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Sex Determining Region Y-Box 2 (SOX2) Is a Potential Cell-Lineage Gene Highly Expressed in the Pathogenesis of Squamous Cell Carcinomas of the Lung

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Abstract

Background: Non-small cell lung cancer (NSCLC) represents the majority (85%) of lung cancers and is comprised mainly of adenocarcinomas and squamous cell carcinomas (SCCs). The sequential pathogenesis of lung adenocarcinomas and SCCs occurs through dissimilar phases as the former tumors typically arise in the lung periphery whereas the latter normally arise near the central airway.

Methodology/Principal Findings: We assessed the expression of SOX2, an embryonic stem cell transcriptional factor that also plays important roles in the proliferation of basal tracheal cells and whose expression is restricted to the main and central airways and bronchioles of the developing and adult mouse lung, in NSCLC by various methodologies. Here, we found that SOX2 mRNA levels, from various published datasets, were significantly elevated in lung SCCs compared to adenocarcinomas (all p<0.001). Moreover, a previously characterized OCT4/SOX2/NANOG signature effectively separated lung SCCs from adenocarcinomas in two independent publicly available datasets which correlated with increased SOX2 mRNA in SCCs. Immunohistochemical analysis of various histological lung tissue specimens demonstrated marked nuclear SOX2 protein expression in all normal bronchial epithelia, alveolar bronchiolization structures and premalignant lesions in SCC development (hyperplasia, dysplasia and carcinoma in situ) and absence of expression in all normal alveoli and atypical adenomatous hyperplasias. Moreover, SOX2 protein expression was greatly higher in lung SCCs compared to adenocarcinomas following analyses in two independent large TMA sets (TMA set I, n = 287; TMA set II, n = 511 both p<0.001). Furthermore, amplification of SOX2 DNA was detected in 20% of lung SCCs tested (n = 40) and in none of the adenocarcinomas (n = 17).

Conclusions/Significance: Our findings highlight a cell-lineage gene expression pattern for the stem cell transcriptional factor SOX2 in the pathogenesis of lung SCCs and suggest a differential activation of stem cell-related pathways between squamous cell carcinomas and adenocarcinomas of the lung.


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Introduction

Lung cancer continues to be the leading cause of cancer-related deaths in the United States and worldwide with over one million deaths each year [1]. The majority of lung cancers (85%) are NSCLCs that include SCCs and adenocarcinomas [2]. The pathogenesis of NSCLC involves the accumulation of genetic and epigenetic alterations in a long multi-step process due in part to chronic exposure to carcinogens such as tobacco smoke. Few early changes that occur during NSCLC pathogenesis have been identified. For example, mutations in KRAS [3] and in the epidermal growth factor receptor (EGFR) [4] typically occur early in the development of lung adenocarcinomas, whereas amplification of EGFR and PIK3CA [2] and epigenetic inactivation of the p16 tumor suppressor [5] are more frequent in SCCG pathogenesis relative to adenocarcinomas. Moreover, the developmental
transcription factor Thyroid transcriptional factor 1 (TITF1) has been shown to be a lineage-survival oncogene over-expressed and amplified in lung adenocarcinoma development [6]. Despite recent progress in the delineation of cellular pathways aberrantly modulated in NSCLC, our understanding of the molecular changes occurring early in NSCLC pathogenesis is still lacking.

Given that the embryonic stem cell SOX2 transcriptional factor [7] plays important roles in tracheal epithelial cells [8] and is only expressed in the main airways and non-branching bronchioles in the developing and adult mouse lung [9], we hypothesized that it may be a cell-lineage gene highly and specifically expressed in SCCs that originate from central and upper airway and bronchial epithelial cells relative to adenocarcinomas that typically arise from the lung periphery [10]. In this study, we found that SOX2 mRNA was largely higher in lung SCCs relative to adenocarcinomas from various microarray datasets. Moreover, when we analyzed an OCT4/SOX2/NANOG stem cell gene signature previously characterized by Boyer et al. [11] in independent publicly available NSCLC datasets, the signature was found to effectively discriminate both major NSCLC subtypes. In addition, we found marked SOX2 protein expression only in the pathogenesis of SCC which was greatly higher in SCCs relative to lung adenocarcinomas following analyses of two independent and large tissue microarray (TMA) sets. Lastly, amplification of SOX2 DNA assessed by quantitative PCR (qPCR) was evident in 20% of lung SCCs studied (n = 40) and was absent in all adenocarcinoma cases tested (n = 17).

**Results**

**Elevated Expression of SOX2 mRNA in Lung SCCs Relative to Adenocarcinomas in Various Microarray Datasets**

Analysis of SOX2 mRNA expression in NSCLC samples of various publicly available datasets revealed the significant elevated expression of this stem cell-related transcriptional factor in lung SCCs compared to adenocarcinomas (all p < 0.001) (Figure 1A). This differential expression pattern was also evident when microarray analysis was performed on FFPE tissue sections of NSCLC (p < 0.001) (Figure S1).

**A Previously Characterized OCT4/SOX2/NANOG Signature Effectively Discriminates Lung SCCs from Adenocarcinomas**

Since SOX2 mRNA levels were largely higher in SCCs than adenocarcinomas of the lung, we questioned whether a SOX2-
related signature can discriminate between the two subtypes of NSCLC. Using only gene features represented in the published dataset platforms, the previously characterized OCT4/SOX2/NANOG signature by Boyer et al. [11] was analyzed alone using human gene expression data from the studies by Bhattacharjee et al and Bild et al [12,13]. In both datasets, the OCT4/SOX2/NANOG signature effectively separated lung tumors based on histology where most SCCs clustered alone (Figures 1B and 1C). In hierarchical cluster analysis of the Bild dataset, 43 out of 55 SCCs clustered together (Figure 1C) \( p = 4.3 \times 10^{-10} \) of the \( \chi^2 \)-test. The sensitivity and specificity for the classification of SCCs and lung adenocarcinomas were 0.81 and 0.78, respectively (Table S1). Moreover, the separation of SCCs from adenocarcinomas by the signature was also evident by principal component analysis in three-dimensional space (Figure 1D). In addition, SOX2 expression in the cluster analyses was higher in lung SCCs relative to adenocarcinomas. Moreover, the expression of SOX2 mRNA correlated with that of genes such as fibroblast growth factor receptor 2 (FGFR2) and parathyroid hormone-like hormone (PTHLH) in cluster analyses of both independent datasets (Figures 1B and 1C). In an attempt to validate these findings, we correlated the protein expression of SOX2 with that of FGFR2 by TMA immunohistochemistry analysis and found that nuclear SOX2 protein levels correlated significantly with cytoplasmic FGFR2 levels in lung SCC histological tissue specimens (Figure S2) but not in adenocarcinomas (data not shown).

Differential Expression of SOX2 Protein between Lung Adenocarcinoma and SCC Development Phases As Revealed by Immunohistochemical Analyses

We next attempted to analyze SOX2 expression at the protein level in histological tissue specimens representing different stages in the pathogenesis of lung adenocarcinomas and SCCs. Strikingly, SOX2 protein expression was absent in all normal alveoli (n = 52) and AAH (n = 37) (Figure 2 and Table 1). In sharp contrast, SOX2 positive expression was mainly nuclear and evident in all normal bronchial epithelia (n = 52), all four alveolar bronchiolization structures and in all (n = 32) but one cases of dysplasia and carcinoma in situ representing the sequence of SCC pathogenesis (Figure 2 and Table 1).

Elevated Expression of SOX2 DNA and Protein in Lung SCCs Relative to Adenocarcinomas

We next sought to analyze SOX2 protein expression in NSCLC tissue microarrays. The characteristics of the NSCLC patients from which the tissue specimens were obtained are summarized in Table S2. Nuclear SOX2 levels were largely and statistically significantly higher in lung SCCs (n = 109, set I; n = 177 set II) relative to the levels in adenocarcinomas (set I, n = 178; set II, n = 334) (both \( p < 0.001 \)) (Figure 3A). Notably, the median level of SOX2 protein was 8.2 and 39.7 higher in lung SCCs relative to adenocarcinomas when analyzed in TMA sets I and II, respectively (set I, adenocarcinoma, 30, SCC, 245; set II, adenocarcinoma 5.8,

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**Figure 2. SOX2 protein is highly expressed in the pathogenesis of lung SCC but not of adenocarcinoma.** A. Representative photomicrographs displaying the immunohistochemical expression of SOX2 protein in histological tissue sections of normal bronchial epithelia, preneoplastic lesions representing SCC development (Hyperplasia, Dysplasia and carcinoma in situ), and in well (Well SCC) and poorly (Poor SCC) differentiated SCCs. B. Representative photomicrographs of SOX2 expression in lung parenchyma (LP), atypical adenomatous hyperplasia (AAH), alveolar bronchiolization structures (AB), and in acinar adenocarcinoma and bronchioalveolar carcinoma (BAC).

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SCC, 230). In addition and irrespective of tumor histology, SOX2 protein expression was statistically significantly higher in ever compared to never smokers (set I, p = 0.002; set II, p < 0.001) (Figure 3B) and was also significantly increased in current or former smokers compared to never smoker NSCLC patients (set I, p = 0.008; set II, p < 0.001) (Figure 3C). Furthermore, in analysis of both TMA sets, SOX2 protein expression was comparable between former and current smoker NSCLC patients.

We also assessed for the levels of SOX2 DNA copy number in 57 NSCLC tumors. We found 20% SCCs had gene copy gain (8/40; 6/29 with high SOX2 protein expression and 2/11 with low SOX2 expression) (Table S3). In contrast, none of the 17 adenocarcinomas tested displayed SOX2 gene copy gain with most cases (83%) exhibiting SOX2 DNA RQs < 1.

**Discussion**

In this study, we sought to investigate the expression patterns of SOX2 in NSCLC pathogenesis based on its role and function in the developing and adult mouse lung and trachea [8,9]. We found that SOX2 mRNA levels are significantly higher in lung SCCs relative to adenocarcinomas or large-cell lung carcinomas from various published microarray datasets. Moreover, a previously characterized OCT4/SOX2/NANOG embryonic stem cell expression signature [11] effectively separated SCCs from lung adenocarcinomas when analyzed in publicly available NSCLC microarray datasets. In addition, we found that SOX2 protein was completely absent in lung adenocarcinoma pathogenesis and highly expressed in SCC development. Lastly, we demonstrated that SOX2 protein expression was largely significantly elevated in lung SCCs relative to adenocarcinomas and its association with smoking patterns.

**Table 1. SOX2 expression in normal and preneoplastic lung lesions.**

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<tr>
<td>Normal alveoli</td>
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<td>Atypical adenomatous hyperplasia</td>
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<td>Alveolar bronchiolization</td>
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<td>4</td>
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<tr>
<td>Squamous dysplasia and carcinoma</td>
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**Figure 3. Increased SOX2 expression in lung SCCs compared to adenocarcinomas and its association with smoking patterns.** Box-plot depicting statistical analysis by the Wilcoxon-rank test of differences in nuclear SOX2 protein score in both TMA sets I and II between lung adenocarcinomas (ADC) and SCCs (A), ever and never NSCLC smokers (B) and between never, former and current smokers (C).

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SOX2 Expression in NSCLC

Materials and Methods

Analysis of SOX2 mRNA in Published Microarray Datasets and Integration of the OCT4/SOX2/NANOG Signature

The integrated cancer microarray database and data-mining platform, Oncomine [17], was utilized to analyze the expression of SOX2 in publicly available microarray datasets of human lung carcinomas available on-line. SOX2 mRNA (probe sets 213721_at and 228038_at) was also compared by microarray analysis between formalin-fixed paraffin embedded (FFPE) lung SCCs and adenocarcinomas (unpublished observations). Genes characterizing an OCT4/SOX2/NANOG expression signature [11] were compiled and queried using NetAffx™ from Affymetrix (http://www.affymetrix.com/analysis/index.affx) to search for corresponding probe set annotations in the HG-U95A and HG-U133 plus 2.0 platforms used in the lung cancer microarray studies by Bhattacharjee et al. [12] and Bild et al. [13], respectively. The OCT4/SOX2/NANOG signature gene features were then analyzed alone in published human gene expression data obtained from the reports by Bhattacharjee et al. and Bild et al. Raw microarray data files from the two published datasets were imported and analyzed using the BRB-ArrayTools v.3.7.0 developed by Dr. Richard Simon and BRB-ArrayTools Development Team [18]. Gene expression data were normalized by Robust multi-array analysis (RMA) in R language environment [19] and median-centered across all samples in each data set before hierarchical clustering analysis. Clustering by average linkage was performed with Cluster 2.11, and results were visualized with TreeView programs (Michael Eisen Laboratory, Lawrence Berkeley National Laboratory and University of California, Berkeley; http://rana.lbl.gov/EisenSoftware.htm). Principal component analysis following gene centering was performed using the BRB-ArrayTools software.

Immunohistochemistry Analysis, Human Lung Tissues and Tissue Microarray Sets I and II

Detailed description of the normal and preneoplastic histological tissue specimens analyzed and two TMA sets is available in Methods S1. Cytoplasmic FGFR2 protein expression was available based on previous analysis [20]. Details of the immunohistochemical analysis for SOX2 protein expression are also available in Methods S1.

DNA Extraction and Quantitative PCR (qPCR)

Tumor tissues (40 SCCs, 17 adenocarcinomas) were dissected from FFPE Hematoxylin-stained tissue sections using manual microdissection to ensure that tumor cell proportions are greater than 70% for subsequent DNA extraction. Tumor DNA was extracted using the PicoPure DNA extraction Kit (Arcturus, Mt View, CA) according to the manufacturer’s instructions. Five μl of DNA was added to a 20 μl final volume reaction mixture consisting of 10 μl Power SYBR® Green PCR Master Mix (Applied Biosystems, Foster City, CA) and 0.5 μmol/l of each of forward and reverse primers which span 102 dinucleotides (613 to 714) of the SOX2 gene (ID: NM 003106) as follows: 5’-GAACCCCGAA-GATGCACACCTC and 5’-CGCTTAGCCTCGTCGATGA-AC. β-actin was used as an endogenous reference gene (TaqMan® Control Human Genomic DNA, Applied Biosystems) and was amplified as a standard control for calibration. All samples and standard DNA reactions were carried out in triplicates. qPCR was performed using an ABI 7300 Real Time PCR System Sequence (Applied Biosystems) at 50°C for 2 min, 95°C for 10 min, followed by 40 cycles at 95°C for 15 s and 60°C for 1 min. The quantity of the target genes was normalized using the level of the β-actin gene, and expressed as relative quantities (RQ) compared with the value of the Human Genomic DNA. RQ equal or larger than 2 was considered as gene copy gain.

Statistical Analyses

The data were summarized using standard descriptive statistics. The rank-based non-parametric Wilcoxon rank-sum test and the Kruskal-Wallis test were used to assess the statistical significance of the differences in nuclear SOX2 staining intensity score between lung SCCs and adenocarcinomas and based on tobacco history (ever vs never smokers) and type of smokers (never vs former vs current). All tests were two sided. p-values <0.05 were considered statistically significant.

Supporting Information

Methods S1 Supplementary methods.

Found at: doi:10.1371/journal.pone.0009112.s001 (0.04 MB DOC)
Increased expression of SOX2 mRNA in lung SCCs relative to adenocarcinomas in FFPE NSCLC specimens. SOX2 levels were analyzed from microarray analysis of FFPE NSCLC specimens using the Affymetrix HG-U133A platform. P-values were obtained by the Student’s t-test.

Correlation of expression of SOX2 and FGFR2 protein in lung SCC tissue specimens. SOX2 and FGFR2 protein levels were assessed by immunohistochemistry as described in Methods S1. Assessment of significance in correlation between SOX2 nuclear and FGFR2 cytoplasmic protein levels was performed using the Spearman Rank correlation test.

Separation of 111 NSCLCs from the study of Bild et al. by the OCT4/SOX2/NANOG signature. *P-value was obtained by Fisher’s exact test. Sensitivity (probability for an SCC sample to be correctly predicted as SCC) = 0.811. Specificity (probability for an ADC sample to be correctly predicted as an ADC) = 0.776.

References

5. Belinsky SA, Nikula KJ, Palmisano WA, Michels R, Saccomanno G, et al. (1998) Increased expression of SOX2 mRNA in lung SCCs relative to adenocarcinomas in FFPE NSCLC specimens. SOX2, FGFR2 gene copy number and protein levels were assessed from microarray analysis of FFPE NSCLC specimens. CN, SOX2 gene copy number assessed as relative quantities (RQs) to b-actin.

Supplementary Figures

Figure S1

Figure S2

Table S1

Table S2

Table S3

Author Contributions

Conceived and designed the experiments: PY HK JDM IIW. Performed the experiments: PY HK CB XT DW LMS MS JF. Analyzed the data: PY HK CB XT DW LMS HS WD LG CM JDM IIW. Contributed reagents/materials/analysis tools: JH EK LG CM WKH JDM IIW. Wrote the paper: PY HK CB XT WD WKH JDM IIW.