Stemness of B-cell Progenitors in Multiple Myeloma Bone Marrow

Kelly Boucher, Nancy Parquet, Raymond Widen, Kenneth Shain, Rachid Baz, Melissa Alsina, John Koomen, Claudio Anasetti, William Dalton, and Lia E. Perez

Abstract

Purpose: In myeloma, B cells and plasma cells show a clonal relationship. Clonotypic B cells may represent a tumor-initiating compartment or cancer stem cell responsible for minimal residual disease in myeloma.

Experimental Design: We report a study of 58 patients with myeloma at time of diagnosis or relapse. B cells in bone marrow were evaluated by multicolor flow cytometry and sorting. Clonality was determined by light chain and/or immunoglobulin chain gene rearrangement PCR. We also determined aldehyde dehydrogenase activity and colony formation growth. Drug sensitivity was tested with conventional and novel agents.

Results: Marrow CD19+ cells express a light chain identical to plasma cells and are therefore termed light chain restricted (LCR). The LCR B-cell mass is small in both newly diagnosed and relapsed patients (≤1%). Few marrow LCR B cells (~10%) are CD19+/CD34+, with the rest being more differentiated CD19+/CD34− B cells. Marrow LCR CD19+ B cells exhibit enhanced aldehyde dehydrogenase activity versus healthy controls. Both CD19+/CD34+ and CD19+/CD34− cells showed colony formation activity, with colony growth efficiency optimized when stroma-conditioned medium was used. B-cell progenitors showed resistance to melphalan, lenalidomide, and bortezomib. Panobinostat, a histone deacetylase inhibitor, induced apoptosis of LCR B cells and CD138+ cells. LCR B cells are CD117, survivin, and Notch positive.

Conclusions: We propose that antigen-independent B-cell differentiation stages are involved in disease origination and progression in myeloma. Furthermore, investigations of myeloma putative stem cell progenitors may lead to novel treatments to eradicate the potential reservoir of minimal residual disease.

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Introduction

The cancer stem cell model predicts that the entire tumor mass emerges from a small proportion of proliferating cells with self-renewal capacity. Early evidence has shown that a small fraction of multiple myeloma (MM) cells is capable of colony formation originating from a single malignant cell in both mice and humans (1). Previous work has identified CD19+ B lymphocytes that express the corresponding light chain of myeloma plasma cells in the peripheral blood of patients with myeloma referred to as clonotypic B cells (2). The clonal relationship among B cells and malignant plasma cells has also been confirmed by molecular methods (3). Clonotypic B cells in myeloma bone marrow have been described in few reports, although not studied in depth (3, 4).

Attempts have been made to study the relationship between clonotypic CD19+ B cells and MM cancer stem cell. Putative MM cancer stem cell has been debated in the literature as being the phenotype of a preswitch and/or a postswitch MM B cell. Evidence for preswitch B-cell progenitors with stem-cell-like properties has been described in CD34+/CD19− cell subsets, which have resulted in xenograft myeloma in immuno-compromised hosts (5). An immature B-cell subset characterized for the coexpression of CD19+/CD34+/CD11b+ in peripheral blood has been shown to have a clonal relation with the original patient’s malignant plasma cells (6), although this has not been consistently identified (7). The existence of a B preswitch isotype species clonally related to myeloma has also been identified in bone marrow (3). B cells expressing clonotypic cytoplasmic immunoglobulin (Ig) M (cIgM) cells (preswitch) in patients with myeloma have been shown to be

Authors’ Affiliations: 1Blood and Marrow Transplantation Program; 2Department of Hematologic Malignancies; 3Experimental Therapeutics Program, H. Lee Moffitt Cancer Center and Research Institute; and 4Eoteric Testing Laboratory, Tampa General Hospital, Tampa, Florida

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Correlated with poor patient outcome (8); however, additional work from the same group has shown that myeloma may originate from a single class switch event in IgM cells with ongoing mutations in the postswitch progeny, suggesting that IgM cells may not be involved in disease progression (9). It has also been suggested that memory B cells represent a clonotypic remnant that is only partially transgenic and/or progression in myeloma. Research studies of putative progenitor stem cell–like cells in myeloma may lead to novel treatments to eradicate myeloma minimal residual disease reservoir. Understanding survival mechanisms of clonotypic B-cell progenitors may expand potential clinical applications of current anti-myeloma approaches.

DNA sequencing revealed somatically hypermutated but homogeneous Ig heavy-chain genes, suggesting that in myeloma, clonal proliferation may occur in cells that have already passed through phases of somatic hypermutation. Clonotypic B cells have been identified in the CD19+/CD38+/CD56−/monotypic Ig light-chain blood differentiation stages may be involved in disease origin. A long-term proliferating compartment of B-cell ontogeny (15). A long-term proliferating compartment of B-cell ontogeny (15). A long-term proliferating compartment of B-cell ontogeny (15). A long-term proliferating compartment of B-cell ontogeny (15). A long-term proliferating compartment of B-cell ontogeny (15). A long-term proliferating compartment of B-cell ontogeny (15). A long-term proliferating compartment of B-cell ontogeny (15). A long-term proliferating compartment of B-cell ontogeny (15). A long-term proliferating compartment of B-cell ontogeny (15).

Controversy arises as both cell subsets, B cells (CD138+/CD19+) and plasma cells (CD38+/CD45−), have been shown to reproduce myeloma in xenograft models (4, 16, 17). Mature plasma cells have been shown to have proliferative and stem cell–like properties. Plasma cells include a subset of proliferating cells present within CD45bright cells; this subset has been postulated to be a growth fraction in myeloma (18). CD138+ cells have been shown to contain a stem cell–like side population with high-proliferation index that is sensitive to lenalidomide (19). Clonogenicity of CD138+ cells has been shown with dendritic cells in coculture support (20).

The clinical significance of monoclonal CD19+ cells remains to be determined. Patients with myeloma have been reported to have increased numbers of circulating B cells, with numbers significantly increased after relapse (12, 21). In contrast, CD19+ blood myeloma cells were not significantly different from median levels shown in normal controls, although CD19+ cell levels convened an improved survival (22). CD19+ cells are not eliminated by any conventional or high-dose chemotherapy regimens (12, 21, 23), although they are undetectable after allogeneic transplant in 1 patient (23).

In this study, we purified light chain-restricted (LCR) CD19+ B cells using multiparameter flow cytometry and cell sorting and confirmed that bone marrow B cells from patients with myeloma are clonally related to malignant plasma cells. Herein, we showed that marrow CD19+/CD34+ and more differentiated CD19+/CD34− B-cell samples exhibited a stem cell–like aldehyde dehydrogenase-positive (ALDH+) phenotype, which were able to grow colonies in colony formation assay (CFC), suggesting that an antigen-independent B-cell maturation stage may be involved in disease origin. We confirmed chemoresistance of B-cell progenitors to conventional myeloma agents and showed that panobinostat, a novel histone deacetylase inhibitor, exhibits activity against progenitor and mature plasma cells.

Materials and Methods

Patient specimens

Human bone marrow and peripheral blood were obtained, with Institutional Review Board approval, by aspiration from the posterior iliac crest of patients with MM either at the time of diagnosis or at the time of clinical evidence of disease relapse. All human participants provided written informed consent. Bone marrow mononuclear cells were isolated by ficoll–hyphaque gradient purification (Mediatech-Cellgro) and kept in Minimum Essential Media (MEMa; Invitrogen) supplemented with 20% FBS (Omega Scientific) and 1% penicillin/streptomycin (Invitrogen) at a concentration of $2 \times 10^6$ cells/mL until use within 18 hours from bone marrow collection. The HS5 human cell line was obtained from American Type Culture Collection and maintained in RPMI 1640 (Invitrogen) supplemented with 10% FBS. HS5 cells were passaged for less than 3 months before renewal from frozen early-passage stocks. Cells were regularly screened for Mycoplasma using a MycoAlert Mycoplasma Detection kit (Lonza).

Compounds

Bortezomib (Fisher Scientific) and panobinostat (LBH 589; Novartis) were reconstituted in dimethyl sulfoxide (DMSO) and stored at −20°C until use. Bortezomib was used at 10 nmol/L for 48 hours. Panobinostat was used at 100 nmol/L for 24 hours. Melphalan (Sigma/M2011) was...
reconstituted in acid-ethanol and stored at −80°C until use (33 mmol/L). Melphalan was used at 25 μmol/L for 24 hours. Apoptotic-induced cell death was determined by flow cytometry using annexin V-PE and 7-amino actinomycin-D. The percentage-specific cell death was calculated as follows: [(experimental apoptosis – spontaneous apoptosis)/(100 – spontaneous apoptosis)] × 100.

**Flow cytometric acquisition and sorting**

Characterization of the progenitor population was conducted using a series of multiple color antibody panels containing up to 7 colors. The panels included: (i) CD138-APC, CD14-FITC, kappa-PE or lambda-PE, CD34-PECy7, CD19-PacificBlue; (ii) CD138-APC, CD27-FITC, kappa-PE or lambda-PE, CD34-PECy7, CD19-PacificBlue; (iii) CD138-APC, CD34-APC, kappa-PE or lambda-PE, CD45-PECy7, CD19-PacificBlue; (iv) CD138-APC, CD34-APC, FITC, kappa-PE or lambda-PE, CD45-PECy7, CD19-PacificBlue; (v) CD138-APC, CD34-APC, FITC, kappa-PE or lambda-PE, CD45-PECy7, CD19-PacificBlue; (vi) CD138-APC, CD14-FITC, kappa-PE or lambda-PE, CD34-PECy7, CD19-PacificBlue; (vii) CD138-APC, CD27-FITC, kappa-PE or lambda-PE, CD34-PECy7, CD19-PacificBlue; (viii) CD138-APC, Notch-1-biotin, streptavidin-FITC, kappa-PE or lambda-PE, CD34-PECy7, CD19-PacificBlue; (ix) CD138-APC, Notch-1-biotin, streptavidin-FITC, kappa-PE or lambda-PE, CD34-PECy7, CD19-PacificBlue; (x) CD138-APC, survivin-AF488, kappa-PE or lambda-PE, CD34-PECy7, CD19-PacificBlue. All antibodies were obtained from BD Biosciences except CD19-PacificBlue (Invitrogen). Notch-1-biotin (eBiosciences), and survivin-AF488 (Cell Signaling Technologies). A minimum of 3 × 10⁵ cells were acquired. All panels included a viability marker, Live/Dead Fixable Yellow Dead Cell Stain kit (Invitrogen). All analyses were conducted using Flowjo software (Treestar). Samples were acquired on a LSRII (BD) equipped with 488, 532, 633, and 405 nm excitation lasers.

To determine ALDH activity of bone marrow mononuclear cells, we used Aldefluor (Stem Cell Technologies), as per manufacturer’s instructions. Activated Aldefluor reagent was added to freshly isolated cells; 30 minutes later, cells were transferred to a tube containing the inhibitor, diethylaminoethylbenzaldehyde (DEAB). Samples were incubated at 37°C for 1 hour and subsequently stained with CD138-APC, kappa-PE or lambda-PE, CD34-PECy7 (BD Biosciences), and CD19-Pacific Blue (Invitrogen). A minimum of 1 × 10⁶ cells were acquired for ALDH analyses.

For sorting, freshly isolated bone marrow mononuclear cells were stained at 10 × 10⁶ cells/mL with CD138-APC, CD14-FITC, kappa-PE or lambda-PE, CD34-PECy7, CD19-Pacific Blue, and a viability marker, Live/Dead Fixable Yellow Dead Cell Stain kit (Invitrogen). Samples were acquired and sorted using a FACSAria-SORP (BD) equipped with 488, 640, 407, 561, and 355 nm excitation lasers. To ensure that only live single cells were collected, we used forward scatter (FSC)-width (W) versus FSC-height (H) and side-scattered (SSC)-W versus SSC-H plots to exclude doublets or cell aggregates. Dead cells were excluded by gating the cells negative for the viability marker. Cells were then gated on CD14-negative cells to exclude monocytes. Finally, cells positive for the light chain of the patient were then gated, and clonotypic cells were sorted into the following populations: (i) LCR CD138+, (ii) LCR CD138–CD19+CD34–, (iii) LCR CD138–CD19+CD34+, (iv) LCR CD138–CD19–CD34+, (v) LCR CD138–CD19+CD27+, and (vi) LCR CD138–CD19+CD27–. We recovered 4 × 10^5 to 2 × 10^6 cells using the above phenotype restrictions, with purity of the sorted populations shown to be greater than 95% (Supplementary Fig. S1). For LCR CD138–CD19+CD34+ cells, purity was not checked after sorting because a low number of cells were recovered.

**Immunoglobulin gene rearrangement detection**

Whole genomic DNA was extracted and amplified from 3 × 10⁴ to 1 × 10⁵ sorted subpopulations using the REPLi-g Mini kit (Qiagen). Sorting gating strategy was first based on light chain expression (Kappa or Lambda) and sorted on the basis of phenotype as follows: A = CD138+/light chain+ and B = CD138–/CD19+/light chain+. To determine Ig heavy chain rearrangements, the amplified genomic DNA was further amplified by PCR using fluorescently labeled primers from the IGH Gene Rearrangement Assay Kit (InVivoscribe Technologies) targeting the joining region (J) and the 3 conserved framework regions between V and J within the IGH gene, as per manufacturer’s instructions. To determine immunoglobulin kappa/lambda light-chain gene rearrangement, fluorescently labeled primers targeting Vκ, Jκ and Vλ, λκ for kappa and conserved regions within Vλ1-3 and Jλ1-3 regions that flank the complementarity determining region 3 for lambda were used (InVivoscribe). No template and amplification controls were run in each test. The resulting PCR products were separated and detected by capillary electrophoresis on the ABI 3130 × l, using GeneMapper 4.0 software (Applied Biosystems).

**Immunoglobulin gene rearrangement sequencing**

The resulting PCR products, as described above, were run in a 2% agarose gel. Clonal bands within the valid assay range were cut and gel extracted using the MinElute Kit (Qiagen) and sequenced on an Applied Biosystems 3130×L genetic analysis system using the primers provided in the IGH Somatic Hypermutation Kit. Sequences were analyzed using VBASE and ClustalW2 multiple sequence alignment.

**Colony formation assays**

Each flow cytometric-sorted population was resuspended in IMEM (Mediatech-CellGro) + 2% FBS (Stem Cell Technologies, catalog #07700) and plated in triplicate in 35 mm² dishes with methylcellulose containing 5% phytohemagglutinin (PHA; Methocult H4553, Stem Cell Technologies) as per the manufacturer’s instructions at a concentration of 1,000 cells/mL for CD34+ cells and at least 100,000 cells/mL for other populations. Conditioned medium from HS5 cells was added where noted, in place of IMEM + 2% FBS. For cultures containing cytokines, IL-2 (50 U/mL), IL-6 (10 ng/mL), IL-10 (50 ng/mL), IL-15 (20 ng/mL), and IL-21 (100 ng/mL; R&D Systems) were added. Cultures were grown at 37°C to 5% CO₂ with a water bath, and colony growth was assessed 14 to 21 days later.

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Colonies morphology was assessed by the Wright–Giemsa staining method using the Hema 3 Stat Pack (Fisher Scientific) in cytopsins slides examined with immunofluorescence microscopy or flow cytometry.

Results

Clonotypic B cells in multiple myeloma bone marrow

Clonotypic B-cell progenitors may contain the putative myeloma cancer stem cell, and represent a malignant, drug-resistant compartment responsible for disease relapse. Characterization of this population(s) is necessary to improve our management of the disease and patient outcomes. We evaluated marrow cells from 58 patients with myeloma for expression of plasma cell and B-cell progenitor surface markers by multicolor flow cytometry and identified distinctive marrow populations based on CD34, CD19, and syndecan-1 (CD138) expression. Plasma cells were shown to be positive for CD138 and negative for CD34 and CD19. Among cells negative for CD138, hematopoietic stem cells (HSC) or multipotent progenitors are CD34+/CD19−, and B cells progenitors encompass CD34+/CD19+ or CD34−/CD19+ subpopulations (24, 25). A minority of the CD19+ marrow cells exhibited a CD34+ phenotype, but most had a differentiated, CD34−, B-cell phenotype. To exclude monocyte contamination, we applied a strict, low SSC gate on CD138− cells (Supplementary Fig. S1). In blood of patients with myeloma (n = 8), we detected very low numbers of circulating plasma cells and a few differentiated CD19+ B cells, but no CD34+/CD19+ cells (Fig. 1A).

To assess for expression of the myeloma clonotype in marrow B cells, we tested initial patients (n = 8) for kappa or lambda light-chain expression using an intracytoplasmic and a surface staining protocol. As expected, cytoplasmic stain was brighter than the surface stain, but percentages of...
Figure 1. (Continued.) B, Ig gene rearrangement of a representative lambda-positive patient. DNA extracted from sorted CD138+/lambda+ and CD138−/CD19+/lambda+ cells followed by PCR amplification using primers targeting all 3 Ig heavy chain (Ig HC) frameworks (FR) and Ig lambda light chain. PCR products were separated and detected by capillary electrophoresis. Peaks shown fall within acceptable ranges for each primer (FR1: 290–360 bp, FR2: 235–295 bp, FR3: 69–129 bp, and lambda: 135–170bp). As a negative control, we used polyclonal DNA, as per manufacturer’s instructions. (Continued on the following page.)
light-chain cells positive by either assay were comparable (data not shown). No light-chain expression was detected in the CD34⁺/CD19⁻/CD138⁻ or the CD34/CD19/CD138-triple negative marrow cells (Fig. 1A). Malignant plasma cells expressed either kappa or lambda light chain. Although the CD19⁺ light chain stain was perhaps skewed in the same direction as the malignant plasma cells, all patients who were tested also had some CD19⁺ cells that expressed the opposite light chain (Fig. 1A).

To determine whether marrow CD19⁺ cells that expressed a surface light chain identical to the plasma cells were clonally related to the myeloma clone, we tested flow-sorted LCR B cells and plasma cells for the Ig heavy- and light-chain gene clonal rearrangements. Fluorescently labeled PCR products were tested by capillary gel electrophoresis; results showed a clonal population of cells yielding the same prominent amplified product within the expected size in both LCR B-cell progenitors and plasma

Figure 1. (Continued.) C, percentages of LCR CD138⁻/CD19⁺ clonotypic cells in whole marrow in patients at time of diagnosis (n = 23) or in patients at time of relapse (n = 21) in kappa (left) and lambda LCR myeloma (right). Statistical analysis was conducted with the Student t test. D, LCR of CD19⁺ cells in bone marrow was determined on the basis of the kappa-to-lambda ratio. Graph compares kappa-restricted (left) and lambda-restricted (right) patients at diagnosis or at relapse compared with healthy marrow cells.
cells (Fig. 1B). Furthermore, both myeloma populations showed identical sequences for IGH somatic hypermutation, confirming the same malignant clone (Supplementary Fig. S2). Therefore, we focused on LCR B cells as they are clonally related to myeloma with the understanding that a proportion of these cells correspond to normal B-cell precursors.

It has been postulated that B-cell numbers are indicative of myeloma burden. In our study, we observed a very low proportion of these cells correspond to normal B-cell cells (Fig. S2). Therefore, we focused on LCR B cells as they are involved in HSC and/or malignant plasma cell survival. B-cell progenitors were characterized by high Notch-1 (90 ± 6%) and survivin (97 ± 2%) expression levels (Fig. 2B) in all patient samples analyzed (n = 4). Expression of Notch-1 and survivin in healthy bone marrow (n = 3) was more than 90% in CD19+/CD34+, CD19+ progenitors, and CD138+ cells (data not shown). In addition, we examined tyrosine-protein kinase c-Kit (CD117) expression levels in B progenitor cells. Historically, normal B-cell progenitors in humans are CD117 negative, findings confirmed in healthy bone marrow (data not shown). B-cell malignancies are characterized as having either negative (B-ALL, lymphoid crisis chronic myelogenous leukemia) or positive CD117 expression (myeloma, B-diffuse large-cell lymphoma; refs. 30, 31). We identified aberrant CD117 expression (n = 3) in a mean of 20.5% (range 11–25) of CD19+/CD34+ cells (n = 3), in 7.8% (range 2.8%–17%) of CD19+/CD34+ B cells (n = 7), and in 4.2% (range 0–15) of CD138+ cells (n = 6; Fig. 2B). Our results showed that CD19 progenitors coexpressed c-Kit in all samples, whereas only 2/6 patient samples coexpressed CD117/CD138. The functional role of Notch, survivin, and c-Kit on clonotypic B-cell progenitors in myeloma remains to be determined.

Stem-like phenotype of clonotypic B-cell progenitors in multiple myeloma bone marrow

We first evaluated the phenotype of LCR CD19+ cells with emphasis on known B-cell progenitors and malignant plasma cell antigens, as presented in Table 1 (n = 7). LCR CD34+/CD19− were characterized by aberrant CD27 and CD20 expression and low levels of CD10 and CD56 markers. ALDH is one of a family of enzymes involved in several detoxifying pathways. Elevated ALDH expression has recently been used to identify a rare stem cell–like population in normal hematopoietic cells and in several tumor types, including leukemia, brain, colon, and breast cancer (26–29) and in MM (16). To determine whether myeloma bone marrow B progenitors contain a high ALDH-expressing stem cell–like population, we used the aldefluor reagent to test for ALDH activity. For each of the tested patients (n = 8), a control sample was run containing a population of cells with fluorescence that is inhibited by the ALDH inhibitor DEAB. High ALDH activity was detected in a mean of 3.05% (0.09%–7.26%) and 2.94% (0.01%–6.9%) of LCR CD34+/CD19+ and CD34−/CD19+ B cells, respectively, and in 8% (1.3%–15.3%) of CD34+/CD19− hematopoietic progenitors. ALDH activity was diminished in CD34+/CD19− progenitor cells from patients with myeloma and increased in myeloma LCRCD19+/CD34+ or CD34− cells when compared with healthy subjects subpopulations (Fig. 2A).

We investigated Notch and survivin expression in LCR B cells as they are involved in HSC and/or malignant plasma cell survival. B-cell progenitors were characterized by high Notch-1 (90 ± 6%) and survivin (97 ± 2%) expression levels (Fig. 2B) in all patient samples analyzed (n = 4). Expression of Notch-1 and survivin in healthy bone marrow (n = 3) was more than 90% in CD19+/CD34+, CD19+ progenitors, and CD138+ cells (data not shown). In addition, we examined tyrosine-protein kinase c-Kit (CD117) expression levels in B progenitor cells. Historically, normal B-cell progenitors in humans are CD117 negative, findings confirmed in healthy bone marrow (data not shown). B-cell malignancies are characterized as having either negative (B-ALL, lymphoid crisis chronic myelogenous leukemia) or positive CD117 expression (myeloma, B-diffuse large-cell lymphoma; refs. 30, 31). We identified aberrant CD117 expression (n = 3) in a mean of 20.5% (range 11–25) of CD19+/CD34+ cells (n = 3), in 7.8% (range 2.8%–17%) of CD19+/CD34+ B cells (n = 7), and in 4.2% (range 0–15) of CD138+ cells (n = 6; Fig. 2B). Our results showed that CD19 progenitors coexpressed c-Kit in all samples, whereas only 2/6 patient samples coexpressed CD117/CD138. The functional role of Notch, survivin, and c-Kit on clonotypic B-cell progenitors in myeloma remains to be determined.

**Table 1.** Phenotypic characterization of clonotypic B cells progenitors in MM bone marrow

<table>
<thead>
<tr>
<th>CD138−/CD34−/CD19− (%) mean (range)</th>
<th>CD138−/CD34+/CD19− (%) mean (range)</th>
<th>CD138+ (%) mean (range)</th>
</tr>
</thead>
<tbody>
<tr>
<td>CD10 7.3 (0.6–16.7)</td>
<td>12.6 (0.6–33.4)</td>
<td>0.62 (0.027–1.68)</td>
</tr>
<tr>
<td>CD20 52 (30.1–99.6)</td>
<td>61.3 (3.2–95.6)</td>
<td>19.6 (1.2–50.4)</td>
</tr>
<tr>
<td>CD27 71.5 (33.6–100)</td>
<td>32.2 (7.6–89.8)</td>
<td>88.8 (72.4–96.7)</td>
</tr>
<tr>
<td>CD56 8.6 (0–15.6)</td>
<td>4.3 (0–10.2)</td>
<td>83.9 (74.7–90.6)</td>
</tr>
</tbody>
</table>

NOTE: Multicolor flow cytometry for detailed phenotypic description of bone marrow subpopulations in patients with MM.
5% lymphocyte-conditioned medium to favor lymphoid differentiation. CD34 cells from patients with myeloma bone marrow (n = 5) were highly efficient, requiring 1,000 cells/plate to successfully grow colonies (Fig. 3A). On the other hand, a minimum of 100,000 cells/plate were needed for colony formation derived from B cells with a colony efficiency estimated in 1 in 25,000 cells. CD138– were unable to form colonies (n = 8) despite increased input number (300,000–1,000,000 cells/plate); however, a few isolated cells persisted in culture. Cells harvested on day 14 are lympho-plasmacytoid (Fig. 3A). As shown in Fig. 3B, a small fraction of CD34+/CD19− cells are able to terminally differentiate into CD138+ cells (8 ± 2%); as opposed to LCR CD19+B cells that differentiated into CD138+ cells (80 ± 5%).

Colony formation of sorted CD34+/CD19+ and CD34−/CD19+B cells was tested in 3 patients with myeloma, with both cell subsets able to grow colonies. Furthermore, B cells, regardless of CD27 expression, successfully grew colonies. Data collected from these studies are shown in Fig. 3C. In summary, LCR B-cell progenitors in myeloma are able to grow colonies and differentiate into mature...
plasma cells (CD138+) regardless of CD34 and/or CD27 expression.

Interactions of hematopoietic progenitors and clonotypic B-cell progenitors in multiple myeloma with stroma-conditioned medium

It has been well established that the tumor microenvironment creates a protective niche that supports myeloma growth (32). In addition, stroma secretes multiple cytokines that support proliferation and differentiation of HSC and committed progenitors. Flow sorted CD34+/CD19– cells from patients with myeloma were grown in methylcellulose supplemented with conditioned medium harvested from HS5 stroma grown for 48 hours (stroma-CM). CFC potential was compared using cytokines known to support plasmablast differentiation (33). Colony efficiency was slightly improved using either stroma-CM or a combination of recombinant human-IL-2, IL-6, IL-10, IL-15, and IL-21. Similar results were obtained when either IL-15 or IL-21 was omitted from the cytokine cocktail (data not shown). Cells harvested from day 14 colonies are CD19+ (35%–50%), and very few terminally differentiated into CD138+ cells (3%–10%; Fig. 4A). We next tested whether CFC efficiency of LCR CD19+ cells could be enriched in the presence of stroma-CM. Stroma-CM significantly improved colony number (3-fold) and size of each individual colony with an estimated colony efficiency of 1:10,000 cells (Fig. 4B).

Apoptosis resistance of clonotypic B-cell progenitors in multiple myeloma bone marrow

We next isolated bone marrow cells by flow sorting to test chemosensitivity of LCR CD19+ cells in patients with myeloma. B cells exhibit relative resistance to melphalan, compared with plasma cells, as determined by annexin V/7-AAD staining (n = 3; Fig. 5A). B cells were less sensitive to apoptosis mediated by bortezomib (n = 4; Fig. 5B). Lenalidomide did not target LCR CD19+ cells (Fig. 5C). We next tested the role of a hydroxamic acid-derived histone deacetylase inhibitor (LBH589, panobinostat), which has been shown to induce in vitro apoptosis in myeloma plasma cells (34) and acute lymphocytic lymphoblasts (35). Panobinostat (100 nmol/L for 24 hours) activity against B-cell progenitors in all treated patients (n = 5) was comparable to CD138+ cells (Fig. 5D).

Discussion

Within the heterogenic cancer cell population, it is hypothesized that only a small subset of neoplastic cells is capable of extensive proliferation and differentiation leading to tumor development. In myeloma, the self-renewal compartment has been described within early B clonotypic progenitors or in memory B cells with the caveat that even CD34+/CD19– cells (5) and mature CD138+/CD38+/CD45– have been shown to reproduce myeloma in xenograft models (17).

Figure 2. (Continued). B, representative contour plots showing fluorescence-activated cell sorting (FACS) labeling with Notch-1, survivin, and CD117 (c-Kit) expression of bone marrow subpopulations. Gates are based on fluorescence minus one (FMO) controls (not shown).
In our study, we provide evidence of the existence of clonotypic LCR B cells, confirmed by molecular studies, in bone marrow from a large series of adult patients, in agreement with previous reports (3, 36, 37). Our analyses of discrete stages of B-cell differentiation by antigen expression patterns in myeloma paralleled normal B-cell development, with a few possible exceptions. Based on combined assessment of the CD19 and CD34 antigens, we showed the existence of clearly defined populations among LCR B cells. Both CD34+/CD19+ and CD34−/CD19+ expressed light chain in all tested patients, suggesting aberrant light-chain processing in myeloma clone and/or aberrant expression of CD34 in mature CD19+ cells. If one assumes CD34+/CD19+ as a more undifferentiated population, the relative number of B-cell subsets increased from more immature cells to more differentiated B cells, indicating that malignant B-cell differentiation parallels normal B-cell development. Multiparameter flow cytometry provides a powerful tool to elucidate different stages of B-cell development. In our study, we used a very strict gate criterion to exclude CD14+ cells, thus avoiding monocyte contamination because of nonspecific coating of M-protein to monocyte cell surfaces that is not completely washed off during specimen processing and/or unspecific binding of monoclonal antibodies, as previously described (38). Our gating strategy, however, excluded myeloma monocytoid B cells characterized by a higher SSC/FSC, which are detected with specific anti-CD19 monoclonal antibody, thus explaining differences in results versus a previous report that used less stringent criteria (39).

The overall number of CD19+ B cells in patients with myeloma is comparable to that shown in healthy

Figure 3. CFC of clonotypic B-cell progenitors in MM bone marrow. A, comparison of colony development in methylcellulose (MC) supplemented with PHA stimulated-5% lymphocyte-conditioned medium (PHA-LCM). Bone marrow (BM) cells were gated and sorted as described in Design and Methods. MC cultures were established with CD138−/CD19−/CD34− (1,000 cells) or LCR CD138−/CD19−/CD34+ (100,000 cells) and CD138+ cells (300,000 cells). Colonies were scored after 14 days of culture. Graph shows results (mean ± SD) from 5 patients with myeloma. Colonies were harvested from each group for morphologic evaluation (hematoxylin-eosin stain, Zeiss Axiovert Inverted Microscope, magnification ×40). B, sorted CD138−/CD19−/CD34− or CD138−/LCR CD19+ and CD138+ cells were cultured for 14 days. After induction stage, developing colonies or CD138+ cells that remained in culture were harvested for fluorescence-activated cell sorting (FACS) analysis. Representative contour plots show CD138 expression on input cells before culture (day 0) and on harvested cells (day 14). C, colony counts in MC PHA-LCM cultures for 14 days with LCR BM cells, sorted on the basis of phenotype as indicated. Results (mean ± SD) show colony numbers of 3 myeloma patients/experiment.
Clonotypic B-cell Progenitors in Multiple Myeloma Marrow

Figure 4. Colony formation cell assay of myeloma CD138+/CD34+/CD19− multipotent progenitors or clonotypic B cells in the presence of marrow-conditioned medium. A, quantification of hematopoietic progenitors in methylcellulose (MC) colony assays with sorted CD138+/CD34+/CD19− cells (n = 3). Culture was supplemented with 5% lymphocyte-conditioned medium (PHA-LCM) in all culture conditions (baseline), and with either HS5 stroma-conditioned medium (stroma-CM) or recombinant human IL-2, IL-6, IL-10, IL-15, and IL-21. Graph represents colony output of triplicate experiments from 3 patients with myeloma at 14 days. Representative contour plots show phenotype (CD34, CD19, and CD138) of plucked cells from MC culture. CD138 cells in each culture were analyzed for light chain expression. Histogram shows kappa (solid line) and lambda (dotted line) light chain (LC) versus condition at 14 days. Representative contour plots show phenotype (CD34, CD19, and CD138) of plucked cells from MC culture. CD138 cells in each culture condition were analyzed for light chain expression. Histogram shows kappa (solid line) and lambda (dotted line) light chain (LC) versus fluorescence minus 1 (FMO) controls (gray shade). B, sorted LCR CD138−/CD19+ CD138+ cells were grown in MC PHA-LCM (baseline) or in the presence of stroma-CM. Colonies were scored at day 14 of culture. Images show representative colonies grown in each condition (Zeiss Axiovert Inverted Microscope, magnification 5×).

individuals (40). Clonotypic B-cell compartment size in patients with newly diagnosed or in patients with myeloma with clinical evidence of relapse remains constant, as previously shown in blood (22). CD34+/CD19+ cells were not detected in circulation, suggesting that these cells reside in the marrow niche. CD34+/CD19+ expressed the TNF receptor CD27, expressed in normal memory B cells, and to a lesser extent CD20, denoting possible differentiation and/or aberrant expression. CD27 has been reported to be expressed in progenitor B cells in other B-cell malignancies; however, its role in malignant growth remains to be defined (41, 42). Work by Sanz and colleagues (24) suggested a dual B-cell development pathway where pro-B cells (CD34+/CD19+/CD10+) are preceded by either a pre–pro B cell (CD34+/CD19+/CD10−) or a early B-cell/common lympoid progenitor (CD34+/CD19−/CD10+) and formerly described in B-cell acute lymphocytic leukemia (43). In MM B progenitors, we identified both CD10-negative and -positive subpopulations within CD34+/CD19+ cells, potentially mimicking 2 distinct pathways. Stroma coculture differentiation studies could help to track the order of emergence of B-cell differentiation stages in MM.

To study "stemness" of LCR B cells, we assessed stem cell-like phenotype and/or evaluated stem cell function by ALDH enzymatic activity and carried out in CFC assays. Myeloma CD19−/CD34+ multipotent progenitors generated polyclonal CD138+ cells in methylcellulose culture, suggesting that early noncommitted CD19−/CD34+ cells in myeloma are not involved in clonal B-cell development. LCR B cells exhibited significantly increased ALDH activity.
versus that shown in healthy donors, and CFC assays showed activity in all stages of B-cell differentiation in myeloma. In addition, hematopoietic stroma-derived cytokines support CFC growth of malignant B progenitors (44). In summary, these finding suggest that a subset of marrow CD19+/CD34+ cells and CD19+/CD34− B cells in myeloma are enriched for cells with a cancer stem cell–like phenotype and/or function.

The cancer stem cell hypothesis postulates that this compartment is intrinsically more resistant to therapy than other tumor cells, constituting a minimal residual disease reservoir responsible for disease relapse. Successful therapy must therefore eliminate these cells, which is hampered by their high resistance to commonly used treatment modalities. In our study, we showed that LCR B cells are relatively resistant to agents commonly used to target CD138+ cells (melphalan, bortezomib, and lenalidomide) as previously shown (4, 16). Panobinostat has been shown to be a potent growth inhibitor against resistant B lymphoblast-promoting histone hyperacetylation and cell growth gene regulation (35). Ongoing panobinostat clinical trials have reported encouraging results in myeloma (45, 46). In this study, we provide information suggesting a potential role of panobinostat to target clonotypic B cells. Strategies to optimize panobinostat-induced apoptosis in synergy with other drugs remain to be explored.

The clinical relevance of targeting cancer stem cell-associated surface markers has been previously shown (47). CD117 seems to be aberrantly expressed in LCR B cells compared with normal B-cell progenitors. We hypothesize that, whereas c-Kit expression is preserved in clonotypic B-cell progenitors as they differentiate into mature malignant plasma cells, its expression is lost on the majority of patients with myeloma. Further studies in a larger series of patients are necessary to confirm these results and more importantly to explore both the functional role of c-Kit and

Figure 5. Drug sensitivity of clonotypic B-cell progenitors in MM bone marrow. A, apoptotic response of myeloma patient’s bone marrow (BM) cells after treatment with melphalan (25 μmol/L) or acid-ethanol (control) for 48 hours (n = 3). Multipotent progenitors were sorted on the basis of CD138+/CD19−/CD34+ expression. To isolate CD138− or LCR CD19− cells, BM was first gated on surface LCR corresponding to each patient’s plasma cells (kappa or lambda). Apoptosis was determined with annexin V-PE and 7-AAD staining. Percentage of each population is indicated in each quadrant of representative contour plots. B, apoptosis responses to treatment of BM subpopulations with bortezomib (10 nmol/L) or DMSO (control) for 48 hours. Graph represents mean ± SD of percentage-specific apoptosis determined by flow cytometry (n = 3). C, apoptosis responses to treatment of BM subpopulations with lenalidomide (10 μmol/L) or DMSO (control) for 48 hours. Graph represents mean ± SD of percentage-specific apoptosis determined by flow cytometry (n = 3). D, apoptosis responses to treatment of BM subpopulation with panobinostat (100 nmol/L) or DMSO (control) for 24 hours. Graph represents mean ± SD of percentage-specific apoptosis determined by flow cytometry (n = 5).
the clinical utility of novel tyrosine kinase inhibitors. Treatment of patients with anti-CD20 antibody failed to achieve clinical response (39, 48), suggesting the existence of myeloma CFC progenitors that are CD20 negative, as we have shown. Notch and survivin are expressed in all B-cell development stages. Novel treatment strategies with monoclonal antibodies, inhibitors, and/or vaccines to target these surface proteins should be explored before drawing any conclusions on the functional role of these molecules on myeloma B-cell progenitors (49, 50).

Cancer chemotherapy is deemed successful if it reduces tumor burden and induces apoptosis of "cancer cells." The challenge remains to identify all cellular components involved in the organized hierarchy of heterogeneous cell populations within myeloma. LCR B cells are relatively rare populations that have been shown to grow colonies in CFC assays and that are chemoresistant, suggesting they potentially fit the cancer stem cell definition. Targeting clonotypic B-cell progenitors in addition to inducing apoptosis of terminally differentiated plasma cells by novel treatment strategies may reduce disease recurrence and may improve long-term survival rates in myeloma.

Disclosure of Potential Conflicts of Interest
No potential conflicts of interest were disclosed.

References

Authors' Contributions
Conception and design: K.H. Shain, R. Baz, C. Anasetti, W.S. Dalton, L. Perez
Development of methodology: K. Boucher, R. Widen, K.H. Shain
Acquisition of data (provided animals, acquired and managed patients, provided facilities, etc.): K. Boucher, N. Parquet, R. Widen, R. Baz, M. Alisa, J. Koomen
Analysis and interpretation of data (e.g., statistical analysis, biostatistics, computational analysis): K. Boucher, N. Parquet, R. Baz, J. Koomen, C. Anasetti, W.S. Dalton, L. Perez
Writing, review, and/or revision of the manuscript: K. Boucher, N. Parquet, K.H. Shain, R. Baz, M. Alisa, J. Koomen, C. Anasetti, W.S. Dalton
Administrative, technical, or material support (i.e., reporting or organizing data constructing databases): K. Boucher, L. Perez
Study supervision: L. Perez

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Kelly Boucher, Nancy Parquet, Raymond Widen, et al.

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