BRIEF REPORT — POLYMORPHISM REPORT

Masami Sato · Yuriko Mori · Akira Sakurada
Shigefumi Fujimura · Akira Horii

A GT dinucleotide repeat polymorphism in intron 1 of the *H-cadherin* (*CDH13*) gene

Received: July 24, 1998 / Accepted: July 29, 1998

Abstract A polymorphic dinucleotide (GT) repeat sequence was isolated from a genomic clone containing the human *H-cadherin* (*CDH13*) gene at 16q24.1-q24.2. This polymorphic marker will be a useful tool in the genetic study of various cancers.

Key words The *H-cadherin* (*CDH13*) gene · GT dinucleotide repeat · Polymorphism · Chromosome 16q

Introduction

Recently, *H-cadherin* (*CDH13*) was cloned, and loss of expression was proven to be closely associated with tumorigenesis in breast cancer (Lee, 1996). We previously reported frequent allelic loss on chromosome bands 16q24.1-q24.2 in human lung cancer (Sato et al. 1998a), and the *CDH13* gene was found to be localized in the common region of allelic loss. We further analyzed the *CDH13* gene and found that this gene was lost and/or hypermethylated at the 5'-flanking region in lung cancer cell lines and primary tumors (Sato et al. 1998b). Genomic analysis of the *CDH13* gene identified a polymorphic GT dinucleotide repeat in intron 1.

M. Sato · Y. Mori · A. Sakurada · A. Horii (✉)
Department of Molecular Pathology, Tohoku University School of Medicine, Sendai, 980-8575 Japan
Tel. +81-22-717-8042; Fax +81-22-717-8047
e-mail: horii@mail.cc.tohoku.ac.jp

M. Sato · A. Sakurada · S. Fujimura
Departments of Thoracic Surgery, Institute of Development, Aging and Cancer, Tohoku University, Sendai Japan

Y. Mori
Department of Respiratory Oncology and Molecular Medicine, Institute of Development, Aging and Cancer, Tohoku University, Sendai, Japan

Isolation of GT repeat sequence

Human genomic clones containing the *CDH13* gene were isolated from the subcloning cosmid library of two YAC clones, y872F3 and y747D4, described by Sato et al. (1998b). We determined the nucleotide sequences of the whole exons as well as exon-intron boundaries and found a GT repeat sequence in intron 1 starting at 203-bp downstream from the donor site. (Accession number in the DDBJ, EMBL, and GenBank databases is AB001090.)

Polymerase chain reaction (PCR) primers

The PCR primers used were: *CDH13*-GT (GT strand): 5'-TCCCACTCTGGCGTGCGT-3', and *CDH13*-CA (CA strand): 5'-TCCTCCCGTTAACGAACGTA-3'.

Table 1 Allele frequency of the GT repeat polymorphism

Number of GT repeats	Frequency
12	0.006
13	0.000
14	0.000
15	0.006
16	0.086
17	0.213
18	0.443
19	0.006
20	0.011
21	0.017
22	0.034
23	0.023
24	0.011
25	0.017
26	0.069
27	0.017
28	0.006
29	0.029
30	0.006

PCR conditions

PCR was performed as follows: 94°C for 2min for the initial denaturation followed by 40 cycles of 94°C for 30s, 55°C for 30s, and 72°C for 30s. Final elongation at 72°C for 5min was also performed. GeneAmp PCR system 9600 (Perkin-Elmer Cetus, Norwalk, CT) was used. The size range of the PCR product in 87 normal Japanese volunteers was 65–101 bp.

Polymorphism and frequency

One hundred and seventy-four alleles were examined and the observed heterozygosity frequency was 0.77. The number of GT repeats and frequency of the alleles are summarized in Table 1.

Mendelian inheritance. Mendelian inheritance was confirmed in three families.

Chromosomal localization. The *CDH13* gene was mapped to chromosome bands 16q24.1-q24.2.

Acknowledgments This work was supported by the Ministry of Education, Science, Sports, and Culture of Japan.

References

- Lee SW (1996) H-cadherin, a novel cadherin with growth inhibitory functions and diminished expression in human breast cancer. *Nature Med* 2: 776–782
- Sato M, Mori Y, Sakurada A, Fukushige S, Ishikawa Y, Tsuchiya E, Saito Y, Nukiwa T, Fujimura S, Horii A (1998a) Identification of a 910kb region of common allelic loss in chromosome bands 16q24.1-q24.2 in human lung cancer. *Genes Chromosom Cancer* 22: 1–8
- Sato M, Mori Y, Sakurada A, Fujimura S, Horii A (1998b) The *H-cadherin (CDH13)* gene is inactivated in human lung cancer. *Hum Genet* 103: 96–101