Molecular pathogenesis of multiple myeloma and its premalignant precursor

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Multiple myeloma is a monoclonal tumor of plasma cells, and its development is preceded by a premalignant tumor with which it shares genetic abnormalities, including universal dysregulation of the cyclin D/retinoblastoma (cyclin D/RB) pathway. A complex interaction with the BM microenvironment, characterized by activation of osteoclasts and suppression of osteoblasts, leads to lytic bone disease. Intratumor genetic heterogeneity, which occurs in addition to intertumor heterogeneity, contributes to the rapid emergence of drug resistance in high-risk disease. Despite recent therapeutic advances, which have doubled the median survival time, myeloma continues to be a mostly incurable disease. Here we review the current understanding of myeloma pathogenesis and insight into new therapeutic strategies provided by animal models and genetic screens.

Introduction

Multiple myeloma (MM) is an age-dependent monoclonal tumor of BM plasma cells (PCs). MM cells are similar to long-lived, post-germinal center (post-GC) PCs, and are characterized by strong BM dependence, extensive somatic hypermutation (SHM) of Ig genes, and absence of IgM expression in all but 1% of tumors (1). However, MM cells differ from healthy PCs because they retain the potential for a low rate of proliferation (1%–3% of cycling cells). MM usually is associated with end-organ damage that can include lytic bone lesions, anemia, immunodeficiency, and decreased renal function (2). It is the second most common hematopoietic malignancy, with an incidence of about 20,000 per year in the United States (3). Despite recent therapeutic advances, MM continues to be a mostly incurable disease, but the median survival has increased from 3 years to over 6 years (4). MM has served as a model for understanding lymphoid tumors because it is characterized by the presence of a premalignant precursor tumor and defined disease stages; researchers have been able to isolate pure tumor cells at all stages. In addition, the study of MM has provided significant knowledge about the critical role of the BM microenvironment in hematopoietic malignancy (5).

Monoclonal gammopathy of undetermined significance is a common premalignant tumor that precedes MM

Monoclonal gammopathy of undetermined significance (MGUS) has a prevalence of 4% in Caucasians over the age of 50 (6, 7). It can be subclassified as lymphoid (15%) or PC (85%) MGUS, which can progress sporadically at average rates of 1% per year to chronic lymphocytic leukemia, lymphoma, lymphoplasmacytoma, or Waldenstrom’s macroglobulinemia, and MM, respectively (8). Lymphoid MGUS and PC MGUS can be distinguished by morphology, but more frequently clinicians use an imperfect method based on the type of monoclonal Ig (mIg detected in serum or urine: mostly IgM for lymphoid MGUS and mostly non-IgM (including Ig light chain only; ref. 6) for PC MGUS. MGUS is distinguished clinically from MM by having no detectable end-organ damage, a serum mIg of less than 3 g/dl, and a BM PC content less than 10% of mononuclear cells (but BM biopsies are not done routinely on these patients) (9).

Although MGUS typically is asymptomatic, some patients develop primary amyloidosis as a result of the accumulation of pathological mlg light chain deposits in various tissues (2, 10). Most — if not all — symptomatic MM tumors are preceded by MGUS (11, 12). Smoldering MM (SMM) also has no detectable end-organ damage, but differs from MGUS by having a serum mlg higher than 3 g/dl or a BM PC content of more than 10% and an average rate of progression to symptomatic MM of 10% per year. Currently there are no tests that measure phenotypic or genotypic markers on tumor cells that predict progression (8). However, two models based on serum and flow cytometric tests stratify patients into groups that progress at yearly rates for MGUS and SMM, respectively, of 0.3% to 12% and 0.8% to 29% (8, 13–15). These models are being used to select high-risk SMM patients for clinical trials (16, 17).

An abnormal immunophenotype distinguishes healthy PCs from tumor cells

Healthy BM PCs are CD38+CD138+CD19+CD45+CD56–. Although MGUS, SMM, and MM tumor cells also are CD38+CD138+, 90% are CD19+, 99% are CD45+ or CD45–, and 70% are CD56+ (14, 18). Perhaps the normal cell that is the target of transformation has this phenotype. Alternatively, it is possible that transformation activates an epigenetic program that includes the changes in expression of these surface antigens. Despite our inability to explain the abnormal immunophenotype, it provides a useful assay for distinguishing tumor and healthy PCs.

The phenotype of the MM stem/tumor-propagating cell

Unlike CD38– or CD138– cells, CD38+ or CD138+ MM cells can proliferate and induce lytic bone lesions when transplanted into ectopic bone in SCID-hu or SCID-rab immunodeficient mouse models (19). This suggests that the tumor-propagating cell has a PC phenotype, with the caveat that it is not possible to serially transplant the cells more than a few cycles. However, recently it was shown that CD138+ but not CD138– cells from two PC leukemia (PCL) tumors could be serially cloned in vitro when cytokines (IL-6 and IGF-1) were included in the media (20). By contrast, others have reported that CD38 CD19 CD27+ cells, but not CD38+ or CD138+ cells, can form in vitro clones or in vivo tumors in immunodeficient NOD/
SCID mice that give rise to CD138+ cells (21, 22). This suggests that there is a tumor-propagating cell with a B cell phenotype, although these experiments have not shown that the in vitro clones or in vivo tumors share both the clonotype and the genomic abnormalities that are present in the bulk of the corresponding MM tumor cells (23). We conclude that tumor-propagating cells have a PC phenotype, although it is unknown what fraction of MM tumor cells is capable of replication. However, it remains possible that tumor cells with a B cell phenotype might contribute to progression of MGUS to MM, to tumor propagation and progression, or to relapse after an apparently complete remission.

Symptomatic MM stages
Progression of symptomatic MM is associated with expanding BM tumor mass and increasingly severe organ impairment or symptoms (2). Despite BM dependence, sometimes the tumor extends to extramedullary locations, such as spleen, liver, and extracellular spaces. Extramedullary MM (EMM) typically is a more aggressive tumor that sometimes is associated with primary or secondary PCL, depending on whether a preceding intramedullary MM was recognized. More than 60 human MM cell lines (HMCLs), which provide a renewable repository of most oncogenic events involved in initiation and progression of the corresponding MM tumor, have been generated, but mostly from EMM tumors (24, 25).

A critical but complex role for the BM microenvironment in MM
Similar to long-lived PCs, MGUS and MM cells are dependent on the BM microenvironment, which includes the extracellular matrix and many kinds of cells, e.g., stromal cells, osteoclasts, osteoblasts, immune cells (T lymphocytes, dendritic cells), other hematopoietic cells and their precursors, and vascular endothelial cells (refs. 1, 26, 27; Figure 1). Reciprocal positive and negative interactions among these cells are mediated by a variety of adhesion molecules, cytokines, and receptors. Additional stimuli such as hypoxia result in activation of HIF-1α and secretion of VEGF (28). For MM, there are several biological phenomena that are affected by these tumor-host interactions, including homing to BM; spread to secondary BM sites by the bloodstream; generation of many paracrine factors that are involved in the survival, differentiation, and proliferation of tumor cells (most notably IL-6, IGF-1, and APRIL); angiogenesis; osteoclastogenesis; inhibition of osteogenesis; enhanced resistance to chemotherapeutic agents; humoral and cellular immunodeficiency; and anemia. Many of these tumor-host interactions (e.g., homing and differentiation/survival) appear to be qualitatively similar for PC and MM tumor cells, whereas the altered composition of the BM microenvironment represents a pathological response to the MGUS and MM tumor cells. Several therapies (such as immunomodulators and proteasome inhibitors) might target not only the tumor cell but also its interaction with the BM microenvironment. Identifying other therapies directly targeting the microenvironment or its interaction with MM tumor cells is an active area of investigation (29, 30).

Seven primary IgH translocations are shared by MM and MGUS tumors
There are three primary IgH translocation groups that involve the cyclin d (CCND) family, the MAF family, and Wolf-Hirschhorn syndrome candidate 1/FGFR3 (MMSET/FGFR3) genes (Table 1 and refs. 8, 31). These mostly balanced translocations position an oncogene under control of the IgH intronic (Emu) and/or 3′ IgH

**Figure 1**
Interactions of MM tumor cells with the BM microenvironment. Five kinds of cells in the BM microenvironment are depicted, as well as a few of the complex interactions among these cells and MM cells. Some of the critical survival and growth factors, such as IL-6, are made by more than one kind of BM cell. External stimuli, such as hypoxia and internal signals resulting from dysregulated MYC, stimulate HIF-1α and VEGF secretion, which in turn stimulate endothelial cells to secrete IGF-1. The hallmark uncoupling of bone remodeling is partially explained by an increase in osteoclast activity (mediated by RANKL/RANK interactions, decreased osteoprotegerin (OPG), and increased MIP-1α) and a decrease in osteoblast activity (mediated by DKK1 and IL-3). The resultant increase in osteoclast activity stimulates the survival and growth of MM cells, at least partially by increased IL-6. Potential therapeutic agents that directly inhibit some of these interactions include bisphosphonates (which inhibit osteoclast function), anti-RANKL antibody, anti-DKK1 antibody, and exogenous OPG.
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Table 1
Comparison of different molecular classifications in MM

<table>
<thead>
<tr>
<th>Group</th>
<th>TC</th>
<th>Gene</th>
<th>Percentb</th>
<th>UAMS</th>
<th>HOVON-GMMG</th>
<th>Comment</th>
</tr>
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<tr>
<td>Cyclin D translocation</td>
<td>11q13a</td>
<td>CCND1</td>
<td>15</td>
<td>CD1, CD2</td>
<td>CD1, CD2</td>
<td>Divergent clinical outcomes for CD1 and CD2</td>
</tr>
<tr>
<td></td>
<td>6p21a</td>
<td>CCND3</td>
<td>2</td>
<td>CD1, CD2</td>
<td>CD1, CD2</td>
<td>Divergent clinical outcomes for CD1 and CD2</td>
</tr>
<tr>
<td></td>
<td>12p13a</td>
<td>CCND2</td>
<td>&lt;1</td>
<td>CD1, CD2</td>
<td>CD1, CD2</td>
<td>Divergent clinical outcomes for CD1 and CD2</td>
</tr>
<tr>
<td>MMSET translocation</td>
<td>4p16</td>
<td>MMSET</td>
<td>15</td>
<td>MS</td>
<td>MS</td>
<td>FGFR3 expressed in 75% of MM patients</td>
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<td>MAF translocation</td>
<td>16q23</td>
<td>MAF</td>
<td>5</td>
<td>MF</td>
<td>MF</td>
<td>Strong transcriptional profile with expression of ITGB7</td>
</tr>
<tr>
<td></td>
<td>20q12</td>
<td>MAFB</td>
<td>2</td>
<td>MF</td>
<td>MF</td>
<td>Strong transcriptional profile with expression of ITGB7</td>
</tr>
<tr>
<td></td>
<td>8q24</td>
<td>MAFA</td>
<td>&lt;1</td>
<td>MF</td>
<td>MF</td>
<td>Strong transcriptional profile with expression of ITGB7</td>
</tr>
<tr>
<td>HRD</td>
<td>D1</td>
<td>CCND1</td>
<td>33</td>
<td>HY</td>
<td>HY, CD-1, NF-κB, CTA, PRL3</td>
<td>NF-κB target gene expression may be ligand dependent or may result from activating mutations</td>
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<tr>
<td></td>
<td>D1+D2</td>
<td>CCND1, CCND2</td>
<td>7</td>
<td>PR</td>
<td>PR, CTA</td>
<td>D1+D2 might occasionally be a progression from D1; PR contains 5%–10% of each TC group, with the exception of D1+D2 and None (contains &gt;40% of each)</td>
</tr>
<tr>
<td>Other</td>
<td>Noneg</td>
<td>No CCND</td>
<td>2</td>
<td>PR</td>
<td>PR CTA</td>
<td>Biallelic RB deletion frequent in None</td>
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<tr>
<td></td>
<td>D2</td>
<td>CCND2</td>
<td>18</td>
<td>PR LB</td>
<td>LB CTA PRL3</td>
<td>PRL3 lacks poor risk features and is enriched for ISS 1® patients</td>
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</table>

*HOVON-GMMG indicates Dutch-Belgian Cooperative Trial group for Hematology-Oncology and German Multiple Myeloma Group. The 11q13 and 6p21 are combined into one TC group; the 12p13 is not usually identified and thus is included in the D2 group. PR, proliferation. bPercent refers to the percent of MM patients in each group. cNone refers to a group of patients with no CCND expression. dISS 1, International Staging System (ISS) 1.

(3'E) enhancers. As the breakpoints usually occur near or within IgH switch regions, but sometimes near VDJ sequences, it seems likely that the translocations are related to errors in class switch recombination or SHM, as normal B cells pass through the GC (1). In rare instances, tumors may have translocations involving two of the primary translocation groups, suggesting that there can be some complementation (25).

It is thought that CCND translocations only dysregulate expression of a CCND gene. In contrast, MAF translocations dysregulate expression of a MAF transcription factor that causes increased expression of many genes, including CCND2 and adhesion molecules that are thought to enhance the ability of the tumor cell to interact with the BM microenvironment (32–34). The contributions of the two genes dysregulated by t(4;14) remain controversial. MMSET is a chromatin-remodeling factor that is overexpressed in all tumors with a t(4;14), whereas about 20% of tumors lack der(14) and FGFR3 expression. The rare acquisition of FGFR3-activating mutations during progression confirms a role for FGFR3 in MM pathogenesis. Although an activated mutant FGFR3 can be oncogenic, it recently was shown that wild-type FGFR3 (as is found in most t(4;14) tumors) can also contribute to B cell oncogenesis (35). It remains to be determined whether FGFR3 is critical early in pathogenesis but becomes dispensable during progression of t(4;14) MM. Preclinical studies suggest that tyrosine kinase inhibitors are active only against t(4;14) HMCL with activating mutations of FGFR3, whereas anti-FGFR3 monoclonal antibodies that inhibit FGFR3 signaling but also elicit antibody-dependent, cell-mediated cytotoxicity are active against HMCLs expressing wild-type FGFR3 (36, 37). Despite an apparently indispensable role in t(4;14) MM, it remains to be determined how MMSET, which sometimes has aminaltermed truncations caused by the translocation, contributes to MM pathogenesis. However, MMSET is a histone methyltransferase for H4K20 and, when overexpressed, results in a global increase in H3K36 methylation and a decrease in H3K27 methylation, which might explain some of the many changes in gene expression associated with t(4;14) tumors (32, 38, 39). In addition, it was recently determined that MMSET has a role in DNA repair (40). Importantly, loss of MMSET expression alters adhesion, suppresses growth, and results in apoptosis of HMCLs, suggesting that it is an attractive therapeutic target (39).

Chromosome content is associated with different oncogenic pathways
Nearly half of MGUS and MM tumors are hyperdiploid (HRD), with 48–75 chromosomes (most have 49–56), including extra copies of three or more odd-numbered chromosomes (chromosomes 3, 5, 7, 9, 11, 15, 19, or 21; ref. 31). Non-HRD (NHRD) tumors have fewer than 48 and/or more than 75 chromosomes. Strikingly, only about 10% of HRD tumors have a primary IgH translocation, whereas about 70% NHRD tumors have an IgH translocation. Tumors with a t(11;14) translocation may represent a distinct category of NHRD tumors, as they often are diploid or pseudodiploid. Curiously, EMM tumors and HMCLs nearly always have a NHRD genotype, suggesting that HRD tumors are more stromal cell dependent than NHRD tumors (41, 42). Although it has been proposed that NHRD and HRD tumors represent different pathways of pathogenesis (31, 43), the timing, mechanism, and molecular consequences of hyperdiploidy are unknown.

Universal CCND dysregulation in MGUS and MM tumors
Despite a low proliferation index, there is increased expression of a CCND gene in virtually all MGUS and MM tumors (Figure 2 and refs. 31, 32). Firstly, this is related to direct or indirect dysregula-
tion, respectively, in tumors with CCND and MAF group translocations. Secondly, although the mechanism is not understood, MMSET/FGFR3 tumors also express moderately increased levels of CCND2. In addition, although normal B cells and PCs do not express CCND1, about two-thirds of MGUS or MM tumors without a primary IgH translocation (virtually all are HRD) express CCND1, and sometimes CCND2, in a biallelic manner. Notably, an extra copy of chromosome 11 is found mainly in HRD tumors that express CCND1. Most of the remaining tumors (about 40% of which are HRD) express increased CCND2 compared with normal PCs. Finally, the infrequent (<5%) tumors that do not express increased levels of a CCND gene often have inactivated RB1, obviating the need for CCND to stimulate proliferation (31).

**Additional oncogenic events in MGUS and MM tumors**

**Chromosome 13 deletion.** A recent study concludes that chromosome 13 deletion can be an early event in MGUS (e.g., in MAF, MMSET tumors) or a progression event (e.g., in t(11;14) tumors) (44). The pathogenic effect of this chromosome deletion is unknown, though it is possible it may lead to progression due to haploinsufficiency of RB1 (31).

**Activating mutations of RAS and BRAF.** The prevalence of activating NRAS or KRAS mutations is about 15%-18% each in newly diagnosed and relapsed MM tumors (31, 45) but is substantially higher in tumors that express CCND1 compared with tumors that express CCND2. For MGUS tumors, the prevalence of NRAS mutations is 7%, but KRAS mutations have not been described (8). This is consistent with increasing evidence that NRAS and KRAS mutations have overlapping but non-identical effects (46), and with the hypothesis that KRAS mutations provide a molecular mark of the transition of MGUS to MM (23, 47). MM tumors depend on signals to long-lived PCs by stimulating TACI, BCMA, and BAFF receptors to activate the NF-κB pathways (56). Most MGUS and MM tumors highly express NF-κB target genes, suggesting a continued role of extrinsic signaling in PC tumors (57, 58). Activating mutations in positive regulators and inactivating mutations in negative regulators of the NF-κB pathway have been identified in at least 20% of untreated MM tumors and approximately 50% of HMCCLs, rendering the cells less dependent on ligand-mediated NF-κB activation (49). Small molecules that inhibit extrinsic signaling (including TACI.Fc, I KKβ, and NIK [MAP3K14]) are being developed as potential therapeutic agents (59, 60). There is also some evidence suggesting that cells addicted to constitutive NF-κB activation may be particularly sensitive to proteasome inhibition (58).

**Chromosome 17p loss and abnormalities of TP53.** Deletions that include the TP53 locus occur in approximately 10% of untreated MM tumors, and the prevalence increases with disease stage (31, 42). TP53 mutations were present in 37% of untreated MM tumors with del17p, but not in patients without del17p (61). It remains to be determined whether the poor prognosis associated with monoallelic del17p but no TP53 mutation is due to haploinsufficiency or to predisposition to complete inactivation of TP53. Recently, decreased expression of microRNAs miR199, miR192, and miR215 in MM was reported to increase MDM2, an inhibitor of TP53 (62).

Gain of chromosome 1q and loss of chromosome 1p. These genomic events frequently occur together in MM, and each is associated with a poor prognosis (31, 63). The relevant genes on 1q are unclear at this time. By contrast, there are potential targets on two regions of 1p that are associated with the poor prognosis: CDKN2C (p18INK4c) at 1p32.3 and FAM46C at 1p12 (64, 65). Homozygous deletion of CDKN2C, which is present in about 30% of HMCL and about 5% of untreated MM tumors, is associated with increased proliferation and a poor prognosis, whereas monoallelic deletion is not. Mutations of FAM46C — often with hemizygous deletion — were identified in 3.4% and 13% of MM tumors in two studies, and in 25% of 16 HMCL (49, 64).

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**Figure 2**

Early and late disruption of the RB pathway. The early dysregulation of a cyclin D gene provides the basis for the TC classification (see text for details). Yet most MGUSs and most MM tumors are minimally proliferative, perhaps a result of the inhibitory effects of p18INK4c, since p16INK4a usually is not expressed. Increased proliferation at late stages of progress sometimes is associated with inactivation of p18 or RB1, but most proliferative tumors have a paradoxically high level of p18INK4c expression and normal levels of RB1.
Other pathogenic events. Secondary Ig translocations, including most IgK and IgL translocations and IgH translocations not involving one of the seven primary partners, can occur at all stages of disease, and with a similar frequency in HRD and NHRD tumors, but apart from MYC, few partner loci have been identified (25). Other genomic rearrangements are frequent, but only a few specific target genes have been identified (63, 66, 67). Changes in DNA methylation are frequent, with one study suggesting that a marked increase in hypomethylation is associated with the MGUS-to-MM transition (68), whereas a second study suggests only a small increase in hypomethylation for MM compared with MGUS (69). Mutations in seven genes regulating RNA metabolism, protein translation, and homeostasis were identified in 16 of 38 patients (49). In addition to previous studies implicating roles for MMSET and KDM6A (UTX), genomic sequencing studies found that other histone-modifying enzymes are frequent targets of mutation, although the epigenetic consequences are unknown (49). Similarly, changes in microRNA expression at different stages have been identified, but more extensive studies are needed (62, 70).

Model for molecular pathogenesis of MGUS and MM
The pathogenesis of MGUS and MM can be considered as occurring in three phases (Figure 3 and refs. 8, 34). Early, partially overlapping genetic events common to MGUS and MM include a minimum primary IgH translocations, hyperdiploidy, and del13 that lead directly or indirectly to dysregulation of a CCND gene. Second, the transition from MGUS to MM is associated with increased MYC expression and sometimes with activating mutations of K-RAS or chromosome 13 deletion. Early and late progression events for symptomatic MM tumors are shown.

Clinical implications of molecular classifications
The presence of primary IgH translocations and the universal overexpression of CCND genes led to the development of the translocations and cyclin D (TC) classification that is focused mainly on early events common to MGUS and MM, and therefore is applicable to the classification of both MGUS and MM tumors (Table 1). Unsupervised analyses of microarray gene expression profiling (GEP) have identified additional MM tumor groups with shared patterns of gene expression (71, 72) that highlight other important secondary events that can occur in each subtype of MM: proliferation and expression of NF-κB target genes, cancer-testis antigens (CTAs), and the phosphatase PTP4A3/PRL3. The University of Arkansas for Medical Science (UAMS) CD1 and CD2 classification groups represent subgroups of patients with t(11;14) and t(6;14) tumors, with the former characterized by arginosuccinate synthetase 1 expression.
and the later by expression of B cell antigens (CD20, VPREB, CD79A). Interestingly, CD1 and CD2 groups identify patients with markedly different clinical outcomes. Of the various genetic events in MM, the one most important clinically is the t(4;14) chromosome translocation. It is associated with a poor prognosis in patients treated with alkylating agents, immunomodulatory drugs (IMiDs), and bortezomib. However, there is a clear survival advantage to the upfront use of bortezomib versus control in these patients (73–76), with a suggestion that prolonged use totally overcomes the adverse prognosis. Numerous randomized, controlled clinical trials of IMiDs in the treatment of thousands of MM patients have been performed, with several studies showing improvements in overall survival (OS) for the cohort receiving IMiDs relative to the control group. Unfortunately, we do not know which molecular subgroups received the maximum benefit from IMiDs versus those that received no benefit. From these studies there are a few reports of the effects of IMiDs on the survival of a molecular subgroup (Table 2). In summary, it appears that thalidomide is no better and often is even worse than placebo in patients with high-risk genetic features (e.g., t[4;14], t[14;16], and del17p). Unlike other GEP-defined risk scores (which all appear to discriminate patients defined as high risk by a GEP index of proliferation or genicity has been described in patients with high-risk MM (67), associated in one case with alternating clonal dominance under selective pressure; these observations have important clinical implications. The findings suggest a competition between subclones for limited resources and raise the possibility that early, suboptimal treatment may eradicate the “good,” drug-sensitive clone, making room for the “bad,” drug-resistant clone to expand. They support the use of aggressive multidrug combination approaches for high-risk disease with unstable genomes and clonal heterogeneity and sequential one- or two-drug approaches for low-risk disease with stable genomes and lacking clonal heterogeneity.

### Challenges for the future

Despite marked progress in understanding the molecular pathogenesis of MM, many important questions remain unanswered. What are the phenotypic and genotypic markers that distinguish MGUS, SMM, and MM, and can they be used to predict progression or suggest therapeutic strategies that will prevent or delay progression? What is the basis for the immunophenotype that distinguishes healthy PCs from tumor PCs? What are the molecular mechanisms and oncogenic consequences of hyperdiploidy? Will studies on cell lines and current animal models provide an adequate way of determining the biological effects — and value as therapeutic targets — of known genetic and epigenetic abnormalities? How can we achieve a more profound understanding of the critical interactions of the BM microenvironment with healthy and tumor PCs? Finally, do current therapeutic regimens show differential activity for tumors with different genetic and phenotypic abnormalities?

Developing new therapeutic strategies is critical. One popular notion is to convert MM to a premalignant MGUS tumor if a complete elimination of MM tumor cells cannot be achieved. However, it will be a challenge to figure out how to effectively monitor this outcome, given our poor understanding of intrinsic differences between MM and MGUS tumors. Simultaneous therapeutic targeting of several genetic and/or epigenetic abnormalities present in individual MM tumors is another attractive concept. But it remains unclear whether initiating or early oncogenic abnormalities are more effective targets than secondary oncogenic abnormalities. Alternatively, it may be possible to target addiction of the tumor cell to the PC phenotype, as illustrated by the dependence of survival of MM cell lines on expression of IRF4 (78). Finally, given that the BM seems to be altered during tumor progression, the possibility of targeting the microenvironment and/or its interaction with tumor cells (including possible enhancement of immune responses) seems attractive, but currently our limited understanding of these interactions hampers this approach. However, the development of an orthotopic, immunocompetent, genetically engineered murine model is a crucial step forward (51, 52).

### Table 2

<table>
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<tr>
<th>Genetic lesion</th>
<th>Arm 1 n/Arm 2 n</th>
<th>Endpoint</th>
<th>Arm 1</th>
<th>Arm 2</th>
<th>Arm 1 OS</th>
<th>Arm 2 OS</th>
<th>Reference</th>
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<tr>
<td>t(4;14)</td>
<td>33/31</td>
<td>3-yr OS</td>
<td>V-A-D/HDM/Thal</td>
<td>Bor-A-D/HDM/Bor</td>
<td>44%</td>
<td>66%</td>
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<td>t(4;14)</td>
<td>98/106</td>
<td>4-yr OS</td>
<td>V-A-D</td>
<td>Bor-D</td>
<td>32%</td>
<td>63%</td>
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<tr>
<td>t(4;14)</td>
<td>21/23</td>
<td>2-yr OS</td>
<td>Thal-TT2</td>
<td>Placebo-TT2</td>
<td>67%</td>
<td>87%</td>
<td>75</td>
</tr>
<tr>
<td>t(4;14)</td>
<td>21/29</td>
<td>2-yr OS</td>
<td>Thal-TT2</td>
<td>Bor-TT3</td>
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<td>97%</td>
<td>75</td>
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<td>del17p</td>
<td>39/19</td>
<td>3-yr OS</td>
<td>V-A-D/HDM/Thal</td>
<td>Bor-A-D/HDM/Bor</td>
<td>17%</td>
<td>69%</td>
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<td>del17p</td>
<td>119/54</td>
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<td>Bor-D</td>
<td>36%</td>
<td>50%</td>
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<td>NHRD</td>
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<td>3-yr OS</td>
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<td>Mel-P-Bor</td>
<td>53%</td>
<td>72%</td>
<td>79</td>
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<td>Unfav. FISH</td>
<td>152/141</td>
<td>3-yr OS</td>
<td>Thal-D-Cyclo</td>
<td>V-A-D-Cyclo</td>
<td>58%</td>
<td>56%</td>
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<tr>
<td>Unfav. FISH</td>
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<td>3-yr OS</td>
<td>Thal-D-Cyclo</td>
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<td>34%</td>
<td>26%</td>
<td>81</td>
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<tr>
<td>Unfav. FISH</td>
<td>99/98</td>
<td>3-yr OS</td>
<td>Thal maint</td>
<td>Placebo maint</td>
<td>45%</td>
<td>69%</td>
<td>82</td>
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</tbody>
</table>

*NHRD status determined by flow cytometry. Unfavorable (Unfav.) FISH includes any of the following: t(4;14), t(14;16), t(14;20), gain(1q), del(1p32), or del(17p). Randomized drugs in each arm are shown in bold. *OSs that are significantly different from control are shown in bold. A, adriamycin; Bor, bortezomib; Cyclo, cyclophosphamide; D, dexamethasone; HDM, high-dose intravenous melphalan; maint, maintenance (implies combination and/or sequential therapies); Mel, low-dose oral melphalan; P, prednisone; Thal, thalidomide; TT2, total therapy 2 (an intense multi-drug combination induction, tandem transplant, and randomization to thalidomide or placebo); TT3, total therapy 3 (similar to TT2 but includes bortezomib). Number shown refers to the total population.
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