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Epigenetic regulation of breast cancer metastasis by miR-106b-BRMS1L-FZD10 signaling.

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Metastasis is responsible for around 90% of breast cancer-associated mortality.



Epigenetic repression of metastasis-associated genes has a significant role in suppressing metastasis.



DNA methylation and chromatin remodeling

Variant histones H2A : HDAC repressor complex

MicroRNAs

SIN3–HDAC complex are important inhibitors in epigenetic silencing of target genes.

core switch-independent 3 (SIN3)–HDAC



BRMS1L (Breast cancer metastatic suppressor 1-like)

Molecular weight: 40KD

A co-suppressor of mSin3A /HDAC complex

Strong histone deacetylase (HDAC) activity

Its biology function is unknown.

AnatolyY. Nikolaev, et al, 2004

BRMS1-Like (BRMS1L) is highly homologous to BRMS1.



- > 57% identity and 79% similarity
- > BRMS1 suppresses metastasis of multiple types of malignancies.
- BRMS1 gene is often deleted or epigenetically silenced in breast cancer.

Cicek M, et al, BBRC, 2004, 323:1216-1222.



Whether BRMS1L plays a functional role in suppressing breast cancer metastasis?

What is the mechanism of BRMS1L(BRL) in breast cancer cells?

BRMS1L expression is much lower in breast cancer tissues.



BM: brain metastasis

LM: liver metastasis

The mRNA and protein level of BRMS1L was much lower in mesenchymal-like breast cells.



Breast cancer patients with high BRMS1L had low metastatic potential and a longer survival.

BRMS1L		IRS>4	IRS≤4	P value	
Age(years)				0.108	
	<u>≤</u> 45	96	106		
	>45	125	101		
Size(cm)				0.005	High BRMS1L (IRS>4)
	≤2	115	80		1.0
	>2	106	127		
Histological					<u> </u>
grade				0.109	
	I	79	56		
	II	95	94		P<0.001
	III	47	57		
Stage				0.021	ja 0.4
	Ι	79	49		Ő
	II	108	116		0.2 -
	III-IV	34	42		
Positive					
Lymph node				< 0.001	0 20 40 60 80
	≤3	185	126		Months
	>3	36	81		
ER				0.287	
	positive	166	146		
	negative	55	61		
HER2				0.238	Median follow-up: 55m
	negative	179	158		
	positive	42	49		
Metastasis				< 0.001	
	no	197	153	<u>تحصیمی</u>	
	ves	24	54		

IRS, immunoreactive score.



Reduced BRL expression is associated With breast cancer metastasis.

Whether BRMS1L exerts a metastatic suppressing function in breast cancer cells?

BRMS1L suppresses migration and invasion of breast cancer cells.



BRMS1L inhibits epithelial-mesenchymal transition (EMT).





BRMS1L inhibits the migration and invasion of breast cancer cells by suppressing EMT.

BRMS1L suppresses FZD10 expression



FZD10: Frizzled10

FZD10 promotes tumor cell growth and metastasis by activation of Wnt pathway.



Figure 2. Non-canonical Wnt signaling pathways

BBRC 1999.

 Highly expressed in cervical cancer , colon cancer , gastric cancer and synovial sarcoma Tumor cell growth, metastasis

Oncogene 2005

• Positive regulator of canonical wnt-β-catenin-TCF signaling pathway

Int J Mol Med (2002)

Activate non-canonical Dvl-Racl-JNK pathway
Oncogene 2009

codes for a seven-transmembrane-receptor of wnt signaling pathway

BRMS1L inhibits breast cancer cell invasion and EMT via suppressing FZD10 expression.



FZD10 expression is inversely correlated with BRMS1L in breast cancer samples.





BRMS1L inhibits EMT and invasion of breast cancer cells via downregulating fzd10.

BRMS1L regulates fzd10 promoter activity by histone deacetylation.

T47D



BRMS1L binds to the fzd10 promoter



BRMS1L increases recruitment of HDAC1 to the *fzd10* promoter.



BRMS1L suppresses the binding of HDAC1 substrates to *fzd10* promoter





BRMS1L increases the recruitment of HDAC1/2 complex to *fzd10* promoter and thus reducing acetylation of HDAC1/2 substrates.



What actives the transcription of *fzd10?*

An SP1-binding site was involved in the full transactivation activity in the FZD10 promoter region.



SP1-mediated transcription is responsible for FZD10 upregulation in breast cancer cells.



BRMS1L suppresses the binding of SP1 to *fzd10* promoter



**



BRMS1L attenuates SP1-mediated FZD10 transcriptional activation probably by reducing histone acetylation at FZD10 promoter.



Whether BRMS1L regulates Wnt signaling pathway via FZD10?

BRMS1L suppresses WNT3/FZD10/β-catenin pathway.





Why BRMS1L is differentially expressed in breast cancers with different metastatic potential ?

Target scan predicts microRNAs targeting BRL-3'UTR

Preferential conservation	microRNAs
High probability	miR-93, miR-20a, miR-106a, miR-106b, miR- 17, miR-20b, miR-519d (position 1128-1135 of p40 3' UTR) (position 576-582 of p40 3' UTR)
Lower probability	miR-520a/b/c/d/e、miR-302a/b/c/d/e、miR-372 (position 575-581 of p40 3' UTR) miR-182 (position 1276-1283 of p40 3' UTR) miR-183 (position 52-58 of p40 3' UTR) miR-223 (position 774-781 of p40 3' UTR)



Increased miR-106b in mesenchymal-like cells silences BRMS1L.



miR-106b suppresses Wnt pathway and EMT by targeting BRMS1L.



miR-106b expression is inversely correlated with BRMS1L.

ISH:106b





miR-106b activates Wnt/β-catenin signaling and promotes EMT by silencing BRMS1L in breast cancer.

Expression of BRMS1L and FZD10 in xenografts



BRMS1L significantly inhibits liver metastasis

	BT-474 (5×10 ⁶)	MDA-MB-231 (2×10 ⁶)			
Groups	Tumors	Liver metastasis	Groups	Tumors	Liver metastasis	
GFP-sh	7/8	1/8	NC-vec	8/8	6/8	
BRL-sh1	6/8	4/8	BRL	7/8	2/8	
BRL-sh2	7/8	5/8				







Signifiance

Our findings highlight the contribution of BRMS1L in epigenetic silencing of oncogenes and its effect in tumor suppression.

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