

Expression of Sonic Hedgehog (SHH) in Human Lung Cancer and the Impact of *YangZheng XiaoJi* on SHH-mediated Biological Function of Lung Cancer Cells and Tumor Growth

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Abstract. Sonic Hedgehog (SHH) is a protein that is aberrantly expressed in various human tumors. SHH and its signaling molecules have been indicated as potential therapeutic targets. In the present study, we evaluated the expression of SHH transcript in human non-small cell lung cancer (NSCLC) tissues and investigated the impact of inhibiting SHH together with a traditional Chinese medicine formula, *YangZheng XiaoJi* (YZXJ), on the function and growth of lung cancer cells. Human NSCLC tissues had significantly higher levels of the SHH transcript compared matched normal lung tissues (n=83). TNM2 tumors and tumors with pleural invasion had higher levels than TNM1 and non-invasive tumors. High SHH levels were associated with a shorter overall survival (OS) of the patients. A SHH inhibitor, cyclopamine, and YZXJ alone or in combination had a marked inhibitory effect on cellular invasion and cellular migration of human lung cancer cells, A549 and SKMES1. *YangZheng XiaoJi* and its combination with cyclopamine also significantly reduced the growth of lung tumors in vivo together with a reduction of SHH and *smoothened* (Smo) proteins in the lung tumors. The present study provides evidence that blocking SHH by way of small inhibitor and by *YangZheng XiaoJi* has a profound influence

on lung cancer cells as seen by in vitro invasion and cell migration and in vivo tumor growth. Together with the aberrant expression of SHH in NSCLC tumors in the patients, it is suggested that SHH is a potential target for therapies for NSCLC.

Sonic Hedgehog (SHH), a mammalian homologue of the Hedgehog (HH), is a lipid modified protein that, via specific signaling pathways, regulates a range of physiological (such as development and tissue regeneration) and pathological (such as cancer and rheumatism) events. After synthesis within the cells, it undergoes autocatalytic cleavage and lipid modification before secretion into the extracellular space. On the target cells, SHH interacts with and activates its receptor, a 12-pass transmembrane protein Patched (Ptch). Activation of the Patched results in its de-coupling from another transmembrane protein, *Smoothened* (Smo), which has 7-transmembrane passes and its functions are inhibited by the non-activated Patched protein (1-5). De-coupled Smo from Patched enables Smo to form a cytosolic protein complex with G-protein receptor proteins and activates downstream proteins including SuFu and transcription factor Gli. Activated Gli then translocates to the nucleus and activates other downstream targets including Wnt, SNA1 and certain ATPases (6-8). This results in transcription activation of a number of genes that are essential for cell and body to function.

The role of SHH and its associated signaling proteins, as well as pathways in cancer, have been explored over the past decade. Its aberrant expression has been reported in a broad range of human cancer types. In retinoblastoma and glioblastoma, SHH was found to be frequently expressed and associated with disease progression (9-12). Medulloblastoma

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is another tumor type strongly associated with the SHH pathway (11-13). In breast cancer, expression of proteins related to SHH is linked to a poor survival (14). In prostate cancer, SHH has been shown to be activated, possibly by the loss of SuFu, and indicated as a possible factor in driving the metastasis and progression of the cancer (15). Other studies have also indicated SHH as a target for therapy in prostate cancer (16, 17). In gastric cancer, SHH and Patched are linked to a poor outcome of the patients and its activation has been linked to *H. Pylori* (18-20). The therapeutic value by targeting SHH in pancreatic cancer is strongly indicated (21-24). The same therapeutic value has also been indicated in clear cell renal cancer (25). These data indicate that the SHH pathway is a promising target in cancer therapies. The past few years have witnessed the discovery and development of a number of therapeutic tools in targeting the pathway with some being currently in late stage clinical trials. The well documented inhibitor to SHH is cyclopamine, a naturally occurring small compound shown to be highly effective in blocking the SHH pathways. Other compounds, including GDC0449 (for skin, colorectal and brain cancers) (26), LDE-225 (for breast cancer), BMS-833923, PF-0449913 (for leukaemia), from the industry are now in early to late clinical trials (27-31).

The role for SHH in the development and pathology of the lungs has been indicated in recent years. In human lung cancer, however, its role remains controversial (32). A study using tissue array (n=248) has shown that SHH staining was correlated with that of Smo, Gli-1 and Gli-2 but did not have correlations with clinical and pathological features of the lung cancer tissues (33). In a study based on immunohistochemical analyses on 81 NSCLC tumors, it has been shown that the staining for SHH, Gli and Smo were weak and that staining for Patched was almost negative. In another immunohistochemically- based study with 40 NSCLC tissues, Hwang *et al.* (35) has shown that SHH and a specific lymphangiogenic marker, LYVE-1, were significantly correlated with pleural invasion and lymphatic thromboembolism. This study has reported that SHH expression levels were significantly correlated with a shorter survival ($p < 0.05$). However, another study that employed a similar method has delivered an opposite observation in that high expression was said to be related to a better survival of the patients (36). It has been shown that smoking-induced lung cancers may be the result of activation of SHH and Wnt (37). In another study, which examined SHH, Gli, Patched, Smo protein expression in NSCLC, all the proteins were found over-expressed in NSCLC compared to their adjacent non-neoplastic lung parenchyma. The study reported that SHH and Patched are associated with node metastasis and that their levels were high in squamous cell carcinoma of the lungs (38).

Recently, we reported that a traditional Chinese medicine formula, *YangZheng XiaoJi*, which has been used in treating patients with liver and lung cancer (39, 40), is able to inhibit

the angiogenic status and migration of cancer cells, including lung cancer cells. The medicine has been found to enhance the efficacy of chemotherapy in liver and lung cancers and reduce the side-effects from the traditional therapies (39, 40). We further demonstrated that the medicine appears to inhibit with intracellular signalling events, including the focal adhesion kinase (FAK) pathway, in both endothelial and cancer cells and the AKT pathway in cancer cells (41, 42) suggesting that the medicine, formulated with 16 herbs, has a tendency to interact with the signaling events. In a screen exercise, in order to identify the key signaling events affected by the medicine, we found that SHH was one such pathway that had response to *YangZheng XiaoJi*. Herein, we investigated the gene transcript expression pattern of SHH in a cohort of human non-small cell lung cancer and then tested the response of lung cancer cells to *YangZheng XiaoJi* *in vitro* and *in vivo*.

Materials and Methods

Materials. A SHH inhibitor, cyclopamine, and a negative control compound, tomatidine, were obtained from Tocris Chemicals (Bristol, England, UK). Antibodies to human SHH, Patched, Gli and Smo were obtained from Santa Cruz Biotechnologies Inc., (Santa Cruz, CA, USA). Fluorescent tagged secondary antibodies were obtained from Sigma Aldrich (Poole, Dorset, England, UK). *YangZheng XiaoJi* extract, referred to as *YZXJ (DME25)*, was prepared from *YangZheng XiaoJi* as we previously reported (41-43). Matrigel was obtained from Laboratory Scientific Suppliers (Hessle, East Riding, Yorkshire, England, UK).

Lung cancer tissues and cell lines. Paired fresh-frozen non-small cell lung cancer (NSCLC) carcinoma tissues at TNM stages of I to III and matched normal tissues were obtained from 83 patients who received a curative resection in Peking University Cancer Hospital from January 2003 to December 2011. Ethical approval was provided by the Peking University Cancer Hospital Ethics Committee. Clinical and pathological information of the patients is given in Table I. These tissues were collected immediately after surgical resection and stored in the Tissue Bank of Peking University Cancer Hospital. Clinical and pathological information, including age, sex, smoking history, histological types of tumors, TNM stage and lymph node metastasis, were collected and stored in the patients' database. Patients were followed up from the day of surgical operation to December 2009. The follow-up intervals were calculated as survival intervals after surgery. Human lung squamous carcinoma SKMES1 and human lung adenocarcinoma A549 cells were obtained from LGC Standard/ATCC (American Type Culture Collection) (Teddington, Middlesex, England, UK). Cells were routinely cultured with Dulbecco's modified Eagle's medium (DMEM) F12 supplemented with 10% foetal calf serum, penicillin and streptomycin (Sigma Aldrich).

RNA isolation and quantitative reverse transcription polymerase chain reaction (QPCR). Total RNA was isolated from the homogenized NSCLC and normal lung tissues and cell lines using a Triagent total RNA isolation reagent (Sigma Aldrich). Reverse transcription was performed using the Reverse Transcription kit

Table I. *SHH* transcript expression and clinical/pathological characteristics of lung cancer.

Clinical/pathological features	Mean±SD	p-Value
Total cohort (n=83 pairs)		
Paired tumor tissue	16.5±15.0	0.01
Paired background tissue	9.7±9.2	
Histology		
Squamous carcinoma	1.9±1.4	0.16
Adenocarcinoma	31.9±30.0	
Other	0.6±0.3	
TNM staging		
I	0.18±0.12	0.03
II	28.4±26.0	
III	1.5±0.09	
Tumor differentiation		
High	0.001±0.01	0.19
Medium/High	37.5±36.1	
Low/Medium	0.3±0.02	
Lymph node status		
Node negative	1.8±1.5	0.30
Node positive	34.5±30.2	
Pleural invasion		
No	0.46±0.3	0.033
Yes	90.8±88.6	
Smoking status		
Former or current smoker	4.5±2.5	0.043
Non smoker	21.6±20.3	

(Primer design). QPCR was performed on the Icyler IQ5 system (Bio-Rad, Hammel Hemstead, UK) to quantify the level of *SHH* transcripts in the NSCLC specimens (shown as copies/l from internal standard). NSCLC cDNA samples were then examined for *SHH* transcript expression, along with a set of standards and negative controls. The QPCR technique utilised the Amplifluor system™ (Intergen Inc., City, England) and QPCR master mix (BioRad). Pairs of primers were designed using the Beacon Design software (PREMIER Biosoft, Palo Alto, CA, USA): The housekeeping control was *GAPDH* (Glyceraldehyde-3-phosphate dehydrogenase) primers (sense: 5'-ctgagtacgtcgtggagtc-3'; antisense: 5' actgaacctgacctacacagatgatgacctttg -3') and *SHH* mRNA levels were assessed using *SHH* specific primers as follow: 5'-caaccccgacatcatatatta -3' and 5'-actgaacctgacctacaactgtttcat caccgaga-'. The underlined sequence in the reverse primers was the additional Z sequence, which is complementary to the universal Z probe (TCS Biologicals Ltd., Oxford, UK). Real-time QPCR conditions were 95°C for 15 min, followed by 60 cycles of 95°C for 20 s, 55°C for 30 s and 72°C for 20 s.

Scratching wounding assay using the EVOS cellular migration system. Cells were seeded into a 96-well plate (Nunc, Fisher Scientific, Paisley, Scotland, UK) at 10,000 per well and allowed overnight in the incubator to reach full confluence. The monolayer was then scratched using a fine-tipped plastic pipette to create a wound of approximate 200 µm. The media, together with the floating cells, were removed and replaced with media together with *YangZheng XiaoJi* extract alone, cyclopamine alone, tomatidine

alone or in combination with *YangZheng XiaoJi*. The plate was immediately placed in the chamber of the EVOS unit (EVOS™ fl Digital Inverted Fluorescence Microscope; Fisher Scientific), which was programmed to supply 5% CO₂ and maintained at 37°C constant temperature. The EVOS was then programmed to memorise the three dimensional position of the wounding position in each well and then automatically tracked the image of each well, every 15 minutes for up to 9 hours. Sequential images were analysed using the Image J software. The net distance that the cell migrated was calculated as: distance migrated=(T₀-T_n)/2, in which T₀ is the distance between two leading wound edges at the beginning of the experiment, T_n is the distance between the wound leading edge of the same wounding point at a given time. The distance is shown here as the number of pixels that cells had migrated. The migration is shown as a time course and the comparison between the experimental settings was based on a fix time point.

Electric cell-substrate impedance sensing (ECIS)-based cellular migration assays. This was modified from a method previously described (44, 45). Briefly, 96-well 96W1E microarrays, which have a gold-plated electrode at the bottom of each well, were used on the ECIS Ztheta instrument (Applied Biophysics Ltd, Troy, NJ, USA). Lung cancer cells were added to the wells of the array, followed by immediate tracking of cell adhesion over a range of frequencies, namely from 1,000 Hz to 64,000 Hz, using an automated module. Once the cells reached confluence, the electric wounding module was activated and applied a current of 2,000 mA for 20 sec for each well (35). The migration of the cells was immediately tracked after wounding, again over a range of frequencies. All the experiments were conducted in triplicate. Cell migration was analysed using the two dimensional and three dimensional models.

In vitro invasion assay. This was based on a matrigel transwell invasion model previously published (46). Transwell invasion insert (Greiner Bio., Gloucester, UK) with pore size at 8.0 µm was first coated with 50 µg Matrigel and allowed to air dry. The gel was then carefully rehydrated. To each insert, 30,000 cancer cells were added together with the test agents or their combinations. After 72 h, Matrigel and non-invading cells were removed using a cotton swab. The invaded cells on the lower surface of the inserts were fixed with 4% formaldehyde and then stained with 1% crystal violet. The number of invaded cells was counted under a microscope.

In vivo tumor model. Athymic female nude mice, CD-1 of 4-6 weeks old were purchased from Charles River Laboratories (Margate, Kent, UK). A549 tumor cells, which were prepared at 5×10⁶/ml in a solution containing 3mg/ml Matrigel, were injected subcutaneously to give 0.5 million cells per injection (47). After one week, when tumors became visible, mice were randomly divided into groups (n=6 in each group). The size of tumors was measured using a digital caliper. Treatments began one week after tumor cell inoculation and included the following: Control group (receiving control buffer), *YangZheng XiaoJi* extract via intraperitoneal injection (IP) or by gavage (oral), cyclopamine, a combination of *YangZheng XiaoJi* extract and cyclopamine. Treatments were given daily. The final concentration for *YangZheng XiaoJi* extract was 1:1,000 and cyclopamine. Mice were weighed and monitored daily. Tumour size was measured weekly for 4 weeks. The procedure was reviewed and approved by the Cardiff University Joint Biological Ethics Committee and conducted under the UK Home Office Project

License (PPL 30/2591). At the conclusion of the experiments, mice were terminated by euthanasia. Tumours were dissected and immediately stored at -80°C for subsequent immunohistochemical analyses. The volume of tumors was calculated by the following formula: tumor volume (mm^3)= $\text{length} \times \text{width} \times 0.54$ (48).

Immunofluorescence staining. Frozen tumors were sectioned using a cryostat (Leica DMR, Bristol, UK) at $10\ \mu\text{m}$ thickness. After fixation, using acetone/methanol fixation buffer, the slides were rehydrated and blocked with a Tris buffer (25 mM, pH 8.4) that contained 10% horse serum for one hour. Primary antibodies (including anti-SHH, anti-Gli, anti-Ptch and anti-Smo), diluted in the blocking buffer, were added to the respective slides that were kept in dark in full humidity on a slow moving platform for one hour and then thoroughly washed. FITC-tagged secondary antibodies were then added to the respective slides together with DAPI for nucleus counter stain. After one hour, the slides were thoroughly washed and mounted using FluoSave™ (Calbiochem, Nottingham, UK). The slides were examined on an Olympus microscope (London, UK) and photographed using a Hamamatsu digital camera (Hertfordshire, UK).

Statistical analysis. This was carried out using SigmaPlot (Version 11; Systat Software Inc., San Jose, CA, USA). The Student's *t*-test and one way analysis of variance (ANOVA) were used where appropriate.

Results

SHH expression in NSCLC. We first evaluated the *SHH* transcript levels in a cohort of paired lung tissues from patients with NSCLC. As shown in Table I, lung tumor tissues expressed high levels of *SHH* transcript ($p=0.01$) compared to matched normal lung tissues. Both TNM-2 and TNM-3 tumors showed high levels of the transcript when compared with TNM-1 tumors, although only TNM-2 showed a statistical difference ($p=0.01$, vs. TNM-1). It is interesting to note that tumors with pleural invasion and tumors from patients with smoking history had high levels of *SHH* transcript than that from the respective non-pleural invasion and non-smoking patients. There are no significant correlations between *SHH*, histological types and the degree of differentiation of the NSCLC tumors. Patients with high levels of *SHH* transcript tends to have shorter survival, although this is not statistically significant ($p>0.05$) (Figure 1).

YZXJ and cycloplamine had marked effects on cellular migration. We employed two independent methods for assessing the migration of cancer cells, namely a scratch wounding-based assay using an EVOS automated tracking system and an electric cell-substrate sensing (ECIS) method both of which provided a human interface-free and automated monitoring of cell migration. Figure 2 shows representative images from A549 cells (top panel: immediately after scratching; Bottom panel: 5 hours after scratching). Over the indicated time period, wounding space in control cells almost closed (Figure 2, left). *YangZheng XiaoJi* treatment and indeed cycloplamine reduced the pace

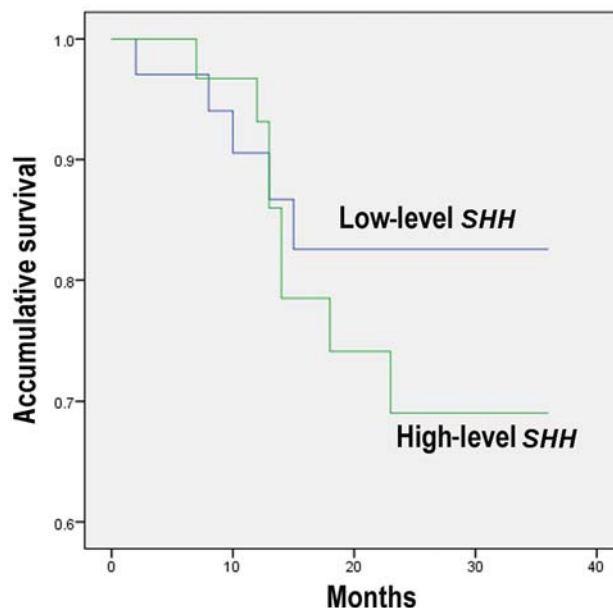


Figure 1. Levels of the *SHH* transcript and the overall survival of the patients with NSCLC. Patients with high levels of *SHH* transcript had a shorter survival, although this yet to reach statistical significance ($p>0.05$).

of cell migration. The combination of both *YangZheng XiaoJi* and cycloplamine reduced the migration (Figure 2, right). Quantitative analyses of cellular migration are shown in Table II in which *YangZheng XiaoJi* and cycloplamine exhibit a significant inhibitory effect on the migration, while the combination of both results in a more profound reduction. It is interesting to note that a control chemical, tomatidine, which has similar chemical structure to cycloplamine but does not interact with *SHH*, showed little effect on the cellular migration (Table II).

Using the ECIS-based method, similar inhibitory effects by *YangZheng XiaoJi* and cycloplamine and their combinations were observed (Figure 3). Over a broad range of frequencies tested, the inhibitory effects were largely consistent (Figure 4).

Cell invasion was also reduced by *YangZheng XiaoJi* and cycloplamine affected cellular invasion. We employed a Matrigel-based method to assess the *in vitro* invasiveness of both cancer cells. As shown in Table II, *YangZheng XiaoJi* and cycloplamine-alone exhibited significant inhibitory effects on the invasion of both lung cancer cells. The combination of *YangZheng XiaoJi* and cycloplamine showed a more profound inhibitory effect than each individual agent when used alone (Table II).

The impact of *YangZheng XiaoJi* and cycloplamine and tumor growth. To further evaluate the effect of *YangZheng XiaoJi*

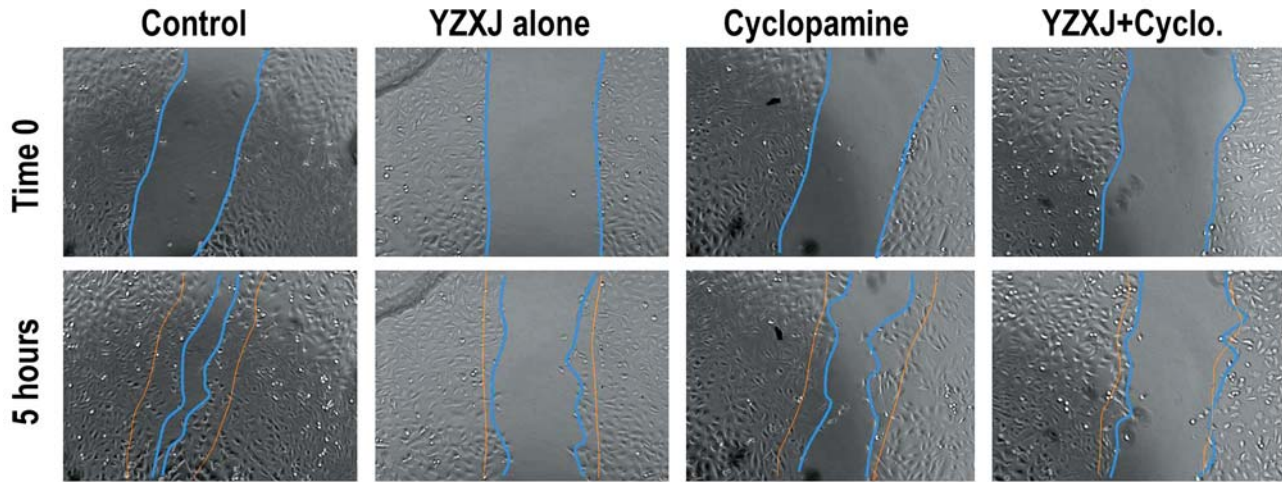


Figure 2. Effect of YangZheng XiaoJi and cyclopamine on the migration of A549 cells. Cells were seeded in a 96-well plate. On reaching confluence, they were scratch-wounded and then immediately and continuously recorded on a EVOS cell imaging system over a 5-h period. Shown here are images of A549 cells immediately after wounding (top panel) and 5 hours after wounding (bottom panel). From Left to Right are: control cells (treated with culture medium only); cells treated with YangZheng XiaoJi ; cells treated with cyclopamine and cells treated with the combination of YangZheng XiaoJi and cyclopamine. Blue lines indicate the leading front of the cells at the time point specified. Light yellow lines in the bottom panel indicate the initial position of the leading front following wounding.

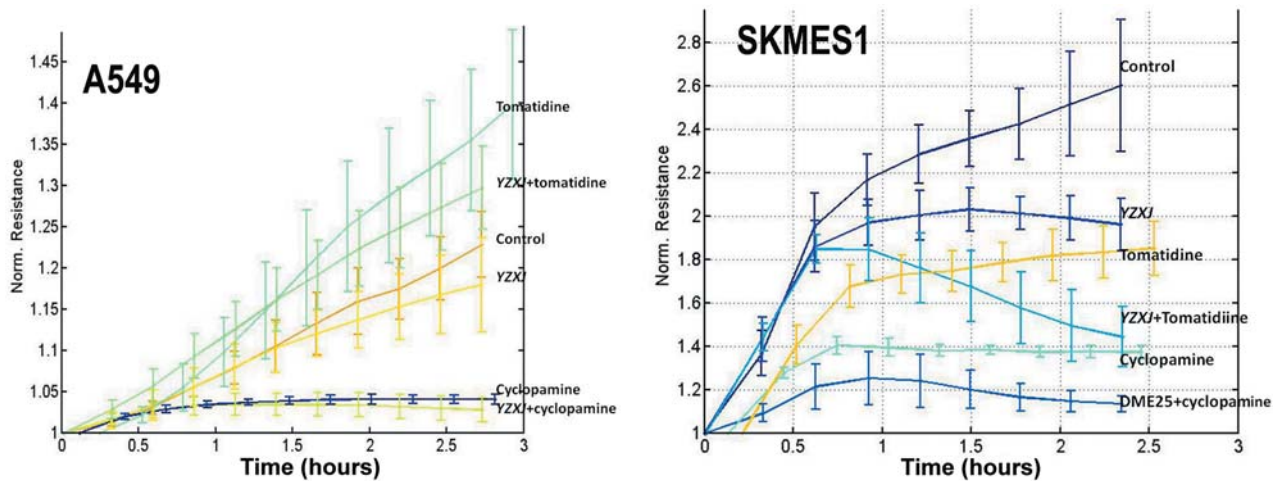


Figure 3. Cell migration assessed by electric cell-substrate impedance sensing (ECIS). Upon reading confluence within the 96WIE ECIS arrays, cells (Left: A549 cells; Right: SKMES1 cells) were electrically wounded and their electrical resistance recorded immediately after wounding. The respective treatment of the cells is indicated in the figure.

and cyclopamine on cancer cells, an *in vivo* tumor model was used in which A549 cells were subcutaneously injected together with Matrigel. When tumor became visible and measurable after one week, the treatment began by delivering the agents *via* intra-peritoneal injections. As shown in Figure 5, after two weeks of treatment, YangZheng XiaoJi had a significant effect on the growth of tumors, so as the YangZheng XiaoJi/cyclopamine combination. Although

cyclopamine demonstrated some degree of inhibitory effect, at the concentration used in the present study, this effect was not statistically significant (Figure 5).

SHH and its signaling molecules in response to YangZheng XiaoJi and cyclopamine. We examined the protein expression of SHH, Ptch, Gli and Smo in lung tumors by immunofluorescence staining of the specific proteins. It was

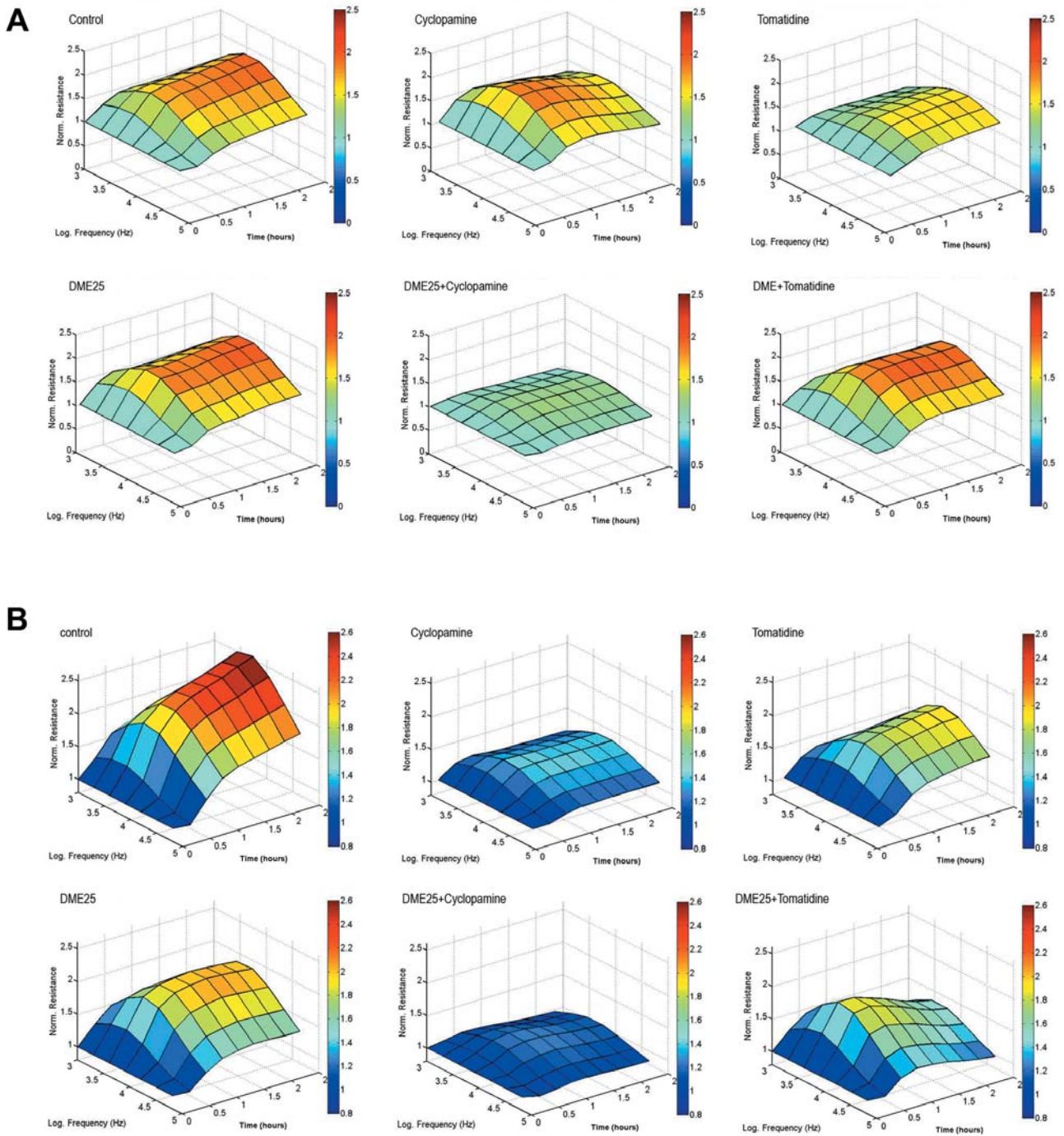


Figure 4. Cell migration assessed by electric cell-substrate impedance sensing (ECIS) and migration demonstrated in a three dimensional graph. The experimental conditions are the same as in Figure 3, except that the responses of the cells are displayed over a three dimensions, namely y-axis for electrical resistance, x-axis for frequencies (shown in Hz) and z-axis for time (in hours). A: A549 cells, B: SKMES1 cells.

found that out of all proteins evaluated, SHH had the most demonstrable change in which *YangZheng XiaoJi*, but not cyclopamine, reduced staining of the protein (Figure 6A). The combination of *YangZheng XiaoJi* and cyclopamine

resulted in almost complete loss of the staining. Reductions of Smo were also seen under both *YangZheng XiaoJi* and cyclopamine (Figure 6C). There were no marked changes in the staining for Gli and Patched (Figure 6B and D).

Table II. Effects of YZXJ and SHH inhibitors on cellular migration and invasion and migration of lung cancer cells, A549 and SKMES1.

	Control	YZXJ	Cyclopamine	Cyclopamine plus YZXJ	Tomatidine	Tomatidine plus YZXJ
Migration ^c						
A549	209.6±32.5	143.2±45.4 ^a	150.8±32.4 ^a	60.5±21.8 ^{a,b}	192.4±28.6	125.8±33.2 ^{a,b}
SKMES1	204.3±42.7	134.0±20.6 ^a	149.7±42.0 ^a	102.5±25.9 ^a	187.5±45.2	130.0±40.5 ^{a,b}
Invasion ^d						
A549	41.2±7.8	25.8±3.0 ^a	30.0±7.6 ^a	24.0±5.1 ^{a,b}	38.7±4.6	39.3±5.2
SKMES1	38.8±3.5	31.0±3.4 ^a	25.0±4.9 ^a	22.5±4.0 ^{a,b}	36.5±2.6	33.8±5.3 ^a

^a*p*<0.05 vs. control; ^b*p*<0.05 vs. YZXJ alone. ^cMigration: shown are pixels that cell migrated in the scratch wounding assay. ^dInvasion: shown are the number of cancer cells invaded through the matrix protein layer.

Discussion

The SHH and its pathways have been implicated as potential therapeutic targets in a number of solid human tumors including neurological, gastrointestinal, pancreatic, breast and prostate cancers in which SHH and its associated signalling molecules are aberrantly expressed and linked to disease progression and prognosis. In lung cancer, the link is far from clear, with some studies showing that it is highly expressed and some showing the opposite. The present study has shown that at transcript level, SHH is significantly raised in non-small cell lung cancer tissues compared with normal tissues. This is in line with previous findings using immunohistochemical methods (33, 35, 37) but in contrast to others in which SHH expression was reported to be a favourable factor for disease progression (36). The controversies in the expression in lung cancer can also be explained by the methods applied and the fact that its activation and expression differ markedly *in vivo* and *in vitro* (49) and that the activation is more likely to exist in a subset of lung cancers (50) and as indicated in early studies (51).

In the present study, we provided compelling evidence to indicate that by blocking the SHH pathway using a SHH inhibitor, cyclopamine, it is possible to markedly reduce cellular migration and invasion *in vitro* suggesting that blocking SHH is indeed a useful approach in combating the aggressive behaviour of lung cancer cells. The findings from *in vivo* tumor models further demonstrate that the SHH pathway is a very useful target in lung cancer therapies.

A major goal of the present study was to investigate if YangZheng XiaoJi is a useful adjunct to anti-SHH treatment. Clinically, YangZheng XiaoJi has been reported to be beneficial to patients with liver and lung cancers when used alone or in combination with chemotherapy (39, 40). In our recent work, we reported that YangZheng XiaoJi can interplay with the FAK and AKT pathways by suppressing the activation of these kinases (41,42). SHH was an alternative signal pathway identified from our screening on the action of YangZheng XiaoJi. Herein, we showed that

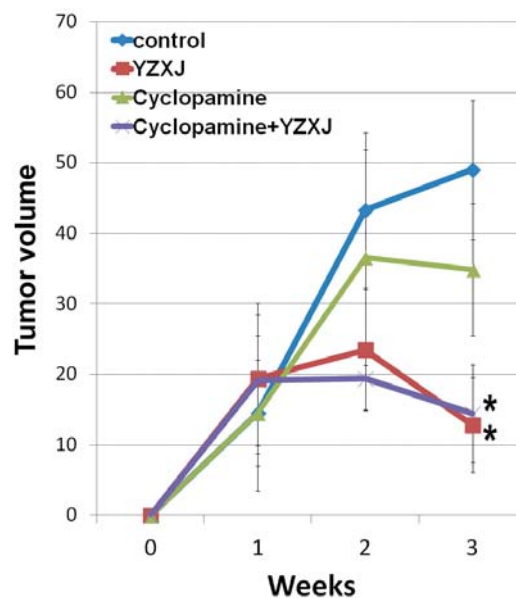


Figure 5. Effect of YangZheng XiaoJi, cyclopamine and their combination on the *in vivo* growth of A549 tumors. Cancer cells were subcutaneously injected (week 0). Treatment (via intra-peritoneal injection) began after one week and was given daily. Shown are tumor volumes in mm³. **p*<0.05 vs. control group by one way ANOVA.

YangZheng XiaoJi was able to reduce the amount of SHH in lung cancer tissues as seen in our *in vivo* tumor models.

Another highlight of the present study is the finding that YangZheng XiaoJi can potentiate the action of cyclopamine on cancer cell, including increased inhibition of cell invasion and cellular migration *in vitro* and tumor growth *in vivo*. This is interesting as it has been suggested that the SHH pathway, in particular Gli1, is a mechanism in inducing drug resistance (52, 53). It is possible, therefore, that the combined use of the SHH inhibitor and YangZheng XiaoJi may assist in overcoming drug resistance, an interesting lead for future studies. Second, in lung cancer, the SHH pathway has been shown to cross-talk with other pathways including the

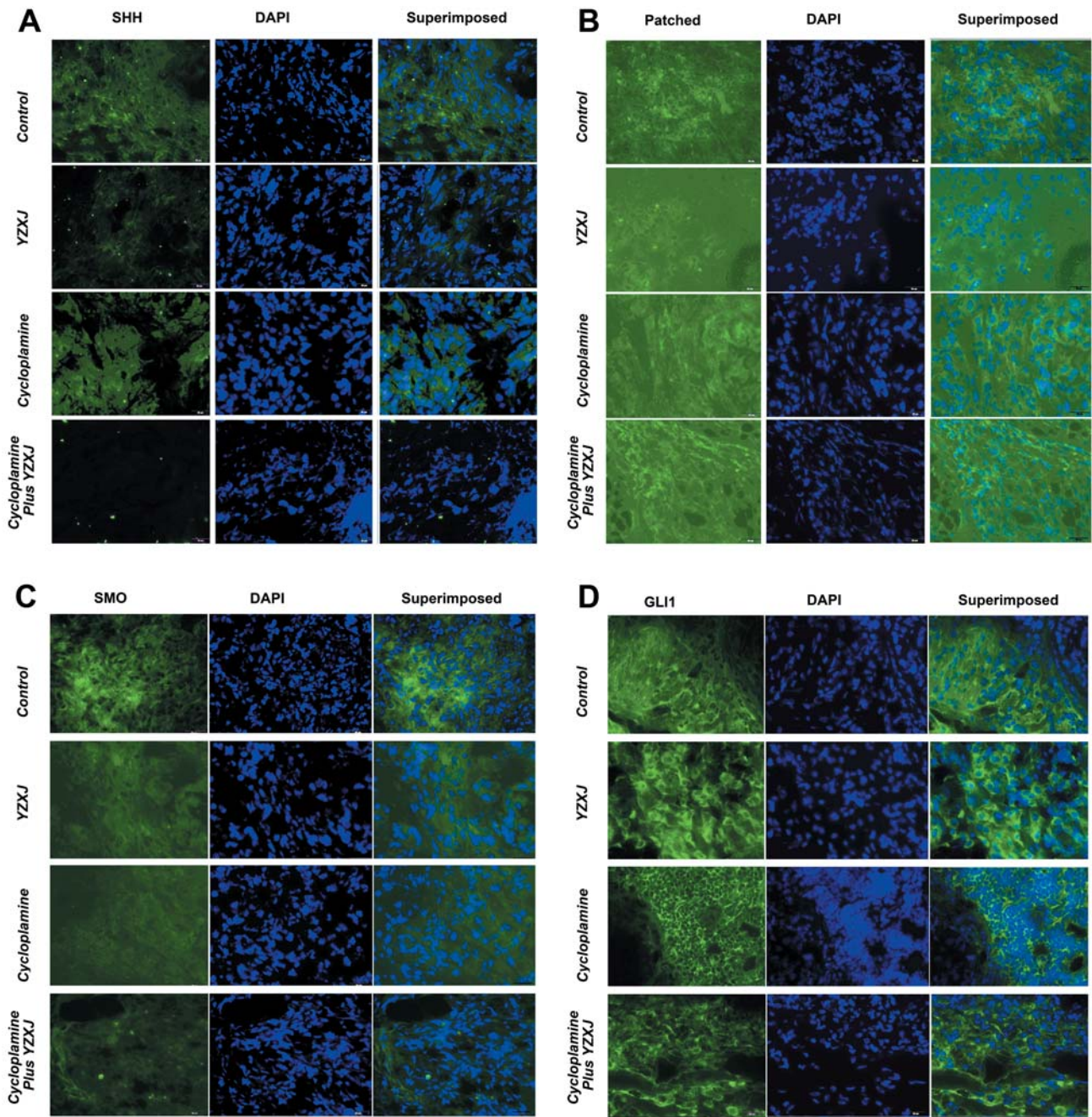


Figure 6. Immunofluorescent staining of SHH (A), Patched (Pch) (B), Smo (C) and Gli (D) in lung tumor tissues from the *in vivo* tumor model. The specific protein staining is seen in green colour (FITC tagged secondary antibody); nucleus staining in blue (DAPI) in the respective panels.

bombesin neuropeptide receptor pathway, which provides other opportunities for combined treatment with other targeted therapies (54). The observed effects of *YangZheng XiaoJi*, namely on the cellular migration and invasion, may further indicate that it plays a role in the process of epithelial to mesenchymal transition (EMT). It has been reported that SHH

up-regulation may contribute to transforming growth factor beta-induced EMT in lung cancer (55, 56) and the effects of *YangZheng XiaoJi* here again indicate the diverse effects of the medicine on cancer cells, including lung cancer cells.

YangZheng XiaoJi is made of natural herbs and is, therefore, comprised of a large number of natural products.

A number of botanical compounds have been indicated as being potential inhibitors for the SHH/Gli pathway (57). These include a broad range of well-known as less well-investigated compounds curcumin, genistein, epigallocatechin gallate, resveratrol, quercetin, baicalen and apigenin, along with novel compounds isolated from Southeast Asian plants, such as the potent sub-micromolar gitoxygenin derivatives. In fact, cyclopamine is also a naturally-occurring product. Thus, the natural products appear to be a rich source of anti-SHH options. Presently, it is not clear which compound or compounds in *YangZheng XiaoJi* result in the anti-SHH effects as observed in the current study, which poses a future challenge. However, given that most modern therapies, including chemotherapy, radiotherapy and targeted therapy, require a combined approach to enhance efficacy, overcome resistance and reduce side-effects, a combined approach using anti-SHH agents and *YangZheng XiaoJi* would be a useful suggestion, when devising new therapies for lung cancer.

In conclusion, SHH is aberrantly expressed in human NSCLC tissues and appears to be linked to disease progression and clinical outcome. We further demonstrated that a traditional Chinese medicine formula, *YangZheng XiaoJi*, is able to potentiate the effect of cyclopamine, an inhibitor for SHH, in the inhibition of cellular migration, invasion and tumor growth of lung cancer cells. The study, thus, suggests that *YangZheng XiaoJi* and inhibitors to SHH pathway would be a viable option in the treatment of non-small cell lung cancer and warrant future investigations.

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