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MMSET is overexpressed in cancers: link with tumor aggressiveness

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Abstract:

MMSET is expressed ubiquitously in early development and its deletion is associated with the malformation syndrome called Wolf-hirschhorn syndrome. It is involved in the t(4;14)(p16;q32) chromosomal translocation, which is the second most common translocation in multiple myeloma (MM) and is associated with the worst prognosis. MMSET expression has been shown to promote cellular adhesion, clonogenic growth and tumorigenicity in multiple myeloma. MMSET expression has been recently shown to increase with ascending tumor proliferation activity in glioblastoma multiforme. These data demonstrate that MMSET could be implicated in tumor emergence and/or progression. Therefore we compared the expression of MMSET in 40 human tumor types – brain, epithelial, lymphoid – to that of their normal tissue counterparts using publicly available gene expression data, including the Oncomine Cancer Microarray database. We found significant overexpression of MMSET in 15 cancers compared to their normal counterparts. Furthermore MMSET is associated with tumor aggressiveness or prognosis in many types of these aforementioned cancers.

Taken together, these data suggest that MMSET potentially acts as a pathogenic agent in many cancers. The identification of the targets of MMSET and their role in cell growth and survival will be key to understand how MMSET is associated with tumor development.
Introduction

MMSET gene is expressed ubiquitously in early development. The Wolf-hirschhorn syndrome is a malformation syndrome associated with a homizygous deletion of the distal short arm of chromosome 4 containing MMSET gene[1].

The MMSET gene is involved in the t(4;14)(p16;q32) chromosomal translocation, which is the most common translocation in multiple myeloma (MM) – occurring in 15% of newly-diagnosed patients – and is associated with poor prognosis[1; 2; 3]. The t(4;14) translocation dysregulates both MMSET and FGFR3 genes that are closely located on chromosome 4p16. FGFR3 has oncogenic activity in vitro and in vivo, but approximately one-third of MM tumors harboring t(4;14) translocation lacks FGFR3 expression, whereas an overexpression of MMSET is a universal characteristic of t(4;14) cases[3; 4; 5]. Furthermore, the poor prognosis of t(4;14) is independent of FGFR3 expression. These data suggest that activation of MMSET, not FGFR3, may be the critical transforming event of this recurrent translocation[1; 3; 5].

MMSET gene encodes for three isoforms including MMSET type I (647 aa) and type II (1365 aa) as a result of alternative splicing, and a 584 aa protein, known as RE-IIB (response element II-binding protein) translated from a second transcription initiation site. MMSET isoforms share various conserved protein domains suggesting a role in DNA-binding and chromatin modification, including PWWP domains, an HMG domain, PHD zinc fingers, and a C-terminal SET domain characteristic of histone methyltransferases[1].

The biological role of MMSET in MM disease is still poorly understood. A direct evidence shows that MMSET expression contributes to cellular adhesion, clonogenic
growth and tumorigenicity in multiple myeloma [1]. MMSET contains a SET domain that is found in many histone methyltransferases and determines their enzymatic activity. Histone lysine methylation promotes or prevents binding of proteins and protein complexes that drive particular regions of the genome into active transcription or repression[6]. MMSET has a transcriptional repressor activity, with increased H4K20 methylation gene and loss of histone acetylation. Consistent with this repressive activity, MMSET could form a complex with HDAC1 and HDAC2, mSin3a and the histone demethylase LSD1 suggesting that it is a component of transcription co-repressor complexes[7]. Moreover, RE-IIB (IL5 response element II-binding protein) has been recently demonstrated to repress IL-5 expression, through the histone H3-K27 hypermethylation around promoter region and H3 hypo-acetylation[8].

Collectively, these data suggest that by acting directly as a modifier of chromatin as well as through binding of other chromatin modifying enzymes, MMSET may influence gene expression and potentially acts as a pathogenic agent in MM. The identification of the targets of MMSET and their role in cell growth and survival will be key to understand how MMSET is associated with tumor development[7].

Recent study has identified an aberrant expression of MMSET mRNA and protein in glioblastoma multiform compared to normal brain cortex samples using proteomic approach[9]. They demonstrated that MMSET expression increased with ascending tumor proliferation activity. Furthermore, RNA interference blocking MMSET expression suppresses glioma cells growth[9]. These data demonstrate that MMSET could be implicated in tumor emergence and/or progression. Therefore, we focussed on MMSET expression in various cancers compared to their normal counterparts and in association with staging.
Methods

Databases
We used oncomine cancer microarray database (http://www.oncomine.org)[10] to study gene expression of MMSET in 40 human tumor types and their normal tissue counterpart as indicated in table 1. To compare the gene expression of a tumor type to its normal counterpart, we used gene expression data from a same study with the same methodology. All data were log transformed, median centered per array, and the standard deviation was normalized to one per array[10] .

Statistical analysis
Statistical comparisons were done with Mann Whitney or student t-test.

Results and discussion
We investigated the expression of MMSET in cancer using publicly available gene expression data. The 40 tumor types investigated corresponded to 4 hematological malignancies and 36 solid tumors (Table 1). We found MMSET overexpression in all hematological cancers and in 12/36 solid tumors (Table 1 and Supplementary figure S1). Overexpression of MMSET was found in glioblastoma compared to normal brain (P = 1.7E-14, P = .009, P = .002)[11; 12; 13]; in hepatocellular carcinoma compared to normal liver (P = 2.9E-7, 1.3E-6) [14; 15]; in head and neck cancer compared to the normal (P = .008, P = 2.7E-5)[16; 17]; in bladder carcinoma compared to normal bladder (P = 4.1E-11, P = 1.8E-7)[18; 19]; in primary colon cancer compared to normal adjacent mucosa (P = 9.5E-6)[20]; in esophagus adenocarcinoma compared to normal esophagus (P = .004)[21]; in breast carcinoma compared to normal breast (P = 3.8E-
in T-cell acute lymphoblastic leukemia compared to normal bone marrow \( (P = 5.1E-7) \)[23]; in B-cell acute lymphoblastic leukaemia compared to normal bone marrow \( (P = .001) \)[23]; in lung adenocarcinoma compared to normal lung \( (P = .009, P = 8.4E-4, 1.7E-6) \)[24; 25; 26]; in lymphoma compared to normal B-cell \( (P = 3.5E-5, 7.3E-5) \)[27]; in cutaneous melanoma compared to normal melanocyte \( (P = 6.46E-13, P = .01, P = .009) \)[28; 29; 30]; in smoldering multiple myeloma compared to normal bone marrow \( (P = 7.3E-4) \)[31]; in prostate cancer compared to normal prostate \( (P = 1.8E-6, P = .039, P = 5.1E-8, P = .002, P = .009, P = .006, P = .009) \)[32; 33; 34; 35; 36; 37; 38]; in yolk sac tumor compared to normal testis \( (P = .003) \)[39]; in ovarian carcinoma compared to normal ovary \( (P = .002, P = 1.1E-4) \)[40; 41] and in clear cell carcinoma compared to normal kidney tissue \( (P = .006) \)[42].

**MMSET** has been shown to be highly overexpressed in MM with t(4;14), in association with poor prognosis. Thus, we looked for whether **MMSET** expression could be associated with tumor progression and prognosis. **MMSET** was significantly overexpressed in oligodendroglioma grade III compared to grade II \( (P = .009) \)[11] (Figure 1) in agreement with previous data[9]; in patients presenting advanced bladder carcinoma (grade II and III) compared to grade I in four independent studies \( (P = 4E-6, P = .0001, P = .004, P = .008) \)[19; 43; 44; 45]; in breast carcinoma grades II and III compared to grade I in four independent studies \( (P = 2.2E-6, P = 9.1E-4, P = .014, P = .017) \)[46; 47; 48; 49]; in advanced prostate carcinoma grades VII, VIII and IX compared to grade VI \( (P = 1.4E-4) \)[50]; in no differentiated hepatocellular carcinoma compared to differentiated hepatocellular carcinoma \( (P = 7.2E-5) \)[15]; in undifferentiated compared to differentiated head and neck cancer \( (P = .002) \)[17]; in undifferentiated compared to
differentiated cervical carcinoma[51]; in advanced papillary renal cell carcinoma stages III and IV compared to stages I and II ($P = .0039$)[52](Figure 1).

Furthermore, as it has been demonstrated in MM, *MMSET* expression is associated with bad prognostic in others cancers (Figure 2). *MMSET* is overexpressed in patients with head and neck squamous cell carcinoma dead at 5 years compared to patients alive at 5 years ($P = 1.2E-4$)[53]; in 1 year relapsing MM patient compared to patients with no relapse ($P = 3.2E-4$)[54]; in MM patients alive compared to dead MM patient at one year ($P = .001$)[54]; in prostate carcinoma patients presenting recurrence compared to prostate carcinoma patients with no recurrence ($P = 1.5E-4$) at 5 years [50] and in dead glioma patients compared to alive glioma patients at 3 years ($P = .009$) [55].

**Correlations between MMSET and HDAC expression in tumor cells**

In patients with MM, it was recently demonstrated that MMSET could form a complex with HDAC1 and HDAC2, mSin3a and the histone demethylase LSD1 suggesting that MMSET is a component of transcription co-repressor complexes. Interestingly, the genes of at least one of these four MMSET partners are overexpressed in cancers presenting a *MMSET* overexpression compared to their normal counterpart (Supplementary Table 1). Furthermore, *HDAC1, HDAC2* and *LSD1* overexpression are associated with tumor aggressiveness, as *MMSET*, in brain and liver cancers (Supplementary Table 2). Furthermore a high expression of the *MMSET* partners is associated with prognosis in brain cancer (Supplementary Table 3). *HDAC2* and *LSD1* overexpression is also associated with breast and lung progression; and they are associated with prognosis in breast cancer (Supplementary Table 3).
Conclusions:

The analysis reported here demonstrates that MMSET mRNA is overexpressed in at least in 15 cancers compared to their normal counterparts, and within a given tumor categories is associated with tumor progression or bad prognosis. The properties of transcriptional co-factor of MMSET appear to be associated with tumorigenesis. The identification of the targets of MMSET and their role in cell growth and survival will be key to understanding how MMSET is associated with tumor development.
Acknowledgements

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**Figure legends**

**Figure 1:** Association between MMSET expression and progression in various cancers

MMSET gene expression in oligodendroglioma [9], bladder[19; 43; 44; 45], breast carcinoma [46; 47; 48; 49], prostate carcinoma[50], in hepatocellular carcinoma [15], head and neck cancer[17], cervical carcinoma[51], papillary renal cell carcinoma[52].

**Figure 2:** Association of MMSET expression with prognosis

MMSET expression in alive patients with head and neck carcinoma, in dead patients with head and neck carcinoma [53], in MM patients with no relapse, in MM patients with relapse[54], in alive and dead patients with MM [54], in prostate carcinoma patients with no recurrence, prostate carcinoma patients with recurrence [50], in alive and dead patients with glioma [55].
References


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Table 1
Expression of MMSET, HDAC1, HDAC2, LSD1, Sin3A in human tumor types to that of their normal tissue counterparts using publicly available gene expression data, including the Oncomine Cancer Microarray database.
Figure 1: Association of MMSET expression with tumor grade

**Oligodendroglioma - Grade**

- Grade 2 (38)
- Grade 3 (12)

*P* = .009

*Sun et al. Cancer cell 2006*

**Bladder Carcinoma - Grade**

- Grade 1 (25)
- Grade 2 (39)
- Grade 3 (11)

*P* = 4E-6

*Lindgren et al. Oncogene 2006*

**Bladder Carcinoma - Grade**

- Grade 1 (12)
- Grade 2 (11)
- Grade 3 (31)

*P* = .001

*Stransky et al. Nat gene 2006*

**Superficial Bladder Carcinoma - Grade**

- Grade 2 (15)
- Grade 3 (14)

*P* = .004

*Dyrskjot et al. Clin Cancer Res 2005*

**Bladder Carcinoma - Grade**

- Grade 2 (19)
- Grade 3 (90)

*P* = .008

*Sanchez-Carbayo et al. J Clin Oncol 2006*

**Breast Carcinoma - Elston Grade**

- Grade 1 (68)
- Grade 2 (126)
- Grade 3 (55)

*Sanchez-Carbayo et al. J Clin Oncol 2006*

*Ivshina et al. Cancer Res 2006*
Prostate Carcinoma - Gleason Score

Breast Carcinoma - Elston Grade

Breast Carcinoma - Grade

Ductal Breast Carcinoma - Grade

Prostate Carcinoma - Gleason Score

Hepatocellular Carcinoma - Differenciation

Head and Neck Cancer - Differenciation

Glinsky et al. J Clin Invest 2004

Miller et al. Proc Natl Acad Sci USA 2005


Zhao et al. Mol Biol Cell 2004

Hepatocellular Carcinoma - Differenciation

Wurmbach et al. Hepatology 2007


P = .014

P = .017

P = 9.1 E-4

P = 1.4 E-4

P = 7.2 E-5

P = .002

P = 7.2 E-5

P = .02
Cervical Carcinoma - Differentiation


P = .0015

Papillary Renal Cell Carcinoma - Stage

Yang et al. Cancer Res 2005

P = .0039
Figure 2: Association of MMSET expression with prognosis

**Head and Neck Squamous Cell Carcinoma Overall Survival - 5 Years**
- Alive (5)
- Dead (15)
- P = 1.2E-4
- Chung et al. Cancer Cell 2004

**Multiple Myeloma - Relapse Status - 1 Year**
- No Relapse (11)
- Relapse (26)
- P = 3.2E-4
- Carasco et al. Cancer Cell 2006

**Multiple Myeloma - Survival - 1 Year**
- Alive (13)
- Dead (16)
- P = .001
- Carasco et al. Cancer Cell 2006

**Prostate Carcinoma - Biochemical Recurrence - 5 Years**
- Negative (42)
- Positive (32)
- P = 1.5E-4

**Glioma - Survival - 3 Years**
- Alive (13)
- Dead (56)
- P = .009