acids), identifying a structure potentially capable of providing multiple contact interfaces, which may partially overlap, for different epitopes (1, 39). Crystallographic analysis has shown that at least in the case of relatively large protein Ags, multiple residues within the H chain CDR3 interface with Ag even in specific (monoreactive) Abs (35, 40, 41). However, as suggested by Chothia and Lesk (26), the important role of the H chain CDR3 in Ab specificity may arise from the central position of this structural element in the binding site rather than from its sheer size (or number of contact residues). In at least some polyreactive Abs, a wide H chain CDR3 loop may be critical for accommodating different Ags, but relatively short H chain CDR3s have been reported in other human polyreactive Abs (5, 7–12). In fact, the H chain CDR3 structures of human polyreactive Abs so far described are highly divergent in length and composition, and do not allow for the identification of any obvious common motif possibly responsible for polyreactivity (5–12). This structural heterogeneity might underlie the functional “uniqueness,” i.e., the discrete Ag-binding features, of each polyreactive mAb (5, 8, 9), but at the same time it raises the possibility that, in certain Abs, polyreactivity is mediated primarily by structures other than the H chain CDR3.

An important role of the H chain CDR3 in providing the structural correlate for multiple Ag-binding has been suggested by Harindranath et al. (6) for human RF IgM autoantibodies, by Ikematsu et al. (8) and by Kasai et al. (10) for other human IgG and IgA autoantibodies, and by Chen et al. (13), who showed that the H chain CDR3 was the most obvious parameter distinguishing polyreactive from monoreactive Ag-induced Abs in a panel of 84 murine mAbs. This hypothesis was substantiated by Martin et al. (14). They generated transfectomas to pair the cross-reactive idiotypic (CR1) 17.109+ κL chain of SMI, a polyreactive IgM RF utilizing a CR1 G6+ Vλ1 segment, with the Ig H chain of SMI or 10 other nonpolyreactive IgMs. All these IgMs had G6+ H chains encoded by the same Vh1 gene as SMI, but different D-Jh (CDR3) sequences. None of the 10 recombinant IgM κ Abs utilizing a H chain other than SMI was polyreactive, suggesting that the polyreactivity of SMI was dependent on the structure of the H chain CDR3. Our findings strengthen these observations by directly demonstrating that the grafting of the H chain CDR3 of a polyreactive Ig onto an originally monoreactive Ig results in multiple Ag-binding, and show further that an appropriate L chain V segment is necessary to fully express the polyreactive potential of the Ig H chain CDR3. Other L chains have been shown to not only contribute to Ag specificity of polyreactivity but also to efficiently bind Ags independently of H chains. Dimers of the MOPC 315 L chain bind e-N-(2,4 dinitrophenyl)-1-lysine and 4-(α-N-N-alanine)-7-nitrobenz-2-oxa-1, 3-diazide (42, 43); and dimers of the L chain Bence-Jones Mcg protein bind dinitrophenyl compounds, e-dansyllysine, colchichine, 1,10-phenanthroline, methadone, morphine, meperidine, 5-acetylsuccinamide, caffeine, theophylline, menadione (vitamin K3), triacetin, and other compounds (44, 45). In the case of mAb55, the direct multiple Ag-binding activity of the V325 segment remains to be defined as this Vλ segment failed to generate a polyreactive Ab when paired with the Vh3 segment of mAb13. The FR1-FR3 sequence of the mAb55-derived κ chain V segment is identical to the FR1-FR3 sequence of the germline kv325 gene, and to that of the V3 (SMI) segment used by Martin et al. (14) to express the polyreactivity of the SMI H chain. In fact, the mAb55 and SMI κ chains are identical not only in their FR1-FR3 sequence, but also in their FR4 sequence, and in the first seven of nine amino acids of the CDR3. The kv325 and other closely related segments of the V1Iib subgroup are frequently utilized to encode natural polyreactive Abs, as well as disease-associated autoantibodies, particularly RFs in autoimmune patients and chronic lymphocytic leukemia patients (20, 24, 46). The FR residues of V1Iib segments, which are putatively involved in the binding of the IgG Fc fragment (47), may also serve in stabilizing or defining the multiple Ag-binding site in polyreactive Abs.

Although limited to a single Ab pair, the present findings suggest that both monoreactive and polyreactive Ag-binding sites can be generated utilizing identical H and L chain V gene segments in conjunction with discrete primary structures of the H chain CDR3 (see Fig. 4, K and L). Previous observations have shown that the pool of Vhλ genes used by polyreactive natural Abs overlaps, at least partially, with that of Vhλ genes recruited in high-affinity immune responses to foreign Ags in healthy subjects or to self Ags in autoimmune patients (1, 5–10, 16, 24, 48). In contrast, the H chain CDR3 constitutes an important source of diversity in the expressed Ab repertoire, since its structure results from complex somatic rearrangement events, often involving more than one D gene in different orientations, and “unencoded” nucleotide additions (19, 49, 50). Computer analysis by Sanz (50) of more than 500 sequences from a CDR3-specific cDNA library revealed that these human Ig H chain sequences have the potential to generate more than 1014 different peptides. In view of the findings of Martin et al. (14), however, only a minority of somatically generated H chain CDR3s would give rise to Abs binding multiple Ags. The frequency of fully polyreactive Abs would be further reduced by the requirement for an appropriate L chain V segment, as shown here, and/or other H or L chain structures. This expected paucity of newly generated polyreactive Abs contrasts with the consistent findings that polyreactive Ab-producing cells account for up to 30% of the adult, and possibly more of the neo-
natal, human B cell repertoire (for a review see reference 51). Polyreactive Ab-producing cell precursors may be positively selected by contact with self Ags in early ontogeny, in a fashion similar to T cells in the thymus, where cells bearing receptors with low affinity for self Ags are recruited along the T cell maturation pathway (52). A somatic selection and amplification of human polyreactive Ab-producing cell clones would be further supported by the findings suggesting that most of the peripheral blood B cells in mice are ligand selected (53). The extension of combined structural and functional studies to other polyreactive Abs may help define the generality of the present findings and elucidate the role of these Abs in development and disease.

References


