Article

Long noncoding RNA PVT1 is Regulated by Bromodomain Protein BRD4 in Multiple Myeloma and is Associated with Disease Progression

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Abstract: Long noncoding RNAs (lncRNAs) are deregulated in human cancers and are associated with disease progression. Plasmacytoma Variant Translocation 1 (PVT1), an lncRNA, is located adjacent to MYC, linked to multiple myeloma (MM). PVT1 is expressed in MM and is associated with carcinogenesis, however, its role and regulation machinery remain uncertain. We examined PVT1/MYC expression through real time PCR in plasma cells purified from 59 MGUS and 140 MM patients. MM cell lines KMS11, KMS12PE, OPM2, and RPMI8226 were treated with JQ1, a MYC superenhancer inhibitor, or MYC inhibitor 10058-F4. The expression levels of PVT1 and MYC were significantly higher in MM than in MGUS (p < 0.0001), and showed positive correlation with disease progression (r = 0.394, p < 0.0001). JQ1 inhibited cell proliferation and decreased the expression levels of MYC and PVT1. However, 10054-F4 did not alter the expression level of PVT1. The positive correlation between MYC and PVT1 in patients, synchronous downregulation of MYC and PVT1 by JQ1, and no effect of MYC inhibitor on PVT1 expression suggest that the expression of these two genes is coregulated by a superenhancer. Cooperative effects between these two genes may contribute to MM pathogenesis and progression.

Keywords: long noncoding RNA, PVT1, MYC, bromodomain, multiple myeloma

1. Introduction

Multiple myeloma (MM) is a plasma cell neoplasm characterized by the proliferation of atypical plasma cells in the bone marrow and the production of monoclonal immunoglobulins. MM progresses from a precancerous state called Monoclonal Gamopathy of Undetermined Significance (MGUS) at a rate of approximately 1% per year [1-3]. The molecular mechanism of MM development is thought to be primarily due to the activation of cancer-related genes by translocations of immunoglobulin heavy chain genes (IgH). These include increased cyclin D1 expression by the translocation t(11; 14) IgH-CCND1, increased FGFR3/MMSET expression by t(4; 14) IgH-FGFR3/MMSET, and increased c-MAF expression by t(4; 16) IgH-c-MAF [4]. These chromosomal abnormalities are observed at the MGUS stage, so additional abnormalities are
required for progression to MM. Recent genomic and transcriptomic analyses have shown that oncogene mutations, such as RAS mutations, and aberrant overexpression of MYC play an important role in the progression of MM [5]. However, not all players have been elucidated yet.

Recent transcriptome-wide analyses have revealed an overwhelming amount of transcribed but not translated non-coding RNAs capable of influencing diverse cellular processes, such as proliferation, apoptosis, and motility [6,7]. Among the non-coding RNAs, long non-coding RNAs (lncRNAs), transcripts >200 nucleotides in length, have emerged as a class of key regulatory RNAs [8]. LncRNAs are deregulated in many human cancers and are associated with disease progression [9-11]; several studies, including ours, have shed light on the role of lncRNAs in MM progression [12-14].

Plasmacytoma Variant Translocation 1 (PVT1) which is an lncRNA longer than 500 nucleotides, was first found in mouse plasmacytoma [15] and then reported to be involved in the oncogenesis of many types of cancers [16,17]. PVT1 is located at the 8q24 locus adjacent to MYC [18], which is highly expressed in many types of cancer and plays an important role in carcinogenesis [19,20]. PVT1 is elevated in MM [5,22] and coamplified with MYC in many cancers [18]; there is an association between PVT1 expression level and poor prognosis in many cancers [16,17,23-25]. High level amplification and/or overexpression of the PVT1 is associated with invasive phenotype of breast cancer and reduced survival time in ovarian cancer patients [21]. These observations are indicative of an involvement of PVT1 in the maintenance of a transformed phenotype. However, its regulation and clinical significance in MM have been poorly documented.

Superenhancers, on which mediator complexes, including activators and coactivators, accumulate at higher densities than on regular enhancers, that control the expression of genes involved in cell identity, determination, and disease, have been described recently [26]. The superenhancers are bound by the bromodomain containing protein 4 (BRD4) which is a member of the bromodomain protein family and is essential for RNA transcription and transcription elongation [27]. The most well-known mechanism of MYC overexpression is the fusion of the IgH enhancer and MYC produced by the chromosomal translocation t(8;14) in Burkitt lymphoma. MYC transcription is controlled by superenhancer [27,28], and BRD4 inhibitors markedly decrease MYC expression in many types of cells including MM cells [28]. Thus, PVT1 is speculated to be regulated by a superenhancer.

In order to clarify the underlying mechanism regulating PVT1 expression and its relationship with progression and prognosis in MM, we investigated the PVT1 expression in plasma and MM cell lines focusing on a superenhancer-related mechanism, and the correlation between PVT1 and MYC expression in MM and MGUS patients.

2. Results

2.1 PVT1 and MYC expression in plasma cells of MM is higher than of MGUS and control

The expression levels of PVT1 and MYC in plasma cells were significantly higher in MM (mean: PVT1 2.58, MYC 0.74), than MGUS (mean: PVT1 0.88, MYC 0.06) and control (mean: PVT1 0.06, MYC 0.07) (p < 0.001, p < 0.001, respectively) (Figure 1A, 1B). PVT1 expression seemed to increase with disease progression, but it did not differ between samples from different stages (stages defined according to the international staging system (ISS) reflecting progression) (p = 0.145) (Figure 1C). We then compared PVT1 expression levels between cell lines with different
chromosomal abnormalities, as detected with fluorescence in situ hybridization (FISH) analysis, including t(11;14), t(4;14), t(14;16), deletion 13q, and deletion 17p, and found no difference \((p = 0.509)\) (Figure 1D). Since PVT1 is located in chromosome 8q24 and a co-occurrence of 8q24 abnormality is sometimes observed in MM, we compared the expression levels between cell lines with 8q24 abnormalities including t(8;14), and tested for 8q24 amplification by FISH analysis. However, no difference was found (Figure 1E). When we analyzed PVT1 and MYC expression levels in the same patients, a positive correlation was found in both MM and MGUS patients \((r = 0.484, p < 0.001; r = 0.423, p < 0.0001; \text{respectively})\) (Figure 1E, F).
Figure 1: RNA expression determined by RQ-PCR in plasma cells isolated from bone marrow specimens and organized by patient status. Each dot shows a patient. RQ-PCR: real time quantitative PCR. MGUS: monoclonal gammopathy of undetermined significance. MM: multiple myeloma. A: PVT1. B: MYC. C: PVT1 expression by international staging system (ISS). D: PVT1 expression according to karyotype determined with fluorescence in situ hybridization (FISH). E: PVT1 expression by chromosome 8q24 abnormality determined with FISH. F: Correlation between PVT1 and MYC RNA expression in plasma cells of MM and MGUS.

2.2 BRD4 inhibitors inhibit MM cell proliferation and downregulate PVT1 and MYC expression

To clarify the mechanisms regulating PVT1 expression, we focused on BRD4 because it is well known that MYC expression is regulated by BRD4. BRD4 inhibitors inhibited the proliferation of eight MM cell lines. JQ1 inhibited the proliferation of KMS11, KMS12PE, KMS12BM, KMS26, KMM1, OPM2, and RPMI8226 cell lines with a concentration of 1 μM (Figure 2A). CPI-203 inhibited the proliferation of KMS11, KMS12BM, KMS26, and OPM2 with a lower concentration (0.1 μM), and inhibited KMS12PE, KMS18, KMM1, and RPMI8226 with 1 μM concentration (Figure 2B).

JQ1 markedly reduced PVT1 mRNA expression with a concentration of 1 μM in KMS11, OPM2, KMS12PE, KMS12BM, KMM1, RPMI8226 and KMS26 (Figure 2C). Similarly to JQ1, another BRD4 inhibitor CPI-203, markedly reduced PVT1 mRNA expression, with a concentration of 1 μM, in KMS11, OPM2, KMS12PE, KMM1, RPMI8226 and KMS26 (Figure 2D).

Consistent with previous reports, 1 μM of JQ1 significantly reduced MYC mRNA expression in KMS11, OPM2, KMS12PE, KMS12BM, KMM1, RPMI8226 and KMS26 (Figure 2E). MYC protein level was also reduced with JQ1 treatment (Figure 2F).
Figure 2: Growth determined using the WST-8 assay and RNA expression determined with RQ-PCR in seven MM cell lines treated with two BRD4 inhibitors JQ1 (0 μM, 1 μM, 10 μM) and CPI-203 (0 μM, 0.1 μM, 1 μM). A: Cell growth under treatment with JQ1. B: Cell growth under treatment with CPI-203. C: PVT1 expression under treatment with JQ1. D: PVT1 expression under treatment with CPI-203. E: MYC expression under treatment with JQ1. F: MYC expression under treatment with CPI-203.

2.3 MYC inhibitor did not reduce PVT1 expression

From the results described above, there were two possibilities for explaining the high PVT1 expression levels in MM. One was that MYC and PVT1 are co-regulated by BRD4 and the other
is that PVT1 is regulated by MYC which is regulated by BRD4. To test these hypotheses, we used the MYC inhibitor, 10058-F4, which inhibits MYC transcription activity by dissociating the MYC-MAX transcription complex. PVT1 expression was not significantly altered by treatment with 10058-F4 in KMS11, OPM2, KMS12PE, and RPMI8226 (Figure 3). Therefore, no contribution of MYC transcriptional activity to PVT1 expression was revealed.

![Figure 3. PVT1 expression in cells treated with the MYC inhibitor 10058-F4. Error bars show the standard error of mean (SEM).](image)

### 2.4 PVT1 downregulation by locked anti-sense nucleotide reduced MYC expression

To determine the role of PVT1 on MYC expression in MM cells, anti-sense locked nucleotide GapmeR™ was used to knockdown PVT1 expression. Three sequences of GapmeR were constructed and five MM cell lines were tested, KMS11, KMS12PE, KMM1, OPM2 and RPMI8226. PVT1 expression was successfully knocked down in two cell lines, KMS11 and OPM2, by one GapmeR product (Figure 4A). In these two cell lines, MYC mRNA expression was significantly reduced (Figure 4B).

![Figure 4. MYC mRNA expression in cells treated with the MYC inhibitor 10058-F4. Error bars show the standard error of mean (SEM).](image)
2.5 Clinical significance of PVT1 expression in MM

To investigate the clinical significance of PVT1 in MM, overall survival (OS) and progression free survival (PFS) of MM patients were analyzed by dividing the two groups according to PVT1 expression levels. Sixty-seven patients were analyzed for OS and 62 patients were analyzed for PFS. Five patients were excluded from PFS analysis due to lack of reliable clinical results for progression. The patients with high PVT1 expression tended to have a shorter OS with a median of 2.7 years compared to 5.0 years in those with low expression (p = 0.09) (Figure 5A), but PFS did not differ between MM patients with high and low PVT1 expression (Figure 5B).

Figure 5. A: Overall survival (OS) and B: progression free survival (PFS) in MM patients divided into two groups by PVT1 expression level.
3. Discussion

In this study, we aimed to clarify the underlying mechanism regulating PVT1 expression and its relationship with progression and prognosis in MM. We found significantly higher PVT1 and MYC expression in MM and MGUS plasma cells compared to that in the control cell line, suggesting that the IncRNA PVT1 is associated with MM pathogenesis and progression. Positive correlation between MYC and PVT1 expression levels suggests that MYC and PVT1 are coregulated by the same mechanism. Two BRD4 inhibitors, JQ1 and CPI-203, markedly reduced both MYC and PVT1 in MM cell lines but the MYC inhibitor did not reduce PVT1 expression, suggesting that PVT1 expression is not controlled by MYC but both genes were regulated by BRD4. Moreover, reduction of MYC mRNA by PVT1 knockdown indicates that PVT1 regulates MYC expression at the transcriptional level.

High expression of PVT1 and MYC in MM cells compared to that in normal plasma cells is consistent with previous studies [17]. A large number of studies have shown that PVT1 levels are higher in many cancers with increased MYC expression compared to normal tissues and are associated with a poor prognosis [16,23-25]. Tissue microarray analysis of primary tumors indicated a high correlation between PVT1 and MYC expression, providing strong evidence for the cooperation of PVT1 and MYC in different human cancers [29]. Nagoshi et al. reported that frequent PVT1 rearrangement and novel chimeric genes, PVT1-NBEA and PVT1-WWOX, occur in MM with 8q24 abnormality [30]. They also found high expression of PVT1 and MYC in most MM cell lines regardless of PVT1 or MYC rearrangement status. Our findings of PVT1 elevation in plasma cells of MM compared to MGUS suggest a role of PVT1 in the pathogenesis of malignant clonal plasma cells and the progression from precancerous stage to cancer.

The precise mechanisms controlling IncRNA PVT1 expression in MM have not been fully clarified. An increased MYC copy number and PVT1 expression occur in more than 98% of cancer cases with increased 8q24 copy numbers, which points to an interaction between PVT1 and MYC, and that they are part of a common signaling pathway. We could not find any correlation between PVT-1 expression level and chromosomal abnormalities including t(8:14) and 8q24 amplification detected with fluorescent in situ hybridization (FISH). This is not conclusive because FISH is not sufficient for the detection of gene amplification; however, positive correlation between PVT-1 and MYC expression implies a common regulation system for both genes, and that upregulation of PVT1 and MYC expression does not solely depend on 8q24 abnormality in MM.

We speculated that a BRD4 inhibitor would downregulate the expression of PVT1 and MYC. JQ1 and CPI-203 significantly reduced the expression of PVT1 in myeloma cell lines. Combined with the high expression of MYC and PVT1 and the positive correlation of MYC and PVT1 in the MM and MGUS patients’ plasma cells, these results suggest that MYC and PVT1 are regulated by the same mechanism. Two possible regulation mechanisms for MYC and PVT1 expression were conceivable. One is that MYC regulates PVT1 expression, and the other is that both MYC and PVT1 are controlled by the superenhancer. To test these hypotheses, we examined the PVT1 expression using 10058-F4, which suppresses the transcriptional activity of MYC by inhibiting the heterodimer formation of MYC and MAX [31].10058-F4 did not decrease PVT1 expression except for in the OPM2 cell line. These results suggest that PVT1 is not transcriptionally regulated by MYC, and that two genes are simultaneously regulated by superenhancers. This result is inconsistent with previous reports that the PVT1 promoter region contains two enhancer E-boxes that serve as MYC binding sites and that E-box 2 mediates the binding of MYC to the PVT1 promoter to promote PVT1 expression [32]. We cannot fully explain this discrepancy, it may be attributed to different cell lineages or the conditions of the cells.

Many studies have revealed a relationship between PVT1 and MYC expression. Our experiments of PVT1 knockdown using the locked nucleotide anti-sense oligo nucleotide resulted
in a decreased expression of MYC mRNA, which is consistent with a previous report showing the effect of PVT1 on MYC transcription [33], but inconsistent with another report where low levels of c-Myc protein were found without significant changes in MYC mRNA levels when siRNA was used to knock down PVT1 [29].

We found a tendency towards worse OS in the high PVT1 group although the PFS did not differ between the high and low PVT1 groups. These results suggest that a high level of PVT1 might be associated with a prognosis of relapse and drug resistance. An association between high PVT1 expression and worse prognosis has been reported in several cancers [16,23,25]. Involvement in drug resistance to anti-cancer drugs has also been documented in several ways [24,34]. For example, PVT1 acts as a competitive endogenous RNA that forms a tight network with protein-coding mRNAs such as CDH1, TP73, TP31, RUNX1, and RUNX via microRNA-200, thereby regulating breast cancer progression [35,36]. Further studies to elucidate PVT1 involvement in drug resistance are warranted.

4. Materials and Methods

4.1 Cell lines

Cell lines used included KMS12PE with t(11;14), KMS11 with t(4;14) and p53 deletion, and OPM2 with t(4;14) + mutated p53 and RPMI8226. The human myeloma cell line RPMI8226 was obtained from the American Type Culture Collection (Rockville, MD, USA), and lines KMS11, KMS12PE, KMS12BM, and KMS18 were kindly provided by Dr Takemi Otsuki (Kawasaki Medical School, Okayama, Japan). OPM2 was kindly provided by Dr Masaki Ri (Nagaya City University, Nagoya, Japan). All lines were cultured in RPMI1640 medium (Sigma-Aldrich, St Louis, USA), supplemented with 10% fetal bovine serum, at 37 °C and 5% CO2.

4.2 Patients

A total of 140 consecutive MM patients, 62 with MGUS, and 21 control patients with lymphoma without bone marrow infiltration or acute myeloid leukemia in complete remission, were included in this study from July 2010 to March 2015. The patient characteristics are summarized in supplementary Table 1. This study was approved by the institutional review board of Gunma University Hospital under the guidelines of the Declaration of Helsinki. Bone marrow (BM) aspirate samples were obtained upon diagnosis after obtaining each patient’s informed consent.

4.3 Treatment with inhibitors

Myeloma cell lines KMS11, KMS12PE, KMS12BM, KMS26, KMM1, OPM2, and RPMI8226 were treated with JQ1 1 μM and CPI203 0.1 μM. KMS11, KMS12PE, KMM1, OPM2, and RPMI8226 were treated for 24 h with MYC inhibitor 10058-F4 (50 μM or 100 μM). Cell growth was determined using the WST-8 assay (Dojindo Laboratory, Kumamoto, Japan) at 24, 48, and 72 h. RNA was isolated from cells incubated for 24 h and gene expression was determined with real time PCR. Experiments were performed in triplicate.

4.4 PVT1 silencing in myeloma cell lines

RNase H-activating Locked Nucleic Acid (LNA) GapmeR™ (Exiqon, Vedbaek, Denmark) was used to silence PVT1 expression in vitro. The cell lines KMS12PE and OPM2 were cultured with GapmeR for 24, 48, and 72 h, after which cell viability was determined using the WST-8 assay.
assay. All experiments were performed in duplicate. Gene expression was determined after 72 h of treatment.

4.5 Isolation of nucleic acids

Plasma cells were purified from the bone marrow mononuclear cells with anti-CD138 antibody conjugated with phycoerythrin (PE) (Beckman-Coulter, Brea, CA) and the Easy Step PE positive selection kit containing anti-PE antibodies conjugated with micro-magnetic beads (STEMCELL Technologies, Vancouver, BC, Canada). RNA was extracted from plasma cells (and one autopsied extramedullary plasmacytoma of the liver) and cell lines using the mirVana RNA Isolation kit (Ambion, Austin, TX, USA). Complimentary DNA (cDNA) was produced using the PrimeScript™ RT reagent kit with gDNA Eraser (TaKaRa Bio, Kyoto, Japan).

4.6 Real-time PCR analysis of PVT1 expression

Transcript levels, including those of PVT1, were determined with real-time PCR using the Power SYBR Green PCR Master Mix (Applied Biosystems, Foster City, CA, USA). Primers used for detection were as follows: PVT1: F-5′-CACTCTGGACGACTTGAGAAC-3′, R- 5′-TCCTCAGATGAACCAGGTGAACA-3′; MYC: F-5′-CCTGGTGCTCCATGAGGAGA-3′, R-5′-CAGTGGGCTGTGAGGAGGGTTT-3′; ACTB: F- 5′-TGGCACCCAGCAATGAA-3′, R- 5′-CTAAGTCATAGTCCGCCTAGAAGCA-3′. The expression levels were calculated using the ΔΔCt method. ACTB was used as an internal control, and cDNA extracted from the HL60 acute myeloid leukemia cell line was used as a calibration sample. Relative RNA expression levels are expressed as 2-ΔΔCt.

4.7 Statistical analysis

EZR version 1.41 (Saitama, Japan) was used for statistical analysis. P values < 0.05 were considered significant. Frequencies were evaluated using Fisher’s exact test, and continuous values were evaluated using the Mann-Whitney U test or Kruskal-Wallis test. Overall survival (OS) and progression-free survival (PFS) were evaluated using the Kaplan-Meier method and log rank test for univariate analysis. The Cox regression hazard model was used for multivariate analysis.

5. Conclusions

Positive correlation between MYC and PVT1 in patients, synchronous downregulation of MYC and PVT1 by JQ1 and CPI203, no effect of MYC inhibitor for PVT1 expression suggest that the expression of these two genes is co-regulated by the BRD4 complex. PVT1 and MYC cooperation may contribute to MM pathogenesis and progression, and our results support the rationale for targeting BRD4 in these patients.

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Conflicts of Interest
The authors declare no conflict of interest.

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