Selective Expression of a V_HIV Subfamily of Immunoglobulin Genes in Human CD5$^+$ B Lymphocytes from Cord Blood

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Summary

Human B lymphocytes expressing the CD5 surface antigen (CD5$^+$ B cells) constitute a subset capable of producing polyspecific antibodies recognizing a variety of self antigens. The repertoire of antibodies produced by CD5$^+$ and CD5$^-$ B cells is different. However, it is not yet established whether this distribution is reflected in different immunoglobulin variable region gene (IgV) use. Rearrangement of heavy chain IgV (IgV_H) genes represents one of the first identifiable stages in the maturation of B cells, and occurs in a developmentally ordered fashion. The repertoire of IgV_H gene expression is highly restricted during fetal life but diversifies progressively after birth. A high frequency of V_H gene use from the relatively small V_HIV gene family has previously been demonstrated in human fetal liver B cells. In the present study, 102 B cell lines established by Epstein-Barr Virus-transformation of separated CD5$^+$ and CD5$^-$ cord blood B cells, were examined for the frequency of IgV expression using monoclonal antibodies to cross-reactive idiotypes (CRI). The results demonstrate a relatively high frequency of V_HIV gene use (30%) in B cells from cord blood. Furthermore, two mutually exclusive CRI associated with distinct subgroups of the V_HIV family are segregated in their association with either subset of B cells. One CRI is exclusively expressed in lines established from CD5$^+$ B cells while the other is associated with lines established from CD5$^-$ B cells.

During the past few years, heterogeneity within B lymphocyte populations has become increasingly apparent. Several studies have demonstrated functional, physiological, and developmental heterogeneity. Studies in the mouse suggested that two separate lineages of B cells may exist (1). One lineage, is defined by cell surface expression of the Ly-1 antigen, characteristic of T lymphocytes, and the secretion of polyspecific antibodies reactive with a variety of self antigens. The second lineage lacks the Ly-1 antigen and produces antibodies, mainly, to exogenous antigens (1). It is not clear, however, if the distinction is also reflected in antibody variable region gene use by the Ly-1$^+$ and Ly-1$^-$ B cell subsets. This question can be approached by analysis of variable region gene segment rearrangements, at the DNA level or through serological markers expressed on the protein products.

In humans, the majority of B lymphocytes in fetal liver, cord blood, and a minority in adult peripheral blood and lymph nodes express surface CD5 molecule, the human equivalent of mouse Ly-1 (2).

In the present study, we have used a number of mAbs that recognize cross-reactive idiotypes (CRI)[1] associated with individual V_H or V_L gene family products to examine IgV gene use in CD5$^+$ and CD5$^-$ B lymphocytes.

Materials and Methods

Preparation and Sorting of B Lymphocytes. B Lymphocytes were enriched from heparinized blood of three full-term donors by centrifugation over Ficoll-Hypaque and rosetting using SRBCs (3). The enriched B cell populations were stained simultaneously with fluorescein-conjugated anti-CD20 (clone Leu-16) and PE-labeled anti-CD5 (clone Leu-1) and sorted using a FACStar® (Becton Dickinson Immunocytometric Systems, Mountain View, CA). Lymphocytes displaying green fluorescence only (CD20$^+$, CD5$^-$ cells) and those displaying green and red fluorescence (CD20$^+$, CD5$^+$ cells) were gated and sorted as CD5$^-$ and CD5$^+$ B cells, respectively.

[1] *Abbreviation used in this paper:* CRI, cross-reactive idiotypes.

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The degree of cell separation was evaluated by re-analysis of the PE-labeled cells by FACSCAN (Becton Dickinson and Co.).

Establishment of Epstein-Barr Virus Transformed Cell Lines. Sorted $CD5^+$ and $CD5^-$ B cells were infected with EBV using supernatant from the B95-8 marmoset line, and cultured in the presence of 2×10^4 irradiated (40 Gy) PBMCs (3). After culture for 2–7 wk, supernatants were harvested and assayed for the presence of Ig using an ELISA. Culture plates with <33% of wells positive for growth and immunoglobulin secretion were further evaluated for the clonality of the Ig product using antibodies specific for the IgM, IgG, IgA, κ, and λ isotypes. Cell lines positive for a single heavy and light chain isotype only were investigated for the expression of V_HI (G6 and G8), V_HIII (B6 and D12), and V_HIV (LC1, R2.1A2, and 9G4) heavy chain subgroup associated CRI.

Production of Murine Monoclonal Antibodies. The production and specificity of all mAbs used has been reported (4–10). Antibodies C7 and 17-109 have specificity for proteins expressing V_HIII subgroup and a V_KIIIb sub-subgroup associated CRI, respectively (5, 6). LC1 (kindly provided by Dr. C. Winearls and Miss D. Brennan, Hammersmith Hospital, London, UK) recognizes a CRI associated with the V_HIV of an IgM rheumatoid factor paraprotein (7); R2.1A2 (9), and 9G4 (10) specific for CRI expressed on 90% of IgM paraproteins with cold agglutinin activity. Mab 9G4 was raised in a Lou rat.

Human Monoclonal Paraproteins and Defined B Cell Clones. Paraproteins with cold agglutinin activity (from patients ODO and HAW) were isolated from the serum of patients with cold agglutinin disease, and specificity established using adult human O^+ red blood cells at 4½ (10). Rheumatoid factor paraproteins (from patients DIN and COR) were isolated from the serum of patients having essential mixed cryoglobulinemia by affinity chromatography. Paraproteins of unknown specificity were isolated from the serum of patients with Waldenstrom's macroglobulinemia by Sephacryl-S200 gel filtration (Pharmacia, Uppsala, Sweden). Proteins from patients ODO, DIN, COR, STR, and CAL were typed, serologically, for expression of heavy and light chain subgroups (11) and kindly provided by Dr. Gregg Silverman (Research Institute of Scripps Clinic, La Jolla, CA). Supernatants from the B cell clones AB26, AB17 and AB44 were a kind gift from Dr. Don Capra (Southwestern Medical Center, University of Texas, Dallas, TX). The clones were established by EBV transformation of sorted $CD5^+$ B lymphocytes from the peripheral blood of a normal individual. The variable region subgroup utilized was determined by cDNA sequencing (12).

Enzyme-Linked Immunosorbent Assay (ELISA). Microtitre ELISA plates (Linbro, Flow Labs, High Wycombe, Bucks, UK), sensitized with polyclonal sheep anti-human μ chain were used to bind IgM in the undiluted culture supernatant of B cell lines. Purified proteins positive or negative for the expression of the probed heavy and light chain isotypes and CRI were included in each assay to confirm specificity. Following three washes with PBS containing 0.05% Tween 20 (PBS/T), murine mAb with specificity for μ, κ, and λ, (clones AF6, 6e1, and C4, respectively; Unipath-Oxoid, Bedford, UK) or CRI were added at 1/500 dilutions in PBS/T. Bound mAb were revealed with horseradish peroxidase conjugated sheep anti-mouse or anti-rat Igs (Binding Site Limited, Birmingham, UK). Plates were read using a Titretek Multiscan reader (Flow Labs, High Wycombe, Bucks, UK) and OD value recorded following subtraction of background control values. The sensitivity of the assays allowed detection of antigen at a concentration of 5–10 ng/ml. Since Ig levels in the supernatants of the EBV lines were 500–5,000 ng/ml the assays provide further evidence suggestive of monoclonality and all profiles obtained were consistent with the establishment of clones.

Statistical Analysis. The expression of CRI were compared in 2×2 tables using the chi-squared test (χ^2) or Fisher's two-tailed test depending on the number of samples examined.

Results and Discussion

Following infection with EBV and culture for 2–7 wk, plates with <33% of wells positive for cell growth were selected for study of the expression of CRI. This cut off point provides for a statistical probability of monoclonality on the basis of Poisson analysis of limiting dilution protocols (13). Additionally, the criterion of expression of a single light and heavy chain isotype was observed for all cell lines studied. Furthermore, none of the cell lines expressed CRI from more than one V_H subgroup of heavy chains. The sensitivity of the ELISA allowed for the detection of Ig produced by <1% of the lymphocytes present; assuming they all have the same capacity to produce Ig. Thus, while monoclonality is not formally proven, all findings are consistent with such a conclusion. By these criteria a total of 102 cell lines were established by EBV transformation of cord blood lymphocytes—53 from the $CD5^+$ population of B cells and 49 from the $CD5^-$ population. Thirty-six of the 53 $CD5^+$ cell lines expressed K light chain, while 17 expressed λ light chain, a κ/λ ratio of 2:1, roughly the ratio found in circulating Igs. For the $CD5^-$ cell lines a considerably lower κ/λ ratio of 1:1.6 was observed.

Previous studies demonstrated a relatively high frequency of V_KIII subgroup expression in B cells from patients with chronic lymphocytic leukaemia which express surface CD5 (14). Within our K-expressing $CD5^+$ lines 12/36 (30%) expressed the V_KIII subgroup of light chain (Table 1), a frequency similar to the expected frequency of this light chain

Table 1. *V_KIII Subgroup Expression within Cell Lines Established from $CD5^+$ or $CD5^-$ B Lymphocytes and Association with 17-109 CRI Expression*

	Lines expressing V_KIII		Lines expressing 17-109		
Cell line origin	Total	% of K lines	Total	% of V_KIII lines	% of K lines
$CD5^+$	12	30	8	67	23
$CD5^-$	5	26	1	20	5

Table 2. *Reactivity of Monoclonal Antibodies Specific for V_HIV Associated CRI with Proteins from the V_HIV Family of Genes*

Protein	Isotype V_H-V_L subgroup	Specificity	Reactivity with anti-V_HIV CRI		
			LC1	R2.1A2	9G4
DIN	IgM-V_HIV V_KIII	Rheumatoid factor	+	−	−
COR	IgM-V_HIV V_KIII	Rheumatoid factor	+	−	−
STR	IgM-V_HIV V_KIII	Unknown	+	−	−
CAL	IgM-V_HIV V_KII	Unknown	+	−	−
ODO	IgM-V_HIV V_KIII	Cold agglutinin	−	+	+
HAW	IgM-V_HIV V_KII	Cold agglutinin	−	+	+
AB26	IgM-V_HIV V_λ	Polyreactive	+	−	−
AB17	IgG3-V_HIV V_KIII	Polyreactive	−	+	+
AB44	IgA-V_HIV V_λI	Polyreactive	−	+	+

Reactivity of monoclonal anti-CRI was determined in ELISA. V_H and V_K subgroup of proteins DIN, COR, STR, CAL, ODO, and HAW were assigned by immunoblot analysis with peptide induced reagents. Expression of V_KIII subgroup was confirmed by reactivity with monoclonal antibody C7. V_H and V_L of proteins AB26, AB17, and AB44 were assigned by DNA sequence analysis.

subgroup in polyclonal IgM. The proportion of V_KIII in the K-expressing CD5$^-$ lines was similar (26%) (Table 1). However, the frequency of V_KIII light chains expressing the 17-109 CRI was higher (Fisher's two-tailed probability = 0.13) in the CD5$^+$ lines compared with the CD5$^-$ ones.

V_H gene usage within the cell lines was investigated using a panel of mAbs specific for V_H subgroup associated CRI. The significant finding was expression of V_HIV–associated CRI. This is of particular interest because recent studies by Sanz et al. (12) have demonstrated a remarkably high frequency of V_HIV gene use in B cell clones established by EBV transformation of CD5$^+$ B cells from the peripheral blood of normal individuals. Furthermore, due to the small number of genes within this family (~10) and the high degree of internal homology (at least 91.5% between the most distant members to a consensus V_HIV sequence) it is probable that the germline gene repertoire would be represented by relatively few CRI.

In this study we applied three anti-CRI reagents, two of which appear to recognize the same or mutually inclusive CRI (R2.1A2 and 9G4). The third reagent (LC1) recognizes a CRI that is mutually exclusive to R2.1A2 and 9G4 (Table 2). Although neither CRI could be formally assigned to reported V_HIV genes, association with some germline genes is possible, on the basis of the present studies and recent studies of cold agglutinins (11) and polyreactive antibodies (12). Thus, the CRI recognized by LC1 may be a phenotypic marker for the 71-2 and 71-4 genes and related genes, whereas R2.1A2/9G4 may be markers for the 4-21 and related genes.

Our analyses reveal that: (*a*) The representation of V_HIV genes in these B cell lines is considerably higher than would be predicted for this relatively small family of genes. (*b*) A relatively higher but insignificant proportion of CD5$^+$ cell lines express V_HIV genes compared to their CD5$^-$ counterparts (35% vs. 28%; $\chi^2 = 0.62$, $p > 0.1$). (*c*) Remarkably, whereas 13/53 (24%) cell lines derived from the CD5$^+$ population coexpressed both R2.1A2 and 9G4, no CD5$^-$ cell lines expressed either of these CRI (Table 3) ($\chi^2 = 13.8$, $p < 0.001$). (*d*) Conversely, 14/49 (28%) CD5$^-$ lines expressed LC1, while only 6/53 (11%) CD5$^+$ lines expressed this CRI ($\chi^2 = 4.8$, $p < 0.05$).

Thus, it appears that a significant proportion of CD5$^+$ B cell lines produce IgM derived from a single gene, or a small number of genes within the V_HIV family for which a CRI associated with anti-I-carbohydrate antigen specificity is a phenotypic marker. Both R2.1A2 and 9G4 were coexpressed on the same molecules and were associated with κ light chain expression in 9/13 (70%) of the cell lines. However, none of the cell lines could be demonstrated to express the V_KIII epitope C7 or 17-109 together with R2.1A2 and 9G4. This appears to be in contrast to the observed association of V_HIV heavy chains and V_KIII light chains in cold agglutinins (15).

Table 3. *V_HIV-associated CRI Expression in CD5$^+$ and CD5$^-$ Cell Lines Established from Cord Blood Lymphocytes*

Cell line origin	Total no.	No. (%) lines expressing		
		LC1	R2.1A2	9G4
CD5$^+$				
IgM κ	36	4 (11%)	10 (28%)	10 (28%)
IgM λ	17	2 (5.5%)	3 (11%)	3 (11%)
Total	53	6 (11%)	13 (24%)	13 (24%)
CD5$^-$				
IgM κ	19	5 (26%)	0 (0%)	0 (0%)
IgM λ	30	9 (30%)	0 (0%)	0 (0%)
Total	49	14 (28%)	0 (0%)	0 (0%)

In this study the expression of heavy chains from the V_HIV family was associated with antibodies that were polyreactive (MacKenzie, L.E., R.A. Mageed, and P.M. Lydyard, unpublished observations). However, V_HIV gene family usage was not seen to be a prerequisite for polyreactivity since heavy chains from other gene families were also expressed in polyreactive antibodies in both $CD5^+$ and $CD5^-$ cell lines.

The significant findings of the present study are: (*a*) The high frequency of V_HIV gene family expression observed in cell lines established from cord blood B cells, and (*b*) The selective expression of a subset of V_HIV genes, characterized by the expression of the R2.1A2 and 9G4 CRI, within $CD5^+$ B cells.

The V_HIV gene family is composed of a maximum of about 10 members, and the incidence of paraproteins derived from this gene family is low in Waldenstrom's macroglobulinemia and multiple myeloma (12). In contrast the frequency of V_HIV gene usage in fetal liver B cells has been estimated to be 21% (16), a frequency not dissimilar to the 30% observed for the cord blood derived B cell lines.

The high frequency of V_HIV gene use in fetal and neonatal life may reflect an evolutionary selective pressure for the early production of antibody specificities encoded by this gene family or programmed expression of V_H genes (17).

It may be presumed that the early antibody repertoire would be generated using rearranged germline gene segments with minimal somatic mutation (18). It has been shown that such germline encoded specificities include recognition of self antigens and it has been suggested that a network of self antigen recognizing antibodies contributes to the further development of the immune repertoire. It may be significant, therefore, that numerous poly-reactive autoantibodies have been shown to use V_HIV gene segments. The data presented in this paper suggests that V_HIV gene use differs between $CD5^+$ and $CD5^-$ B cells in cord blood. It remains to be determined whether the CD5 antigen is a marker for a distinct lineage of B cells expressing a restricted repertoire of antibody specificities or is an activation marker such that the gene usage observed in early B cells reflects stimulation by a restricted number of self antigens.

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