REARRANGEMENT OF EXOGENOUS IMMUNOGLOBULIN \( V_H \) AND DJ\( _H \) GENE SEGMENTS AFTER RETROVIRAL TRANSDUCTION INTO IMMATURE LYMPHOID CELL LINES

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The variable regions of Ig and T cell receptor chains are encoded in the germ line by discrete elements that are brought together by site-specific recombination during lymphoid differentiation (1, 2). As a consequence of this process, a diverse set of variable regions can be specified by a relatively small number of gene segments. In the case of Ig H chains, for example, the variable regions are encoded by three germ line elements: \( V_H \), D, and \( J_H \). During B cell differentiation, individual segments from each group are joined to form a complete \( V_H\)-D-\( J_H \) variable region (3–9).

Unrearranged Ig and T cell receptor gene segments are accompanied by similar sequences that lie near the sites of recombination and are presumed to mediate rearrangement (3, 4, 10–15). These putative recombinational signals consist of three elements: a heptamer sequence, a spacer region, and a nonamer sequence. The heptamer and nonamer sequences are highly conserved, both among gene families and among vertebrate species (1, 2, 16, 17). The spacer regions are less well conserved with respect to sequence, but in length they fall into two classes of ~12 and 23 bp. Gene segments that are associated with 12-bp spacer regions normally recombine with segments that carry 23-bp spacer regions (3). The generality of these observations suggests that rearrangements of all Ig and T cell receptor gene segments are catalyzed by a common apparatus.

While the structural features of Ig gene segments have long been defined, the mechanism of rearrangement remains unknown. It has recently been demonstrated that exogenous Ig or T cell receptor gene segments can undergo rearrangement after they are stably introduced into lymphoid cells (18–22). In one experiment, a retroviral vector was used to deliver unrearranged kappa chain gene segments to a B cell precursor cell line; selection for integration was linked to the activation of a selectable marker, which in turn was dependent on rearrangement (18, 20). These results suggested a functional approach to the study of Ig gene rearrangement, by manipulation of model substrates in vitro and subsequent assay for their recombination in cultured cells. To facilitate this approach, we have devised an assay for the joining of exogenous Ig H chain gene segments in vivo. A retroviral vector is used to deliver the substrate to recipient...
cells; selection for viral integration is independent of rearrangement. We dem-
strate joining of the exogenous segments in cell lines that represent three
distinct stages in B cell ontogeny. In addition, we directly observe that the joining
of H chain gene segments occurs by means of a nonreciprocal recombinational
mechanism. Our results suggest that Ig H and L chain gene segments are joined
by a common mechanism that is more active in B cell precursors than in mature
B cells. The assay described here, which permits selection for retroviral integra-
 tion regardless of rearrangement, should be of particular use in defining the
nucleotide sequence requirements for Ig gene assembly.

Materials and Methods

DNA Constructions and Probes. The retroviral vector pDOL* (23) was a gift of Richard
Mulligan, Whitehead Institute, Cambridge, MA. The vector (see Fig. 1A) is based on
sequences derived from the Moloney murine leukemia virus (Mo-MLV)1, including: the
5' and 3' long terminal repeats (LTRs), which are required for initiation and polyadenyl-
ation of viral transcripts and for viral integration; the minus and plus strand primer-
binding sites necessary for replication (24, 25); and sequences required for packaging of
viral RNA (Ψ site) (26, 27). The 5' splice donor sequence has been mutationally inactivated
to prevent the generation of subgenomic RNA. Located between the LTRs is a Bam HI–
Hind III fragment containing the SV40 early promoter and origin of replication. Imme-
diately adjoining this fragment is a 1,321-bp Hind III–Eco RI fragment containing the
neomycin (neo) resistance gene of Tn5 (28, 29); in this vector the neo gene is under
control of the SV40 early promoter. Also present is an Eco RI–Xho I fragment containing
the pBR322 origin of replication.

The substrate for Ig H chain gene rearrangement, pLJHCR, was derived from pDOL*
by the insertion of a 2.0-kb cassette at the unique Bam HI site of the vector. This cassette
is diagrammed in Fig. 1B, and contains three elements. The 750-bp Bam HI–Eco RI
fragment is the former Bgl II–Hind III fragment of p40E4-2-5.2 (30); it contains the
recombined Dasp and Jα3 Ig gene segments of BALB/c mouse. The Vn-containing Eco
RI–Bam HI fragment was derived from the 246-bp Eco RI–Pst I fragment of p40E4-2-
26-8.0 (30); it contains the terminal 204 bp of the Vn81X coding sequence from BALB/c
mouse (31) and 42 bp of 3' flanking DNA. Between these two segments of mouse DNA
we inserted the xanthine–guanine phosphoribosyl transferase gene (gpt) of Escherichia coli
(32–34), which was derived from the 1,057-bp Hind III–Bam HI fragment of pPT-1 (32)
by the attachment of synthetic Eco RI linkers. In pLJHCR, the gpt gene lies in antisense
orientation relative to the 5' LTR.

To prepare the gpt probe, pLJHCR was cut with a mixture of Eco RI and Kpn I, and
the resulting 740-bp fragment was purified by electrophoresis through 1.0% agarose. To prepare the neo probe, pLJHCR was cut with Hind III and Eco RI, and the resulting 1,321-bp fragment was isolated by electrophoresis through 0.8% agarose. The locations
of these probes with respect to the pLJHCR restriction map are indicated in Fig. 3.

All plasmids were propagated as monomers in the E. coli strain DH1 (35). Plasmid DNA
was prepared by a detergent lysis procedure (36) and purified over two CsCl equilibrium
gradients.

Cell Lines. The Ha-MSV-transformed cell line HAFTL-1 (37), the Ab-MuLV–trans-
fomed cell lines 40E4-2 (30) and PD31 (38), the B cell lymphomas M12.4.1 clone 4.5
(39) and A20-2f (40), and the B cell hybrid line SP2/0 (41) were cultured in RPMI 1640
medium supplemented with 10% FCS and 50 μM 2-ME (RPMI-10). The cell lines Ψ-2
(26) (a gift of Richard Mann, Whitehead Institute, Cambridge, MA) and NIH-3T3 were

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1 Abbreviations used in this paper: LTR, long terminal repeats; Mo-MLV, Moloney murine
leukemia virus.
propagated in DME supplemented with 10% FCS (DME-10). Lymphoid cells were cloned by limiting dilution at a concentration of 0.2 cell/microtiter well.

**Packaging of Recombinant Retrovirus.** The plasmid pLJHCR was transfected into the Ψ-2 cell line by the calcium phosphate technique of Graham and van der Eb (42), as modified by Parker and Stark (43), except that salmon sperm DNA was omitted from the transfection cocktail. 2 d after transfection, the cells were trypsinized, suspended in fresh DME-10, and diluted 10-fold into DME-10 containing G418 at 1 mg/ml (28). At 5, 8, and 11 d after transfection, cells were fed with fresh medium containing G418 at 1 mg/ml. Clones of G418-resistant (G418') cells were evident by 14 d after transfection; these were transferred to individual microtiter wells and propagated in DME-10 containing G418 at 1 mg/ml. To harvest recombinant LJHCR virus, stably transfected Ψ-2 cells were grown in a 78.5-cm² dish in the presence of G418 at 1 mg/ml until the cells had reached 75% confluence. The selective medium was then removed and 10 ml DME-10 was added. After incubation for 16 h, the culture supernatant was collected and filtered through nitrocellulose (0.45-μm pore size). The supernatant was stored in 1-ml aliquots at -70°C. Viral stocks were stable under these conditions for at least 6 mo.

Virus was quantitated by infection of NIH-3T3 cells followed by selection in G418, as described by Cepko et al. (44). Viral titers are expressed as the number of G418' NIH-3T3 colonies obtained per ml Ψ-2 culture supernatant (G418' cfu/ml).

**Infection of Lymphoid Cell Lines.** Cultures of lymphoid cells at 1-2 × 10⁶ cells/ml were collected by centrifugation and suspended in RPMI-10 at a concentration of 10⁷ cells/ml. To infect cells, 1 ml Ψ-2 culture supernatant and 0.1 ml (10⁶) lymphoid cells were combined in a 20-cm² dish and incubated at 37°C in the presence of 8 μg/ml polybrene. After 2.5 h, 3 ml RPMI-10 was added and the culture was incubated for 48 h. Cells were then split 1:5 into selective medium containing G418 at 2 mg/ml. At 5, 8, and 11 d after infection, cells were transferred to fresh selective medium containing G418 at 2 mg/ml. Growth of G418' cells was usually apparent by 14 d after infection.

**Preparation and Analysis of Genomic DNA.** Genomic DNA was prepared as described (45). DNA probes were labeled with ³²P by synthesis from random oligonucleotide primers as described by Feinberg and Vogelstein (46). Hybridization reactions were undertaken in 50% formamide, 0.6 M NaCl, 0.075 M sodium citrate, 0.065 M K₂HPO₄, 0.005 M Na₂-EDTA, 0.02% (each) BSA, Ficoll, and polyvinylpyrrolidone 360, 100 μg of denatured salmon sperm DNA per ml, and 10⁵ cpm of heat-denatured probe per ml for 16-24 h at 42°C. Filters were washed in 0.3 M NaCl, 0.03 M sodium citrate, and 0.1% SDS at 68°C for 45 min; °²P was detected by autoradiography.

**Isolation and Characterization of Genomic DNA Clones.** Genomic DNA from the HAFTL-1/LJHCR-e-I and PD31/LJHCR-m-10 cell lines was digested with Hind III and fractionated by electrophoresis through a preparative 0.8% agarose gel (Bull's Eye preparative gel unit, Hoefer, San Francisco). Selected fractions were pooled and DNA was ligated to λ2001 DNA (47), which had previously been digested with Hind III and Bam HI (Strategene, San Diego, CA). The products of ligation were encapsidated in vitro; the packaging extract (Gigapack, Stratagene, San Diego, CA) was used according to the supplier's instructions. The resultant bacteriophages were propagated in the E. coli strain LE392. Plaques were screened by the method of Benton and Davis (48). Bacteriophage were isolated by two additional rounds of plaque purification.

**Results**

**Structure of the Retroviral Substrate for V[to]-to-DJα Joining.** The recombination substrate used in these experiments, pLJHCR, was constructed in the retroviral vector pDOL⁻ (see Materials and Methods and Fig. 1A) (23). The vector contains the LTR sequences of the Mo-MLV, which are required for integration and transcription of the viral genome, and an element necessary for encapsidation of viral RNA (Ψ site) (26, 27). The vector also carries the neo gene of E. coli (28, 29) under control of the SV40 early promoter.
Two separate Ig sequences are present in pLJHCR; one contains the product of a D-to-J<sub>R</sub> fusion and the other contains a portion of an unarranged V<sub>H</sub> gene, including 42 bp of its 3'-flanking DNA (Fig. 1 B and Materials and Methods). These two segments have been shown to undergo V<sub>H</sub>-to-DJ<sub>R</sub> joining in cultured lymphoid cells (30). The Ig gene segments in pLJHCR lie in opposite transcriptional orientations; between them is located the gpt gene of E. coli (32), in antisense orientation with respect to the 5' LTR.

**Transfection of pLJHCR into Helper Cells and Production of Infectious Recombinant Virus.** The virus encoded by pLJHCR is defective; its propagation requires that a number of viral functions be supplied in trans. The helper cell line ψ-2 (26) expresses all Mo-MLV proteins necessary for viral packaging and replication. To propagate the recombination substrate as a retrovirus, pLJHCR was introduced into the ψ-2 cell line by transfection in the presence of calcium phosphate (42, 43). Stable derivatives of ψ-2 containing pLJHCR DNA were selected in medium containing G418 (28). The resulting G418<sup>+</sup> cell clones were expanded to ~10<sup>7</sup> cells in the presence of G418; the cells were then grown for one doubling time in the absence of G418. The titer of virus in culture supernatants was measured by infection of NIH-3T3 cells and selection in G418 as described in Materials and Methods. Of eight independent G418<sup>+</sup> ψ-2 lines tested, three were found to be stable producers of recombinant retrovirus; viral titers in culture supernatants ranged from 1 × 10<sup>3</sup> to 9 × 10<sup>3</sup> G418<sup>+</sup> cfu/ml. One such cell line, ψ-2/LJHCR-1, was the source of the virus used in the experiments described here.

**Transmission of the LjHCR Virus to Immature B Lymphoid Cells.** To determine whether the LJHCR substrate could be transmitted by infection to immature lymphoid cells, we initially used two cell lines, HAFTL-1 and 40E4-2, representative of cells at early stages of B lymphoid differentiation. The HAFTL-1 cell line was established by transformation of mouse fetal liver with the Harvey murine sarcoma virus (Ha-MSV) (37, 49). This line expresses a number of surface markers characteristic of members of the B cell lineage (50); it undergoes continuing Ig D-to-J<sub>H</sub> rearrangement during propagation in culture (37). The 40E4-2 cell line was established by transformation of mouse fetal liver with the
Abelson murine leukemia virus (A-MuLV) (51). Like HAFTL-1, the 40E4-2 cell line expresses B lymphoid surface markers, but it possesses DJ \(_n\) fusions on both chromosomes and undergoes V\(_{\text{int}}\)-to-DJ\(_{\text{int}}\) joining in culture (30, 52).

These cell lines were infected with the LJHCR virus at a ratio of \(1 \times 10^2\) (infections “a”) and \(1 \times 10^3\) (infections “b”) G418\(^\prime\) cfu to \(10^6\) cells. After growth for 2 d in nonselective medium, cells were transferred to medium containing G418 at 2 mg/ml; G418\(^\prime\) derivatives of HAFTL-1 and 40E4-2 were evident at \(~14\) d. Samples of cells (\(~2 \times 10^7\) ) were taken from the G418\(^\prime\) populations for analysis of proviral DNA. Single cell clones were obtained from the same populations by limiting dilution.

To establish the presence of proviral DNA in G418\(^\prime\) derivatives of HAFTL-1 and 40E4-2, genomic DNA was digested with Xba I, fractionated by electrophoresis in agarose, transferred to nitrocellulose, and hybridized to a neo-specific probe (Fig. 2). The Xba I restriction enzyme was expected to cut LJHCR DNA once within each LTR to yield a single 6.0-kb fragment containing the entire internal proviral sequence (see Fig. 1). Each of the G418\(^\prime\) cell populations we
examine (40E4-2/LJHCR infections a and b; HAFTL-1/LJHCR infections a and b) yielded a 6.0-kb neo-containing fragment (Fig. 2, lanes 4a, 4b, Ha, and Hb) that comigrated with the fragment detected in a mixture of uninfected HAFTL-1 DNA and pLJHCR (Fig. 2, lane H+P). The fragment was not found in DNA from uninfected cells (Fig. 2, lanes 4 and H). In 3 of the 4 infected cell populations examined (40E4-2/LJHCR infections a and b; HAFTL-1/LJHCR infection a), this was the only neo-containing fragment detected (Fig. 2, lanes 4a, 4b, and Ha). In one of the two infected HAFTL-1 pools (HAFTL-1/LJHCR infection b; Fig. 2, lane Hb) at least two neo-containing fragments were found that differed in length from the intact proviral fragment. The additional fragments may have arisen by recombination between internal proviral sequences and neighboring mouse DNA (S. V. Desiderio and K. Wolff, unpublished data).

This observation prompted us to examine the stability of proviral sequences in other infected cell populations. In 14 clones derived from HAFTL-1/LJHCR infection a, and 23 clones derived from 40E4-2/LJHCR infection a, only the 6.0-kb neo-containing DNA fragment was seen (data not shown). Thus, the arrangement of the proviral DNA with respect to flanking sequences appeared to be stable in these cells.

**Joining of Exogenous V\textsubscript{\textit{\textmu}} and DJ\textsubscript{\textmu} Elements in the HAFTL-1 Cell Line.** To detect specific recombination between the V\textsubscript{\textit{\textmu}} and DJ\textsubscript{\textmu} sequences that had been introduced into the HAFTL-1 cell line, we used a direct physical assay, illustrated in Fig. 3. The LJHCR provirus contains three Kpn I restriction sites; one site lies within each LTR and a third site lies within the gpt gene, between the unrearranged V\textsubscript{\textmu} and DJ\textsubscript{\textmu} elements. Thus, digestion of unrearranged proviral DNA with Kpn I should create a 1.9-kb fragment that hybridizes to a gpt-specific probe and a 4.1-kb fragment that is detected by a neo-specific probe (Fig. 3A). Joining of the proviral V\textsubscript{\textmu} and DJ\textsubscript{\textmu} elements should result in an inversion of the intervening DNA. Digestion of proviral DNA with Kpn I after V\textsubscript{\textmu}-to-DJ\textsubscript{\textmu} rearrangement is therefore expected to yield two fragments; a 1.2-kb fragment and a 4.8-kb fragment that hybridizes to both the gpt probe and the neo probe (Fig. 3B).

Genomic DNA from clones of LJHCR-infected HAFTL-1 cells was cut with
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FIGURE 4. Rearrangement of LJHCR proviral sequences in the HAFTL-1 cell line. Genomic DNA (12 μg) from clones of LJHCR-infected HAFTL-1 cells was digested with Kpn I and assayed for V_{H}-to-DJ_{H} joining by hybridization to DNA probes as outlined in Fig. 3. (A) Hybridization to the gpt probe. Lanes a, b, e, and g. DNA from HAFTL-1/LJHCR-a, HAFTL-1/LJHCR-b, HAFTL-1/LJHCR-e, and HAFTL-1/LJHCR-g, respectively. Lane 0, DNA from HAFTL-1. Lanes 1 and 2, DNA from HAFTL-1 to which 23 pg or 46 pg of pLJHCR, respectively, was added before digestion. (B) Hybridization to the neo probe. The filter used in A was washed in 0.5 M NaCl, 0.05 M NaOH, and 0.002 M Na_{2}EDTA for 30 min at 28°C to remove the gpt probe. The filter was neutralized and hybridized to the neo probe. Lanes are designated as in A. The positions of DNA standards (in kb) are indicated.

Kpn I, fractionated by electrophoresis, transferred to nitrocellulose, and hybridized to the gpt probe. Fig. 4 shows the results obtained with four of these clones, designated a, b, e, and g. In all four samples, a major 1.9-kb species was detected (Fig. 4 A, lanes a, b, e, and g). In clone e (and faintly in clone a) a second, 4.8-kb species was found (Fig. 4 A, lanes a and e). When the filter was stripped of the gpt probe and hybridized to the neo probe, a predominant species of 4.1 kb was found in all clones, as expected (Fig. 4 B, lanes a, b, e, and g). In addition, the minor 4.8-kb fragment that was detected with the gpt probe in clones a and e also hybridized to the neo probe (Fig. 4 B, lanes a and e). These results are consistent with the occurrence of V_{H}-to-DJ_{H} joining within the LJHCR provirus. In all, 14 clones of LJHCR-infected HAFTL-1 cells were assayed; in two clones the rearranged provirus was detected. That these rearrangements represent joining of the V_{H} and DJ_{H} elements present within the LJHCR provirus was directly demonstrated by molecular cloning of the recombination products (see below).
Integration of murine retroviruses occurs at a large number of sites in the host genome (53). Therefore, when two cells are infected independently they are likely to differ with respect to their proviral integration sites. Conversely, among the progeny of a single infected cell, the site of proviral integration will be the same. We used this fact to demonstrate that the rearrangement of exogenous Ig sequences occurred after their integration into the HAFTL-1 genome, rather than at an earlier stage in the experiment. Genomic DNA from clones a, b, e, and g was digested with Bam HI, fractionated by electrophoresis, transferred to nitrocellulose, and hybridized to the neo probe. The resulting neo-containing fragments are defined at one end by a Bam HI site within the LJHCR provirus and at the other end by a Bam HI site in the flanking mouse DNA. In the experiment shown in Fig. 5, all four clones share a common 4.4-kb neo-containing Bam HI fragment (sample g shows a minor band at 5 kb, and is probably not derived from a pure cell clone). Thus, at least clones a, b, and e are derived from the same infected cell. This fact, together with the presence of rearranged substrate in clones a and e, but not in b, indicates that rearrangement occurred after retroviral integration. In addition, homogeneous subclones of clone e containing rearranged or unrearranged provirus (see below) showed identical proviral integration patterns, further demonstrating that rearrangement occurred after retroviral integration (data not shown).
Assay for Rearrangement of the LJHCR Substrate in Other Cell Lines. Rearrangement of the LJHCR substrate was assayed in two cell lines that, together with HAFTL-1, represent intermediate states in B cell ontogeny (40E4-2 and PD31), in cell lines derived from mature B cells (M12.4.1 clone 4.5, A202J, and SP2/0), and in a fibroblastoid cell line (NIH-3T3). The 40E4-2 cell line, as described above, undergoes the second step in Ig H chain gene assembly: the joining of V\textsubscript{H} segments to DJ\textsubscript{H} elements (30, 52). The PD31 cell line represents a stage in B cell differentiation after the assembly of H chain genes, and undergoes continuing rearrangement of V\textsubscript{H} and J\textsubscript{H} segments in culture (38). The cell lines M12.4.1 clone 4.5 (39) and A202J (40) are derived from primary and secondary B cell lymphomas; they represent stages of differentiation after the assembly of Ig genes. The cell line SP2/0 (41) is derived from a hybrid between a mature B cell and a myeloma cell. Each of these lymphoid cell lines was infected with the LJHCR virus and G418\textsuperscript{R} derivatives were obtained. Single cell clones were isolated from the G418\textsuperscript{R} populations and assayed for rearrangement of the proviral substrate. Rearrangement was detected in 40E4-2 (4 positive clones out of 23 examined) and in PD31 (1 in 21 clones). We did not detect rearrangement of the substrate in the mature B cell lines M12.4.1 clone 4.5 (none in 32 clones) and A202J (none in 29 clones), or in the B cell hybrid line SP2/0 (none in 22 clones). We also failed to detect rearrangement of the provirus in the fibroblastoid cell line NIH-3T3 (none in 26 clones). Every cell clone that was positive for rearrangement contained a mixture of recombined and unrecombined substrate. Thus, the rearrangements we observed occurred during the expansion of the cell clones, and each positive cell clone represents at least one recombinational event.

Molecular Analysis of the Products of Recombination. To define precisely the products of recombination, we carried out molecular cloning of rearranged proviral DNA from LJHCR-infected HAFTL-1 and PD31 cells. For these experiments we used the HAFTL-1/LJHCR-e and PD31/LJHCR-m cell lines; these comprise a mixture of cells that contain either rearranged or unrearranged provirus (Fig. 6A, lane e and 6B, lane m). To obtain homogeneous populations of cells, subclones of HAFTL-1/LJHCR-e and PD31/LJHCR-m were isolated. Genomic DNA from these subclones was cut with Kpn I and assayed for recombination of proviral Ig segments. In some of these subclones we found only the 4.8-kb (rearranged) fragment (Fig. 6A, lane e and 6B, lane m), while in others only the 4.1-kb (unrearranged) fragment was detected (Fig. 6A, lane e9 and 6B, lane m2). Thus, from clones exhibiting a mixture of rearranged and unrearranged copies of the LJHCR provirus, we could obtain subclones in which all cells contained only the rearranged provirus.

To demonstrate directly V\textsubscript{n}-to-DJ\textsubscript{n} recombination within the LJHCR substrate, we carried out molecular cloning of rearranged proviral sequences from HAFTL-1/LJHCR-e-1 and PD31/LJHCR-m-10. The restriction maps of the fragments recovered from these cell lines were identical to the restriction map expected after joining of the Ig gene segments in LJHCR (Fig. 7, a–c). In each example, V\textsubscript{n}-to-DJ\textsubscript{n} joining gave rise to two products: a coding joint and a noncoding joint. We determined the nucleotide sequences of these regions. From this analysis it was clear that the LJHCR rearrangements observed in the HAFTL-1/LJHCR-
e-1 and PD31/LJHCR-m-10 cell lines were the result of $V_n$-to-$DJ_n$ joining (Fig. 8). At the $V_n$-$DJ_n$ junction recovered from HAFTL-1/LJHCR-e-1, the coding sequences of the $V_n$ region and part of the $DJ_n$ region are identical to the sequences that had been introduced into the cell line (Fig. 8A, a). As is typical of $V_n$-$DJ_n$ joints (9), some nucleotides were lost from the $DJ_n$ coding sequence. The $V_n$-$DJ_n$ junction obtained from PD31/LJHCR-m-10 was similar (Fig. 8B, a); nucleotides were lost from both the $V_n$ and $DJ_n$ coding sequences. The sequences at the noncoding junctions from HAFTL-1/LJHCR-e-1 and PD31/LJHCR-m-10 revealed that the flanking sequences, in contrast to the coding sequences, had been precisely fused (Fig. 8A, b, and B, b). No loss or addition of nucleotides was observed in either case.
we have used a recombinant retroviral substrate to examine the rearrangement of exogenous Ig V\(_h\) and DJ\(_h\) elements in a series of cell lines. The retrovirus carries a neomycin resistance marker whose expression is independent of the arrangement of the resident Ig gene segments. The ability to select for retroviral integration independently of rearrangement made it possible to quantitate the virus present in culture supernatants of the transfected helper cell line. More importantly, this feature permitted us to introduce the substrate into a variety of cell lines regardless of their ability to support rearrangement. Joining of the exogenous gene segments was detected by a stringent hybridization assay that allowed us to simultaneously observe the rearranged and unrearranged substrate present in a cell population.

The assembly of Ig genes occurs by means of an ordered program of rearrangement (38, 52, 54, 55). The earliest step is the joining of a D segment to a J\(_h\) segment at the H chain locus; this is followed by the appendage of a V\(_h\) segment to the DJ\(_h\) element, to produce an intact \(\mu\) transcriptional unit. The assembly of L chain genes from separate V and J segments begins only after productive H chain gene assembly has occurred. Thus, at each of these stages, rearrangement appears to be restricted to particular gene segments. The retroviral substrate for V\(_h\)-to-DJ\(_h\) joining was introduced into three cell lines that exhibit continuing rearrangement of endogenous gene segments: HAFTL-1, 40E4-2, and PD31. In each of these cell lines, rearrangement of endogenous genes is representative of a specific stage in Ig gene assembly. All of these cell lines supported rearrangement of the exogenous substrate, regardless of the nature of their endogenous rearrangements. Our results suggest that specific V\(_h\) and DJ\(_h\) sequences, removed from their normal environments and placed within the context of a Mo-MLV transcriptional unit, are able to escape the regulation imposed on the rearrangement of intact gene segments in situ. This escape may...
FIGURE 8. Nucleotide sequences at the recombinant junctions recovered from the HAFTL-1/LJHCR-e-1 and PD31/LJHCR-m-10 cell lines. (A) Products of V_h-D_JH joining in the HAFTL-1/LJHCR-e-1 cell line. (a) Top line and bottom line, partial sequences of the unrearranged V_h X_31 and Dsr_2.7 JH_3 5' flanks; middle line, nucleotide sequence at the coding joint in HAFTL-1/LJHCR-e-1. Sequences derived from the V_h-coding region are shaded; those from the DJH_3 coding region are boxed. (b) Top line and bottom line, partial sequences of the unrearranged Dsr_2.7 JH_3 5' flank and the V_h X_31 3' flank; middle line, sequence at the noncoding joint in HAFTL-1/LJHCR-e-1. Sequences derived from the DJH_3 5' flank are boxed; those from the V_h 3' flank are shaded. The lengths of spacer regions are marked in bp. (B) Products of V_h-D_JH joining in the PD31/LJHCR-m-10 cell line. (a) Top line and bottom line, partial sequences of the unrearranged Dsr_2.7 JH_3 5' flank and the V_h X_31 3' flank; middle line, nucleotide sequence at the coding joint in PD31/LJHCR-m-10. Sequences derived from the DJH_3 5' flank are boxed; those from the V_h 3' flank are shaded. The lengths of spacer regions are marked in bp. (B) Products of V_h-D_JH joining in the PD31/LJHCR-m-10 cell line. (a) Top line and bottom line, as described in A; middle line, sequence at the noncoding joint in PD31/LJHCR-m-10. Sequences are marked as in A. These sequence data have been submitted to the EMBL/GenBank Data Libraries under the accession number Y00642.

be directly related to the unusual transcriptional setting of the exogenous segments (56), or may result from the removal of cis-acting elements required for developmental ordering of rearrangement. We have so far observed no rearrangement of the LJHCR substrate in three cell lines representative of
mature B cells, or in the fibroblastoid cell line NIH-3T3. The present data support the idea that Ig H and L chain gene segments are joined by a common apparatus that is more active in B cell precursors than in mature B cells.

The \( V_{\gamma 1}X \) gene segment is one of the most \( J_{H} \)-proximal \( V_{H} \) segments in the BALB/c mouse germline (31). Joining of the \( V_{\gamma 1}X \) segment to a DJ\(_{H} \) unit is accompanied by deletion of the intervening DNA (31). Thus, in the unrearranged state, the \( V_{\gamma 1}X \) gene segment appears to lie in the same transcriptional orientation as the \( J_{H} \) locus. In the L\( J_{H} \)CR substrate, the \( V_{\gamma 1}X \) and DJ\(_{H} \)3 sequences are inverted with respect to their orientation in the germline; nonetheless, they are able to undergo joining when introduced into appropriate cells. This result agrees with the observation that exogenous \( V_{\gamma} \) and \( J_{H} \) gene segments are joined when they are introduced in opposing orientation into a lymphoid precursor cell line (18, 20). Examples of inversionsal recombination in vivo at the \( \kappa \) locus and the T cell receptor \( \beta \) locus (58) have recently been described. Taken together, the evidence suggests that the joining reaction can occur independently of the relative orientation of the participating gene segments. The available data do not, however, rule out the possibility that the frequency of rearrangement may be orientation dependent.

In experiments that used a model substrate for recombination, the joining of \( V_{\gamma} \) and \( J_{H} \) segments was shown to be asymmetric; the coding joints are generally variable, while the reciprocal joints are invariant (20). We were able to examine the coding joints and the reciprocal joints produced by rearrangement of the H chain segments present in the L\( J_{H} \)CR substrate. We observed that these rearrangements are similar to \( V_{\gamma} \)-to-\( J_{H} \) rearrangements in that nucleotides may be lost at the coding joints, but not at the reciprocal joints. Thus, rearrangement of the \( V_{\gamma} \) and DJ\(_{H} \) elements in the L\( J_{H} \)CR substrate is asymmetric. Our data are consistent with models in which reciprocal joints are formed by site-specific cleavage at the borders between the coding sequences and the conserved heptamer sequences, followed by direct joining of the heptamers (20).

Junctions between \( V_{\gamma} \)- and \( J_{H} \)-flanking sequences have been isolated at random from a variety of mouse and human lymphoid cell lines (57, 59–62). In general, these resemble the reciprocal joints formed during recombination of exogenous substrates, in that the heptamer sequences are precisely fused. In one case, however, the heptamer sequences are separated by several nucleotides (62). Another exception to the precise joining of heptamer sequences was found in a product of rearrangement at the T cell receptor \( \beta \) locus (58). It is difficult to tell whether these exceptional sequences are products of the normal mechanism of rearrangement, however, because the recombination events that gave rise to these structures were not directly observed and can only be inferred.

The coupling of site-directed mutagenesis with a functional assay for recombination is likely to be a powerful approach to the problem of Ig gene rearrangement. The L\( J_{H} \)CR substrate is suited for such an approach, in that mutations that affect rearrangement should not interfere with selection for stable integration of the provirus. This feature has recently enabled us to introduce a series of mutant substrates into lymphoid cells (Morzycka-Wroblewska, E., and S. V. Desiderio, unpublished results). Thus, it seems likely that the assay described
here will be of use in defining the nucleotide sequences that direct rearrangement of Ig gene segments.

Summary

A model substrate for the joining of Ig V<sub>H</sub> and DJ<sub>H</sub> elements has been constructed in a retroviral vector carrying a selectable marker whose expression is independent of the arrangement of the resident Ig gene segments. The substrate was introduced into lymphoid and nonlymphoid cells, and site-specific recombination between the V<sub>H</sub> and DJ<sub>H</sub> elements was monitored by a direct hybridization assay. Joining of the exogenous gene segments was observed in cell lines representative of three distinct stages in early B cell differentiation. Rearrangement was not observed in three cell lines derived from mature B cells, or in a fibroblastoid cell line. The V<sub>H</sub> and DJ<sub>H</sub> elements were initially arranged so that the V<sub>H</sub>-DJ<sub>H</sub> junction and the recombined flanking sequences could be recovered after rearrangement. By molecular cloning and nucleotide sequence determination, V<sub>H</sub>-DJ<sub>H</sub> junctions formed upon rearrangement of the substrate were found to resemble closely similar junctions in functional H chain genes. The joining of V<sub>H</sub> and DJ<sub>H</sub> elements was observed to be asymmetric; loss of nucleotides occurred at the coding joints, but not at the junctions between flanking sequences. Our results suggest that Ig H and L chain gene segments are joined by a common mechanism that is more active in B cell precursors than in mature B cells. These observations provide further evidence that the rearrangement of Ig gene segments occurs by a nonreciprocal recombinational mechanism. The model substrate described here is likely to be of use in defining the nucleotide sequences that mediate rearrangement and in examining the developmental specificity of this process.

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