Background: The peroxiredoxin (PRDX) protein family is involved in cancer cell invasion and metastasis, but its prognostic value in lung cancer remains elusive.

Methods: In this report, we accessed the overall survival (OS) of each individual PRDX mRNA expression through the Kaplan–Meier plotter (KM plotter) database, in which updated gene expression data and survival information include a total of 1,926 lung cancer patients.

Results: Our results indicated that PRDX1 and PRDX2 mRNA expressions were associated with improved OS in all lung cancer patients, especially in lung adenocarcinoma patients, whereas PRDX5 and PRDX6 mRNA expressions were associated with poor OS in all lung cancer patients. In addition, the prognostic value of PRDXs in the different clinicopathological features according to smoking status, pathological grades, clinical stages, and chemotherapeutic treatment of lung cancer patients was further assessed in the KM plotter database by the multivariate cox regression analysis.

Conclusion: Our finding will elucidate the prognostic role of PRDXs in lung cancer and might promote development of PRDX-targeted inhibitors for the treatment of lung cancer.

Keywords: PRDX, expression, prognostic, KM plotter, smoking status, lung cancer

Introduction

Lung cancer is one of the most common cancers and the leading cause of cancer death worldwide. It is generally classified as small-cell lung cancer and non-small-cell lung cancer (NSCLC), accounting for 15% and 85% of all lung cancers, respectively. 1 NSCLC includes adenocarcinoma (Ade), squamous cell carcinoma (SCC) and large cell carcinoma. While standard treatment and better supportive care have improved overall survival (OS) and life quality, the prognosis of lung cancer is still unfavorable with an overall 5-year survival rate <15%. 2 Therefore, there is much interest in identifying a more accurate prognostic assessment and molecular biomarkers for lung cancer.

Peroxiredoxins (PRDXs) are a ubiquitous family of small (22–27 kDa) non-seleno peroxidases which catalyze peroxide reduction to balance cellular hydrogen peroxide (H₂O₂) levels. 3,4 They are divided into two classes: 2-Cys PRDXs and 1-Cys PRDX. Six PRDX isoforms have been identified. 5 Increased or decreased levels of PRDXs have been demonstrated in many human cancers. 6–10 Studies performed in vitro or in vivo models have demonstrated that overexpression of PRDXs may either inhibit cancer development or promote cancer growth, depending on the specific PRDX family member and the cancer context. 11–15 However, the prognostic value of mRNA expression of individual PRDXs in lung cancer patients is still elusive. In this study, we determined the prognostic roles of mRNA expression of six PRDXs in lung cancer patients.

KM plotter database generated data from The European Genome-phenome Archive (EGA), Gene Expression Omnibus (GEO), and The Cancer Genome Atlas (TCGA,
http://cancergenome.nih.gov) cancer data sets, which include gene expression data and survival information from a total of 1,926 lung cancer patients. In the present study, we used the KM plotter database and accessed the prognostic roles of individual PRDX mRNA expression in patients with lung cancer.

Materials and methods

The Kaplan–Meier plotter (KM plotter, http://kmplot.com/analysis) has information of 54,675 genes on survival using 10,461 cancer samples, which include breast, ovarian, gastric, and lung cancer patients with a mean follow-up of 69, 40, 49, and 33 months, respectively. Gene expression data and OS information are downloaded from EGA, GEO (Affymetrix microarrays only), and TCGA, which is handled by a PostgreSQL server and integrates clinical data and gene expression information simultaneously. The database collected survival information of 1,926 lung cancer patients, which comprises clinical data such as gender, age, histology, grade, stage, and chemotherapy of all patients in WinStat 2013.

In our study, the prognostic values of the individual mRNA expression of PRDXs in lung cancer were speculated using the KM plotter online database. In addition, we evaluated the correlation between OS of lung cancer patients and specific PRDXs based on smoking status, pathological grades, clinical stages, and chemotherapeutic treatment. Briefly, the JetSet probe IDs representing the six genes of PRDXs (PRDX1, PRDX2, PRDX3, PRDX4, PRDX5, and PRDX6) individually entered into the database (http://kmplot.com/analysis/index.php? service&cancer=lung) to analyze Kaplan–Meier survival curves. With the purpose to determine the prognostic value of a particular gene, certain gene mRNA expression between the lower and upper quartiles were computed, and the best performing threshold was used as the final cutoff in a univariate cox regression analysis. Smoking status, pathological grades, clinical stages, and chemotherapeutic treatment were calculated in the multivariate analysis. Finally, the expression cutoff points of the PRDX genes were determined according to the median expression of the gene from the selected lung cancer samples. PRDX expression were split into “low” and “high” depending on the comparisons between expression values with established cutoffs. The number of cases, median values of mRNA expression levels, HR, 95% CI, and log rank P were determined and presented on the webpage. P-value of <0.05 was deemed to be statistically significant to reduce the false-positive rate.

Results

In our present study, all the six PRDX family Kaplan–Meier survival information can be determined on www.kmplot.com. We used KM plotter and determined the prognostic value of PRDX1 in the database. The valid Affymetrix ID is 208680_at (PRDX1). Survival curves are drafted for all lung cancer patients (n=1,926) (Figure 1A), Ade patients (n=720) (Figure 1B), and SCC patients (n=524) (Figure 1C). PRDX1 mRNA high expression was correlated with worse OS for

![Figure 1](image-url) The prognostic value of PRDX1 expression in the database.

**Notes:** The valid Affymetrix ID is 208680_at (PRDX1). Survival curves are plotted for (A) all patients (n=1,926), HR=1.33 (95% CI: 1.17–1.51); (B) adenocarcinoma (n=720), HR=1.11 (95% CI: 0.88–1.4); and (C) squamous cell carcinoma (n=524), HR=1.22 (95% CI: 0.97–1.55).
all lung cancer patients who were followed for 20 years (HR = 1.33, 95% CI: 1.17–1.51, P = 8.9e–6). Nevertheless, with regard to Ade and SCC patients, there was no significant difference in HR estimates between study strata.

We next determined the prognostic value of PRDX2 in the database. The valid Affymetrix ID is 39729_at (PRDX2). PRDX2 mRNA high expression was significantly correlated with worse OS for all patients (HR = 1.19, 95% CI: 1.05–1.35, P = 0.0077; Figure 2A). PRDX2 mRNA high expression was also correlated with worse OS in Ade patients (HR = 1.34, 95% CI: 1.05–1.7, P = 0.018; Figure 2B), but not in SCC patients (HR = 0.91, 95% CI: 0.72–1.15, P = 0.44; Figure 2C).

Figure 3 demonstrates the prognostic value of PRDX3 in the database. The valid Affymetrix ID is 201619_at (PRDX3). PRDX3 mRNA high expression was significantly correlated with worse OS for all patients (HR = 1.01, 95% CI: 0.8–1.28, P = 0.92; Figure 3C).
(PRDX3). PRDX3 mRNA high expression was not significantly correlated with OS for all lung cancer patients (HR=0.9, 95% CI: 0.79–1.02, P=0.088; Figure 3A), SCC patients (HR=1.01, 95% CI: 0.8–1.28, P=0.9174; Figure 3B). However, PRDX3 mRNA expression predicted a better OS in Ade patients (HR=0.68, 95% CI: 0.54–0.86, P=0.0011; Figure 3C).

Figure 4 shows the prognostic value of PRDX4 in the database. The valid Affymetrix ID is 201923_at (PRDX4). PRDX4 mRNA high expression was not significantly correlated with OS for all lung cancer patients (HR=0.98, 95% CI: 0.87–1.12, P=0.79; Figure 4A), Ade patients (HR=0.93, 95% CI: 0.73–1.17, P=0.5238; Figure 4B), as well as patients with SCC (HR=0.79, 95% CI: 0.62–1.01, P=0.0556; Figure 4C).

Figures 5 and 6 present the prognostic significance of PRDX5 and PRDX6, respectively. Affymetrix IDs were as follows: 1560587_s_at (PRDX5) and 200845_s_at (PRDX6). Both elevated PRDX5 and PRDX6 mRNA expressions are associated with a favorable OS for all the lung cancer patients (PRDX5: HR=0.7, 95% CI: 0.59–0.82, P=1.8e–5, Figure 5A; PRDX6: HR=0.71, 95% CI: 0.63–0.81, P=1.5e–7, Figure 6A). In addition, only PRDX6 mRNA high expression was significantly associated with worse OS in Ade patients (HR=0.45, 95% CI: 0.35–0.57, P=2.8e–11).

To further assess the association of PRDXs with other clinicopathological profiles, we determined the correlation with the patients’ smoking status (Table 1), clinical different stages (Table 2), and chemotherapeutic treatment. As from Table 1, PRDX1 and PRDX6 are significantly correlated with the smoking status. PRDX3 and PRDX6 are significantly associated with lung cancer patients without smoking history. From Table 2, PRDX1, PRDX2, PRDX3, and PRDX6 are significantly correlated with clinical stage I of the patients. Only PRDX6 is significantly associated with clinical stage II of lung cancer patients. However, none of the PRDXs was associated with chemotheraphy of lung cancer patients.

Discussion

PRDX1 was first reported as an antioxidant enzyme. Recent studies have shown that abnormal expression of PRDX1 has been observed in several human cancers, including breast, esophageal, liver, lung, and prostate cancers. PRDX1 is expressed at significantly higher levels in lung cancer tissues compared with normal lung tissues, and elevated PRDX1 associated with shorter survival in lung cancer. Furthermore, PRDX1 is upregulated in NSCLC tissue interstitial fluid, and high level of PRDX1 expression is related to lymph node metastasis and tumor differentiation. Knockdown of PRDX1 in lung cancer cells significantly inhibits TGF-β1-induced epithelial-mesenchymal transition (EMT) and cell migration, whereas PRDX1 overexpression enhances TGF-β1-induced EMT and cell migration. In addition, in vivo studies have shown that silencing of PRDX1 leads to tumor suppression of growth and metastases by reducing the activation of c-Jun.
Consistent with these findings, our data suggested that high mRNA expression of PRDX1 was associated with worse OS in patients with stage I lung cancer. Furthermore, PRDX1 is significantly correlated with the smoking status of patient with lung cancer.

PRDX2, also named as NKEF-B, was the most homologous molecule of PRDX1 and showed similar cellular localization. Lu et al demonstrated that PRDX2 overexpression in colorectal cancer tissues was strongly correlated with a more aggressive cancer behavior, tumor metastasis, and the tumor–node–metastasis (TNM) stage. PRDX2 overexpression was an independent prognostic indicator for stage I–III colorectal cancer patients. However, the biologic role and the prognostic effect of PRDX2 in lung cancer...
Table 1 Correlation of PRDX mRNA expression with smoking status of lung cancer patients

<table>
<thead>
<tr>
<th>Gene</th>
<th>Smoking history</th>
<th>HR (95% CI)</th>
<th>Log rank P</th>
</tr>
</thead>
<tbody>
<tr>
<td>PRDX1</td>
<td>Smoke</td>
<td>1.24 (1.01–1.53)</td>
<td>0.039*</td>
</tr>
<tr>
<td></td>
<td>Never smoke</td>
<td>1.17 (0.67–2.05)</td>
<td>0.5783</td>
</tr>
<tr>
<td>PRDX2</td>
<td>Smoke</td>
<td>1.08 (0.87–1.32)</td>
<td>0.4917</td>
</tr>
<tr>
<td></td>
<td>Never smoke</td>
<td>1.3 (0.75–2.28)</td>
<td>0.35</td>
</tr>
<tr>
<td>PRDX3</td>
<td>Smoke</td>
<td>1.14 (0.92–1.4)</td>
<td>0.2282</td>
</tr>
<tr>
<td></td>
<td>Never smoke</td>
<td>0.34 (0.18–0.63)</td>
<td>0.00035*</td>
</tr>
<tr>
<td>PRDX4</td>
<td>Smoke</td>
<td>0.89 (0.72–1.09)</td>
<td>0.26</td>
</tr>
<tr>
<td></td>
<td>Never smoke</td>
<td>1.08 (0.62–1.87)</td>
<td>0.7966</td>
</tr>
<tr>
<td>PRDX5</td>
<td>Smoke</td>
<td>0.91 (0.61–1.37)</td>
<td>0.6625</td>
</tr>
<tr>
<td></td>
<td>Never smoke</td>
<td>2.17 (0.93–5.06)</td>
<td>0.067</td>
</tr>
<tr>
<td>PRDX6</td>
<td>Smoke</td>
<td>0.72 (0.58–0.89)</td>
<td>0.002*</td>
</tr>
<tr>
<td></td>
<td>Never smoke</td>
<td>0.33 (0.18–0.62)</td>
<td>0.00028*</td>
</tr>
</tbody>
</table>

Note: *P<0.05.
Abbreviation: PRDX, peroxiredoxin.

PRDX3 was mainly located in mitochondria. Several studies have indicated that PRDX3 is overexpressed in several human cancers, including lung cancer. However, its role in prognosis of lung cancer is barely explored. In the present study, overexpressed PRDX3 mRNA only predicted a better OS in Ade patients, but not in SCC patients.

Wei et al demonstrated that Srx-PRDX4 axis plays a very important role in tumor progression and metastasis in lung cancer through the modulation of specific phosphokinase signaling. However, our results showed that PRDX4 was not significantly related to OS in patients with lung cancer.

Increased levels of PRDX5 have been reported in breast cancer and malignant mesothelioma. PRDX5 overexpression was associated with larger tumor size, positive lymph node status, poor differentiation, and a shorter patient survival in breast cancer patients. PRDX5 was involved in the regulation of several mitochondrial processes, which is essential in the protection of lung cancer cells against apoptosis induced by anticancer drugs. In this report, we observed that PRDX5's high mRNA expression was found to be significantly correlated with worse OS for all lung cancer patients.

PRDX6 is a bifunctional enzyme with both GSH peroxidase and phospholipase A2 activities. PRDX6 is the only mammalian 1-Cys member of the PRDX family and is expressed in all major organs with a particularly high level in lung.

In our present study, we comprehensively investigated the prognostic value of six PRDX members in patients with lung cancer through the modulation of specific phosphokinase signaling. However, our results showed that PRDX4 was not significantly related to OS in patients with lung cancer.

PRDX6 promotes lung tumor progression via its GPx and iPLA2 activities and promotes lung tumor development via activation of the JAK2/STAT3 pathway in a carcinogen-induced mouse lung tumor model. Our recent study demonstrated that high mRNA expression of PRDX6 was associated with worse OS in lung cancer patients, Ade patients, and those with early stage I–II.

Conclusion

In our present study, we comprehensively investigated the prognostic value of six PRDX members in patients with lung cancer by using the KM plotter database. In which, we revealed that PRDX1 and PRDX2 mRNA expressions were associated with improved OS in all lung cancer patients especially with Ade patients, whereas PRDX5 and PRDX6 mRNA expressions were associated with poor OS in all lung cancer patients. The prognostic value of the PRDX protein should be further evaluated in clinical studies.
finding provides new insights into the prognostic functions of PRDX proteins in lung cancer and might promote the development of PRDX-targeted inhibitors for the treatment of lung cancer.

Disclosure
The authors report no conflicts of interest in this work.

References

