DOUBLE ISOTYPE PRODUCTION BY A NEOPLASTIC
B CELL LINE

II. Allelically Excluded Production of \( \mu \) and \( \gamma_1 \) Heavy Chains Without
\( C_m \) Gene Rearrangement

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Ig class switching is a process in which a single clone of B lymphocytes
synthesizes IgM antibody, and subsequently synthesizes another isotype other
than IgD with the same specificity for antigen. Thus, the same heavy chain
variable region gene (\( V_\mu \)) formerly associated with the \( C_\mu \) gene is subsequently
associated with one of several constant region genes (\( C_{\gamma}, C_{\alpha}, C_\delta \)) (reviewed in
reference 1). Expression of \( C_\mu \) genes downstream to \( C_\delta \) (e.g., \( C_{\gamma}, C_\alpha, C_\delta \)) in
transformed cell lines involves deletion of DNA 5' to the expressed \( C_\mu \) gene (1, 2). Studies of the structure of Ig genes in myelomas or hybridomas (reviewed in
references 3 and 4) have led to the conclusion that the isotype switch is mediated
by DNA recombination between tandemly repeated switch (S) sequences located
5' to each \( C_\mu \) gene, with the exception of \( C_\delta \) production (5, 6). Cloned cell lines,
including BCL, B1 (7), simultaneously express both \( \mu \) and \( \delta \) genes in the same
unrearranged DNA context as in \( \mu \)-producing cells, and therefore, must produce
these isotypes by alternative RNA processing and/or termination of a 26-kb
RNA transcript (7-11).

Mitogen- or antigen-activated cells are reported to express IgM in combination
with isotypes other than \( \delta \) (12-18). Southern blot analyses have raised the issue
of whether these normal cells use downstream \( C_\mu \) genes, either singularly or in
combination, in the same manner as plasmacytomas and hybridomas. Yaoita et
al. (17) presented evidence that \( C_\mu \) is not deleted in surface IgM* IgE* (sIgM*sIgE*)
spleen cells from SJL/J mice infected with parasites. Their finding
that all \( C_\mu \) genes were retained in the germline context suggested that the
expression of IgM and IgE is mediated by the splicing of an 180-kb RNA

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Abbreviations used in this paper: s, switch region; sIg, surface Ig; UT, untranslated region.
transcript. Because of the induction of avid Fc receptors for IgE after infection of SJA/9 mice with such parasites, there is a strong possibility that the majority of the ~10% slgE+ cells were not synthesizing IgE, but were absorbing it from the culture medium. This hypothesis is strongly supported by recent data of Katona et al. (19). Studies by Perlmutter and Gilbert (18) also support the long-transcript model. Using a combination of cell sorting, Southern blotting, and sandwich RNA hybridization, they concluded that slgG1+ splenic cells have long RNA transcripts generated from unrearranged DNA that contain both γ and μ sequences. However, as in the case of the report by Yaoita et al., their interpretations depend upon cell homogeneity. For example, they claimed to have successfully sorted 1–3% slgG1+ cells to 99% purity, yet no data were shown to estimate the level of contaminating slgM+ cells in their slgG1+ population.

The mechanism of double isotype production could give insights into the genetic regulation of Ig synthesis in differentiating B cells. To analyze such mechanisms requires a constitutively expressing clonal analogue. In our accompanying paper, we described a switch variant derived from the BCL1.B1 in vitro line in which each cell expresses both surface IgM and surface IgG1 and also secretes both isotypes. The IgM and IgG1 share the same idiotype and use the same VDJ rearrangement. In this paper, we present evidence, based on the Cγ gene context of several independently isolated IgM/IgG1-producing clones (collectively termed BCL1.B), that both μ and γ1 heavy chains are transcribed in germline DNA configuration from a single copy of chromosome 12.

**Materials and Methods**

**Cell Lines and Subcloning.** The derivation of the two BCL1.B subclones, BCL1.2.62 (IgM producer) and BCL1.2.58 (IgM/IgG1 producer), is described in the accompanying paper. BCL1.2.54 is a sister subclone of BCL1.2.58. For DNA analysis, we have employed additional independently derived IgM/IgG1 subclones of the parental BCL1.B1 line. The subclone BCL1.13.92 was one of the BCL1.B subclones obtained at a frequency of 1.35 x 10^-2 (12/888) by depositing one cell per well using a FACS III. The medium used for subcloning is the same as described in the accompanying paper. The subclone BCL1.6.1 is a subclone of BCL1.2.58, derived in the same way. The subclones BCL1.15.9 and BCL1.15.19 were two of the seven BCL1.B2 subclones derived similarly at a frequency of 5 x 10^-3 (7/1429), except that no WEHI 274 SN was added to the medium. As in the case of BCL1.2.58, all subclones except BCL1.6.1 secrete more IgM than IgG1 and preliminary data of surface immunofluorescence indicate that all subclones express slgM and slgG1. BCL1.6.1 secretes more IgG1 than IgM (Y.-W. Chen et al., unpublished data).

**Southern Hybridization Analysis.** Procedures for genomic DNA isolation and blotting were described in the preceding paper. All washings were done in 3x SSC plus 0.1% SDS, three times at room temperature, followed by washing in 0.1x SSC, 0.1% SDS at 42°C for 1 h, with the exception of the pre (see probes) probed filter, which was washed at 65°C. Restriction endonucleases were purchased from Boehringer Mannheim Biochemicals (Indianapolis, IN), New England Biolabs (Beverly, MA), and Bethesda Research Laboratories (Gaithersburg, MD) and used according to the manufacturer’s instructions. Electrophoresis was carried out as described in the accompanying paper (in 1% agarose at 40 V for 18 h).

**Probes.** Genomic or cDNA probes were prepared by gel isolation (20) of restriction fragments from previously characterized recombinant clones, except for py1 and pe where the whole plasmids were used. To insure that no repetitive sequences were present in the probes, particularly in fragments derived from introns, DNAs were digested with various
enzymes and subjected to Southern analysis with $^{32}$P-labeled mouse genomic DNA as a probe. Only nonhybridizing fragments were employed for further experiments.

Relative positions of the probes are shown in Figs. 2, A–R and 6, S–U. Ali DNAs were labeled by nick translation (21) to a specific activity of ~$10^6$ cpm/µg. Probe A: A 700-bp Pvu II/Pst I fragment of pu3741 (cDNA clone) (22) containing 18 bp of C,3, the entire C,2 and half of the C,4 region of $\mu$ chain mRNA. Probe B: A mixture of 1.35-kbp and 1.25-kbp Hha I/Bam HI fragments from pB2 (genomic clone) (P. Fell, personal communication) containing the C,4, C,2, C,3, and C,4 exons of C,4. Probe C: A 900-bp Pst I/Pst I fragment of p5451 (cDNA clone) (23) containing C,1, $\delta$, C,3 and the secreted carboxyl terminus ($\delta$s) of $\delta$ chain mRNA. Probe D: A 1.3-kbp Bam HI/Bam HI fragment of pCp13 (genomic clone) (24) containing the carboxyl terminal membrane (M) exons $\delta$M1 and $\delta$M2 of the C,6 gene. Probe E: A 1.2-kbp Eco RI/Eco RI fragment of $\gamma$3-13 (genomic clone) (25) containing C3-Cy3 intronic sequences. Probe F: A 1.0-kbp Eco RI/Eco RI fragment of $\gamma$3-13 (25), located downstream of probe E. Probe G: A 2.0-kbp Hind III/Hind III fragment of pH311 (subcloned from genomic phage $\gamma$3-25) (25) containing 5' flanking region of the Cy3 gene. Probe H: A 1.0-kbp Xba I/Hind III fragment of pJW7 (genomic clone) (26) containing the 5' flanking region of the Cy3 gene. Probe I: A 473-bp BstE II/Sph I fragment of pDRI (genomic clone) (27) containing most of C,3 and 3' untranslated region (UT) of the Cy3 gene. Probe J: A 1.4-kbp Xba I/Hind III fragment of pJW7 (genomic clone) (26) containing Cy3, M2 segment and 3' UT. Probe K: A 1.0-kbp Sac I/Hind III fragment of $\gamma$1-6 (genomic clone) (25) containing the flanking region 5' to $\delta$I (switch region of Cy1 gene). Probe L: A 1.7-kbp Xba I/Eco RI fragment of py1 (genomic clone) (27) containing the 5' flanking region of the Cy1 gene (3' to the Cy1 region). Probe M: py1 (27); pBR322 plasmid containing a 6.6-kbp Eco RI insert of the entire Cy1 gene and its 5' and 3' flanking regions. Probe N: A 2.1-kbp Xba I/Sac I fragment of py1 (genomic clone) (27) containing the Cy1 structural gene. Probe O: A 1.2-kbp Sac I/Eco RI fragment of py1 (genomic clone) (27) containing the 3' flanking region of the Cy1 gene. Probe P: A 1.0-kbp Bam HI/Kpn I fragment of py2b (11') (cDNA clone) (28) containing the entire coding sequence of $\gamma$2b chain message. Probe Q: pC (29); pBR322 plasmid containing a 4.4-kbp Bam HI insert of the Cy structural gene and its 5' and 3' flanking regions. Probe R: A 900-bp BstE II/BstE II fragment of pC(1558) (cDNA clone) (30) containing C,1, C,2, and most of C,5 of a chain mRNA. Probe S: A 2.0-kbp Bam HI/Eco RI fragment of pJ,3,4,4 (subcloned from genomic clone GH1A-127) (31) containing J,3,4,4 and ~1.5 kb of 3' flanking sequence. Probe T: A 674-bp Eco RI/Hind III fragment located just 3' to probe S subcloned from genomic clone CH-28.289.1 (27; P. W. Tucker, unpublished data). Probe U: A 760-bp Hind III/Hind III fragment located just 3' to probe T (subcloned from genomic clone CH-28.289.1) (P. W. Tucker, unpublished data). Probe V: 1.774-bp Sph I/Bam HI fragment of pDRI (26) containing the entire C,4 coding region and 3' UT of the secreted terminus.

Karyotyping. Cells from the BCL, B, and BCL, 2.58 lines were grown to exponential phase and cells were harvested for karyotypic G-banding analysis (32, 33).

Densitometry. For band quantification, autoradiographs were scanned with a densitometer (model GS 300, Hoefer Instruments), and densities were calculated using a Bio-Rad model 33E2A integrator.

**Results**

*BCL, B, and BCL, 2.58 Cells Carry Two Copies of a Translocated Chromosome 12*. Two reports (34, 35) of the karyotype of the in vivo BCL, cell line were in conflict with respect to the copy number and constitution of the IgH-bearing chromosome 12 (36). The single J,3 rearrangement observed in the Eco RI blots of the in vitro lines (Fig. 5 of companion report) was consistent with either a single copy of VDJ or multiple copies of the same VDJ. Resolution of this question, imperative for evaluation of the Southern blotting data presented...
below, required a careful cytogenetic evaluation of the in vitro–adapted parental and variant lines.

Chromosome analysis of BCL1.B1 and one of the IgM/IgG1-producing subclones, BCL1.2.58, was performed by Giemsa banding techniques. The modal chromosome number in BCL1.B1 was 62 (with 55–63 chromosomes in 52 cells analyzed). The modal chromosome number in BCL1.2.58 was 63 (57–66 chromosomes in 65 cells analyzed). We karyotyped 25 cells from BCL1.2.58 and 19 cells from BCL1.B1. We found that the in vitro BCL1.B1 line has two copies of chromosome 12 per cell. These two chromosomes appear to be identical, and both have an unusual translocation to chromosome 16 [t(12;16)], which carries the λ light chain gene (37) (Fig. 1b). Likewise, in BCL1.2.58, 24 out of 25 cells carry two t(12;16) chromosomes (Fig. 1c). One of 25 cells has only one t(12;16), probably due to a random loss of this chromosome during the preparation of the slides. It appears that at the microscopic level both t(12;16) chromosomes identified in BCL1.2.58 are indistinguishable from those of BCL1.B1. One normal chromosome 16 was found in every cell karyotyped.

The breakpoint on chromosome 12 is in the distal region (12F2), telomeric to the Vμ region cluster (Fig. 1a) (36, 38). The breakpoint on chromosome 16 is at a region proximal (16B3) to the centromere, based on the ideogram proposed by Nesbitt and Franke (39). Presumably, this would translocate λ genes to chromosome 12, although their definitive band location on chromosome 16 has not been established. Therefore, heavy chain expression in BCL1.B1 and BCL1.B2 is derived from either one or two copies of an apparently identical translocated chromosome 12, but the breakpoint of the translocation is 5′ to the rearranged Vμ gene(s). Light chain expression (λ3) could conceivably be generated from either the translocated or normal chromosome 16.

Strategy for Determining the Jμ, Cμ Gene Context of BCL1.B1 and BCL1.B2. In the accompanying paper we have shown that all BCL1.2.58 cells synthesize both IgM and IgG1, and both isotypes carry the same serologically defined idiotype. To determine whether the expression of μ and γ1 genes is allelically excluded and, if so, the DNA context of the Cμ locus, we have carried out an extensive overlapping Southern blotting analysis of BCL1.B1, BCL1.2.58 and several other independently derived IgM/IgG1-producing subclones (Materials and Methods). Fig. 2 summarizes the probes and restriction digestions employed with respect to the composite germline Cμ map of Shimizu et al. (25). Considerable care was taken to insure the absence of repetitive sequences.

All Cμ Alleles Are Present in Germline Configuration. As shown in Fig. 2 and lane 1 of Fig. 3, Bam HI cleaves within Cμ, generating a germline 9.4-kbp 5′ fragment that spans the Sμ region, and a 10.5-kbp 3′ fragment that extends into the Cδ locus. Only these two germline bands are present in BCL1.B1 (lane 2), BCL1.2.62, an IgM-secreting subclone (lane 3), BCL1.2.58 (lane 7), and in four other BCL1.B2 subclones (lanes 4–6, 8). As expected from the published maps of the Cμ-Cδ region, rehybridization of this blot to Cδ (probe C) detected the 10.5-kbp fragment, insuring that no rearrangement had taken place between Cμ and Cδ or within Cδ (data not shown). Similarly, Eco RI digests probed for Cμ gave only the 12.5-kbp germline fragment in all DNAs. From these results, in
Figure 1. Translocation of the IgH-bearing chromosome 12 to the Igλ-bearing chromosome 16 in both alleles of BCL₁, B₁ and BCL₁, 2.58 cell lines. (A) Representative normal chromosomes 12 and 16. Indicated on the schematic ideograms (39) are the mapped positions of heavy chain C and V loci (38). The λ genes on chromosome 16 have not been precisely mapped. (B) Representative pair of t(12;16) alleles from the IgM-producing parental line. The translocation breakpoint (12F2;16B3) is denoted by a solid horizontal line on the ideogram. (C) Representative t(12;16) from an IgM/IgG₁ variant cell line.
Figure 2. Summary of genomic Southern hybridization analyses of the IgH allele responsible for both IgM and IgG1 production. The map in the center is to the scale according to Shimizu et al. (25). Structural genes are shown as closed boxes and corresponding switch recombination regions are shown as open boxes. Above the map, solid lines (1–24) depict the location and length of the restriction fragment (or fragments, as indicated by redundant numbers) that hybridize to the probes whose size and position are indicated below the map as narrow boxes (A–R). Dashed lines above the map represent fragment sizes inferred by crosshybridization. The wavy line represents a segment of repetitive DNA that, in addition to the expected fragments (fragments 5 and 6), yielded many other bands that migrated identically in all DNAs. Numerous attempts to confirm this 7.9-kbp repetitive region employing alternative digestions and probes were unsuccessful. The table below the map correlates fragment location with its size and the enzyme(s) and probe(s) used in a particular experiment. Most of the data were generated from the complete panel of BCL3-B2 subclones described in Materials and Methods.
EXPRESSION OF IgM AND IgG1 WITHOUT GENE REARRANGEMENT

FIGURE 3. Analysis of Cy gene context. High molecular weight DNAs were digested with Bam HI (see Figs. 2 and 6 for relative location of sites), and were fractionated and blotted as described in Materials and Methods, then were hybridized with Cy (probe B). Lane 1, BALB/c liver DNA; lane 2, BCL, B1; lane 3, BCL, 2.62; lane 4, BCL, 15.19; lane 5, BCL, 15.9; lane 6, BCL, 13.92; lane 7, BCL, 2.58; lane 8, BCL, 2.54. kb markers are shown in margin.

conjunction with data from Kpn I digestions presented below, we conclude that no rearrangement involving Sµ, Cy, or Cδ alleles contribute to double production of µ and γ1 in BCL1.B2.

All Cµ Genes 3′ to Cµ, including Cγ1, are in Germline Configuration. The lack of Cµ rearrangement suggested that γ1 expression in BCL1.B2 subclones does not occur by prototypic class-switch recombination. To resolve the issue directly, we carried out an exhaustive set of CH probings, which overlapped the entire region (~100 kbp) between Cδ and Cγ1 as well as the DNA downstream to Cγ1. The complete analysis was performed on Balb/c liver, BCL1.B1, BCL1.2.62 and BCL1.2.58, and partial analyses were carried out on additional BCL1.B2 subclones. The data are summarized in Fig. 2, with the most crucial blots for the region between Cγ3 and Cγ1 presented in Fig. 4. Digestion with Hind III generates a diagnostic fragment (fragment 15 in Fig. 2) which spans the γ1 switch region and generally detects rearrangement of this locus. This is shown in Fig. 4a by the two rearranged bands (15 and 16 kbp) in the control digestion of an IgG1 secreting hybridoma (lane 1). In contrast, we detect only the germline band of Cγ1 (23 kbp) and the more faintly crosshybridizing germline fragments of Cγ2a, Cγ3 and Cγ2s (9.2, 6.6, and 6.4 kbp, respectively) in liver (lane 2), BCL1 IgM producers (lanes 4 and 5) and BCL1.B2 (lanes 3, 6–8). Likewise, with the more upstream probes L, K and J (Fig. 4b–d), the BCL1 and BCL1.B2 patterns are identical to those of the liver.

Although no rearrangement occurred between γ3 and γ1, it still remained possible that expression of γ1 might be affected by a recombination between δ and γ3. For example, a deletion within this region would appreciably reduce the length of a putative Jδ-Cµ-Cγ transcription unit. As summarized in Fig. 2, we detected no rearrangements in BCL1.B1 and BCL1.B2 relative to liver within this ~55 kbp area with the exception of only 7.9 kbp of repetitive DNA (between fragment 4 and 7) that was difficult to confirm. Similarly, in the BCL1.B2 cells, downstream genes from Cγ1 to Ca remain in germline context. Taken together, these results strongly argue that DNA rearrangement of Cµ genes is not responsible for expression of γ1 in BCL1.B2 cells.

Deletion of the Majority of the Cµ Locus Has Occurred on the Nonproductive Chromosome 12 of BCL1.B2. As noted above, the Cµ and Cδ genes of both BCL1.B1 and BCL1.B2 are unarranged and are linked on a Bam HI fragment
FIGURE 4. C₃ genes and the region between C₃ and C₄ are unarranged in BCL₁, B₂ double producers. (A) Hybridization of a Hind III digest (Fig. 2, fragment 15) to C₃ probe M. Lane 1, 9B12 (IgG1-secreting hybridoma); lane 2, BALB/c liver; lane 3, BCL₁, 2.58; lane 4, BCL₁, B₁; lane 5, BCL₁, 2.62; lane 6, BCL₁, 2.54; lane 7, BCL₁, 15.92; lane 8, BCL₁, 15.9. (B) Hybridization of an Xba I digestion (Fig. 2, fragment 14) to C₃-C₄ intronic probe L. Lane 1, BCL₁, 2.62; lane 2, BCL₁, B₁; lane 3, BCL₁, 2.58; lane 4, BCL₁, 6.1; lane 5, Balb/c liver DNA. (C) Hybridization of a Sac I digestion (fragment 13, Fig. 2) to C₃-C₄ intronic probe K. Lane 1, BCL₁, B₁; lane 2, BCL₁, 2.58; lane 3, BCL₁, 6.1; lane 4, Balb/c liver DNA. (D) Hybridization of a Kpn I digestion (fragment 12, Fig. 2) to C₃ 3′ probe J. Lanes are as in B. The additional bands seen in Fig. 4C (15.1 kbp) and 4D (5.6 kbp) are residual hybridization from the previous probeds of the same filters. kb markers are shown for A–D.
FIGURE 5. BCL₁₂ clones carry two different alleles of chromosome 12. Southern blots of Kpn I-digested DNAs (see Fig. 6 for positions of sites) were hybridized in A to probe S (J₅-J₆/₄) and in B to probe B (Cμ). Lane 1, BALB/c liver; lane 2, BCL₁₂₀; lane 3, BCL₁₂₂; lane 4, BCL₁₂₁₅.₁₉; lane 5, BCL₁₂₁₅.₉; lane 6, BCL₁₂₁₃.₉₂; lane 7, BCL₁₂₂.₅₈; lane 8, BCL₁₂₂.₅₄. Cμ and C₃μ genes are not linked in μ only (lanes 4-6, BCL₁₂₂.₆₂) and μγ₁- (lanes 1-3, BCL₁₂₂.₅₈) producing subclones. DNAs were digested with Bgl II and were hybridized to J₅ (probe S) (lanes 1 and 4), C₃μ (probe V) (lanes 3 and 6), and a mixture of probes S and V (lanes 2 and 5). In Fig. 5c, lanes 2, 3, 5, and 6, the 17 kbp and 7.5 kbp fragments were C₃μ gene crosshybridizations with probe W. The 6.2 kbp fragment is the Bgl I fragment containing VDJ sequences located on the H' allele (see Fig. 6). kb markers are shown.

(Fig. 3). Both lines contain two copies of the t(12;16) chromosome. But a single, apparently identical variable region rearrangement is observed when Eco RI blots of BCL₁₂₂.₅₈, BCL₁₂₂ and BCL₁₂₂.₆₂ DNA are probed with a Jn region fragment (probe S and Fig. 6 of accompanying paper). In addition, a single VDJμ-containing band was obtained in Xba I, Hind III, Bam HI and Bgl I digests of all the BCL₁₂₂ subclones probed with Jn (accompanying paper and data not shown). These data suggested that each BCL₁₂₂ allele possessed an identically rearranged VDJ. However, Kpn I digests revealed a rearrangement of one of the two BCL₁₂₂ alleles with respect to BCL₁₂₀. As shown in Fig. 5a, in addition to the rearranged 17.8-kbp Kpn I fragment found in BCL₁₂₀ (lane 2) and BCL₁₂₂.₆₂ (lane 3), we detected a 12.5-kbp fragment in BCL₁₂₂.₅₈ (lane 7). The identically rearranged band is present in the other BCL₁₂₂ subclones (lanes 4-6, 8), suggesting that all BCL₁₂₂ lines, although independently cloned, were derived from a common parental variant. When a similar Kpn I blot was probed with Cμ (Fig. 5b), only a single hybridizing band, corresponding to the
17.8-kbp fragment from the unrearranged allele of BCL1.B1, was detected in BCL1.B2. To map the rearrangement more precisely, we performed similar Kpn I blots with probes (T and U) that extend directly from the Eco RI site in the Jn-Cμ intron. In all cases, only the 17.8-kbp fragment hybridized (data not shown). Since there is only a single Eco RI band in Jn3Jα4 blots, the rearrangement had to occur just 3’ (<50 bp) to the Eco RI site in the Jn-Cμ intron. Otherwise, the 12.5-kbp band would have been detected by probe T or U in BCL1.B2.

Hybridization of the Kpn I digests to probe M had shown that the 12.5-kbp fragment did not contain Cγ1 (Fig. 2, fragment 18). However, there are a number of Kpn I sites between Cγ3 and Cα1 in germline DNA (25), and there is a slight possibility of fragment comigration in the analysis of Fig. 4. Therefore, we digested BCL1.B1 and BCL1.B2 DNAs with Bgl I, an enzyme that generates a fragment that spans the entire Cγ5-Sγ1 germline region (Fig. 2, fragment 20a), and cuts at a single site between Jn and Cα, ~480 bp downstream of the Eco RI site of the rearrangement junction (P. W. Tucker, unpublished results). As seen in Fig. 5c, hybridization either separately or jointly with JH (probe S) and Cγ3 (probe V) gave different sized bands (30 and 32 kbp, respectively). These data prove that Jn and Cγ1 are not linked on either allele of the IgM/IgG1 producing variants.

Simultaneous Expression of μ and γ1 in BCL1.B2 is Allelically Excluded. The above results, taken with the analyses of the Cα genes, suggest that the observed rearrangement on one allele of BCL1.B2 is unusual. It deletes, at a minimum, part of Jn-Cμ intron, all Cμ and, by direct inference of the Cμ-Cδ linkage (Fig. 3), Cδ. However, the germline patterns (Figs. 2 and 4) and the analysis of Fig. 5c show unequivocally that this rearrangement is not accomplished by recombination into downstream Cα sequences. Therefore, the 3’ side of the rearrangement in BCL1.B2 appears to be unrelated to Ig C H DNA, yet it is not large enough to be detected cytogenetically.

A proposed map of the two IgH alleles in BCL1.B2 is shown in Fig. 6. The model predicts that downstream Cα genes on the productive chromosome (i.e., on the H+ allele) exist in single copy in BCL1.B2 but in double copy in BCL1.B1, BCL1.2.62, or liver. On the other hand, Jn genes should exist in double copy in parental, variant, and germline DNA. To test this hypothesis, we hybridized Eco RI digests (Fig. 7a) of the appropriate DNAs to a mixture of Jn (probe S) and Cγ3 (probe V), and Hind III digests (Fig. 7b) to a mixture of Jn (probe S) and Cγ1 (probe M). The hybridization intensities were quantified by densitometry and the ratio of Jn/Cγ3 (4 kbp:18 kbp, Fig. 7a) and Jn/Cγ1 (2.55 kbp:23 kbp, Fig. 7b) were determined. As shown in Table I, the Jn/Cγ3 and Jn/Cγ1 ratios in BCL1.B1, BCL1.2.62 are approximately twice those in the IgM/IgG1-producing variants, BCL1.2.58 and BCL1.13.92. We conclude that allelic exclusion is operative in BCL1.B2 in generating both μ and γ1 chains from a single rearranged VDJ.

Discussion

Two major conclusions can be drawn from the results of our studies: (a) IgG1 is expressed in the BCL1.B2 clones in the absence of DNA rearrangement of the constant region genes; and (b) the heavy chains of both IgM and IgG1 are
**Figure 6.** Schematic representation of the productive (H+) and nonproductive (H-) heavy chain alleles of BCL and B2 double producers. Location and lengths of probes S, T, U, and B are indicated. The hatched DNA to the right of the H- Eco RI site is of undetermined (?) origin.
expressed from a single rearranged VDJ segment on the same chromosome 12. Therefore, we conclude that simultaneous production of IgM/IgG1 in BCL1.B2, as in the case of IgM and IgD in BCL1.B1, is controlled exclusively at the RNA level.

Our findings provide the first example of allelically excluded, double isotype expression in a neoplastic B cell clone. A similar conclusion was drawn to explain dual μ and γ2b production in a derivative of a μ-producing Abelson murine leukemia–transformed cell line (40). Contrary to the initial report, it is now clear (41, 42) that γ2b synthesis in this line is accompanied by deletion of sequences between Jμ and Cγ2b, and thus cannot be explained by differential RNA processing. Our data also support the observations of Yaoita et al. (17) and Perlmutter and Gilbert (18), who used purified populations of normal lymphocytes. The caveats associated with these studies (19) are overcome here since we have shown that virtually all cells in BCL1.2.58 synthesize, express, and secrete IgM and
IgM and IgG1 without gene rearrangement

Furthermore, the clonal BCL1.B2 lines have provided the opportunity for a more extensive analysis of the DNA context. In addition to establishing germline configuration of sequences anticipated to undergo rearrangement during switch recombination (e.g., $S_\alpha$, $C_\mu$, and $S_\gamma$), we have also shown that the remainder of the $C_\mu$ locus is unrearranged on the productive allele. This observation argues against the hypothesis that $C_\mu$ genes might be translocated, via nonclassical switch sequences and deletion of $C_\delta$, to a position downstream to $C_\mu$, possibly replacing $\delta$ with another isotype (7, 11).

Although we have provided strong evidence for use of a single VDJ, it resides on a chromosome 12 that has undergone an unusual translocation, distal to the Ig locus, with chromosome 16. At the microscopic level, the t(12;16) appears to be identically duplicated in both the BCL1.B1 and BCL1.B2 cell lines. However, our blotting data define the nonproductive t(12;16) allele ($H^-$ in Fig. 6) by virtue of its loss of Ig-related sequences 3' to the Eco RI site within the JH intron. These findings have important implications in considering both the derivation of the in vivo BCL1 leukemia, its subsequent in vitro adaptation, and the eventual mechanism for allelic exclusion in BCL1.B2. The in vivo BCL1 leukemia cells appear to have a stable karyotype, with the exception of chromosome 12. Two early reports (34, 35) are in agreement with our data (Y.-W. Chen and G. V. Dev, unpublished results), with respect to the modal chromosome number (35 chromosomes in reference 34 and our data, and 36 chromosomes in reference 35). However, Schroeder et al. (34) reported a single normal chromosome 12 and a translocated chromosome 12 to an unidentified recipient in early passages of the line. One year later, Voss et al. (35) found no evidence for normal copies of chromosome 12, but identified three translocated alleles. We observed a single copy of the same t(12;16) in the in vivo line (Y.-W. Chen and G. V. Dev, unpublished results) that is duplicated in the in vitro BCL1.B1 and BCL1.B2 lines, both of which have a modal chromosome number of ~60. We suggest that the precursor to the original leukemic cell carried a normal chromosome 12 as nonproductive and retained it during early passages, at which time the productive chromosome 12 underwent translocation(s). Adaptation to cell culture resulted in a duplication of most of the karyotype, including t(12;16), and may have required a second more subtle event (e.g., somatic mutation), which was undetectable at the cytogenetic or DNA rearrangement level, to effect allelic exclusion in BCL1.B1. Alternatively, both of the t(12;16) alleles remain active in BCL1. If the former is true, then the third event, the rearrangement 3' to VDJ on the $H^-$ allele of BCL1.B2, is not required for allelic exclusion, but may instead reflect some trans-acting regulatory requirement for switching the productive allele from $\mu/\delta$ to $\mu/\gamma 1$. The significance of this DNA rearrangement is underscored by the fact that all independent BCL1.B2 variants maintain it.

Aside from its unusual karyotype, do the BCL1.B2 variants have a counterpart amongst normal B cells? Based on its surface Ig phenotype, its low level of constitutive IgM secretion (reviewed in reference 43), and its heavy chain gene transcription profile (44), the parental BCL1.B1 line appears to represent an immature B cell. It has been employed as a model for numerous functional studies by virtue of its ability to undergo further differentiation when cultured...
with LPS (45), anti-Ig (46), or T cell-derived lymphokines (47). The fact that all BCL1.B2 variants isolated for IgG secretion secrete both IgM and IgG1, as well as express them on their surface, may reflect their derivation from a single precursor. It may also denote a basic difference between these cells and the nonsecreting memory cell populations analyzed by others (17, 18) at the molecular level. Regardless of whether these differences in mode of expression are real or are a consequence of the transformed state, the BCL1.B2 phenotype shows that high expression of the secreted and the membrane form of γ mRNA can be generated from Cμ genes in germline configuration.

Finally, with regard to mechanisms, the only plausible explanation for the present data is that μ and γ1 mRNA are expressed with a common VDJ gene by alternative RNA processing. This could be accomplished by a discontinuous mechanism in which the RNA polymerase translocates from the template to transcribe discrete segments of DNA, as proposed for trypanosome variable antigen (48) and certain viral genes (49, 50). Alternatively, there could be a continuous transcription mechanism (i.e., long transcript model), such as that apparently used by the drosophila bithorax locus (51), which has been invoked by others (17, 18) to account for their results in normal B cells. In the latter scenario, the γ1 chains could then be translated from mRNA derived by processing a primary transcript that includes sequences from both Cμ and Cγ1 genes. The μ mRNA may be derived either from an identical transcript of ~120 kb or from one that terminates in the intervening sequence between Cμ and Cδ. Based on nuclear transcription studies in BCL1.B1 cells (44) and other IgM/IgD double producers (52, 53), we favor the latter alternative. This would require differential regulation of transcriptional termination, perhaps at two points. First, the majority of the RNA polymerases would unload 3′ to Cμ, since in BCL1.B2 cells, μ RNA abundance is greater than γ1 RNA abundance (accompanying report and data not shown). Second, a small proportion of the polymerases would read through the μ termination region and exit the template downstream of the Cμ gene to be expressed (Cγ1 in BCL1.B2). A choice in the second polymerase unloading event may dictate (and simplify) not only the subsequent RNA splicing decision, but may also bear on the acquisition of isotype commitment; i.e., once a cell expresses an isotype other than IgM and IgD, it is then committed and restricted to secretion of that isotype upon stimulation (54).

The best clonal example of this model is the 1.29 B cell lymphoma, which undergoes spontaneous and/or inducible switch recombination from IgM to IgA (55). The Cα gene is preferentially open, as defined by hypomethylation, in the IgM-synthesizing cells that are committed to switch to this isotype (56). Similarly, in the transition of BCL1 to BCL1.B2, Cγ1 appears to be exclusively selected. Perhaps transcription through, and equally important, termination beyond a Cμ gene (Cγ1 in BCL1.B2) is critical in inducing an active chromatin structure for subsequent expression of that same Cμ gene. The resulting prediction is that BCL1.B2 cells, on receiving the appropriate signal, would undergo exclusive switch recombination to Cγ1. This cell line, therefore, provides us with the opportunity of testing the mechanisms of double isotype production and its consequences.
EXPRESSION OF IgM AND IgG1 WITHOUT GENE REARRANGEMENT

Summary
In our accompanying paper, we described a switch variant (BCLI .2 .58) that expresses membrane and secreted forms of IgM and IgG1. Both IgM and IgG1 share the same idiotype and use the same VDJ rearrangement. Here, a detailed Southern blot analysis of the entire constant region of the Ig heavy chain (Ig C\text{H}) locus of parental (BCLI .B1) and variants (BCLI .B2) DNA showed no detectable rearrangement. Similar analysis of the J_{\text{H}}-C\text{H} region led to the conclusion that two heavy chain alleles present in the IgM/IgG1-producing variants carried the same VDJ rearrangement but differed in their 3' flanking regions. One chromosome 12 did not carry any Ig C\text{H} genes, whereas, the other chromosome 12 carried one copy of C\text{H} genes. In BCLI .B1, however, each of the chromosome 12 alleles carried a full copy of C\text{H} genes. Karyotypic analysis confirmed the presence of two translocated t(12:16) chromosomes in both BCLI .2 .58 and BCLI .B1 cells, with a break 5' to the V\text{H} locus at the distal region (12F2) of chromosome 12, and at the proximal region below the centromere (16113) of chromosome 16. We conclude that double production of IgM and IgG1 in BCLI .B2 is accomplished by transcription of the corresponding C\text{H} genes in germline configuration using a single VDJ on the same chromosome 12.

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Note added in proof: Results of sandwich hybridization and nuclear run-on transcription are consistent with the long transcript model for dual \mu and \gamma1 expression in BCLI .B2.

References


