Serial Analysis of Gene Expression in Human Gastric Cancer

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It is important to identify genes responsible for metastasis of gastric cancer, as this disease is one of the leading causes of cancer death in the world. Here we analyzed gene expression in human gastric cancer by serial analysis of gene expression (SAGE). SAGE is a method for comprehensive analysis of gene expression patterns. A short sequence tag (10-14bp) contains sufficient information to uniquely identify a transcript. The tag is obtained from a unique position within each transcript. Sequence tags can be linked together to from long serial molecules that can be cloned and sequenced and quantitation of the number of times a particular tag is observed provides the expression level of the corresponding transcript. We obtained primaly tissue, normal mucosa, and lymph node metastasis from a advanced gastric cancer patient. Total RNA was isolated and SAGE was performed. Tag sequences were analyzed using SAGE software. A total of 60621 transcripts were identified. We show tags which highly expressed, in primaly tumor, normal mucosa, and lymph node metastasis. The lymph node metastasis library was compared with primaly tumor library, we could identify certain set of genes up-regulated in lymph node metastasis in tag ratio of two fold or more. Validation by RT-PCR on RNA from another patients shows higher expression of SIAT6, APOC1, galectin-1 and COL1A1 in lymph node metastasis versus primaly tumor. These results together with currently accumulating data would provide basic knowledge toward understanding molecular mechanism underlying progression and metastasis of gastric cancer.

Summary of SAGE tag libraries

Library	Sequences	Total Tags	Unique Tags
Normal	731	14843	5243
Tumor	933	22681	8337
LN meta	1030	23097	7976