SKA3 promotes lung adenocarcinoma metastasis through the EGFR-PI3K-Akt axis

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Abstract

The processes that lead to lung adenocarcinoma (LUAD) metastasis are poorly characterized. Spindle and kinetochore associated complex subunit 3 (SKA3) plays a key role in cervical cancer development, but its contribution to LUAD is unknown. Here, we found that SKA3 is overexpressed in LUAD and its expression correlates with lymph node metastasis and poor prognosis. SKA3 silencing experiments identified SKA3 as an oncogene that promotes the metastasis of LUAD cell lines and tissues. SKA3 was found to induce the expression of matrix metalloproteinase (MMP)-2, -7, and -9 which activate PI3K-AKT. SKA3 was also found to bind to ands activate EGFR to activate PI3K-AKT. In summary, we identify a role for SKA3 in LUAD metastasis through its ability to bind EFG and activate PI3K-AKT signaling.

Keywords: EGFR; LUAD; cancer; metastasis; PI3K-AKT; SKA3.
Introduction

Lung cancer (LCa) remains the major cause of cancer mediated fatalities globally, with 5-year survival rates less than 20% \[^{[1]}\]. Approximately 234,030 new LCa cases were diagnosed in the US alone in 2018, of which 154,050 are expected to die \[^{[2]}\]. Non-small cell lung cancer (NSCLC) is the major subtype of LCa, with lung adenocarcinoma (LUAD) the major NSCLC subtype \[^{[3]}\]. Despite progress in LUAD therapeutics, the molecular mechanisms governing LUAD progression and development are poorly understood \[^{[4, 5]}\]. Further mechanistic studies to fully understand LUAD progression are therefore urgently required.

SKA3 is present in the kinetochore layer of the SKA complex, and is a key mediator of mitotic exit in cooperation with NDC80 \[^{[6-8]}\]. SKA3 is also key to the migration of meiotic spindles and the stability of the spindles during anaphase \[^{[9]}\]. It has been shown that SKA3 mediates cancer development and progression. SKA3 mutations are common in breast cancer where they regulate cell growth \[^{[10]}\]. Studies have shown that SKA3 mediates the metastatic profile and outcome of several cancers \[^{[11, 12]}\]. Using the GEPIA database to analyze LUAD tissue, SKA3 mRNA expression was elevated and correlated to poor survival outcomes in LUAD patients. The molecular mechanisms underlying the oncogenic effects of SKA3 in LUAD were not however characterized.

Here, we confirm that SKA3 is overexpression in LUAD and shows a negative association with the survival of LUAD patients. Using SKA3 silencing approaches, we highlight that SKA3 acts as an oncogene through direct binding to EGFR, and the subsequent activation of pro-cancer signaling pathways to promote LUAD metastasis.

2. Methods

2.1 Patients and sample collection

We analyzed 26 LUAD tissues and their corresponding healthy tissue in samples
collected from our local hospital. Our local ethics committee approved the study protocols and all participants provided informed consent. Patient information that could lead to patient identification remained confidential throughout the study.

2.2 qRT-PCR analysis

Trizol was added to cell/tissues for RNA extraction which was quantified on a nanodrop. cDNA synthesis was then performed and gene expression was quantified through qRT-PCR analysis [13]. Primer sequences are shown in Table 1.

2.3 Cell based assays

MRC-5 cells (non-cancer) and H226 and SK-MES-1 cells (LUAD) were grown in complete culture media (DMEM plus 10% FBS at 37°C 5% CO₂). Cells were stimulated with recombinant human EGF (Abcam). siRNAs targeting SKA3 were synthesized by Gene Pharma Co. Overexpression plasmids for HA-tagged EGFR, pmyr-AKT, and shSKA3 were synthesized by Genechem. Cells were transfected with the indicated plasmids and packaged lentivirus was collected. Cells were then infected with each lentivirus and PI3K activity was assayed as previously described [14].

2.4 Cell cycle assessments

LUAD cells were transfected with siRNA-SKA3 or scrambled controls. Ten hours post-transfection, cells seeded into 96-well plates (~1x10⁴ cells/well). Cells were BrdU labeled (CST) to assess cell cycle progression. Experiments were repeated on a minimum of three independent occasions.

2.5 Assessment of the invasiveness and migratory ability of LUAD cells

Assays were performed in Boyden chambers with pore sizes of 8 mm in PET membranes. LUAD cells were counted and assessed via transwell assays. After 48 h, non-invasive cells in the upper Matrigel membrane were removed with cotton-tipped swabs and cells in the bottom wells were fixed in methanol and
toluidine blue stained. Cells were invasive when they passed through the lower membrane surface. All cells were imaged on an inverted light microscope (200 x magnifications) and quantified from three widefield images. Data shown are the averages of three independent experiments.

2.6 Co-immunoprecipitation assays

Post-thawing, LUAD cells were harvested in lysis buffer containing NaF, 50 mM; NaCl, 100 mM; Tris-HCl pH 7.5, 50 mM; Na3VO4, 1 mM; Na4P2O7, 30 mM; 0.5% NP-40 and PMSF, 0.5 mM supplemented with protease inhibitors. Antibodies were added to the lysates as previously described [15] and Co-IPs were assessed by western blot analysis to confirm interactions. Antibodies used in the study are listed in Table 2.

2.6 In vivo metastasis assays

All animal experiments were carried out in Shanghai Kaixue Biological Technology Development Co., Ltd., Shanghai, China (Experiment code: 2018-03-07). In vivo assessments were performed in male nude mice aged 6 weeks (Beijing Vitonlihua Experimental Animal Technology Co. Ltd, Beijing, China). Animals were housed in specified cages that were approved by the national animal guidelines of our institute. Mice were injected with either H226-shSKA3 (Group 1) or H226-shNT (Group 2) cells (4×10^5 cells, 5 mice per group) in the tail vein to produce the pulmonary metastasis model. Ten weeks following injection, mice were humanely killed in accordance with ethical study requirements and H&E stained to identify the presence of metastatic foci in the lungs. None anaesthetics were used during animal experiments.

2.7 Statistical analysis

SPSS19.0 was used for data analysis. Student’s t-tests were used for repeated variance assessments. Wilcoxon signed-rank tests and Mann Whitney U tests were performed for group comparisons. Kaplan-Meier curves were constructed
to assess patient survival. Log rank tests were employed for subgroup comparisons. Unless otherwise stated, data are the mean ± SE. P < 0.05 were deemed statistical significance.

3 Results

3.1 SKA3 is up-regulated in LUADs

Analysis of the GEPIA suggested that SKA3 is upregulated in LUAD vs. normal tissue (Fold-change > 2, p-value < 0.05, Figure 1A). To confirm this observation, SKA3 mRNA was quantified by qRT-PCR in 26 human LUAD and adjacent normal tissues (ANTs). Significantly higher expression of SKA3 mRNA was observed in LUAD vs. ANT tissue (Figure 1B). SKA3 mRNA expression across LUAD tissue positively correlated with the occurrence of lymph node metastasis (Figure 1C). We further noted that SKA3 expression was elevated in vitro LUAD cell lines (H226 and SK-MED-1 cells) compared to non-lung cancer cells (MRC-5, Figure 1D). To confirm the prognostic value of SKA3 LUAD, the GEPIA database was analyzed which indicated that elevated SKA3 expression leads to a reduced OS vs. tumors with low expression levels of SKA3 (Figure 1E). An intimate relationship therefore was observed between SKA3 overexpression, LUAD metastasis, and poor patient prognosis.

3.2 SKA3 promotes LUAD metastasis

The data to this point inferred a role for SKA3 during LUAD metastasis. To fully define the role of SKA3 in LUAD tumorigenesis, we performed silencing experiments in in vitro and in vivo models of LUAD. To this end, we designed shRNAs targeting SKA3 to silence its expression in the H226 and SK-MES-1 LUAD cells (Figure 2A). SKA3-silencing strikingly inhibited the in vitro proliferation of H226 and SK-MES-1 cells (Figure 2B). Similarly, SKA3-silencing reduced the metastatic phenotypes of these LUAD lines, as decreased motility was observed in silenced vs. shNT (shRNA non-target control) cells (Figure 2C-D). To confirm these findings, in vivo assessments of SKA3 expression in situations of LUAD
metastasis were performed. In these experiments, SKA3 was silenced in H226-shSKA3 which was subcutaneously injected into the tail veins of nude mice to assess metastatic growth. Ten weeks post-injection, lungs were H&E stained and micro-metastases assessed (Figure 2E). Mice injected with H226-shSKA3 cells showed fewer numbers of metastatic foci which upon examination were of smaller size vs, the H226-shNT group (Figure 2F). This suggested that SKA3 mediates the metastasis of LUAD cells.

3.3 SKA3 controls matrix metalloproteinase -2, -7, and -9 expression through PI3K-AKT activation

To study the regulation of LUAD via SKA3, we examined its role(s) in EMT, a key process during cancer metastasis. The data revealed that SKA3 did not influence the expression of vimentin, N-cadherin or E-cadherin (Figure 3A) suggestive that the metastasis induced by SKA3 occurs independently of EMT processes. A key process during tumor invasion is the enhanced proteolytic activity of cancer cell expressed MMPs that mediate the degradation of the stroma of neighboring cells and enhance the spread of tumor cells. In LUAD cells overexpressing SKA3, a marked increase in MMP-2, -7, and -9 proteins was observed, which decreased in response to SKA3-silencing (Figure 3B). In terms of other known oncogenic pathways, we observed low levels of active p-AKT in H226-shSKA3 and SK-MES-1-shSKA3 cell lines, whilst the levels of JAK, STAT3, and p38 did not differ between SKA3 silenced cells or shNT cells (Figure 3C). Upon the exogenous transfection of H226 and SK-MES-1 cells with shSKA3, shNT, or pmyr-AKT for overexpression studies, the overexpression of AKT enhanced the expression of MMP-2, -7, and -9 mRNA in cells silenced for SKA3 (Figure 3D). No such effects on PTEN expression were observed (Figure 3E-F). These findings suggested that SKA3 mediated its effects on tumor metastasis through MMPs, mediated via the PI3K-AKT signaling axis.
3.4 Enhanced SKA3-mediated PI3K-AKT signaling requires SKA3 binding to EGFR

PI3K-AKT signaling occurs via RTKs and their downstream interactions with cognate ligands. We further explored the role of SKA3 in response to HGF and EGF. As shown in Figure 4A-B, SKA3-silencing strongly inhibited EGF mediated AKT activation in LUAD-shSKA3 cells, vs. shNT cells, whilst HGF stimulation led to no such observable changes. To assess a possible interaction of SKA3 with EGFR, FLAG-tagged SKA3 was co-transfected into LUAD cells with or without HA-EGFR or empty vector controls. Co-IPs were performed to investigate potential interactions (Figure 4C). We found that EGFR enhances AKT activation via SKA3, evidenced through the enhanced phosphorylation on TYR992, TYR1045, and TYR1068, that decreased following SKA3-silencing in LUAD cells (Figure 4D). These data confirmed that the oncogenic effects of SKA3 were mediated through its binding to EGFR, which would promote PI3K-AKT activation and enhance EGFR-phosphorylation.

4 Discussion

Despite improvements in LUAD diagnostics, treatment and subsequent patient prognosis, LUAD frequently metastasizes and tumor recurrence is common [16-21]. Despite this, the molecular basis of LUAD metastasis is poorly characterized. Biomolecular markers that that can predict both tumor recurrence and patient outcomes are urgently required for efficient patient management and the exploration of new therapeutic targets. Here, we investigated the role of SKA3 in LUAD and highlighted its critical requirement for LUAD metastasis. At a mechanistic level, we found that SKA3 increased MMP-2, -7, and -9 expressions in a PI3K-AKT dependent manner. SKA3 also interacted with EGFR to enhance its activation and protein pro-oncogenic PI3K-AKT signaling. These data highlight SKA3 as a novel therapeutic target to inhibit the metastasis of LUAD.

We investigated human LUAD samples and in vitro cell lines for SKA3 expression
to fully define its role during LUAD metastasis. Analysis of the online database showed that SKA3 expressed was enhanced in clinical LUAD samples, and higher levels of lymph node metastasis were observed in LUAD cell lines. SKA3 expression positively correlated with survival time’s post-curative resection. Moreover, SKA3 silencing impaired the motility and invasion of LUAD cells both in vivo and in vitro. This implicated SKA3 in the pro-metastatic phenotypes of LUAD, and suggested that SKA3 acts as a biomarker to predict LUAD prognosis. SKA3 therefore represents a putative therapeutic target for LUAD treatment.

We further assessed the role of SKA3 in EMT processes but no associations were observed. Upon further analysis, we found that AKT activation strongly correlated with SKA3 expression, and that the expression of MMP following SKA3 silencing decreased in a manner that could be rescued by exogenous AKT overexpression, suggestive that SKA3 influences MMP-2, -7 and -9 to promote of LUAD occurrence and development. These data further suggested that the selective modulation of SKA3 during EGFR-PI3K-AKT signaling in LUADs leads to EGF modulation, with no effects on HGF-signaling. Co-IPs indicated an interaction between SKA3 and EGFR, which influenced EGFR phosphorylation and activation. Similar to this study, recent findings indicated that SKA3 promotes cell proliferation and migration in cervical cancer tissue through its ability to activate PI3K/Akt signaling. However, we found that SKA3 interacts with EGFR to enhance PI3K-AKT activity, which was a novel finding. The mechanisms governing this EGFR interaction now require further exploration.

In summary, we report for the first time that LUAD metastasis is enhanced by SKA3/EGFR mediated PI3K-AKT signaling. This reveals new information on the mechanisms of metastasis in LUAD and highlights SKA3 as an exciting anti-LUAD therapeutic.

**Abbreviations**

LUAD: lung adenocarcinoma; SKA3: Spindle and kinetochore associated complex
subunit 3; MMP: matrix metalloproteinase; LCa: Lung cancer; NSCLC: Non-small cell lung cancer; ANT: adjacent normal tissue; GEPIA: Gene Expression Profiling Interactive Analysis

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Author Contribution

Guo-liang Yang performed conception and design, and was responsible for experiments performance. Dan-dan Hu and Li-ming Lou contributed to experiments performance. Hai-ling Chen performed data analysis. Hong Zhang contributed to conception and design, data analysis, manuscript writing. Guo-liang Yang contributed to financial support and final approval of manuscript.

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**FIGURE 1 SKA3 is upregulated in LUAD.** (A) Gene Expression profiling Interactive Analysis (GEPIA) indicated that the SKA3 expression is enhanced in LUAD tissues compared to normal tissue (Fold-change>2, p-value<0.05). (B) SKA3 mRNA in 26 paired LUADs and ANTs examined by qRT-PCR. Data were compared via a Student’s t test. (C) SKA3 mRNA in 19 LUADs lacking lymph node metastasis and 7 with lymph node metastasis. (D) SKA3 expression in MRC-5, H226, and SK-MES-1 cells. (E) GEPIA analysis revealing the association of high SKA3 expression with a poor OS. Data were compared via two-sided log-rank tests.

**FIGURE 2 SKA3 enhances the metastatic phenotypes of LUAD.** (A) SKA3 silencing (KD, shSKA3) in the indicated cell lines. (B-D) Effects of SKA3 silencing on cell proliferation (B). A one way ANOVA was used for data comparisons. (C & D) Migration and invasion assays of H226 and SK-MES-1 cells, respectively. Data were compared via a Student’s t test. (E) H & E staining of mouse lung tissues from H226-shNT and H226-shSKA3 groups (40×, metastatic nodules are indicated by arrows). (F) Numbers of metastatic foci observed in each group (n = 5). Data were analyzed through a student’s t-test.

**FIGURE 3 SKA3 modulates MMP-2, -7, and -9 expressions through PI3K-AKT activation.** (A) Expression of the indicated EMT markers. (B) Expression of MMP-2, -7, and -9. GAPDH was probed as a loading control. (C) AKT (p-AKT), JAK2 (p-JAK2), STAT3 (STAT3), and p38 (p-p38) were evaluated by western blot analysis. GAPDH was probed as a loading control. (D) Relative mRNA expression of MMP-2, -7, and -9. (E) PI3K kinase activity in the specified cell lines. (F) Western blot analysis of PTEN expression.

**FIGURE 4. SKA3 and EGFR interact to enhance PI3K-AKT signaling.** (A-B) Cells were stimulated with EGF (A) or HGF (B) for 0, 5, or 15 min and assessed for the expression of the indicated proteins. GAPDH was probed as a loading
control. (C) Co-IPs using anti-FLAG antibodies in LUAD cells co-transfected with FLAG-SKA3 along with HA-EGFR or empty vector controls, as specified. (D) Cells were EGF treated for 0 or 5 min.
A

|        | H226 | SK-MES-1 |
|--------|------|----------|
| E-Cadherin |     |          |
| N-Cadherin |     |          |
| Vimentin  |     |          |
| GAPDH    |     |          |

B

|        | H226 | SK-MES-1 |
|--------|------|----------|
| MMP-2  |     |          |
| MMP-7  |     |          |
| MMP-9  |     |          |
| GAPDH  |     |          |

C

|        | H226 | SK-MES-1 |
|--------|------|----------|
| p-AKT  |     |          |
| AKT    |     |          |
| p-STAT3 |     |          |
| STAT3  |     |          |
| p-JAK2 |     |          |
| JAK2   |     |          |
| p-p38  |     |          |
| p38    |     |          |
| GAPDH  |     |          |

D

Relative mRNA level

E

|        |
|--------|
| Relative PI3K activity(%) |

F

|        | H226 | SK-MES-1 |
|--------|------|----------|
| PTEN   |     |          |
| GAPDH  |     |          |
### Table 1. Sequence of Primers for qRT-PCR

| Primer            | Sequence (5' to 3')             |
|-------------------|---------------------------------|
| SKA3 forward primer | CAGATCCCTCTTCACCTACGA          |
| SKA3 reverse primer | TCAACGTTTAAAGGGGACA            |
| MMP2 forward primer | TCTTGACCAGAATACCATCG           |
| MMP2 reverse primer | TACTTCACACGGACCACCTTG         |
| MMP7 forward primer | AGTGGTCACCTACAGGATCGTA         |
| MMP7 reverse primer | ATCTCCTCCGAGACCTGTCC          |
| MMP9 forward primer | CAACACTACCTATGGATCC           |
| MMP9 reverse primer | GGTGTAGAGTCTCTCGCTG          |
| GAPDH forward primer | TGTGGGCATCAATGGATTGG         |
| GAPDH reverse primer | ACACCATGTATTCCGGGTCAAT       |
Table 2 The primary antibodies used for WBs and the antibodies used for IP were as follows:

| Antibody                      | Supplier                  |
|-------------------------------|---------------------------|
| SKA3                          | ab186003, Abcam, 1:1,000  |
| GAPDH                         | ab181602, Abcam, 1:1,000  |
| vimentin                      | ab193555, Abcam, 1:1,000  |
| E-cadherin                    | ab194982, Abcam, 1:1,000  |
| N-cadherin                    | ab202030, Abcam, 1:1,000  |
| PTEN                          | ab32119, Abcam, 1:1,000   |
| STAT3                         | ab119352, Abcam, 1:1,000  |
| JAK2                          | ab108596, Abcam, 1:1,000  |
| total p38 (T-p38)             | ab31828, Abcam, 1:1,000   |
| total Akt (T-Akt)             | ab179463, Abcam, 1:1,000  |
| phosphorylated EGFR (p-EGFR, at Y992) | ab81440, Abcam, 1:1,000 |
| phosphorylated EGFR (p-EGFR, at Y1045) | ab24928, Abcam, 1:1,000 |
| phosphorylated EGFR (p-EGFR, at Y1068) | ab40815, Abcam, 1:1,000 |
| phosphorylated p38 (p-p38)    | ab4822, Abcam, 1:1,000    |
| phosphorylated STAT3 (p-STAT3) | ab76315, Abcam, 1:1,000  |
| phosphorylated JAK2 (p-JAK2)  | Ab32101, Abcam, 1:1,000   |
| phosphorylated Akt (p-Akt)    | ab38449, Abcam, 1:1,000   |
| HA-probe                      | sc-2362, Santa Cruz Biotechnology; 1:800 |
| FLAG-probe                    | F1804, Sigma-Aldrich; 1:2,000 |
| EGFR                          | ab52894, Abcam, 1:1,000   |
| FLAG M2-affinity gel          | A2220, Sigma-Aldrich; 20 ml per reaction |