Reduced Expression of the let-7 MicroRNAs in Human Lung Cancers in Association with Shortened Postoperative Survival

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Abstract

In this study, we report for the first time reduced expression of the let-7 microRNA in human lung cancers. Interestingly, 143 lung cancer cases that had undergone potentially curative resection could be classified into two major groups according to let-7 expression in unsupervised hierarchical analysis, showing significantly shorter survival after potentially curative resection in cases with reduced let-7 expression (P = 0.0003). Multivariate COX regression analysis showed this prognostic impact to be independent of disease stage (hazard ratio = 2.17; P = 0.009). In addition, overexpression of let-7 in A549 lung adenocarcinoma cell line inhibited lung cancer cell growth in vitro. This study represents the first report of reduced expression of let-7 and the potential clinical and biological effects of such a microRNA alteration.

Introduction

Cells contain a variety of noncoding RNAs, which perform a multitude of functions. Recently, microRNAs (miRNAs), an abundant class of small noncoding RNAs of about 22 nucleotides in length, have been recognized as being numerous and phylogenetically well conserved (1). The miRNA species are encoded by genes that are presumably transcribed into single or clustered miRNA precursors, which are converted to mature forms of miRNAs through stepwise processing including generation of a ~70 nucleotide pre-miRNA with a characteristic hairpin structure from the longer nascent transcripts (pri-miRNA) and the following Dicer-mediated processing into mature forms (2–5). Although thus far over 300 miRNA genes have been discovered in various organisms (6–10), including humans, their precise physiological functions are largely unknown except for a handful of miRNAs (11–17), and their potential pathological involvement including oncogenesis is yet to be explored.

The Caenorhabditis elegans let-7 miRNA is to date the best-studied example along with lin-4, which are converted to mature forms of miRNAs through stepwise processing including generation of ~70 nucleotide pre-miRNA with a characteristic hairpin structure from the longer nascent transcripts (pri-miRNA) and the following Dicer-mediated processing into mature forms (2–5). Although thus far over 300 miRNA genes have been discovered in various organisms (6–10), including humans, their precise physiological functions are largely unknown except for a handful of miRNAs (11–17), and their potential pathological involvement including oncogenesis is yet to be explored.

The let-7 miRNA, which starts to be expressed during the late developmental stage, acts as a post-transcriptional repressor of lin-41, hbl-1/lin-57 and perhaps other genes that contain sequences imprecisely complementary to the miRNA in their 3′ untranslated regions. The expression levels of the human let-7 gene have been shown to vary among various adult tissues, lung being one of the tissues with most abundant expression of let-7 (18).

In this study, we show for the first time that expression levels of let-7 are frequently reduced in lung cancers both in vitro and in vivo. Furthermore, lung cancer patients with reduced let-7 expression were found to have significantly worse prognosis after potentially curative resection, and this prognostic impact of reduced let-7 expression appears to be independent of disease stage in multivariate COX regression analysis. In addition, we show that overexpression of let-7 inhibits growth of lung cancer cells in vitro.

Materials and Methods

Study Population. This study dealt with 159 nonsmall cell lung carcinoma (NSCLC) tissue specimens collected with the approval of the institutional review board of the Aichi Cancer Center. The specimens from 143 cases (105 adenocarcinomas, 25 squamous cell carcinomas, 9 large cell carcinomas, and 4 adenosquamous cell carcinomas), which had been followed up for >5 years after potentially curative resection, were used specifically for studying the prognostic significance of let-7. These 143 cases consisted of 90 female and 53 male patients with a median age of 62 (range, 32–84), and with 75 in stage I, 19 in stage II, and 49 in stage III.

Preparation of Cell Line and Tissue Samples. All of the human NSCLC cell lines analyzed were cultured with 5% (v/v) FCS-containing RPMI 1640 at 37°C with 5% CO2. BEAS-2B and HPL1D (19) cells were cultured with 1% (v/v) FCS-supplemented Ham’s F-12 supplemented with bovine insulin (5 μg/ml), human transferrin (5 μg/ml), 10−7 m hydrocortisone, 2 × 10−10 m triiodothyronine, penicillin (100 IU/ml), and streptomycin (100 μg/ml) at 37°C with 5% CO2. The tumor specimens were homogenized in guanidine isothiocyanate homogenization buffer immediately after resection and stored at −80°C until use with the approval of the institutional review board. Processing of all cell lines and tissue samples for RNA extraction were performed according to the standard procedures.

Northern Blotting. Ten μg of RNA were separated on a 15% denaturing polyacrylamide gel. The RNA was then transferred to Zeta-Page GT Blotting Membranes electrophoretically overnight. Probes (let-7; 5′-TACTATA-CAACCTACTACCTCAATTGGC and 5′-TTGCTTCCCCGATGATC-GAGA) were generated by T4 polynucleotide kinase (New England Biolabs, Beverly, MA) mediated end-labeling of DNA oligonucleotides with [γ-32P]ATP. Prehybridization and hybridization were carried out using hybridization buffer (0.25 m sodium phosphate (pH 7.2), 7% SDS, 0.5% sodium PP).

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Note: J. Takamizawa and H. Konishi contributed equally to the present study. H. Konishi is currently at the Sidney Kimmel Comprehensive Cancer Center, Johns Hopkins University, Baltimore, MD.

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transfected into A549 lung adenocarcinoma cell line using the FuGENE 6 reagent (Roche, Inc. Basel, Switzerland) according to the manufacturer’s instructions. Cells were selected by the addition of puromycin (2 μg/ml) 3 days after the transfection and cultured at 37°C for 2 weeks. After 2 weeks of puromycin selection, the plates were stained with Giemsa and scored for the number of resistant colonies.

Results

Reduced Expression of let-7 in Human Lung Cancers in Both in Vitro and in Vivo. Northern blot analysis was first performed to analyze let-7 expression in 20 human lung cancer cell lines as well as in two immortalized human normal lung epithelial cell lines (Fig. 1A). The mature form of let-7 miRNA was readily detectable in both immortalized lung epithelial cell lines at a level comparable with that in normal lung tissues. In marked contrast, a significant reduction (>80%) in the expression levels of let-7 was observed in 60% (12 of 20) of lung cancer cell lines. Expression levels of let-7 in primary human lung cancer tissues taken directly from surgically treated patients, in which sufficient RNA were available, were further analyzed by Northern blot analysis. Consequently, 44% (7

Fig. 1. Northern blot analysis of let-7 expression in primary lung cancers. A, representative Northern blot analysis in lung cancer cell lines in vitro. BEAS-2B and HPL1D, immortalized human normal bronchial and peripheral lung epithelial cell lines, respectively. HNLEC, human normal lung epithelial cell lines. B, representative Northern blot analysis of primary lung cancer specimens in vivo. 5S rRNA served as a loading control. N, normal lung; T, lung cancer.

CAGTCGGAGAAGAAGTGTAC); and 5S–S (sense; 5′-TACCGCCATACTACCCCTGAA) and 5S–AS (antisense; 5′-TAACCCGCCCAGCCCTG)

To quantify the expression level of the let-7 genes, standard curves were made using serially diluted pBluescriptIIISK (−) inserted with each PCR product into the EcoRV site. PCR amplification consisted of 55 cycles (95°C for 30 s, 56°C to 60°C optimized for each primer set for 30 s and 72°C for 15 s) after the initial denaturation step (95°C for 10 min). Expression levels of the let-7 genes were based on the amount of the target message relative to the 5S RNA control, to normalize the initial input of total RNA.

Hierarchical Clustering. We used the Eisen CLUSTER and TREEVIEW programs for hierarchical clustering and visualization of data sets. Before applying the clustering algorithm, we log-transformed the fluorescence ratio for each expression and then average centered the data for all samples. Agglomerative hierarchical clustering was applied using the complete linkage method to investigate whether there was evidence for natural groupings of tumor samples based on correlations between gene-expression profiles.

Statistical Analysis. The Kaplan-Meier method was used to estimate survival as a function of time, and survival differences were analyzed by the log-rank test. Cox regression analysis of factors potentially related to survival was performed to identify which independent factors might jointly have a significant influence on survival.

Colonies Formation Assay. The let-7 expression construct and a control plasmid were constructed by the cloning of annealed oligonucleotides of let-7a (sense, 5′-GATCCCCCTGAGTGTTGATGGTATGATTATT and antisense, 5′-GCTAAAAACTATACAACTACCATCTCAGGG), let-7f (sense, 5′-GATCCCCCTGAGTAGTATGTTAGTTT and antisense, 5′-GCTAAAAACTATACAACTACCATCTCAGGG), or control (sense, 5′-GATCCCTGAGTGTTGATGGTATGATTATT and antisense, 5′-GCTAAAAACTATACAACTACCATCTCAGGG), into pBl-RNApuro, in which expression of a gene is under the control of the RNA polymerase III H1-RNA gene promoter prepared by PCR amplification of human genomic DNA. The let-7a and -7f expression constructs were
of 16) of the cases examined were found to exhibit >80% reduction in let-7 expression when compared with that in the corresponding normal lung tissues (Fig. 1B). A more frequent occurrence of reduced let-7 expression in cell lines in vitro may be related to the inevitable contamination of normal stromal/inflammatory cells in tumor tissues in vivo or, alternatively, this may reflect in vitro selection of cells with reduced let-7 in the process of the establishment of cell lines. These findings thus clearly showed the frequent occurrence of a significant reduction in let-7 miRNA expression in lung cancers.

Prognostic Impact of Reduced let-7 Expression in Surgically Treated Lung Cancer Patients. We next wished to investigate whether reduced let-7 expression has any relation to clinicopathological characteristics of lung cancers in an isomorf-specific manner. To this end, 143 lung cancer cases, which had undergone potential curative resection of NSCLCs, were examined by real-time reverse transcription-PCR analysis using let-7 isoforms-specific oligonucleotide primers. Expression levels of let-7 pri-miRNAs were consequently shown to vary significantly among lung cancer cases, although they tended to be coordinately regulated. The most abundant species were let-7a-1 and let-7f-1, which are known to be clustered within a few hundred bases in the human genome (6) and could be amplified together by reverse transcription-PCR (data not shown). We used unsupervised hierarchical clustering to classify the 143 resected human NSCLC cases in an unbiased manner without using any information on the identity of the samples. This procedure resulted in the classification of NSCLC cases into two major classes based on similarities in let-7 expression (Fig. 2A). Except for a significant association between cluster 1 with low let-7 expression and higher disease stages (P = 0.004 by the χ² test), no other significant associations were found between the clusters and various clinicopathological features including age, sex, histology, primary tumor status (pT), and differentiation grade. Of special interest was a striking difference in the postoperative survival of patients between the two clusters. The Kaplan-Meier survival curves demonstrated that patients belonging to cluster 1 were at a significantly greater risk of an earlier death than those classified as cluster 2 (P = 0.0003 by the log-rank test; Fig. 2B). A separate study analyzed the prognostic significance of let-7 in adenocarcinomas, which constitute the major proportion of lung cancers in Japan as well as in other countries such as the United States. We found that adenocarcinoma cases can also be divided into two major clusters, again showing that patients in cluster 1AD with low let-7 expression had significantly shorter survival than those in cluster 2AD with high let-7 expression (P = 0.03 by the log-rank test; Fig. 2, C and D).

Univariate Cox regression analysis was then performed for the entire cohort and showed that, in addition to disease stage (P < 0.001; Table 1), classification into cluster 1 with characteristic low let-7 expression is a significant predictive factor for poor prognosis (P < 0.001). Cox proportional hazards modeling was then conducted to identify which independent factors would jointly have a significant influence on survival (Table 1). The inter-relationship of possible prognostic factors was analyzed, using age, sex, histological type, smoking history, disease stage, and the let-7-defined cluster as variables, resulting in the identification of let-7-defined cluster as a significant, independent prognostic factor in surgically treated NSCLC patients after potentially curative resection (P = 0.009) in addition to disease stage (P < 0.001). The hazard ratio of earlier death was 2.17 (95% confidence interval, 1.21–3.89) for clusters 1 versus 2 and 3.49 (95% confidence interval, 1.89–6.42) for pathological stage II/III versus pathological stage I. Taken together, expression levels of let-7 seemed to have a significant impact on the postoperative survival of NSCLC patients.

Growth Suppression of Lung Cancer Cells by Overexpression of Exogenous let-7. The identification of a reduced expression of let-7 in lung cancers, in association with a shortened survival, prompted us to explore the possible biological significance of let-7 in lung cancer development. As an initial step, we introduced let-7 into a lung cancer cell line by using expression constructs, which were designed to synthesize mature miRNAs of two predominant let-7 isoforms, let-7a and let-7f, under the control of the RNA polymerase-III H1-RNA gene promoter. We confirmed that these expression constructs could work as expected using 293T cells (Fig. 3A). Overexpression of let-7f in A549 lung adenocarcinoma cell line resulted in a 78.6% reduction in the number of colonies, whereas the introduction of let-7a also showed similar but a more modest growth-inhibitory effect (Figs. 3, B and C). Similar results were obtained in five independent assays done in triplicate. C, representative dishes showing reduced colony formation by overexpression of exogenously introduced let-7.

**Table 1** Cox regression analysis of various prognostic factors for postoperative survival of lung cancer patients.

<table>
<thead>
<tr>
<th>Variables</th>
<th>Hazard ratio (95% CI)</th>
<th>Unfavorable/favorable</th>
<th>P</th>
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<td><strong>Univariate analysis</strong></td>
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<tr>
<td>Age (yr)</td>
<td>1.70 (0.97–2.99)</td>
<td>≥62/62</td>
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<td>Sex</td>
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<td>Male/female</td>
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<td>1.30 (0.67–2.52)</td>
<td>Squamous/non-squamous</td>
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<td>Smoking history</td>
<td>1.42 (0.80–2.51)</td>
<td>Smoker/non-smoker</td>
<td>0.233</td>
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<tr>
<td>Disease stage</td>
<td>3.89 (2.14–7.08)</td>
<td>II/III</td>
<td>&lt;0.001</td>
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<td>let-7</td>
<td>2.78 (1.56–4.89)</td>
<td>Cluster 1/cluster 2</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td><strong>Multivariate analysis</strong></td>
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<tr>
<td>Age (yr)</td>
<td>1.68 (0.95–2.97)</td>
<td>≥62/62</td>
<td>0.076</td>
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<tr>
<td>Sex</td>
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<td>0.741</td>
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<tr>
<td>Histology</td>
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<td>Non-squamous/squamous</td>
<td>0.942</td>
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<tr>
<td>Disease stage</td>
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<td>II/III</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>let-7</td>
<td>2.17 (1.21–3.89)</td>
<td>Cluster 1/cluster 2</td>
<td>0.009</td>
</tr>
</tbody>
</table>

*95% CI, 95% confidence interval.

**Discussion**

It has become apparent that genomic information for transcribing miRNAs is indeed implemented in the human genome (6, 9), but extremely little information is available regarding their physiological...
Reduction in the expression of let-7 microRNA in various human tumors was observed, indicating its potential role in cancer development. This microRNA is known to regulate the expression of several genes involved in tumor suppressor pathways, such as the let-7 family. The reduced expression of let-7 in tumors suggests that it may play a role in the pathogenesis of cancer.

However, the exact mechanisms by which let-7 microRNA regulates gene expression in the context of cancer are not fully understood. Further experimental evidence is required to clarify the role of let-7 microRNA in cancer development.

References

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