

***MEN1* Gene Mutation and Reduced Expression Are Associated With Poor Prognosis in Pulmonary Carcinoids**

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Context: *MEN1* gene alterations have been implicated in lung carcinoids, but their effect on gene expression and disease outcome is unknown.

Objective: Our objective was to analyze *MEN1* gene and expression anomalies in lung neuroendocrine neoplasms and their correlations with clinicopathologic data and disease outcome.

Design: We examined 74 lung neuroendocrine neoplasms including 58 carcinoids and 16 high-grade neuroendocrine carcinomas (HGNECs) for *MEN1* mutations ($n = 70$) and allelic losses ($n = 69$), promoter hypermethylation ($n = 65$), and mRNA ($n = 74$) expression. Results were correlated with disease outcome.

Results: *MEN1* mutations were found in 7 of 55 (13%) carcinoids and in 1 HGNEC, mostly associated with loss of the second allele. *MEN1* decreased expression levels correlated with the presence of mutations ($P = .0060$) and was also lower in HGNECs than carcinoids ($P = .0024$). *MEN1* methylation was not associated with mRNA expression levels. Patients with carcinoids harboring *MEN1* mutation and loss had shorter overall survival ($P = .039$ and $P = .035$, respectively) and low *MEN1* mRNA levels correlated with distant metastasis ($P = .00010$) and shorter survival ($P = .0071$). In multivariate analysis, stage and *MEN1* allelic loss were independent predictors of prognosis.

Conclusion: Thirteen percent of pulmonary carcinoids harbor *MEN1* mutation associated with reduced mRNA expression and poor prognosis. Also in mutation-negative tumors, low *MEN1* gene expression correlates with an adverse disease outcome. Hypermethylation was excluded as the underlying mechanism. (*J Clin Endocrinol Metab* 99: E374–E378, 2014)

Pulmonary neuroendocrine neoplasms (NENs) include well-differentiated carcinoids, classified into typical carcinoid (TC) and atypical carcinoid (AC) subtypes, with a relatively favorable prognosis (1, 2), and aggressive high-grade neuroendocrine carcinomas (HGNECs), ie, large-

cell neuroendocrine carcinoma (LCNEC) and small-cell lung cancer (SCLC).

Lung carcinoids occur in 5% of patients with multiple endocrine neoplasia (MEN) type 1 syndrome with *MEN1* germline mutations (3). *MEN1* mutations have been re-

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Abbreviations: AC, atypical carcinoid; HGNEC, high-grade neuroendocrine carcinoma; LCNEC, large-cell neuroendocrine carcinoma; MEN, multiple endocrine neoplasia; MSP, methylation-specific PCR; NEN, neuroendocrine neoplasia; NGS, next-generation sequencing; SCLC, small-cell lung cancer; TC, typical carcinoid.

ported in approximately 16% of sporadic lung carcinoids (4–6) but are exceptional in HGNECs (7, 8). Allelic losses of the *MEN1* locus are detected more frequently (~36%) than gene mutations (5), suggesting that alternative mechanisms might lead to *MEN1* gene inactivation. So far, the association of *MEN1* gene alterations with clinical follow-up has not been reported in lung NENs.

Here we report a comprehensive analysis of *MEN1* alterations, methylation status, and transcriptional expression in 74 lung NENs. Results are compared with tumor characteristics and clinical outcome.

Materials and Methods

Tissue samples

Seventy-four sporadic lung NENs (34 TCs, 23 ACs, 1 unclassified carcinoid, 9 LCNECs, 6 SCLCs, and 1 mixed LCNEC-SCLC), including 71 with follow-up (median 52 months), were studied. Institutional review board approval for the study was obtained by each contributing center following local ethical requirements. Nine neuroendocrine cell lines were included for *MEN1* mRNA expression analysis.

MEN1 mutational analysis

The entire coding region and splice junctions of *MEN1* were analyzed on tumor and matched normal DNA by Sanger sequencing, as described (9) (Supplemental Table 1A).

MEN1 deletion analysis

Fluorescent in situ hybridization on frozen sections was performed using the *MEN1* locus BAC probe CTD-222019, and centromere probes for chromosomes 1, 11, 3, and 7 as described (10).

Quantitative real-time PCR

Quantitative real-time PCR was performed using mRNA on *MEN1*, menin interactors *JUND* and *MLL*, and menin targets *HOXC8*, *P18*, *P21*, and *P27*, using primers listed in Supplemental Table 1B. Expression levels were normalized to *ACTB* and *CYPB* housekeeping genes as described (11).

Methylation-specific PCR and next-generation sequencing

MEN1 promoter methylation analysis was performed on all cases by nested methylation-specific PCR (MSP) (Supplemental Table 1C) and by next-generation sequencing (NGS) on methyl-CpG binding domain-immunoprecipitated DNA of 10 primary carcinoids and carcinoid cell lines NCI-H720 and NCI-H727 (focusing on the *MEN1* gene).

Statistical analysis

Correlations between *MEN1* data and follow-up were determined using IBM SPSS Statistics (version 20.0.0; IBM) setting the *P* values cutoff for significance at $\leq .05$. Differences in mean *MEN1* mRNA levels were determined by Student's *t* test, and the optimal cutoff point was determined using area under the re-

ceiver operating characteristic curve analysis. Associations between clinical and molecular parameters were calculated using logistic and linear regression, Fisher's exact, or χ^2 tests, as appropriate. Associations between relative expression levels of *MEN1* and other genes were calculated using Pearson's correlation.

Survival curves were created by the Kaplan-Meier method and compared using the log-rank test. The prognostic value of age at diagnosis, histopathology, sex, smoking status, tumor diameter, and *MEN1* mutation, deletion, and gene expression were tested in univariate and multivariate settings using Cox regression. Only variables with a *P* value $< .10$ in univariate analyses were included in multivariate analyses.

Results

MEN1 gene mutations and deletions are more frequent in ACs

MEN1 mutations were searched in 70 tumors, including 7 previously published cases (5). Eight cases (11%) showed nonsynonymous somatic alterations: 2 of 32 TCs (6%), 5 of 23 ACs (22%), and 1 of 7 LCNECs (14%). Mutations included 3 small deletions, 3 single-nucleotide substitutions, and 2 insertions (Supplemental Tables 2 and 3). Patient 35 showed the same *MEN1* mutations in the primary tumor and 2 distant metastases removed 8 and 10 years later.

Ploidy status and *MEN1* deletion were analyzed by fluorescent in situ hybridization in 69 tumors (Table 1 and Figure 1, A–C). Most carcinoids were disomic, whereas HGNECs were more frequently polysomic. Among carcinoids, 8 of 57 (14%, 1 TC and 7 ACs) showed *MEN1* allelic loss. In HGNECs, *MEN1* was deleted in 3 of 12 cases (25%). *MEN1* deletion was more frequent in ACs than in TCs ($P = .0060$) and was significantly associated with the presence of mutations in both the total group of NENs ($P = .0022$) and in carcinoids ($P = .0063$) (Supplemental Table 3).

MEN1 gene expression is heterogeneous in lung NENs

Quantitative RT-PCR performed on all 74 NENs showed that relative *MEN1* expression levels in lung NENs ranged from 0.031 to 0.85, generally lower than exocrine pancreas (mean 0.58; Figure 1D) but higher than normal lung (mean 0.078). A gradual decrease in mean *MEN1* expression values was apparent from TCs to ACs and HGNECs (Figure 1, D and E). Similarly, *MEN1* expression levels in SCLC NCI-H69 and LCNEC NCI-H460 cell lines were lower than in lung carcinoid NCI-H720 and NCI-H727 cells (Figure 1D). *MEN1* gene expression levels were inversely correlated to the presence of mutations and deletions (Supplemental Table 3) in the

Table 1. Univariate and Multivariate Analysis of Clinical Data and *MEN1* Parameters Correlated With Outcome of Patients With Pulmonary NENs

	Lung NENs, <i>P</i> Values		Carcinoids, <i>P</i> Values	
	Univariate	Multivariate ^a	Univariate	Multivariate ^a
Age at diagnosis	.0003	NS	.0021	NS
Diameter	.086	NI	NS	NI
Histopathology	<.0001	<.0001	.011	NS
Sex	.049	NS	NS	NI
Smoking status	NS	NI	NS	NI
Stage	.0002	NS	.0013	.0009
<i>MEN1</i> deletion	.013	NS	.047	.013
<i>MEN1</i> mutation	.060	NI	.050	NI
<i>MEN1</i> gene expression	.0068	.017	.035	NS

Abbreviations: NI, not included in multivariate analysis; NS, not significant.

^a Only parameters displaying a *P* value < .05 are included in multivariate analysis, and in the final model all *P* values needed to be < .05.

complete group of lung NENs ($P \leq .0060$) and carcinoids ($P \leq .025$).

No correlation between *MEN1* methylation and gene expression

Because low *MEN1* expression levels were present in tumors with neither *MEN1* mutation nor deletion, we analyzed *MEN1* promoter methylation by MSP. No methylation-specific product was seen in 65 primary NENs, cell lines, and 15 normal lungs from noncancer patients. NGS in 10 primary carcinoids and lung carcinoid cell lines NCI-H720 and NCI-H727 showed some methylation signals in *MEN1* promoter region and gene body but not at the locus used for MSP analysis (Supplemental Figure 1). No methylation signals were found in CpG islands. There were no differences in methylation between samples with high and low *MEN1* mRNA levels.

Deregulation of *MEN1* is associated with metastatic disease and poor prognosis

MEN1 gene mutations and deletions and decreased gene expression were associated with the presence of distant metastasis in both the total group of NENs and the carcinoids subgroup but were not related to sex, age, and smoking status (Supplemental Table 4). In particular, *MEN1* mRNA levels were significantly lower in patients with distant metastasis and/or patients who died from their tumor, both in the entire group (0.162 vs 0.318, $P = .00080$) and within the carcinoid subgroup (Figure 1E).

Univariate survival analysis showed in both the complete group of NENs and the carcinoid subgroup that age, histopathology, stage, presence of *MEN1* deletions, and decreased gene expression were significantly associated with higher risk of death (Table 1). At multivariate survival analysis, histopathology and decreased *MEN1* gene expression in lung NENs overall and stage and *MEN1*

deletion in the carcinoid subgroup retained statistical significance. Kaplan-Meier survival analysis confirmed that the 15-year overall survival of lung carcinoids was significantly shorter in patients with *MEN1* mutation (Figure 1F), decreased mRNA levels (Figure 1G), and deletion ($P = .035$).

Menin interactors and target genes

Within the complete set of NENs, *MEN1* gene expression was correlated with that of its interactors *JUND* ($P = .016$) and *MLL* ($P = .026$) but not of its targets *HOXC8*, *P18*, *P21*, and *P27*. Significant associations between *MEN1* deletion and low *HOXC8* expression ($P = .010$) and low *P18* gene expression ($P = .017$) were also found. *MEN1* mutational status and menin protein expression were not associated with mRNA levels of interactors and downstream targets.

In the complete group of NENs, as well as within carcinoids, lower levels of *P18* expression ($P = .0074$ and $P = .0011$, respectively) were associated with lower 15-year survival.

Discussion

Our study on pulmonary NENs shows that the presence of *MEN1* mutation and/or a lower *MEN1* gene expression is associated with distant metastasis and lower 15-year survival in both the entire cohort of NENs and lung carcinoids considered separately.

MEN1 mutations were found in 13% of carcinoids (7 of 55), in line with previous reports (4, 5), with most mutations occurring in ACs. All mutations were of the loss-of-function type, and most mutated cases also displayed deletion of the second *MEN1* locus. Only 1 of 15 HGNECs was mutated, confirming that *MEN1* mutations do not play a major role in HGNECs (7, 8).

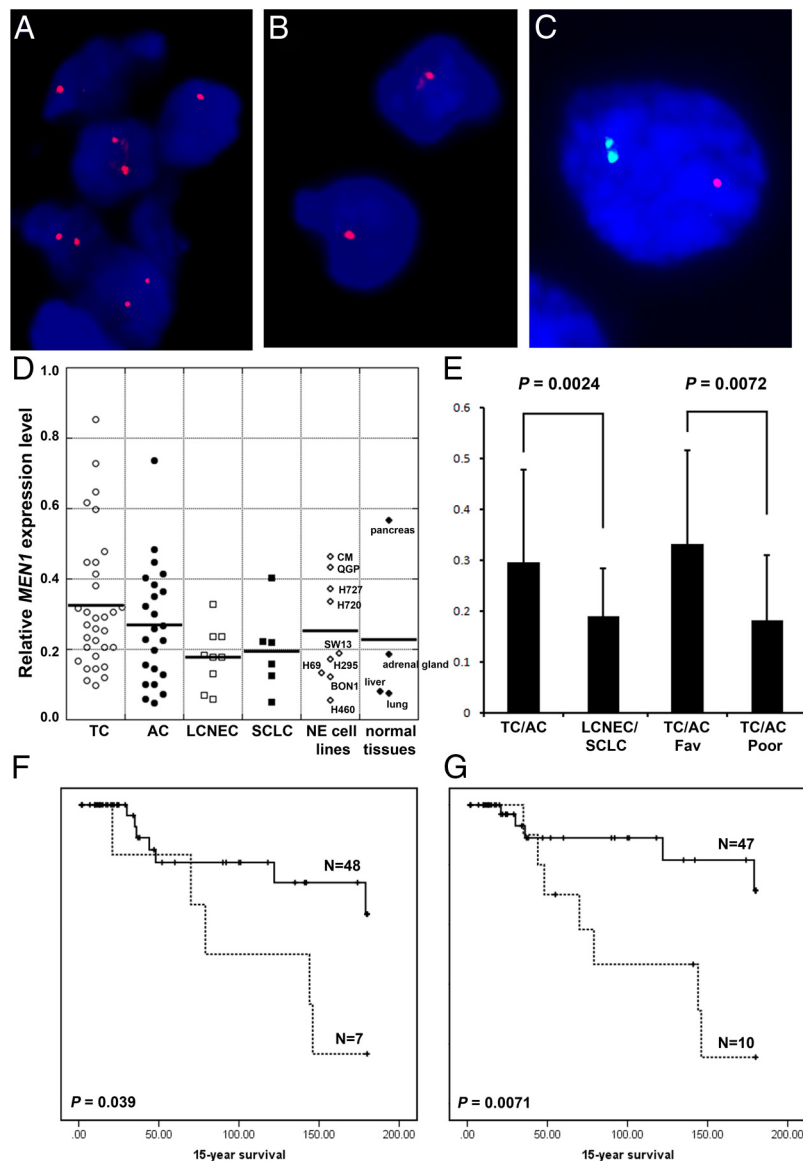


Figure 1. *MEN1* gene alterations and expression in lung NENs and association with survival. A–C, Fluorescence in situ hybridization for the *MEN1* locus (in red), showing a case with an *MEN1* mutation but retention of 2 copies of the *MEN1* gene (A) and 2 cases with *MEN1* mutation and associated loss of the *MEN1* locus (B and C), the latter in the presence of 2 copies of chromosome 7 (centromeric probe of chromosome 7 in green). D, Scatterplots showing the relative mRNA expression values of *MEN1* for TCs, ACs, LCNECs, SCLCs, neuroendocrine (NE) cancer cell lines, and normal tissues compared with the geometric mean of the expression levels of the housekeeping genes *ACTB* and *CYPB*. The horizontal bars represent the mean expression values. E, Differences between the mean values \pm SD of *MEN1* gene expression levels between the total group of carcinoids (TC/AC) and NE carcinomas (LCNEC/SCLC) (left; 95% confidence interval, -0.175 to -0.0400) and of carcinoid patients (TC/AC) with a favorable (Fav) and a poor disease outcome (right; 95% confidence interval, 0.0423 – 0.257). F and G, Kaplan-Meier analyses depicting 15-year overall survival in the group of carcinoids according to the presence of *MEN1* gene mutations (F, dotted line) or *MEN1* gene expression levels below the cutoff point of 0.136 (G, dotted line).

The large majority of neoplasms with the wild-type *MEN1* gene had high mRNA levels. However, not all cases with low mRNA levels harbored mutations or deletions, indicating that other mechanisms might unbalance *MEN1* expression in these tumors. No hypermethylation was seen in CpG islands within the *MEN1*

promoter with MSP analysis, whereas methylated regions outside the CpG island were identified by methyl-CpG binding domain sequencing. However, such methylation was not associated with reduced *MEN1* mRNA levels, suggesting that *MEN1* hypermethylation unlikely underlies *MEN1* downregulation.

MEN1 gene alterations and reduced expression were significantly associated with tumor stage, presence of distant metastases, and patient survival. At multivariate analysis, decreased *MEN1* gene expression was an independent predictor of disease outcome in both the complete group of NENs and in the group of carcinoids alone. This finding seems specific for lung NENs because it is not observed in pancreatic NENs (10).

The mechanisms underlying the role of *MEN1* gene loss of function and the acquisition of clinical aggressiveness in lung carcinoids deserves further investigation. We identified correlations between *MEN1* and *JUND/MLL* mRNA levels but not with menin targets *P18*, *P21*, and *P27*, suggesting that lung-specific mechanisms might be active, such as the E-cadherin/ β -catenin pathway, which interacts with menin and is frequently deregulated in lung NENs (7).

In conclusion, our comprehensive overview of *MEN1* molecular alterations in lung NENs demonstrates a significant association between *MEN1* gene deregulation and clinical aggressiveness in lung carcinoids and postulates different mechanisms of gene regulation in well-differentiated and poorly differentiated NENs.

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