Original Article

High-level expression of MYH9 predicts poor prognosis in patients with colon cancer

Rengeng Liu^{1,2}, Qianyu Zhang^{1,2}, Yuehong Lang^{1,2}, Zibo Tang^{1,2}, Zhongzhong Peng³, Xiaojun Cai^{1,2}, Zhaojian Fu⁴, Weiyi Fang^{1,2}, Libo Li^{1,2}

¹Cancer Center, ²Traditional Chinese Medicine-Integrated Hospital, Southern Medical University, Guangzhou 510315, China; ³Department of Oncology, Ningbo No. 2 Hospital, Ningbo, Zhejiang, China; ⁴Department of Oncology, Dali Bai Autonomous Prefecture People's Hospital, Dali, China

Received January 9, 2017; Accepted March 14, 2017; Epub May 1, 2017; Published May 15, 2017

Abstract: MYH9 (myosin, heavy chain 9, non-muscle) as a gene encodes NM II-A (non-muscle II-A) protein, exists primarily in the cytoplasm. MYH9 consists of 2 mysoin heavy chains with a relative molecular mass of 230 kDa. Previous studies have shown that MYH9 is involved in a number of diseases, including cancer. However, the exact role of MYH9 in colon cancer is still unclear. Therefore, we used a tissue microarray of 90 colon cancer cases using immunohistochemistry and western blotting on four cases of paired fresh tissues. After analyzing both the immunohistochemical scores and clinical data, the results suggest that colon cancer tissues had higher expression of MYH9 than normal colon tissues. Higher expression of MYH9 in colon cancer patients predicted a worse N classification and clinical stage. Additionally, colon cancer patients with high expression of MYH9 had a shorter survival time than those with low MYH9 expression. Further, subgroup analysis revealed that the expression level of MYH9 was associated with colon cancer patients' survival time in the $T_{3.4}$ stage, the $N_{0.1}$ stage, and the clinical stages I-II. Univariate and multivariate analyzes of regression showed that MYH9 is an independent prognostic factor for colon cancer patients. These findings suggested that MYH9 is an oncogene and may be used as an indicator for clinical diagnosis in colon cancer patients. We also demonstrated that MYH9 could serve as an independent prognostic factor for colon cancer patients.

Keywords: MYH9, immunohistochemistry, colon cancer, prognosis

Introduction

Colon cancer has a high prevalence worldwide. In the USA, the American Cancer Society (ACS) estimated that 134,490 patients will be diagnosed with colon cancer and 49,190 patients with colon cancer will die during 2016 [1]. The Chinese Center for Disease Control and Prevention (CDC) has estimated that 376,300 new colon cancer cases would be diagnosed, and 191,000 patients with colon cancer would die during 2015 [2]. Thus, early diagnosis and targeted therapy are extremely important for colon cancer patients. In previous studies, MYH9 (myosin, heavy chain 9, non-muscle) was reported to be involved in cancer metastasis.

MYH9 as a gene encodes NM II-A protein which exists primarily in the cytoplasm. MYH9 consists of 2 myosin heavy chains, with relative

molecular mass of 230 kDa. MYH9 is related to a number of diseases, including focal segmental glomerulosclerosis [3], HIV-associated collapsing glomerulopathy [3], human non-syndromic hereditary deafness [4], macrothrombocytopenia [5], cataracts [5], anaplastic large cell lymphoma [6], and cancers. A study showed that MYH9 plays a protective role for patients with squamous carcinomas by suppressing squamous cell carcinoma migration in headneck squamous cell carcinoma [7]. However, other studies have reported that MYH9 is harmful to patients with adenocarcinomas through promotion of adenocarcinoma migration in various adenocarcinomas [8-12].

Studies have revealed that MYH9 promoted breast cancer metastasis [9]. Additionally, high-level expression of MYH9 in lung cancer patients was associated with a poor prognosis,

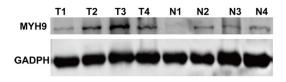


Figure 1. MYH9 is highly expressed in colon cancer tissues compared to normal colon tissues. T stands for colon cancer tissues, N stands for normal colon tissues. Results are from paired tissues from 4 cases of colon cancer patients.

indicating worse pathological stages and increased tumor invasion into the vessels [8]. Moreover, invasion and metastasis of gastric cancer was prevented through the use of microRNA Let-7f, which interfered with MYH9 expression, thus demonstrating that high-level MYH9 expression led to a poor prognosis in gastric cancer [10, 11]. Based upon the work in other cancers, MYH9 is likely to be a poor prognostic indicator for adenocarcinomas. Moreover, it has been shown that the expression of MYH9 in colon cancer is higher than that in normal colon tissues [13]. Although several studies on MYH9 and cancer have been done, the relationship between MYH9 expression and colon cancer and the prognosis of the colon cancer patients is still unclear.

In this study, we examined the expression MYH9 in colon cancer tissues using immuno-histochemistry and Western blotting. We also investigated correlations between the MYH9 expression and the clinicopathologic features and the survival period of the colon cancer patients.

Materials and methods

Sample collection

A tissue microarray containing 90 paired colon cancer and normal colon tissues with clinical data was purchased from Shanghai Outdo Biotech Co., Ltd. (Shanghai, China). This tissue microarray included tissues from 45 males and 45 females between 47 and 90 years of age, with a duration of clinical follow-up of 84 months. All specimens were pathologically-confirmed and were classified according to the 7th edition of the American Joint Committee on Cancer (AJCC) criteria. Four cases of paired fresh tissues from colon cancer patients were collected from the Traditional Chinese Medicine-Integrated Hospital of Southern Medical University (Guangzhou, China).

Immunohistochemistry (IHC) and evaluation of staining

The tissue microarray was deparaffinized in 100% xylene and rehydrated in a descending ethanol series and water according to standard protocols. Heat-induced antigen retrieval was performed in 10 Mm citrate buffer for 2 min at 100°C [14]. Endogenous peroxidase activity and nonspecific antigens were blocked with a peroxidase-blocking reagent containing 3% hydrogen peroxide and serum, followed by incubation with rabbit anti-human MYH9 antibody (1:200) overnight at 4°C. After washing, the sections were incubated with a biotin-labeled goat anti-rabbit antibody for 20 min at room temperature, and were subsequently incubated with a streptavidin-conjugated horseradish peroxidase (Maixin, Fuzhou, China). A 3, 3-diaminobenzidine chromogen solution in with DAB buffer substrate was used to add color to the sections. The sections were visualized with DAB and counterstained with hematoxylin, mounted in neutral gum, and analyzed using a bright field microscope.

Two independent pathologists who were blinded to the origination of the samples and subject outcomes assessed the IHC results. The cell staining was semi-quantitatively expressed as an immunohistochemical score in combination with the percentage of based upon the percentage of positive cells (<10%, 0; 10%-25%, 1; 26%-75%, 2; and >76%, 3), and staining intensity (none, 0; weak yellow, 1; brown-yellow, 2; and brown-auburn, 3). The staining intensity and average percentage of positive tumor cells were assayed for 5 independent high magnification (×400) fields. The points for the percentage of positive cells and staining intensity were multiplied. Samples were then assigned to 1 of 2 groups according to the overall score (0-4 points, low expression or 5-6 points, high expression) [15, 16].

Western blot analysis

For protein analysis, 40 mg of tissues were used. The tissues were then cut into pieces and milled using a bead mill homogenizer. Finally, the tissues were lysed in RIPA buffer (50 Mm Tris-HCI [pH 8.0], 1 mM EDTA [pH 8.0], 5 mM DTT, and 2% SDS) at $4\,^{\circ}\text{C}$. All protein concentrations were determined using the BCA assay (Beyotime, Beijing, China). Total protein (30 $\mu\text{g})$ was resolved using 10% SDS-polyacrylamide

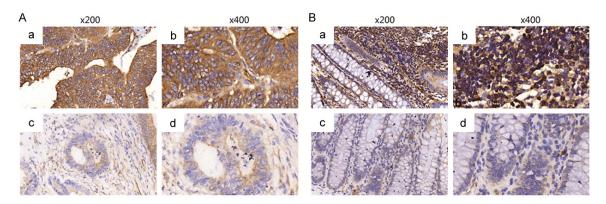


Figure 2. A. It has been observed that MYH9 expression primarily occurs in the cytoplasm of colon cancer. Aa and Ab (high power field) show high MYH9 expression. Ac and Ad (high power field) show low MYH9 levels. B. MYH9 expression occurs in the cytoplasm of normal colon tissue. Ba and Bb (high power field) show high MYH9 expression. Bc and Bd (high power field) show low MYH9 expression.

Table 1. Protein levels of MYH9 between colon cancer tissues and normal colon tissues

Group		P value		
	Case	High	Low	
	Case	expression	expression	
Cancer	90	43 (47.8%)	47 (52.2%)	
Normal	90	5 (5.6%)	85 (94.4%)	<0.001

gel electrophoresis and bands were electrotransferred to polyvinylidene fluoride membranes (Invitrogen, Los Angeles, CA, USA). The membranes were blocked with 5% BSA in Trisbuffered saline (pH 7.5), followed by immunoblotting overnight at 4°C with MYH9 (1:1000; Proteintect Group, Chicago, IL, USA) or GADPH (1:1000; Santa Cruz Biotechnology, Inc., Santa Cruz, CA, USA). Horseradish peroxidase-conjugated anti-rabbit IgG and anti-mouse IgG antibodies were used as secondary antibodies (Zhongshan, Beijing, China). Signals were detected using enhanced chemiluminescence reagents (Pierce, Rockford, IL, USA).

Statistical analysis

All data were analyzed by SPSS (version 19.0). A x^2 test was used to analyze MYH9 expression between colon cancer and normal colon tissues. The relationship between clinicopathologic characteristics and the MYH9 expression in individuals with colon cancer was also analyzed using a x^2 test. Survival curves were plotted using the Kaplan-Meier method and compared using a log-rank test. Multivariate survival analysis was performed for all parameters that were significant based upon univariate

analyzes using a Cox regression model. A P<0.05 was considered statistically significant.

Results

High-level expression of MYH9 in colon cancer tissues

In order to evaluate the role of MYH9 in colon cancer, we used western blot analysis on four cases of paired fresh colon cancer and normal colon tissues. Results showed that MYH9 expression in colon cancer tissues is higher than that in the normal colon tissues (See Figure 1), suggesting that MYH9 is an oncogene in colon cancer.

IHC analyzes of MYH9 in colon cancer and normal colon tissues

We measured the subcellular localization of MYH9 and MYH9 protein levels in the tissue microarray of colon cancer tissues and normal colon tissues using immunohistochemical staining. Highly specific levels of MYH9 appeared in the cytoplasm of colon cancer tissues and normal colon tissues (**Figure 2**). The level of MYH9 in colon cancer tissues (47.8%) was significantly higher than that of normal colon tissues (5.6%, P<0.001; **Table 1**).

The relationship between the clinicopathologic characteristics of colon cancer patients and the cytoplasmic expression of MYH9 in colon cancer tissues

Table 2 provides a summary of results on the relationship between the clinicopathologic

Table 2. Relationship between clinicopathological characteristics and MYH9 expression levels in individuals with colon cancer (n = 90)

Observantariation		MYH			
Characteristics	n	High expression Low express		m P	
Gender					
Male	45	23 (51.1%)	22 (48.9%)	0.527	
Female	45	20 (44.4%)	25 (55.6%)		
Age (years)					
≥65	57	31 (54.4%)	26 (45.6%)	0.099	
<65	33	12 (36.4%)	21 (63.6%)		
T classification					
$T_1 + T_2$	6	3 (50.0%)	3 (50.0%)	1.000	
$T_3 + T_4$	84	40 (47.8%)	44 (52.2%)		
N classification					
$N_0 + N_1$	78	33 (42.3%)	45 (57.7%)	0.008	
N_2	12	10 (83.3%)	2 (16.7%)		
Distant metastasis					
Mo	89	43 (48.3%)	46 (51.7%)	1.000	
$M_\mathtt{1}$	1	0 (0%)	1 (100%)		
Clinical stage					
I-III B	80	35 (43.8%)	45 (56.3%)	0.030	
III C-IV	10	8 (80.0%)	2 (20.0%)		

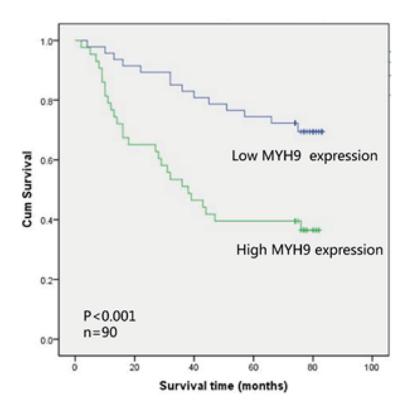


Figure 3. A Kaplan-Meier survival curve with data from 90 patients with colon cancer. Patients with colon cancer expressing low MYH9 levels had achieved better survival times when compared to those with high MYH9 expression (*P*<0.001, log-rank test).

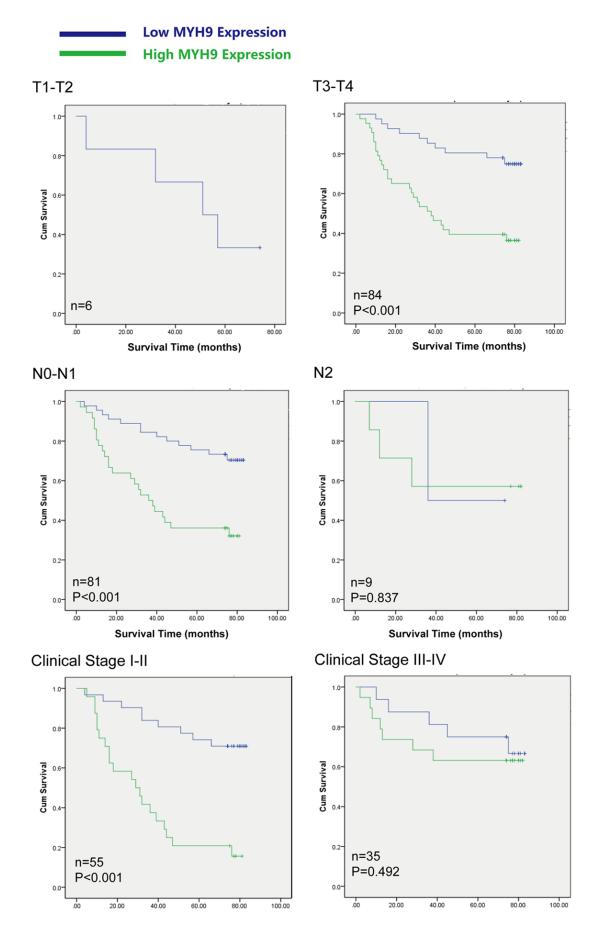
characteristics of colon canpatients and MYH9 expression in colon cancer tissues. The expression level of MYH9 was not correlated with the gender, age, T classification, or M classification of the 90 patients with colon cancer. However, we did observe a positive correlation between the expression level of MYH9 and the N classification $(N_0-N_1 \text{ vs. } N_2; P = 0.008)$ and clinical stage (I-III B vs. III C-IV: P = 0.030: Table 2).

MYH9 expression is associated with the survival time of colon cancer patients

To investigate the prognostic value of MYH9 expression in colon cancer patients, we analyzed the relationship between MYH9 expression and survival time of the colon cancer patients, using a Kaplan-Meier analysis with a log-rank test. MYH9 expression was significantly correlated with the 90 patients' overall survival. Moreover, tumors with high MYH9 expression had a worse prognosis than those with low MYH9 expression (P<0.001; **Figure 3**).

Subgroup analysis suggested that MYH9 expression was inversely associated with survival time for colon cancer patients with T_{3-4} and N_{0-1} tumors and those in clinical stage I and II

We analyzed the correlation between the cytoplasmic expression of MYH9 and the prognosis of colon cancer patients according to T classification, N classification, and clinical stage (**Figure 4**). High MYH9 expression was related to a shorter survival time in colon cancer patients with $T_{3.4}$ (P<0.001) and $N_{0.1}$ stage



MYH9 expression in colon cancer

Figure 4. Correlation of MYH9 expression with colon cancer patients' survival time, stratified by T classification, N classification and clinical stage. MYH9 protein expression was associated significantly with a shorter survival for patients in stages $T_{3,4}$, stages $N_{0,1}$, and clinical stages I-II, but did not correlate with the survival of those in stages $T_{1,2}$, stage $N_{0,1}$, or clinical stages I-II.

Table 3. Summary of univariate and multivariate Cox regression analysis of overall survival duration (n = 90)

D	Univariate analysis			Multivariate analysis		
Parameters	Р	HR	95% CI	Р	HR	95% CI
Age						
≥65 vs. <65	0.124	1.766	0.855-3.649			
Gender						
Male vs. Female	0.082	1.783	0.930-3.421			
T classification						
T_1 - T_2 vs. T_3 - T_4	0.979	505492.552	0.000-			
N classification						
N_0 - N_1 vs. N_2	0.932	1.045	0.381-2.864			
M classification						
M_0 vs. M_1	0.926	1.114	0.113-10.929			
Clinical Stage						
I-II vs. III-IV	0.009	2.528	1.267-5.047	0.002	0.374	0.201-0.695
MYH9 expression						
High vs. Low	0.002	0.335	0.167-0.671	0.001	0.322	0.168-0.617

(P<0.001) tumors and those in clinical stage I-II (P<0.001).

High expression of MYH9 is an independent prognostic factor for colon cancer patients

Univariate analysis showed that clinical stage (P = 0.009) and cytoplasmic expression of MYH9 (P = 0.002) were significantly correlated with the survival time of colon cancer patients (**Table 3**). In order to identify whether MYH9 is an independent prognostic factor for colon cancer, we carried out a multivariate analysis on the variation of MYH9 expression in the clinical stages. The results showed that the expression level of MYH9 was indeed an independent prognostic factor (P = 0.001).

Discussion

MYH9 promotes cancer metastasis by lamellipodia formation at the leading edge of the cell [17]. Lamellipodia formation is controlled by Rac1, the WAVE complex, and the Arp2/3 complex [18]. Previous studies have reported that high MYH9 expression is a poor prognosis indicator in non-small cell lung cancer [8], gastric cancer [10, 11], bladder cancer [12], and breast

cancer [9]. Moreover, MYH9 promoted cancer metastasis. In contrast, others have shown that high MYH9 expression plays a protective role in squamous cell carcinoma, potentially due to its ability maintain the post-transcriptional stability of p53 [7] or maintain the mitotic stability of the chromosomes during karyomitosis [19]. The explanation of the role of MYH9 in squamous cell carcinoma versus other tumors is not clear. Additionally, the role of MYH9 expression in colon cancer and its influence on the survival period of colon cancer patients has not been examined.

In this study, we have showed that MYH9 expression in colon cancer tissues is higher than that in normal colon tissues using western blotting. These results agree with previous research in lung cancer [8], breast cancer [9], and gastric cancer [10].

Further, we evaluated the expression of MYH9 protein in colon cancer tissues immunohistochemical staining. MYH9 expression was mainly located in the cytoplasm, which matches similar findings in lung cancer [8], gastric cancer [10, 11], and breast cancer [9]. Since MYH9

can promote cell migration by forming lamellipodia at the edge of the cell, we analyzed the correlation between MYH9 expression and the clinical features of the colon cancer patients. We found that although MYH9 expression was not related to patient age, gender, T classification, or distant metastasis, it had a positive correlation with N classification and clinical stage, indicating that MYH9 is a potential oncogene.

Moreover, a negative correlation between MYH9 expression in colon cancer tissues and the survival period of colon cancer patients was noted, suggesting that high expression of MYH9 may act as an important clinical biomarker for colon cancer patients with poor prognosis. Additionally, the relationship with prognosis and the MYH9 levels were assessed further by the stratification of T and N classification and clinical stage. The results showed that MYH9 expression had a reverse correlation with the survival period of colon cancer patient in T_{3-4} stage, N_{0-1} stage, and clinical stage I-II, indicating that high MYH9 expression may promote colon cancer cell proliferation in advanced stages and promote cell migration in the early stages of colon cancer.

Finally, we assessed whether MYH9 is as an independent prognostic factor for patients with colon cancer. According to univariate analysis, the survival period of patients was inversely correlated to clinical stage and MYH9 expression. Moreover, multivariate analyzes showed that high MYH9 expression is a significant indicator of poor prognosis for colon cancer patients, which agrees with observations in lung [8], breast [8], gastric [10], bladder [11], and esophageal cancers [20].

In summary, we have confirmed that high MYH9 expression is associated with the clinical progression of colon cancer patients. MYH9 suggests a poor prognosis for colon cancer patients. Furthermore, data indicate that MYH9 may serve as an independent prognostic indicator for colon cancer patients.

Disclosure of conflict of interest

None.

Address correspondence to: Dr. Libo Li, Traditional Chinese Medicine-Integrated Hospital, Southern Medical University, Guangzhou 510315, China. Tel: 86-13632101888; E-mail: niuniu_dhd@163.com

References

- [1] Smith RA, Andrews K, Brooks D, DeSantis CE, Fedewa SA, Lortet-Tieulent J, Manassaram-Baptiste D, Brawley OW and Wender RC. Cancer screening in the United States, 2016: a review of current American Cancer Society guidelines and current issues in cancer screening. CA Cancer J Clin 2016; 66: 96-114.
- [2] Chen W, Zheng R, Baade PD, Zhang S, Zeng H, Bray F, Jemal A, Yu XQ and He J. Cancer statistics in China, 2015. CA Cancer J Clin 2016; 66: 115-132.
- [3] Winkler CA, Nelson G, Oleksyk TK, Nava MB and Kopp JB. Genetics of focal segmental glomerulosclerosis and human immunodeficiency virus-associated collapsing glomerulopathy: the role of MYH9 genetic variation. Semin Nephrol 2010; 30: 111-125.
- [4] Lalwani AK, Goldstein JA, Kelley MJ, Luxford W, Castelein CM and Mhatre AN. Human nonsyndromic hereditary deafness DFNA17 is due to a mutation in nonmuscle myosin MYH9. Am J Hum Genet 2000: 67: 1121-1128.
- [5] Marigo V, Nigro A, Pecci A, Montanaro D, Di Stazio M, Balduini CL and Savoia A. Correlation between the clinical phenotype of MYH9related disease and tissue distribution of class Il nonmuscle myosin heavy chains. Genomics 2004; 83: 1125-1133.
- [6] Lamant L, Gascoyne RD, Duplantier MML, Armstrong F, Raghab A, Chhanabhai M, Rajcan-Separovic E, Raghab J, Delsol G and Espinos E. Non-muscle myosin heavy chain (MYH9): a new partner fused to ALK in anaplastic large cell lymphoma. Genes Chromosomes Cancer 2003; 37: 427-432.
- [7] Schramek D, Sendoel A, Segal JP, Beronja S, Heller E, Oristian D, Reva B and Fuchs E. Direct in vivo RNAi screen unveils myosin iia as a tumor suppressor of squamous cell carcinomas. Science 2014; 343: 309-313.
- [8] Katono K, Sato Y, Jiang S, Kobayashi M, Nagashio R, Ryuge S, Fukuda E, Goshima N, Satoh Y, Saegusa M and Masuda N. Prognostic significance of MYH9 expression in resected non-small cell lung cancer. PLoS One 2015; 10: e121460.
- [9] Derycke L, Stove C, Vercoutter-Edouart A, De Wever O, Dollé L, Colpaert N, Depypere H, Michalski J and Bracke M. The role of non-muscle myosin IIA in aggregation and invasion of human MCF-7 breast cancer cells. Int J Dev Biol 2011; 55: 835-840.
- [10] Liu D, Zhang L, Shen Z, Tan F, Hu Y, Yu J and Li G. Clinicopathological significance of NMIIA overexpression in human gastric cancer. Int J Mol Sci 2012; 13: 15291-15304.
- [11] Liang S, He L, Zhao X, Miao Y, Gu Y, Guo C, Xue Z, Dou W, Hu F, Wu K, Nie Y and Fan D.

MYH9 expression in colon cancer

- MicroRNA let-7f inhibits tumor invasion and metastasis by targeting MYH9 in human gastric cancer. PLoS One 2011; 6: e18409.
- [12] Xiong D, Ye YL, Chen MK, Qin ZK, Li MZ, Zhang H, Xu LH, Xu ZZ and Zeng MS. Non-muscle myosin II is an independent predictor of overall survival for cystectomy candidates with earlystage bladder cancer. Oncol Rep 2012; 28: 1625-1632.
- [13] Mu Y, Chen Y, Zhang G, Zhan X, Li Y, Liu T, Li G, Li M, Xiao Z, Gong X and Chen Z. Identification of stromal differentially expressed proteins in the colon carcinoma by quantitative proteomics. Electrophoresis 2013; 34: 1679-1692.
- [14] Geng Q, Peng H, Chen F, Luo R and Li R. High expression of Sirt7 served as a predictor of adverse outcome in breast cancer. Int J Clin Exp Pathol 2015; 8: 1938-1945.
- [15] Jiang Q, Mai C, Yang H, Wu Q, Hua S, Yan C, Long Y, Zhang Y, Long X, Fang W and Liu Z. Nuclear expression of CDK4 correlates with disease progression and poor prognosis in human nasopharyngeal carcinoma. Histopathology 2014; 64: 722-30.

- [16] Schaal C and Chellappan S. Nicotine-mediated regulation of nicotinic acetylcholine receptors in non-small cell lung adenocarcinoma by E2F1 and STAT1 transcription factors. PLoS One 2016; 11: e156451.
- [17] Yamaguchi H, Wyckoff J and Condeelis J. Cell migration in tumors. Curr Opin Cell Biol 2005; 17: 559-564.
- [18] Ridley AJ. Rho GTPases and actin dynamics in membrane protrusions and vesicle trafficking. Trends Cell Biol 2006; 16: 522-529.
- [19] Anne Conti M, Saleh AD, Brinster LR, Cheng H, Chen Z, Cornelius S, Liu C, Ma X, Van Waes C and Adelstein RS. Conditional deletion of nonmuscle myosin II-A in mouse tongue epithelium results in squamous cell carcinoma. Sci Rep 2015; 5: 14068.
- [20] Xia ZK, Yuan YC, Yin N, Yin BL, Tan ZP and Hu YR. Nonmuscle myosin IIA is associated with poor prognosis of esophageal squamous cancer. Dis Esophagus 2012; 25: 427-436.