High Frequency of Coexistent Mutations of PIK3CA and PTEN Genes in Endometrial Carcinoma

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Abstract

The phosphatidylinositol 3′-kinase (PI3K) pathway is activated in many human cancers. In addition to inactivation of the PTEN tumor suppressor gene, mutations or amplifications of the catalytic subunit α of PI3K (PIK3CA) have been reported. However, the coexistence of mutations in these two genes seems exceedingly rare. As PTEN mutations occur at high frequency in endometrial carcinoma, we screened 66 primary endometrial carcinomas for mutations in the helical and catalytic domains of PIK3CA. We identified a total of 24 (36%) mutations in this gene and coexistence of PIK3CA/PTEN mutations at high frequency (26%). PIK3CA mutations were more common in tumors with PTEN mutations (17 of 37, 46%) compared with those without PTEN mutations (7 of 29, 24%). Array comparative genomic hybridization detected 3q24-qter mutations in nine tumors. Knocking down PTEN expression in the K-Ras mutations, further enhances phosphorylation of Akt (Ser473), indicating that double mutation of PIK3CA and PTEN has an additive effect on PI3K activation. Our data suggest that the PI3K pathway is extensively activated in endometrial carcinomas, and that combination of PIK3CA/PTEN alterations might play an important role in development of these tumors.

Introduction

The phosphatidylinositol 3′-kinases (PI3K) are widely expressed lipid kinases that catalyze the production of the second messenger phosphatidylinositol 3,4,5-triphosphate (PIP3), which in turn con-tribute to the recruitment and activation of a wide range of downstream targets, including Akt (1). PTEN is a lipid phosphatase that counteracts the activity of PI3K (2). PTEN is frequently mutated in various tumors, including endometrial carcinoma (34-55%; refs. 3, 4). Recent studies showed an inverse correlation between loss of PTEN expression and Akt activation (5). Increased PI3K activity via gain of function has also been shown in a number of human cancers: PIK3CA, which encodes the catalytic subunit p110α of PI3K, is located on chromosome 3q26.3, and amplification of this locus was suggested to increase PI3K activity (6). Moreover, Samuels et al. identified somatic mutations of PIK3CA in several types of human tumors (7). Functional analysis revealed that several “hotspot” mutants of p110α (E542K, E545K, and H1047R) increase lipid kinase activity and induce oncogenic transformation (8). Simultaneous mutation in PIK3CA and PTEN has been thought to be mutually exclusive, as reported in breast carcinoma and glioblastoma (9, 10). However, in this study, we show the frequent coexistence of PIK3CA and PTEN mutations in endometrial carcinomas. We also show that PIK3CA copy number may change in endometrial carcinomas.

Materials and Methods

Tumor samples and genomic DNA. Surgical samples were obtained from 66 patients with primary endometrial carcinomas who underwent resection of their tumors at the University of Tokyo Hospital. All of the patients provided informed consent for the research use of their samples and the collection, and use of tissues for this study was approved by the appropriate institutional ethics committees. Genomic DNA was extracted by a standard SDS-proteinase K procedure. The clinical status was described previously (4). Detailed distribution of the histologic subtypes was as follows: 58 (88%) endometrioid carcinomas, one squamous cell carcinoma, and three mixed carcinomas.

PCR and sequencing. Primer sequences and PCR conditions of exons 9 and 20 of PIK3CA have been described previously (7). PCR products were sequenced with the BigDye terminator method (Applied Biosystems, Foster City, CA) on an autosequencer (ABI PRISM 3700).

Statistical analysis. Survival curves were constructed using the Kaplan-Meier method and compared with a log-rank test. The analyses were carried out using the JMP 5.1J statistics package (SAS Institute, Cary, NC). The association of variables was evaluated by the Fisher’s exact test. P values obtained in all tests were considered significant at \( P < 0.05 \).

Cell lines. AN3CA, KLE, HEC-1B, and RL95-2 were obtained from the American Type Culture Collection (Manassas, VA). Ishikawa3-H-12 was a generous gift of Dr. Masato Nishida (Kasumigaura Medical Center, Ibaraki, Japan). Ishikawa3-H-12, AN3CA and HEC-1B cells were maintained in Eagle’s MEM with 10% fetal bovine serum (FBS). KLE and RL95-2 cells were grown in 1:1 mixture of DMEM and Ham’s F12 medium with 10% FBS. We confirmed PTEN and K-Ras mutations (entire coding lesion of Pten and exons 1 and 2 of K-Ras) by PCR and sequencing, using genomic DNA or cDNA of each cell line. Only HEC-1B possesses K-Ras mutation (G12D). PTEN mutation was detected in AN3CA [codon 130 and 1-bp (G) del], Ishikawa3-H-12 [codon 289, 1-bp (A) del and codons 318-319, 4-bp (CTTA) del], and RL95-2 [codon 322, 1-bp (A) del and codon 322, 1-bp (A) ins].

Western blotting. Cells were lysed in 500 μL of buffer A [50 mmol/L Tris-HCl (pH 7.5), 150 mmol/L sodium chloride, 5 mmol/L EDTA, 2 mmol/L sodium orthovanadate, and 10 mmol/L sodium fluoride] containing 1% Triton X-100. Western blotting was done with 15 μg of each extract and antisera specific for PTEN (138606; Cell Signaling, Beverly, MA; 1:1,000), phospho-Akt (Ser473; Cell Signaling; 1:1,000), phospho-PDK1 (Ser417; Cell Signaling; 1:1,000), and phospho-GSK3β (Ser9; Cell Signaling; 1:1,000), -actin (Sigma, St. Louis, MO; 1:5,000), and K-Ras (Santa Cruz Biotechnology, Santa Cruz, CA; F234; 1:500) in TBST/0.5% milk followed by anti-rabbit-horseradish peroxidase (HRP; Amersham Biosciences, Piscataway, NJ; 1:5,000) or anti-mouse HRP (Amersham; 1:5,000). Immunoreactive proteins were detected by chemiluminescence (Enhanced Chemiluminescence Plus, Amersham) and autoradiography.

Note: Supplementary data for this article are available at Cancer Research Online (http://cancerres.aacrjournals.org/).

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Small interfering RNA transfection. Small interfering RNA (siRNA) was used to inhibit the expression of the K-Ras or PTEN gene in HEC-1B cell line. The targeted sequence of K-Ras siRNA and PTEN siRNA is 5'-AACCTGTCTC-TTGGATATTCT-3' and 5'-AACAGTAGAGGAGCCGTCAAA-3', respectively. Cells were seeded at 2.0 x 10^5 per six-well plate 24 hours before transfection and transfected with 80 or 160 nmol/L siRNA duplexes, using LipofectAMINE 2000 (Invitrogen, Carlsbad, CA). After 6 hours of transfection, the growth media were replaced to Eagle's MEM with 10% FBS. Cells were collected 72 hours after transfection and analyzed by immunoblotting.

Array comparative genomic hybridization. Array comparative genomic hybridization (array CGH) was carried out using arrays of 2464 BAC clones each printed in triplicate (HumArray2.0) according to published protocols (11). The tumor genomic DNA and normal male reference DNA (300 ng each) were labeled by random priming in separate 50 μL reactions to incorporate Cy3 and Cy5, respectively. For each tumor, the data are plotted as the mean log 2 ratio of the triplicate spots for each clone normalized to the genome median log 2 ratio. The clones are ordered by position in the genome beginning at 1p and ending with Xq.

Results and Discussions

We have analyzed mutations in exons 9 and 20 of PIK3CA gene in 66 endometrial carcinoma patients. We specifically examined these two exons, because four fifths of the mutations of PIK3CA gene are clustered in these regions (7). Direct sequencing identified mutations in 24 of 66 (36%) patients, as summarized in Table 1. These data suggest that the incidence of PIK3CA mutation in endometrial carcinoma is one of the highest among all tumors examined. Most of the mutations were identified in exon 20 (20 of 24, 83%). All of these mutations except one were missense mutations, and the most common mutation detected in this study was H1047R (Table 1), in agreement with previous reports (10, 12, 13).

Coexistence of loss of PTEN expression and PIK3CA mutation has been rarely detected in other cancers (9, 10). However, we identified coexistence of PTEN and PIK3CA mutations in 26% (17 of 66) of patients, making use of the data of previously published PTEN mutations (4). Figure 1A shows the sequences of a tumor in which both genes are mutated. Tumors with PTEN mutation showed a tendency to carry PIK3CA mutation more frequently (17 of 37, 46%) than tumors without PTEN mutation (7 of 29, 24%), although statistical significance is not reached (P = 0.078 in Fisher’s exact test). Subsequently, we evaluated the relationship between PIK3CA mutation and other clinicopathologic factors. There was no evidence of an association of PIK3CA mutations with histologic grade, International Federation of Gynecology and Obstetrics (FIGO) stage, lymph node metastasis, and estrogen/progesterone receptor status (Supplementary Data 1). These data are in striking contrast to previous reports (10, 12, 13).

Table 1. PIK3CA mutations in endometrial cancer

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A, coexistence of PIK3CA and PTEN mutations. Sequence traces of one case for exon 20 of PIK3CA (left) and exon 7 of PTEN (right). B, PIK3CA mutational status and survival in endometrial carcinomas calculated according to Kaplan-Meier method. Survival of patients with PIK3CA mutations (n = 24) was compared with those with wild-type PIK3CA (n = 42). C, survival of PIK3CA mutant patients with PTEN mutations only outside exons 5 to 7 (n = 9) compared with those with PTEN mutations in exon 5, 6, or 7 (n = 8) or those with wild-type PTEN (n = 7).
to those of breast carcinoma, showing that PIK3CA mutations correlate with expression of hormone receptors and node metastasis and are mutually exclusive with loss of PTEN expression (10). However, two of eight (25%) PTEN mutant breast carcinomas also possessed PIK3CA mutations, suggesting that coexistence of PTEN/PIK3CA mutations could occur in other tumors as well.

Next, we analyzed prognosis according to PIK3CA and PTEN status. Kaplan-Meier analysis suggested that PIK3CA mutation itself was not a marker of poor prognosis (Fig. 1B), although the sample size is small. Moreover, PIK3CA mutation did not affect the prognostic difference caused by PTEN mutational status (Fig. 1C). The group with PTEN mutation only outside exons 5 to 7 and PIK3CA mutation still showed better prognosis compared with the other groups with PIK3CA mutation. These results suggest that activated PI3K pathway alone is not a poor prognostic factor in endometrial carcinoma. The disparity of prognosis according to PTEN status, regardless of PIK3CA status, might indicate that PTEN mutation is not only associated with the PI3K pathway but also with other pathways.

Mutations in both PTEN and PIK3CA are most unexpected, because loss of PTEN and activation of PI3Ks are thought to have similar effects on the PI3K pool. We could not find any correlations between types of PIK3CA mutations, such as H1047R or H1047Y, and PTEN mutations. Furthermore, previous clonal analyses showed that adenocarcinomas of uterine endometrium are monoclonal in composition (14). We propose three hypotheses to account for this controversial discovery. First, more than one input activating the PI3K/Akt pathway is required to completely activate this pathway. In breast carcinoma, PIK3CA mutations correlate with ErbB2 overexpression, suggesting that another activating event might be necessary to fully activate the PI3K pathway (10). The second hypothesis is that either PTEN or p110α possesses additional function(s) distinct from the PI3K pathway. In support of this, lipid phosphatase independent role for PTEN, including protein phosphatase activity, have been reported. Raftopoulou et al. showed that PTEN can inhibit cell migration through its C2 domain, depending on the protein phosphatase activity (15). Freeman showed that PTEN can interact with p53 and modulate p53 function independently of its phosphatase activity (16). Okumura et al. reported that the PTEN COOH-terminal domain physically interacts with the oncogenic MSP58 protein (17). These findings suggest that impairment of other PTEN function(s) might play a key role in endometrial carcinoma. Finally, other isoforms of p110 might have important roles in endometrial carcinogenesis. Mammals have three genes for the class IA p110 subunits encoding p110α, p110β, and p110δ and one gene for the class IB p110 subunit encoding...
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