## Serial analysis of gene expression (SAGE) in human stomach cancer

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## 2000 Fiscal Year Final Research Report Summary

# SERIAL ANALYSIS OF GENE EXPRESSION (SAGE) IN HUMAN STOMACH CANCER

Project/Area Number 11671218 **Research Category** Grant-in-Aid for Scientific Research (C) **Allocation Type** Single-year Grants Section 一般 Research Field Digestive surgery **Research Institution** KANAZAWA UNIVERSITY **Principal Investigator** MINAMOTO Toshinari KANAZAWA UNIVERSITY, CANCER RESEARCH INSTITUTE, ASSOCIATE PROFESSOR, がん研究所, 助教授 (50239323) Co-Investigator(Kenkyū-buntansha) MAI Masayoshi KANAZAWA UNIVERSITY, CANCER RESEARCH INSTITUTE, PROFESSOR, がん研究所, 教授 (80092807) YAMASHITA Kaname KANAZAWA UNIVERSITY, CANCER RESEARCH INSTITUTE Project Period (FY) 1999 - 2000 Keywords

#### **Research Abstract**

STOMACH CANCER / GENE EXPRESSION / SERIAL ANALYSIS OF GENE EXPRESSION (SAGE)

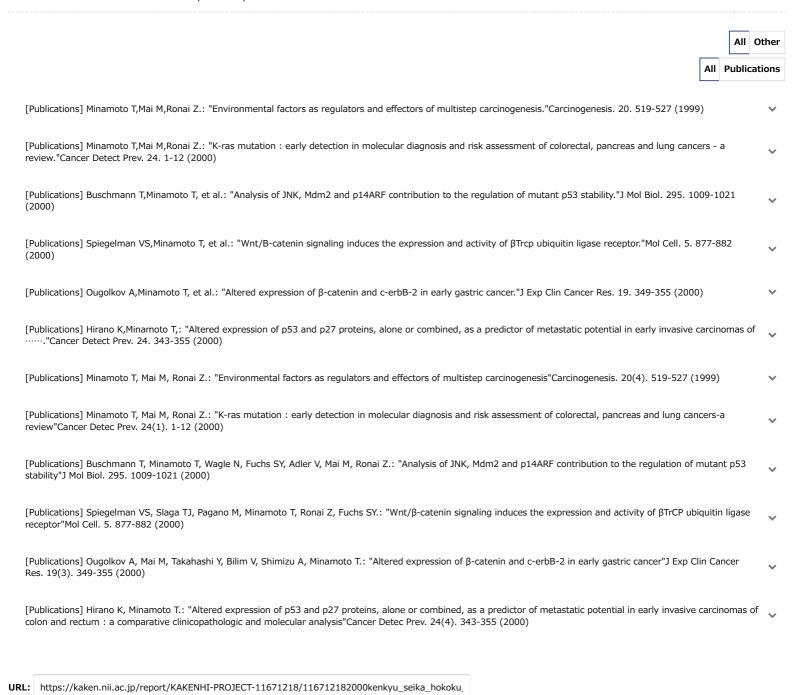
Research Project

The purpose of this project is to conduct serial analysis of gene expression (SAGE) for human stomach cancer. Applying SAGE, that was originally developed in the tissue culture system, for global analysis of gene expression in clinical stomach cancer requires purification of high quality mRNA from tissue samples that contain minimal amount of stromal cells. In 1999, prior to examine tissue samples, we analyzed by SAGE for gene expression in a cancer cell line, KKLS that was established from undifferentiated stomach carcinoma in our institute. This preliminary analysis could quantitatively identify 2969 unique genes expressed among 5182 SAGE tags obtained from the cell line, with a linker ratio of 1.02%. Among highly expressed genes were included mitochondrial genes and several unknown genes unregistered to the Gene

Bank. We assume that the gene expression profile of KKLS would be fundamental for further analysis of gene expression in human stomach cancer showing different histological types.

In 2000, human stomach cancer tissues has been subjected to SAGE. During this analysis we have had difficulty in preparation of highly purified mRNA from the surgical materials, which was later overcome by modification of our method for extraction and purification of mRNA. Similar to the gene expression pattern in KKLS cell line, unknown nuclear genes and mitochondrial genes were quantitatively detected in the library of SAGE tags yielded from human stomach cancer samples. Recent reports showing frequent genetic alteration in mitochondrial DNA suggest an involvement of altered expression of mitochondrial genes in development and progression of stomach cancer. Although we could not complete this project in the given term (1999 to 2000), SAGE for human stomach cancer is being in progress in our laboratory, targeting nuclear as well as mitochondrial genes.

### Research Products (12 results)



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