HEMCAM, an Adhesion Molecule Expressed by c-kit⁺
Hemopoietic Progenitors

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Abstract. We have characterized the adhesion molecule HEMCAM, which is expressed by hemopoietic progenitors of embryonic bone marrow. HEMCAM belongs to the immunoglobulin superfamily and consists of the V-V-C2-C2-C2 Ig domains. There are three mRNA splice variants. One has a short cytoplasmic tail; another has a long tail; while the third seems to lack transmembrane and cytoplasmic regions. Except for the NH₂-terminal sequence, HEMCAM is identical to gicerin, a molecule involved in neurite outgrowth and Wilm’s kidney tumor progression in the chicken and it is significantly homologous with MUC18 a molecule involved in melanoma progression and metastasis in human beings.

In the bone marrow the HEMCAM⁺ cell population contains c-kit⁺ subsets. HEMCAM⁺ cells coexpressing the receptor tyrosine kinase c-kit give rise to T cells at a frequency of 0.17 when injected intrathymically in congenic animals. As HEMCAM⁺, c-kit⁺ cells differentiate into myeloid and erythroid CFU’s the double-positive cell population seems to contain precursors for multiple lineages. HEMCAM promotes cell–cell adhesion of transfected cells. Cross-linking of murine HEMCAM leads to cell spreading of T-lymphocyte progenitors adhering to the vascular adhesion molecules, PECAM-1 and VCAM-1. Thus, HEMCAM is likely to be involved in cellular adhesion and homing processes.

A large proportion of immunoglobulin superfamily (IgSF) molecules serve as adhesion receptors on the cell surface. In the recent literature there has emerged a prominent subgroup with a characteristic V-V-C2-C2-C2 Ig domain structure. Important representative members of this subgroup of molecules are B-CAM (human), Lutheran blood group antigen (human), BEN/DM-GRASP/SC1 (chicken), ALCAM (human), KG-CAM (rat), irreC-rst (drosophila), Neurolin (goldfish), Gicerin (chicken), and MUC18 (human) (3-5, 26, 28, 38, 41, 45, 47, 57, 60). Although most of these molecules are involved in adhesion and migration processes of neural cells, several of them are also found directly or indirectly associated with cells of the immune system, with epithelial cells, and/or with vascular endothelium.

BEN is expressed by embryonic hemopoietic progenitor cells from the bone marrow and immature thymocytes, but it is absent from most mature leukocytes (8). BEN-positive bone marrow cells develop macrophage, granulocyte, thrombocyte, and erythrocyte colonies when allowed to differentiate in vitro in the presence of appropriate factors. Mature resting peripheral T-lymphocytes are virtually negative for BEN expression, however this can be overcome by mitogenic or allogeneic stimulation of these cells; thus BEN is a T cell activation marker (7). ALCAM (activated leukocyte-cell adhesion molecule), the human homologue of BEN, has recently also been identified as an adhesion ligand for CD6 (3) that functions as an accessory protein in T cell activation; antibodies against CD6 can prevent transplant rejection of kidney and bone marrow (2, 25, 48).

Gicerin is transiently expressed in the developing nervous system and kidney (57, 58). Cloning and transfection experiments have demonstrated that the adhesive interactions mediated by gicerin include homophilic (gicerin-gicerin) or heterophilic contacts between gicerin and neurite outgrowth factor (NOF), a 700-kD extracellular matrix glycoprotein of the laminin family (18). Antibodies against...
To initiate T cell differentiation, hemopoietic stem cells must migrate to the thymus (37, 39). Several studies have shown that hemopoietic progenitors are transported via the blood to the vicinity of the thymus when adhesion molecules result in the attachment to the thymic endothelium. Both α6 integrin and CD44 expressed on vascular endothelium are involved in this process (10, 51). Extravasation and migration of progenitors in the perivascular space through the perithymic mesenchyme towards the thymic epithelium requires interaction with extracellular matrix molecules (52). Another adhesion step between the progenitor T cell and the thymic epithelium is thought to occur before the progenitor cell enters the thymus. Identification of the adhesion molecules involved in thymic homing requires the isolation of hemopoietic progenitor cells from the tissue in which they are most abundant.

Attempts to characterize hemopoietic stem cells have been made with mouse and human tissue. In the adult mouse, bone marrow stem cells, which can reconstitute all hemopoietic cell lineages, are of the phenotype Thy-1+ Sca-1+ and lineage marker negative (lin-) (20). A similar stem cell population was isolated from human bone marrow although the type of marker molecules was different (CD34+, lin-) (20). In both cases, the proportion of stem cells to total leukocytes is very low (<0.05%) (20) although it is significantly increased in embryonic tissue. The bone marrow and the blood of human embryos contains CD34+ cells that give rise to lymphocytes in SCID mice with human thymus transplants (40). From mouse blood at embryonic day 15.5 (E15.5), it was recently possible to separate pro-thymocytes (Thy-1+, c-kit+ and CD3+ cells) from pluripotent hemopoietic progenitors (Thy-1-, c-kit-) (49). With birds, unlike mammals, one can obtain experimental access to precisely staged embryos. Hemopoietic stem cells emerge in chicken bone marrow as early as E10, and the percentage of pro-T cells that can migrate to the thymus peaks at E13 (11). In the present work, we measured the T cell differentiation potential of hemopoietic progenitors by intrathymic injection into congenic animals. Using this method, we show that an E13 embryonic bone marrow population expressing c-kit and the antigen recognized by a monoclonal antibody (mAb) c264 gives rise to T cells at frequencies of 0.17. The mAb c264 facilitated the cloning and sequencing of the antigen which we call hemopoietic cell adhesion molecule (HEMCAM). This adhesion protein of the V-V-C2-C2 IgSF subgroup was highly homologous to the human melanoma progression molecule MUC18 and gicerin.
**Immunofluorescence and Cell Sorting**

For single, two-, or three-color analysis cells (10⁶) were incubated with hybridoma supernatants or purified mAb, washed, and incubated with FITC-conjugated anti-mouse Ig isotype specific antibodies (Southern Biotechnology). After washing, the cells were washed again and incubated with a biotin-conjugated mAb followed by streptavidin-Tricolor reagent (Caltag Labs, South San Francisco, CA). A FACScan was used for immunofluorescence analysis, a FACStar Plus (Becton Dickinson, Mountain View, CA) was used for sorting.

**Intrathymic Injection and Differentiation of Embryonic Bone Marrow Cells**

To prepare bone marrow cells from congenic ov⁻ mice, cells were flushed from the cavity of the isolated femurs and tibiae with a 25G 5/8-inch long syringe containing medium (DMEM containing 10% FCS), washed twice in PBS, counted, and adjusted to the required cell concentration (11). The recipient, 14-day-old ov⁻ congenic chicks were injected into two upper lobes on each side. Each lobe was injected with 10⁵ cells/thymus lobe in 1 ml syringe (Insulin syringe, Becton Dickinson, San Jose, CA) placed into a Tridek Stepper (Tridek, Brookfield, CT). The incision was closed with three wound clips (Autoclip, Clay Adams, Becton Dickinson Primary Care, Sparks, MD). After the operation, the chickens were kept under an infra-red radiator, Atomic Energy of Canada, Ottawa, Canada) about 6 h before radiating with the mAb llA9 (isotype IgM) directed against the ov⁺-antigen. The animals recovered rapidly and no special care was necessary for housing. 2-4 wk after chimera construction the chickens were sacrificed and cells from the injected thymus lobes isolated. Donor-derived cells were identified by immunofluorescence with the mAb 11A9 (isotype IgM) directed against the ov⁻-antigen.

**cDNA Cloning and Sequencing**

mRNA from E13.5 H.B19ov⁻ thymocytes was prepared by a FastTrack mRNA isolation kit (Invitrogen, De Schelp, Netherlands). A library of cDNA was constructed from 15 μg of the mRNA in the COS cell expression vector pCD3 (Invitrogen). The library consisted of 2.2 × 10⁵ primary clones, was amplified once, and had an average cDNA size of 1.0 kb. Transfection of adherent COS.7 cells with the library and screening of the transfected cells with mAb was done as described earlier (64). Briefly, COS cells were grown to 75% confluence in 35-mm tissue culture flasks (Falcon, Becton Dickinson, Franklin Lakes, NJ) at ~80% confluence were transfected with 10 μl cell suspension in PBS (3×10⁵ cells/ml). The transfected cells were incubated with the mAb llA9 (isotype IgM) directed against the ov⁺-antigen. The cells were washed and then stained with PE-conjugated mAb followed by streptavidin-Tricolor reagent (Caltag Labs, South San Francisco, CA). A FACScan was used for immunofluorescence analysis, a FACStar Plus (Becton Dickinson, Mountain View, CA) was used for sorting.

**Semiquantitative PCR**

From day 9 onwards embryonic tissues were carefully microdissected and total RNA was prepared. For cDNA synthesis, standard protocols and universal primers were used (51). Semiquantitative PCR was done as described by Keller et al. (24, 51). The amount of CDNA synthesized was calibrated from the relative expression level of 3 β-actin as a standard. The two actin oligonucleotide primers, 4611 and 4612, generated a band of 646 nucleotides (13). A series of 10-fold dilution was used to standardize the cDNA. The oligonucleotides covering the coding sequence of HEMCAM were: 11169 (HEMCAM, from nucleotide 195) ATGCTGGGGGGCCAGGCGGC; 11260 (HEMCAM, from nucleotide 609) GGAGAGGGCCAAGGCTTACACCC; 11261 (HEMCAM, from nucleotide 634, antisense) GGCTTAGGCTGGTGCGGCTCTCC; 11188 (HEMCAM, from nucleotide 1097) GAGGAGAGCTGGGGGGCCAGGCGGC; 11106 (HEMCAM, from nucleotide 1363, antisense) GCTTGAAGGGGCTCTGGG; 11898 (HEMCAM, from nucleotide 1597) TGCAAAGGCATCGCCTC; 11902 (HEMCAM, from nucleotide 2100, antisense) AAAGCTTAAAGGAGCC; GIC (HEMCAM, from nucleotide 2448, antisense) AAAAGAACCCT-CCATAGCAG; 4611 (5′ of actin, from nucleotide 3598) TACCACATG-TACCCGGGC; and 4612 (3′ of actin, from nucleotide 4246, antisense) CTCGCTCTTGTTTATGCGG. PCR reaction mixtures in 30 μl with 1 U Taq polymerase (Perkin-Elmer Cetus, Norwalk, CT) were denatured by heating to 96°C for 5 min, and then subjected to 30 rounds of amplification using a Biometra Protocol thermocycler under the following conditions: 96°C for 15 s, 50°C for 40 s, and 72°C for 1 min for cDNA amplification. Final extension was done at 72°C for 10 min. Amplified DNA fragments were gel purified and cloned into pCR II (Invitrogen). Sequences were determined from denatured double-stranded recombinant plasmid DNA using Sequenase (USB) in the chain termination reaction.

**Generation of Soluble Recombinant HEMCAM**

The vector pCD3 containing the cloned HEMCAM cDNA was used as a PCR template for the amplification of the sequence encoding the extracellular domains of HEMCAM. The PCR primers were: 5′-ATTAGAGCTCACCATGTGGGCCAGGCGGC-3′ (5′ primer) and 5′-TACCTACCTCTTTGGTCGTTTG-3′ (3′ primer). The amplified product was purified and inserted into the vector pHT4 containing the mouse Igκ constant region as a fusion partner, and the junctional regions were analyzed by nucleotide sequence analysis. The vector was cloned into competent E. coli K803 cells then transfected into J558L myeloma cells by protoplast fusion. Supernatants of the transfected mycoplasma-producing cell clones were screened by ELISA with goat anti-mouse κ reagents (Southern Biotechnology). Supernatants were purified by affinity chromatography with a monoclonal rat anti-mouse Cκ antibody (clone 187.1). The purified molecules were equilibrated with PBS and used for NIH-terminal amino acid sequencing and for immunizations of mice in order to produce mAb. For sequencing, the protein was transferred to Immobilon-P membrane (Millipore, Bedford, MA) and loaded into the cartridge of 475A protein sequencer (Applied Biosystems, Foster City, CA).
Polyclonal Antibody

Soluble recombinant HEMCAM protein was injected into a rabbit at 100 μg in complete Freund’s adjuvant followed by three injections of 100 μg protein each in incomplete adjuvant. The specific serum, but not the pre-immune serum, reacted with chicken thymocytes and HEMCAM-transfected L cells at a dilution of 1:3,000, and it cross-reacted with mouse pro-T lymphocytes at 1:1,000. The polyclonal antibodies were purified on protein A columns, and anti-mouse κ IgG was removed by absorbing the purified antibodies on a κ containing affinity column.

Transfection of L Cells

The liposome-mediated transfection method was used to introduce pc264 DNA into mouse L cells for stable expression of HEMCAM. A day before transfection, L cells (3 × 10^6 in 2 ml DMEM, 10% FCS) were plated on a six-well plate (Costar, Cambridge, MA). Plasmid DNA (5 μg) was mixed with 20 μl lipofectin (Lipoctam, Gibco BRL, Gaithersburg, MD) in a total volume of 100 μl H2O and left at room temperature for 30 min. Then, 800 μl Opti-MEM medium (Gibco BRL) was added to the DNA-liposome mixture, and after rinsing the L cells once with pre-warmed Opti-MEM medium, the mixture was overlayed on them and incubated at 37°C 5% CO2 for 5 h. After incubation 1 ml DMEM, 20% FCS was added to the well. At 24 h after transfection, the medium was replaced with fresh DMEM, 10% FCS. At 72 h after transfection, the cells were trypsinized and plated at a 1:20 dilution into 96-well plates in DMEM, 10% FCS, and 1 mg/ml G418 (Geneticin, Gibco BRL). Growing G418-resistant clones were tested for HEMCAM surface expression by flow cytometry.

Progenitor Cell Assays

Plasma clot assays for colony forming units were performed as described previously (9). Briefly, sorted cells were seeded in 1.2 ml of “Media Mix” (33) composed of DMEM (Gibco BRL), 10% FCS (Sigma), 2.5% chicken serum (Sigma), 0.15% NaHCO3, 56 μg/ml conalbumin (Sigma), 80 mM 2-mercaptopethanol, 0.9 μg/ml insulin, and penicillin-streptomycin (Gibco BRL). 120 μl of citrated bovine plasma (Gibco BRL) and 10 μl thrombin (100 i.u./ml, Sigma) were added rapidly, and two 600-μl aliquots from this mixture were seeded in a 24-well tissue culture plate (Nunc). Cultures were incubated for 3 d at 37°C, harvested, and air dried onto microscope slides according to the methods described previously for collagen cultures (27). Slides were stained for hemoglobin using diaminobenzidine (32), and counterstained with May-Grünwald-Giemsa; colony types were assessed by morphology. In some experiments, cultures were supplemented with anemic serum (46) as a source of erythropoietin, chicken myelomonocytic growth factor (cMGF) (29), or stem cell factor (SCF) (55). Liquid culture experiments were performed as above, but bovine plasma and thrombin were omitted. The frequency of eosinophils and erythrocytoid cells in liquid culture experiments were determined by sensitive, in situ stains for eosinophil-peroxidase (15, 23) and hemoglobins (36).

Cell Aggregation and Spreading

Adherent HEMCAM-transfected L cells were rapidly trypsinized and removed from culture flasks by moderately vigorous pipetting with PBS. Cells were aggregated at 2 × 10^6 cells/ml in DMEM (Gibco BRL) containing 10% FCS at 37°C in popypropylene tubes (Falcon, Becton Dickinson, Basel, Switzerland). Particles were enumerated at intervals in aliquots taken after gently turning the tube in order to resuspend the sedimented aggregates. Aliquots were taken by pipettes with widened tips in order to avoid shear forces during aggregate collection. Aggregates were counted in a Malassez chamber. Untransfected L cells were labeled by the fluorescent dye BCECF/AM (Calbiochem, San Diego, CA) by adding 2 μl stock solution (1 mg/ml in DMSO) to 1 ml cell suspension in full medium and incubated at 37°C for 20 min. After one wash the cells were ready to use for aggregation.

Purified recombinant HEMCAM, PECAM-1, and VCAM-1 were directly coated onto microtiter wells (Costar Corp., Cambridge, MA) at 10 μg/ml in 50 ml D-PBS for 2 h at room temperature (43). The wells were blocked with 20% BSA for 1 h at room temperature and washed with D-PBS. FITC mouse pro-T cells (a generous gift of R. Palacios, Houston, TX) were loaded in full medium (42) to the coated wells. The plates were then put under a microscope (Zeiss) equipped with a heated humid chamber at 37°C and a video-recording system (Panasonic).

Results

The Antigen Recognized by mAb c264 Is Expressed on Hemopoietic and Vascular Endothelial Cells

To follow migration and differentiation of chicken T cell precursors, mAb were raised against surface molecules of embryonic thymocytes (E15). At this stage of development many pro-T lymphocytes have already migrated from the bone marrow, the site of emergence, to the embryonic thymus (6, 11). One of the antibodies, c264, was selected because it detected an antigen on embryonic bone marrow cells, spleen cells, and thymocytes (Fig. 1). In embryonic bone marrow and spleen, many cell types, including erythrocyte precursors, expressed the antigen recognized by mAb c264 (not shown). In the adult thymus, the c264 antigen is highly expressed by 80% of CD4+ , CD8-
Table I. Growth and Myeloid/Erythroid Differentiation Assay in Liquid Medium

<table>
<thead>
<tr>
<th>Cell type</th>
<th>SCF</th>
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<th>SCF</th>
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<tr>
<td></td>
<td>cMGF</td>
<td>EPO</td>
<td>cMGF</td>
</tr>
<tr>
<td>HEMCAM+/c-kit⁺</td>
<td>10.5</td>
<td>8.7</td>
<td>6.5</td>
</tr>
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<td>0.6</td>
<td>0.5</td>
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<td>HEMCAM-/c-kit⁻</td>
<td>0.1</td>
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Embryonic E13.5 bone marrow cells were sorted for the expression level of HEMCAM and c-kit. The sorted cells were then cultured in liquid suspension at 10³ cells per well in the presence of hemopoietic growth factors: stem cell factor (SCF), chicken erythropoietin (EPO), and chicken myelomonocytic growth factor (cMGF). The number of cells after culturing for 5 d is indicated.

Table II. Colony Differentiation Assay in Semisolid Medium

<table>
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<th>Cell type</th>
<th>Growth factors</th>
<th>Type of colony</th>
</tr>
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<tbody>
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<td></td>
<td>Mac</td>
<td>Gran</td>
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<tr>
<td>HEMCAM+/c-kit⁺</td>
<td>SCF/EPO</td>
<td>49</td>
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<td></td>
<td>SCF/cMGF</td>
<td>37</td>
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<tr>
<td>HEMCAM+/c-kit⁻</td>
<td>SCF/EPO</td>
<td>6*</td>
</tr>
<tr>
<td></td>
<td>SCF/cMGF</td>
<td>5*</td>
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<tr>
<td>HEMCAM-/c-kit⁻</td>
<td>SCF/EPO</td>
<td>1*</td>
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<tr>
<td></td>
<td>SCF/cMGF</td>
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</tbody>
</table>

Embryonic E13.5 bone marrow cells were sorted for the expression level of HEMCAM and c-kit. These cells were placed into semisolid medium containing bovine plasma and the following growth factors; stem cell factor (SCF), chicken erythropoietin (EPO), and chicken myelomonocytic growth factor (cMGF). Cultures were incubated for 3 d, harvested, dried, stained by May-Grünwald Giemsa solutions to visualize myeloid cells, and diaminobenzidine to stain erythroid cells. Colonies were then counted and analyzed by microscopy. Colonies contained: Macrophages (Mac), Granulocytes (Gran), Macrophages and Granulocytes (Mac/Gran), Immature Myeloid cells and Macrophages (Myl/Mac), Immature Myeloid cells (Myl), Erythrocytes and Thrombocytes (Ery/Thro), Erythroid burst forming cells (BFU-E), and Stromal cells (Stromal). *small mature colonies; + immature colonies.

Figure 2. Immunohistochemistry of c264 antigen expression in the thymus. Frozen tissue sections of the thymus from a hatched chick were stained by mAb c238 specific for c264 antigen and best suitable for histochemistry. The bound antibody was visualized by a staining kit containing a peroxidase-conjugated reagent. The immune reaction appears in brown, the counterstaining of the tissue in blue. (a) The cortical region of the thymus contained c264-antigen-positive thymocytes. (b) Thymocytes in the corticomedullary junction were negative for c264 antigen expression but the vascular endothelium of thymic blood vessels were stained. (oc) outer cortex; (m) medulla. Bar represents 50 μm.

(double negative) as well as on all double positive thymocytes. The c264 antigen was also expressed albeit at lower levels, by CD4−, CD8+ cells but was absent from CD4+ and CD8− single positive cells (data not shown). The antigen was expressed at 100-fold lower levels, as determined by relative fluorescence intensity, on cells of the B lymphocyte lineage (data not shown). For immunohistochemistry, we used mAb c238 because it recognized the C264 antigen and it was most suitable for histochemistry. It reacted most strongly with thymocytes in the outer cortex of the thymus of newly hatched chicks (Fig. 2 a). Staining of cells in the inner cortex was clearly weaker, and most medullary thymocytes appeared to be c264-negative. The antigen was also expressed at high levels by vascular endothelial cells, as exemplified by thymic capillary endothelial cell staining (Fig. 2 b). Thus, mAb c264 seems to be specific for an antigen that is most prominently expressed on cells of the T lymphocyte lineage and on vascular endothelium. The expression of the c264 antigen was not exclusively restricted to the thymus since it was also found in other tissues such as spleen, bursa of Fabricius, gut, muscle, and brain of 3-wk-old chicks (Fig. 3). In all these tissues the antigen is expressed by vascular endothelium, although it was also found in epithelial cells of the bursa (Fig 3, b and c) and in myocytes (Fig. 3 e). In the brain however, only vascular endothelium was stained by the antibody (Fig. 3 f). Antibody c264 precipitates a molecule with an apparent molecular mass of 98 kDa, under both reducing (Fig. 4) and non-reducing conditions (not shown). After treatment with N-glycanase, the core protein migrated at ~84 kDa; thus, 14 kDa are due to N-linked glycosylation.

T Cell Differentiation of c264-positive Bone Marrow Cells

As the c264 antigen is highly expressed by immature thymocytes as well as by embryonic bone marrow cells, we assayed the c264 positive bone marrow cells for hemopoietic precursors able to differentiate into T cells. To this end, we
Figure 3. c264 antigen expression in various tissues. Frozen tissue sections of a 3-wk-old chick were stained by mAb c238 as described for Fig. 1. (a) Spleen, it showed prominent staining of blood vessels; capillaries (C), arterioles (A). The T-lymphoid tissue in periarteriolar lymphoid tissue, PALS (Pa), and the B-lymphoid tissue in pericapsidal lymphoid tissue, PELS (Pe), are not stained. The stroma in the red pulp (R), mainly sinuses, are strongly stained. (b) Bursa of Fabricius, note the strong staining in the cortico-medullary junction. (c) Bursa of Fabricius at 4× higher magnification. All the cortical-medullary capillaries and the thin epithelial monolayer are stained. (d) Intestinal villus, the blood vessels in the lamina propria are stained. (e) Skeletal muscle, the arterioles (A), and the venules (V) are strongly stained. All plasma membranes of myocytes are stained (f). Brain, all the blood vessels are stained, neural tissue was generally negative. Bars represent 50 μm.

sorted c264+ and c264− E13.5 bone marrow cells (H.B19ov+ animals) and injected them intrathymically into 14-d-old H.B19ov− congenic animals. Thymus reconstitution by the ov+ donor bone marrow cells was measured by flow cytometry with the anti-ov mAb 11A9 at 2 wk after injection. In a representative experiment, 500 sorted c264+ cells led to 5% thymocyte chimerism while up to 10,000 c264− cells induced no chimerism (Fig. 5). To obtain a similar recon-
Figure 4. Biochemical analysis of \(c_{264}\) antigen. The thymocytes from a three-wk-old chicken of the strain H.B19 were \(^{125}\text{I}\)-labeled, and the lysate precipitated with mAb \(c_{236}\) obtained by immunization with soluble recombinant HEMCAM protein. Immunoprecipitates were analyzed by SDS-PAGE on a 7.5% gel under reducing conditions (a). In b, the precipitated protein was digested by N-glycanase before analysis by SDS-PAGE. The molecular weight standards are indicated on the left.

To test whether the \(c_{264}\) antigen\(^{+}\), c-kit\(^{+}\) bone marrow cell population also contained progenitors for the myeloid and/or the erythroid lineages, we assayed growth and differentiation in vitro in the presence of chicken stem cell factor (SCF), myelocytic growth factor (cMGF), and erythropoietin (EPO). All the combinations stimulated proliferation of the sorted \(c_{264}\)\(^{+}\), c-kit\(^{+}\) cells but not single positives or double negatives (Table I). Culturing of \(1 \times 10^{5}\) double positive cells for 5 d resulted in \(6.5-10.5 \times 10^{5}\) differentiated cells of all myeloid or erythroid lineages (Table I and not shown). When the double positive cells were cultured under semi-solid growth conditions, there was a high frequency of mixed colonies (Table II). These results suggest that \(c_{264}\) antigen and c-kit are present on hematopoietic progenitors of all lineages.

The \(c_{264}\) Antigen Is Homologous to the Human Melanoma Progression Marker MUC18

Since embryonic thymocytes showed the highest expression level of the \(c_{264}\) antigen, a cDNA library was made from E13.5 thymus polyA\(^{+}\) mRNA. The library was constructed into the pCDA3 vector, which allowed expression of cDNA in eukaryotic cells (COS 7). Using expression screening with mAb \(c_{264}\), we isolated one clone from transiently transfected COS cells. This clone has an open reading frame of 1,878 bp that corresponded to a recently isolated cDNA encoding gicerin, a molecule involved in neurite outgrowth. Among nucleotide differences, at position 326 of the gicerin sequence, one C was missing whereas at position 466 another C was inserted changing the reading frame between amino acid residues 43 and 77 (Fig. 7 and not shown) (56, 57). We confirmed the cDNA sequence by NH\(_2\) terminus amino acid sequencing of the recombinant soluble protein produced in J558L myeloma cells (28 amino acid residues). The leader peptide was unusually long (35 amino acids) and it contained six cysteine residues. In the NH\(_{2}\) terminus \(c_{264}\) sequence a new putative N-linked glycosylation site was found.

The predicted amino acid sequence of the \(c_{264}\) protein identified this molecule as a member of the type I transmembrane protein of the IgSF, with five extracellular Ig domains, two of them of the V-like and three of the C2-like, in the order V-V-C2-C2-C2. The extracellular domains showed nine putative N-glycosylation and seven
myristylation sites. Among the IgSF molecules in the EMBL data base MUC18 showed high homology (39%) with the c264 protein (Fig. 7). MUC18 is a human member of the V-V-C2-C2-C2 family and is a marker for human melanoma tumor progression (28). Significant but lower homology was also found with other five Ig-domain proteins from various species: B-CAM (27%, human), AL-CAM (25%, human), BEN (25%, chicken), and neurolin (28%, fish). There was much higher homology between chicken c264 and human MUC18 in the transmembrane (66%) and cytoplasmic regions (69%). Exon 13 of MUC18, which encodes 34 amino acid residues located between the last Ig domain and the transmembrane region is not present in c264 (Fig. 7). Because of the expression by hematopoietic cells, the structural similarity and the high sequence homology to MUC18, we call the c264 protein HEMCAM (Hemopoietic, MUC18 related, Cell Adhesion Molecule). It was interesting to note that HEMCAM showed higher sequence homology to MUC18 in the NH2-terminal region than gicerin to MUC18. As two different cytoplasmic sequences have been observed in gicerin and HEMCAM, we searched for the presence of cDNA splicing variants (56) with reverse transcriptase PCR (RT-PCR) on several tissues. Three differ-
Table III. Expression of HEMCAM Transcripts during Chicken Development

<table>
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The pattern has been established with a semiquantitative PCR technique using oligonucleotide primers 1188 and 1106 which allow amplification of an invariant part of HEMCAM transcripts (see Materials and Methods). The PCR products have been analyzed by agarose gels and the intensity of the appearing bands is indicated by a grading from (−) no band to (+ (+++ +) band at saturation levels.

Figure 8. Predicted amino acid sequences of three mRNA splicing variants of HEMCAM. The sequences shown start from residues 481. "Long" and "short" indicate the long and short forms of the cytoplasmic tails of HEMCAM; soluble corresponds to the putative soluble form of HEMCAM ending at residue 504. +, *; and −, indicate possible phosphorylation sites for protein kinase C, casein kinase II, and calmodulin kinase II, respectively.

Figure 9. Expression of HEMCAM mRNA encoding the cytoplasmic variants during embryogenesis. RT-PCR analysis of embryonic bone marrow and thymus from day 9 (E9) of development onwards was done with a combination of two primers depicting mRNA coding for the long or short cytoplasmic forms (1188-11902). After 30 cycles of amplification, PCR products were separated on a 1.2% agarose gel. The short form appears as the lower band at 384 bp and the long form at 503 bp. (M) DNA molecular weight markers 1 kb ladder. (C) Control sample containing the primers but no templates. nd, not determined.

HEMCAM Confers Cell Spreading and Cell Adhesion by Homophilic Interaction

HEMCAM cDNA coding for the short and the long cytoplasmic variants were transfected into mouse L cells. Both forms of HEMCAM led to cell–cell adhesion in a suspension assay (Fig. 10 A). In transfected cell lines, the average size of aggregates was four cells, while in control, untransfected cell lines, the average was 1.2 cells. The largest aggregates were 30 cells in the transfected lines, while aggregates larger than four or five cells were never seen in the controls. Soluble recombinant HEMCAM molecules and anti-HEMCAM antibodies blocked cell adhesion confirming that the adhesion was HEMCAM specific (Fig. 10 B). And finally, the aggregation of transfected L cells was mediated by homophilic interaction of HEMCAM molecules, since untransfected cells were not found in aggregates formed by HEMCAM expressing cells (Fig. 10 C).

A mouse pro-T lymphocyte cell line (FTF1) bound to recombinant chicken HEMCAM, mouse PECAM-1, and mouse VCAM-1, all molecules found on vascular endothelia (21). When HEMCAM of adherent pro-T cells was cross-linked by a purified polyclonal antibody that recognizes chicken and mouse HEMCAM (see Materials and Methods), the cells exhibited significant spreading on PECAM-1-, VCAM-1-, and HEMCAM–coated surfaces but not on control BSA (bovine serum albumin) (Fig. 10 D). Thus, HEMCAM seems to be able to mediate adhesion and induce cell spreading, probably by activating cytoskeletal elements after signal transduction.

Discussion

We have characterized and cloned HEMCAM, a molecule expressed by hemopoietic progenitor cells in embryonic bone marrow, thymocytes, and capillary endothelial cells. HEMCAM-expressing cells sorted from bone marrow were enriched in progenitors able to differentiate into T cells when transferred into the appropriate thymic microenvironment. An extremely high frequency of T cell precursors of 0.17 was found among embryonic bone marrow cells expressing both HEMCAM and the receptor tyrosine kinases.
kinase c-kit. Three putative splice variants of HEMCAM were observed; two have transmembrane domains with cytoplasmic tails of 63 or 21 amino acids, and one lacks both transmembrane and cytoplasmic regions. HEMCAM which is almost identical to gicerin, a molecule involved in neural outgrowth (57), is also homologous to human MUC18, a molecule expressed by highly metastatic melanoma cells (28). The function of HEMCAM seems to be mediation of cell–cell adhesion as well as cell spreading of pro-T lymphocytes. We concluded that HEMCAM could be involved in the colonization of the thymus by hemopoietic progenitor cells.

Although progenitor cells represent an extremely small population in the mouse, <0.05% of leukocytes in adult bone marrow, a much higher frequency was found in fetal tissues (e.g., 8% of all leukocytes in fetal blood [20, 34, 49]). Embryonic bone marrow cells, which are easily obtainable in the chicken, are also highly enriched in hemopoietic progenitors (11). Here we have characterized the phenotype of these progenitor cells, and, as expected from mouse and human data, hemopoietic progenitors expressed c-kit. More importantly, we showed that the c-kit+ progenitors coexpressed the adhesion molecule HEMCAM.

Three V-V-C2-C2-C2 IgSF molecules are known in human beings: BCAM, ALCAM, and MUC18. Two forms of BCAM are generated by alternative splicing; BCAM and the Lutheran blood group antigen. (5, 38). BEN, DM-GRASP, and SC1 are homologues of ALCAM in the chicken, or KG-CAM in the rat and neurolin in the fish (Fig. 11). HEMCAM differs from gicerin by a stretch of 35 amino acids at the NH2 terminus. However, this difference is due to an insertion and a deletion of one nucleotide at each side of the borders of this stretch, leading to a frame shift. The few nucleotide substitutions observed between the two sequences make it likely that HEMCAM and gicerin are the same molecular entity. The high GC percentage in the NH2 terminus region may account for the possible errors encountered in the gicerin sequence (57). Two different clues suggest that our nucleotide sequence is the correct one: first, the determined amino acid sequence of our recombinant HEMCAM protein fits with the cDNA sequence and second, the amino acids 43 to 77 of HEMCAM and not those of gicerin are homologous to MUC18, a human metastatic melanoma marker (28). The function of HEMCAM seems to be mediation of cell–cell adhesion as well as cell spreading of pro-T lymphocytes. We concluded that HEMCAM could be involved in the colonization of the thymus by hemopoietic progenitor cells.

Figure 10. HEMCAM, an adhesion molecule involved in cell spreading. (A) Aggregation of HEMCAM-transfected cell lines. Control and transfected L cells (HEMCAM cytoplasmic short and long variant) were cultured in suspension at 2 × 106 cells/ml in full medium at 37°C. At indicated time points, the cell suspension was gently agitated, and the number of particles (cell aggregates) were counted in a small aliquot in a hemocytometer. (B) L cells transfected with the long variant form of HEMCAM were allowed to aggregate at 2 × 106 cells/ml for 100 min at 37°C in the presence of control mouse IgG (co), soluble HEMCAM (sol), or polyclonal anti-HEMCAM antibody (anti). The aggregation was blocked when the cells were incubated in the presence of 50 μg/ml of recombinant soluble HEMCAM (sol) or 50 μg/ml of purified polyclonal rabbit anti-HEMCAM antibody (anti). (C) HEMCAM mediates L cell aggregation by homophilic interaction. L cells, transfected with the long variant form of HEMCAM were allowed to aggregate at 2 × 106 cells/ml for 100 or 200 min, respectively (hatched bars). In a simultaneous experiment transfected L cells at 2 × 106 cells/ml which have been previously labeled with the fluorescent dye BCECF. The average number of cells per aggregate was assessed by a microscope equipped by epifluorescence (solid bars). In 30 aggregates the number of fluorescent and unstained cells were counted and expressed as an index given on top of the bars, it is calculated as the number of labeled cells (control L cells) divided by the number of unlabeled cells (transfected L cells). Note that the aggre-
gates in 1:1 cell mixtures were smaller and contained mostly transfected cells. (D) Soluble recombinant HEMCAM, PECAM-1, VCAM-1, or control BSA were coated onto culture dishes. FITF1 pro-T lymphocytes were allowed to adhere to the coated dishes for 20 min at 37°C, and the nonadhering cells were removed. The spreading of adherent cells was observed over 2 h by video-microscopy; photographs were taken at the end of this observation time (control). Then, polyclonal anti-HEMCAM antibody was added at 50 μg/ml to cross-link HEMCAM. Cell spreading occurred after a further 15–20 min at 37°C, and photographs were taken at 20 min after (crosslinked). Bar, 10 μm.
The transcript encoding the short cytoplasmic form would be generated by direct junction of the exons. As it is an adhesion molecule and it belongs to the MUC18 family. In fact, these 34 amino acids correspond exactly to a mucin repeat found in human molecule SMUC-40. Such structural differences have been previously encountered in homologous molecules in different species. For example, in the mouse MAdCAM-1, a large mucin domain replaced an Ig domain present in human MAdCAM-1. Thus, taken together, our data suggest that HEMCAM is the chicken homologue of human MUC18.

We identified three HEMCAM mRNA splice variants. Two of them encode transmembrane proteins that vary in their cytoplasmic tail. This may be of importance for the protein function since the cytoplasmic domain of the long form has three protein kinase C (PKC) and two casein kinase II (CKII) phosphorylation sites, the short form has only one of these PKC sites in common along with a calmodulin kinase 2 phosphorylation site. The capacity for differential phosphorylation of the short and long cytoplasmic forms of HEMCAM might have consequences for signal transduction into the cell and/or inside out signaling leading to different ligand specificities. This is further emphasized by the fact that the two forms have temporally different expression patterns in the thymus. It remains to be determined whether or not differentiating thymocytes and thymic vascular endothelial cells express both forms of HEMCAM. The nucleotide sequence missing from the short cytoplasmic HEMCAM transcript corresponds exactly to exon 15 of MUC18. It suggests that MUC18 and HEMCAM genes have the same structure. In this context the generation of the two alternative transcripts is easy to understand. The transcript encoding the short cytoplasmic form would be generated by direct junction of the exons homologous to exons 14 and 16 of MUC18, while the transcript encoding the soluble form would result in the absence of splicing of the intron homologous to intron 11 of MUC18.

As HEMCAM is expressed by hemopoietic progenitor cells and has mostly disappeared in differentiated T cells, we think this molecule might contribute to a specific mechanism allowing hemopoietic progenitors to colonize the thymus. As it is an adhesion molecule and it belongs to the

\[ \text{V-V-C2-C2-C2-IgSF} \]

HEMCAM would likely be involved in an adhesion process allowing hemopoietic progenitor cells to attach to the luminal plasma membrane of the vascular endothelial cells. As it is a variant of gicerin, HEMCAM should exhibit similar adhesion specificities; e.g., homophilic interactions and heterophilic interaction with NOF, a laminin-like molecule. Interestingly, HEMCAM is expressed on vascular endothelium, which may allow progenitor/endothelial cell adhesion. Moreover, as is the case with many other adhesion molecules of the IgSF family, a physiological soluble form of HEMCAM can be produced. Soluble HEMCAM may play a role in the regulation of thymus homing, inhibiting progenitor/endothelial cell adhesion by competitive binding to its ligand on the plasma membrane. It remains to be determined whether the two cytoplasmic domains are involved in inside out signaling leading to different ligand specificity. For example, it has recently been shown that alternatively spliced tails of PECAM-1 determine whether the molecule interacts in a homophilic or heterophilic manner. At present, we are testing such a regulation of ligand specificity with HEMCAM. The strength of HEMCAM adhesion is weak in comparison to adhesion with selectins, integrins, and other IgSF proteins such as ICAMs, VCAM-1, and PECAM-1. The main role of HEMCAM, whether it is a proper adhesion molecule or whether it acts as a modulator of adhesion through association with other adhesion molecules or they are involved in outside-in signaling, remains to be tested.

Like HEMCAM, two molecules involved in thymus homing of pro-T cells, α6 integrin and the adhesion molecule CD44 play a role in tumor metastasis. The α6β1 integrins are mediators of metastatic melanoma cell adhesion to the vascular endothelium, and the expression of a variant of CD44 confers metastatic potential to rat carcinoma cells. Gicerin, the homologue of HEMCAM has been described in tumorigenesis. Both HEMCAM and its human homologue MUC18 participate in organogenesis during development. At the adult stage their expression is restricted to a few tissues, but it may be induced during tumor progression. Understanding the normal function of these molecules ought to contribute to the understanding of their malfunction in tumors.

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