Prostate cancer is the most common malignancy in males and the second leading cause of cancer-related deaths in the United States and Europe (1). Detection of prostate cancer at an early stage by serum test for prostate-specific antigen (PSA) and subsequent surgery, and radiation therapy can cure the localized disease, but nearly 30% of treated prostate cancer patients suffer relapse (2–4). Relapsed or advanced prostate cancers are usually treated with androgen ablation therapy and subsequent surgery, and radiation therapy can cure the localized disease, but nearly 30% of treated prostate cancer patients suffer relapse (2–4). Relapsed or advanced prostate cancers are usually treated with androgen ablation therapy and reveal relatively good response, but some of them eventually become androgen independent and progress very rapidly.

Because there is at present no effective therapy available for such advanced tumors, it is crucial to develop novel therapeutic tools against prostate cancers.

To attempt to identify novel molecular targets or biological markers for prostate cancers, we previously analyzed the precise gene expression profiles of prostate cancer cells purified by laser microdissection using a genome-wide cDNA microarray (5). In the present study, we report the identification and characterization of molecule interacting with CasL-2 prostate cancer variants (MICAL2-PV), which are novel splicing variants of MICAL2 belonging to the MICAL family, overexpressed in prostate cancer cells. MICAL1 was initially identified as a CasL-interacting molecule and was shown to associate with vimentin, a cytoskeletal regulator that connects CasL to intermediate filaments (6). In addition, Terman et al. have reported that Drosophila MICAL1 interacts with the neuronal plexin A receptor and is required for semaphorin 1a/plexin A–mediated repulsive axon guidance during neural development (7). It is also known that semaphorins and plexins are involved in control of invasive growth of cancer cells through making a complex with and activating c-Met (hepatocyte growth factor receptor; refs. 8–10). Although MICAL2 and its novel variants MICAL2-PVs have a high degree of homology and share several important domains with MICAL1, little is known about their pathophysiologic roles in growth of tumor cells or in neuronal guidance and development.

Expression of Novel Molecules, MICAL2-PV (MICAL2 Prostate Cancer Variants), Increases with High Gleason Score and Prostate Cancer Progression

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Abstract

Purpose: The aim of this study is to identify novel molecular targets for development of novel treatment or diagnostic markers of prostate cancer through genome-wide cDNA microarray analysis of prostate cancer cells purified by laser microdissection.

Experimental Design and Results: Here, we identified molecule interacting with CasL-2 prostate cancer variants (MICAL2-PV), novel splicing variants of MICAL2, showing overexpression in prostate cancer cells. Immunohistochemical analysis using an antibody generated specific to MICAL2-PV revealed that MICAL2-PV was expressed in the cytoplasm of cancer cells with various staining patterns and intensities, whereas it was not or hardly detectable in adjacent normal prostate epithelium or prostatic intraepithelial neoplasia. Interestingly, immunohistochemical analysis of 105 prostate cancer specimens on the tissue microarray indicated that MICAL2-PV expression status was strongly correlated with Gleason scores (P < 0.0001) or tumor classification (P < 0.0001). Furthermore, the expression levels of MICAL2-PVs were also concordant to those of c-Met, a marker of tumor progression, with statistical significance (P = 0.0018). To investigate its potential of molecular therapeutic target for prostate cancers, we knocked down endogenous MICAL2-PVs in prostate cancer cells by small interfering RNA, which resulted in the significant reduction of prostate cancer cell viability.

Conclusions: Our findings suggest that MICAL2-PV is likely to be involved in cancer progression of prostate cancer and could be a candidate as a novel molecular marker and/or target for treatment of prostate cancers with high Gleason score.

Prostate cancer progression and diagnostic markers of prostate cancer through genome-wide microarray analysis of prostate cancer cells purified by laser microdissection.

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In this study, through intensive immunohistochemical staining, we show the relationship between MICAL2-PVs expression and clinicopathologic variables, including Gleason score and the expression status of c-Met. Our studies disclose the biological significance of MICAL2-PVs overexpression in progression of prostate cancer cells.

**Materials and Methods**

**Cell lines.** Human prostate cancer cell lines LNCaP, PC-3, DU145, and COS-7 were obtained from the American Type Culture Collection (Rockville, MD). All of them were cultured as monolayers in appropriate medium supplemented with 10% fetal bovine serum. Cells were maintained at 37°C in an atmosphere of humidified air with 5% CO2.

**Selection of a candidate gene and Northern blot analysis.** Using the gene expression profile analysis of 20 clinical prostate cancers (5), we selected several up-regulated genes whose expression ratio was >5.0 in >50% of informative cases, and we focused on one expressed sequence tag (EST) (accession no. AF052170). To confirm overexpression of a gene corresponding to this EST, we extracted total RNAs from prostate cancer cell lines using TRizol reagent (Invitrogen, Carlsbad, CA) and did Northern blot analysis. After treatment with DNase I (Nippon Gene, Osaka, Japan), mRNA was purified with Micro-FastTrack according to the manufacturer’s protocols. A 1-μg aliquot of each mRNA from prostate cancer cell lines and those isolated from (Invitrogen), according to the manufacturer’s protocols. A 1-μg aliquot of each mRNA from prostate cancer cell lines and those isolated from normal human heart, liver, kidney, lung, bone marrow, pancreas, and prostate (BD Biosciences, Palo Alto, CA) were separated on 1% agarose gels and transferred onto nylon membranes. The 252-bp probes specific to AF052170 were prepared by PCR using the following primer set: forward, 5'-TGAAGCACAAGAGAGCAGGGAGAG-3' and reverse, 5'-CCGGTGCCACTGTTAATGGATTA-3'. Hybridization with a random-primer, α-DCTP-labeled probe was carried out according to the instructions for Megaprime DNA labeling system (Amersham Biosciences, Buckinghamshire, United Kingdom). Prehybridization, hybridization, and washing were done according to the supplier’s recommendations. The blots were autoradiographed with intensifying screens at -80°C for 7 days. Human multiple-tissue Northern blots (BD Biosciences) were also hybridized with the 32P-labeled AF052170-specific probe and analyzed.

**Cloning the full length of MICAL-PVs.** The further 3' portion of this cDNA clone, AF052170, was obtained by 3'-rapid amplification of cDNA ends (RACE) using a Marathon cDNA amplification kit (BD Biosciences). One microgram of mRNA from the human prostate cancer cell line LNCaP was reversely transcribed using Marathon cDNA synthesis primer and avian myeloblastosis virus reverse transcriptase (BD Biosciences). Marathon cDNA adaptors were added to the 5' and 3' end of the cDNA by T4 DNA ligase (BD Biosciences). The cDNA was amplified by PCR using the adaptor primer AP1 and the primer specific to AF052170, GSP1 (5'-CCCTAACCCTGGGAGCCAGGAC3'-3'). The product was amplified by nested PCR using the nested adaptor primer AP2 and the nested primer specific to AF052170, GSP2 (5'-CGCTGTGACCTGATG-GAAGGTGGA-3'). The amplified cDNA fragments were directly sequenced using ABI 3700 DNA Analyzer (Applied Biosystems, Foster City, CA). The cDNA sequences were determined as described in the instructions of the kit. The 5' region of AF052170 was obtained by exon connection experiments using cDNA prepared from LNCap as a template.

**Preparation of polyclonal antibody to MICAL-PVs.** Plasmid clone designed to express His-tagged 137-amino-acid peptide (codon 827-963) corresponding to COOH-terminal of MICAL2-PVa was designed to express His-tagged MICAL2-PVs (AN-2427) and MICAL2-PVb (AN-2428) were transfected with pcDNA3.1-MICAL2-PVb-myc/His or pcDNA3.1-MICAL2-PVb-myc/His (for exogenous myc/His-tagged MICAL2-PV protein) were used as a positive control, and those transfected with pcDNA3.1 vector (mock) were used as a negative control of MICAL2-PV. The blots were autoradiographed with intensifying screens at -80°C for 7 days. Human multiple-tissue Northern blots (BD Biosciences) were separated on 1% agarose gels, transferred to nitrocellulose membranes (Amersham Biosciences), and incubated with a 1:500 diluted solution of anti-MICAL2-PV polyclonal antibody (pAb; 100 μg/mL) as a primary antibody. After incubation with sheep anti-rabbit IgG-horseradish peroxidase as a secondary antibody (Amersham Biosciences), signals were visualized with enhanced chemiluminescence kit (Amersham Biosciences).

**Tissue samples and immunohistochemical study.** Twenty-seven specimens of primary prostate cancer were obtained with the appropriate informed consent by radical prostatectomy at Department of Urology, Kochi Medical School and Kochi Prefectural Aki Hospital between 2001 and 2004. Representative section slides were obtained from the 27 specimens after fixation by formalin and being embedded in paraffin and then used for estimating the proportion of immunostaining staining positive cells in the carcinoma, prostatic intraepithelial neoplasia, and normal tissue. To further investigate MICAL2-PV expression in a larger number of tumor specimens, tissue microarray samples containing 78 prostate cancer specimens (AccuMax Array, Petagen, Inc., Seoul, Korea), for which the mean age of the patients was 63.1 years (range, 43-79 years), were obtained also. Histopathologic classifications, including Gleason score, were done using the tumor-node-metastasis system (Tumor-Node-Metastasis Classification of Malignant Tumors, 6th edition, 2002). Immunohistochemical study was carried out using the Ventana automated immunohistochemical systems (Discovery, Ventana Medical Systems, Inc., Tucson, AZ). Sections were incubated with a 1:20 diluted solution of purified anti-MICAL2-PV pAb (100 μg/mL) or a 1:50 diluted solution of anti-c-Met pAb (c-12, Santa Cruz Biotechnology, Inc., Santa Cruz, CA), for 16 minutes. The automated protocol is based on an indirect biotin-avidin system using a biotinylated universal secondary antibody and diaminobenzidine substrate with hematoxylin counterstaining. The specificity of the binding was confirmed by negative staining using rabbit nonimmune serum as primary antibody.

**Scoring of immunohistochemical staining.** To evaluate both the intensity of staining and the proportion of the positive-stained cells, we used a scoring method reported previously (14). Regarding the morphology and the intensity of MICAL2-PV or c-Met expression, positive staining of anti-MICAL2-PV or anti-c-Met antibody was defined as follows: score 1 for variable weak cytoplasmatic staining, score 2 for segmental and apical granular cytoplasmatic staining, and score 3 for diffuse continuous and intense cytoplasmatic staining. For each score, the proportion of cells with the score was estimated visually. A combined weighed score (MICAL2-PV immunohistochemical score or c-Met immunohistochemical score) consisting of the sum of the proportion of cells with each score was calculated for each sample as described previously (14). For example, a case with 70% score 3 staining, 20% score 2 staining, and 10% score 1 staining would be scored as follows: 70 x 3 + 20 x 2 + 10 x 1 = 260. The maximum score should be 300.

**Statistical analysis.** The correlations between MICAL2-PV expression levels and clinicopathologic variables (age, preoperative serum prostate-specific antigen, tumor classification, lymph node metastasis, Gleason score, and lymphatic or vascular invasion) were evaluated using the Kruskal-Wallis and Mann-Whitney U tests. Association
between MICAL2-PV immunohistochemical scores and c-Met immunohistochemical scores was determined using the Spearman rank correlation coefficient test.

**Small interfering RNA—expressing constructs and colony formation/MITT assay.** We used small interfering RNA (siRNA) expression vector (psiU6BX3.0) for examining RNA interference effect to the target gene, MICAL2-PV, as described previously (12). The target sequences for MICAL2-PV were 5'-GCTGCTGGCCTCCATATCA-3' (si#1) and 5'-TGCTTACAACTACTGCTAC-3' (psiU6BX3.0) for examining RNA interference effect to the target sequence of EGFP or MICAL2-PV using FuGene6 reagent (Roche Diagnostics, Mannheim, Germany). Cells were selected in the culture medium containing 0.8 mg/mL Geneticin for 1 week and harvested 48 hours after transfection for reverse transcription-PCR analysis to validate knockdown effect on MICAL2-PV expression in prostate cancer cell lines. The primers of reverse transcription-PCR were 5'-GACGAGATATCTTGGAGAA-3' and 5'-CCAGGATCAGACAAATACA-3' for MICAL2-PV and 5'-TGAGCAGTTGGGTTTG-3' and 5'-TGACCTGGAGAAGCTG-3' for β-actin, which was used to quantify the amount of cDNA input. After 7 days of incubation, these cells were fixed with 100% methanol and stained with Giemsa solution to evaluate the colony formation, and cell viability was evaluated by 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide (MTT) assay. Cells (5 x 10^4) on six-well plates were transfected with siRNA-expressing vector or control vector using FuGene6 (Roche Diagnostics) according to the supplier’s protocol. Cell-counting kit 8 (DOJINDO, Kumamoto, Japan) was added to each dish at a concentration of 1:10 volume, and the plates were incubated at 37°C for an additional 2 hours. Absorbance was then measured at 490 nm, and at 630 nm as reference, with a Microplate Reader 550 (Bio-Rad Laboratories, Hercules, CA).

**Results**

**Identification and cloning of the full-length MICAL2-PVs.** Through our earlier genome-wide expression analysis of prostate cancers using a cDNA microarray (5), we identified several genes commonly up-regulated in prostate cancer cells, and we here focused on one gene corresponding to an EST sequence (accession no. AF052170). Northern blot analysis revealed that a 7-kb transcript was commonly overexpressed in prostate cancers compared with other normal adult tissues, including the prostate. On the other hand, about 4-kb transcript was expressed in prostate cancer cell lines. The 7-kb transcript was expressed abundantly in normal testis and prostate cancer cell lines, whereas the 4-kb transcript corresponding to the MICAL2 was observed in heart, brain, and skeletal muscle. C. genomic structure of MICAL2 and its novel variants MICAL2-PVa and MICAL2-PVb. Expressed sequence tag AF052170 was the probe for the microarray analysis. Full-length cDNA sequences of MICAL2 (accession no. NM014632), MICAL2-PVa (accession no. AB126828), and MICAL2-PVb (accession no. AB126829) were 3,885-, 6,805-, and 6,742 bp long, respectively. Exons are represented by black boxes. Black arrowheads indicate the stop codon and open arrowheads the first methionine.

**Fig. 1.** A, Northern blot analysis of a gene corresponding to expressed sequence tag AF052170 in prostate cancer cell lines (LNCaP, DU145, and PC-3) and normal human tissues (heart, liver, kidney, lung, bone marrow, pancreas, and prostate). About 7-kb transcript corresponding to the full-length MICAL2-PV was observed abundantly in three prostate cancer cell lines (LNCaP, PC-3, and DU145) and normal bone marrow, compared with other normal adult tissues, including the prostate. On the other hand, about 4-kb transcript corresponding to the previously reported MICAL2 was not expressed in prostate cancer cell lines. B, Northern blot analysis of a gene corresponding to expressed sequence tag AF052170 in normal adult human tissues. The 7-kb transcript corresponding to the full-length MICAL2-PV was observed abundantly in normal testis and prostate cancer cell lines, whereas the 4-kb transcript corresponding to the MICAL2 was observed in heart, brain, and skeletal muscle. C, Genomic structure of MICAL2 and its novel variants MICAL2-PVa and MICAL2-PVb. Expressed sequence tag AF052170 was the probe for the microarray analysis. Full-length cDNA sequences of MICAL2 (accession no. NM014632), MICAL2-PVa (accession no. AB126828), and MICAL2-PVb (accession no. AB126829) were 3,885-, 6,805-, and 6,742 bp long, respectively. Exons are represented by black boxes. Black arrowheads indicate the stop codon and open arrowheads the first methionine.

**Fig. 2.** Immunoblot analysis using purified polyclonal antibody specific to the novel variants MICAL2-PVs. Specificity of ant–MICAL2-PV pAb was indicated by detection of exogenous MICAL2-PVs in COS7 and endogenous MICAL2-PVs expression in three prostate cancer cell lines. Lane 1, COS7 cells transfected with mock pcDNA3; lane 2, COS7 cells transfected with pcDNA3/psiU6BX3.0; lane 3, COS7 cells transfected with pcDNA3/psiU6BX3.0-MICAL2-PVa; lane 4, LNCaP prostate cancer cell line cells; lane 5, DU145 prostate cancer cell line cells; lane 6, PC-3 prostate cancer cell line cells. The 112- and 109-kDa bands correspond to MICAL2-PVa and MICAL2-PVb, respectively.
prostate cancer cells comparing with normal prostate (Fig. 1A), whereas a 4-kb transcript corresponding to the previously reported MICAL2 cDNA (accession no. NM_014632) was not expressed in prostate cancer cell lines. Among the adult normal organs, this 7-kb transcript was most abundant in testis (Fig. 1B) and expressed in bone marrow (Fig. 1A), whereas the faint expression of this transcript was detectable in other organs, including vital organs. We attempted to isolate the full-length cDNA corresponding to the 7-kb transcript by exon connection experiments and 3’-RACE using cDNA prepared from prostate cancer cell line LNCaP. Then, we isolated two novel splicing variants of MICAL2 that were different from the MICAL2 transcript corresponding to NM_014632 reported previously. We named them MICAL2-PVs (prostate cancer variants), MICAL2-PVa and MICAL2-PVb, because they were overexpressed in prostate cancer. The MICAL2 transcript is composed of 28 exons, whereas one of the MICAL2 splicing variants, MICAL2-PVa, has 21 exons with a large last exon (3885 bases), and the other variant, MICAL2-PVb, consisted of 20 exons as shown in Fig. 1C. Full-length cDNA sequences of MICAL2-PVa (accession no. AB126828) and MICAL2-PVb (accession no. AB126829) were 6,805-bp long and 6,742-bp long, respectively (Fig. 1C), encoding 976-amino-acid and 955-amino-acid proteins with a monooxygenase motif at its NH2-terminal, a CasL domain, and a LIM domain that are conserved in members of the MICAL family.

**Generating pAb specific to MICAL2-PV protein.** To investigate the detailed expression pattern of MICAL2-PV protein and characterize its biological functions, we generated pAb specific to MICAL2-PV, using the recombinant protein of the COOH-terminal region of MICAL2-PV, which was common in both MICAL2-PV variants but not contained in MICAL2, as an immunogen. We first did the immunoblot analysis to examine whether the purified anti-MICAL2-PV pAb (anti-MICAL2-PV
We used the exogenously introduced myc/His-tagged MICAL2-PVa and MICAL2-PVb proteins as positive controls. As shown in Fig. 2, this study validated that our anti-MICAL2-PV pAb could recognize both endogenous MICAL2-PVa and MICAL2-PVb (112 and 109 kDa, respectively) with high specificity and sensitivity.

**Immunohistochemical study of prostatectomy specimens.** We further did immunohistochemical staining of 27 clinical prostate cancer cases with anti-MICAL2-PV pAb. All 27 cases of prostate cancers expressed MICAL2-PV mainly in the cytoplasm, although staining patterns and intensities varied in individual cases (Fig. 3A-C). On the other hand, adjacent normal prostatic epithelium or prostatic intraepithelial neoplasia in the same patient revealed very weak or no signal for MICAL2-PV. Because each prostate cancer specimen apparently showed a different degree of staining intensity and different proportion of the staining-positive cell, we took these heterogeneity into consideration and applied the immunohistochemical scoring system; a combined weighed score was given by the sum of the proportion (0-100%) of stained cells for which the score 1, 2, or 3 was given according to the signal intensity as described previously (11). MICAL2-PV immunohistochemical scores were calculated for 105 specimens on the tissue microarrays, based on this scoring criteria (see Materials and Methods); representative staining lesions scored as 1, 2, or 3 according to the intensity, and their morphologic evaluation are shown in Fig. 3.

To investigate the clinicopathologic significance of MICAL2-PV expression in prostate cancer tissues, we analyzed the relationship between the calculated immunohistochemical scores for MICAL-PV2 and the clinicopathologic variables of 105 prostate cancer specimens, which is summarized in Table 1. Significant associations between MICAL2-PV immunohistochemical scores and several clinicopathologic factors (P < 0.05) were observed; in particular, it is notable that MICAL2-PV immunohistochemical scores was strongly correlated with tumor classification (P < 0.0001) and Gleason scores (P < 0.0001). We further divided these tumors into groups at the T2 (n = 41) or T3 (n = 60) stage by the size and confirmed that MICAL2-PV immunohistochemical score still revealed a strong correlation with Gleason score (P < 0.0001; Table 2), independent of the tumor size. Through immunohistochemical study, we noted that the cell staining pattern in each Gleason grade lesion was very homogeneous. Hence, we investigated the relationship between the Gleason grade and the MICAL2-PV intensity score and found that MICAL2-PV expression level was strongly correlated with Gleason grade (P < 0.0001; Table 3); higher Gleason-grade prostate cancers revealed higher expression levels of MICAL2-PV. There was no relationship between MICAL2-PV immunohistochemical score and preoperative serum PSA level (P = 0.0865; Table 1), which does not reflect the clinical behavior of prostate cancers (13).

### Table 1. Summary of the relationship between MICAL-2PV immunohistochemical scores and clinicopathologic factors in 105 patients with prostate cancers

<table>
<thead>
<tr>
<th>Tumor classification</th>
<th>Gleason score</th>
<th>MICAL-2PV immunohistochemical score</th>
<th>P*</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>n</td>
<td>Mean (SD)</td>
<td></td>
</tr>
<tr>
<td>T2</td>
<td>2-6</td>
<td>221 (47)</td>
<td>0.0001</td>
</tr>
<tr>
<td></td>
<td>7</td>
<td>216 (55)</td>
<td>0.0001</td>
</tr>
<tr>
<td></td>
<td>8-10</td>
<td>37 (44)</td>
<td></td>
</tr>
</tbody>
</table>

**NOTE:** Tumor classification was referred from Tumor-Node-Metastasis Classification (2002).

*Statistical significance was determined using Kruskal-Wallis and Mann-Whitney U tests.

† Data available in 92 cases.
of bone metastasis (14, 15). Similarly to the evaluation of MICAL2-PV expression, we also calculated c-Met immunohistochemical scores in 27 specimens from standard slides and examined the correlation between MICAL2-PV expression and c-Met expression (Fig. 3D). Interestingly, MICAL2-PV expression was positively correlated with c-Met expression ($\rho = 0.612$, $P = 0.0018$; Fig. 3E), suggesting a possible biological link between MICAL2-PV and c-Met expressions that affect prostate cancer progression (14, 15).

Knockdown of MICAL2-PV by siRNA suppressed prostate cancer cell viability. To investigate its potential of molecular therapeutic target for prostate cancers, we knocked down its endogenous expression in prostate cancer cell line PC-3 by mammalian vector-based RNA interference technology. The transfection of one of the siRNA-expressing vectors, si#2, clearly reduced the endogenous expression of MICAL2-PV (Fig. 4A). This knockdown effect by the siRNA on MICAL2-PV mRNA resulted in drastic growth suppression in colony formation assay as well as MTT assay (Fig. 4B and C). The similar results were obtained when we used another prostate cancer cell line LNCaP (data not shown). These findings strongly suggest that overexpression of MICAL2-PV in prostate cancer cells is likely to be associated with prostate cancer cell viability and support its potential of molecular therapeutic target for prostate cancers.

**Discussion**

MICAL family was initially identified as a molecule interacting with CasL and vimentin, a major component of the intermediate filaments, implicating its role as a cytoskeletal regulator that connects CasL to intermediate filaments (6). Recently, Fischer et al. (16) reported a possible association of MICAL1 and MICAL3 with microtubule cytoskeleton in their immunofluorescence analysis. Although the results in these reports suggest a possible association between MICAL2-PV and cytoskeleton, we observed no change in the cell morphology or cytoskeletal structure of cells in which MICAL2-PV was overexpressed or knocked down (data not shown).

*Drosophila* MICAL interacts with plexin A and is required for semaphorin 1a/plexin A–mediated repulsive axon guidance. Vertebrate orthologues of *Drosophila* MICAL was also indicated to interact with plexins (7). Semaphorins are secreted and membrane-bound proteins that control axon guidance through their receptors, plexins (8, 17), and these molecules play essential roles in axon guidance and neuronal development. Invasive growth is a hallmark during the development of the nervous system (8), and these molecules mentioned above, including MICALs, are likely to function in promotion and invasion of cancer cells in the similar manner. Furthermore, a novel biological function of semaphorins and plexins was recently documented; plexin B1 (semaphorin 4D receptor) was shown to form a complex with c-Met, which shares structural homology with plexins in the extracellular domain. Binding of semaphorin 4D to plexin B1 was indicated to activate c-Met and then make tumor cells more invasive (9). Overexpression

<table>
<thead>
<tr>
<th>Gleason grade</th>
<th>MICAL2-PV expression level</th>
<th>$P^*$</th>
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</thead>
<tbody>
<tr>
<td></td>
<td>Score 1</td>
<td>Score 2</td>
</tr>
<tr>
<td>2</td>
<td>5</td>
<td>0</td>
</tr>
<tr>
<td>3</td>
<td>14</td>
<td>6</td>
</tr>
<tr>
<td>4</td>
<td>1</td>
<td>12</td>
</tr>
<tr>
<td>5</td>
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*Statistical significance was determined using $\chi^2$ test.

Table 3. Relationship between MICAL2-PV expression level and Gleason grade in 53 lesions of prostate cancers

![Image of a diagram](image_url)
of c-Met was frequently observed in a wide spectrum of malignancies, including prostate cancers, and it plays a key role in cancer progression (8, 18, 19). Our immunohistochemical study evidently showed that MICAL2-PV expression status was strongly associated with progressive nature of the disease, such as tumor classification, lymph node metastasis, lymphatic or vascular invasion, and Gleason score (Tables 1-3), and our findings prompted us to investigate a possible association of MICAL2-PVs with c-Met in prostate cancer progression. Interestingly, the MICAL2-PV expression levels were also significantly concordant with the c-Met expression levels (P = 0.0018). Considering the relationship between c-Met expression and high-grade prostate cancers (14) or high incidence of bone metastasis in prostate cancers (15), our results of the coexpression of c-Met and MICAL2 suggest that MICAL2-PVs may be involved in cancer progression of prostate cancer as well as Gleason score, probably in association with the activation of the c-Met pathway. Gleason grading system is one of the established indicators for progression and prognosis of prostate cancers, and high Gleason score implies that cancer cells are more proliferative, lose cell-to-cell contact for scattered growth, and become more invasive (20). Our immunohistochemical data suggested that MICAL2-PV expression might associate with progression of prostate cancers (Tables 1-3) in the similar manner with Gleason score, and that it should have therapeutic implications especially in patients having prostate cancers with high Gleason score. Indeed, our siRNA study, which knocked down MICAL2-PV expression in prostate cancer cells, supports its potential of molecular therapeutic target for prostate cancer treatment. Because MICAL2-PVs have the conserved monoxygenase domain at its NH2-terminal, this enzymatic activity, if it has, could be a good therapeutic target to inhibit the MICAL2-PV function as well as MICAL1 (7). At present, the functional significance of MICAL2-PVs in prostate cancers remains unclear both in terms of cancer epidemiology and molecular pathology, and more detailed investigation into its function in prostate cancers, with or without the association to c-Met, is required. Because the most prevalent prostate cancer marker, PSA, is not related to the volume or grade of prostate cancers and does not reflect well the clinical behavior of prostate cancers (13), novel markers reflecting the pathologic and clinical outcome of prostate cancers are required. Our results have indicated that MICAL2-PVs should represent a promising novel molecular marker for prostate cancer progression as well as Gleason score, at least, and could be a promising candidate for development of novel treatment to prostate cancers with high Gleason score.

References

Expression of Novel Molecules, MICAL2-PV (MICAL2 Prostate Cancer Variants), Increases with High Gleason Score and Prostate Cancer Progression

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