Aberrant DNA Methylation In Oesophageal Cancer And Barrett's Oesophagus

by

Eric Smith Cert Med Lab Sc, Ass Dip Med Lab Sc, BSc

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ABSTRACT

Oesophageal cancer is the eighth most common cancer and the sixth most common cause of death from cancer worldwide. There are two main histological types of oesophageal cancer: squamous cell carcinoma (ESCC), adenocarcinoma (EAC). In the developing world the major histological type is ESCC, whilst in the developed world EAC is increasing rapidly in incidence and is now the major type. Both histological types have a similarly poor prognosis, with a high morbidity and mortality.

Barrett's oesophagus (BE) is considered a precursor to EAC. It is found in up to 1.5% of the general population, and in up to 12% of patients who are investigated for chronic reflux symptoms. Approximately 0.5 to 1% of patients with BE will develop EAC each year, and patients with BE have 30- to 125-fold increased risk of EAC compared to the general population. Gastro-oesophageal reflux is the major risk factor for the development of BE and EAC, and medical and surgical anti-reflux therapies are available to relieve symptoms of the reflux and prevent reflux-related complications, although it is not certain if they will prevent the development of cancer.

The development of oesophageal cancer is associated with an accumulation of genetic abnormalities, with some reports suggesting a stepwise progression of genetic changes involving the up-regulation and down-regulation of critical genes. Methylation of cytosine residues in CpG dinucleotides of the promoter regions of genes, DNA methylation, is a genomic change associated with silencing of gene expression.

In the studies described in this thesis I have developed a simple quantitative method to assess DNA methylation using the melt data obtained following amplification of bisulphite modified DNA. I identified eight genes (BNIP3, FBN2, ID4, MLF1, PRDM2, RBP4, RARRES1, TFAP2C) that had been reported methylated in other cancers, but not before in BE or EAC, and four genes (CLDN6, DCBLD2, FNBP1 and MGC16824) that had not previously been reported as methylated in any cancer. I have shown that in non-dysplastic (metaplastic) BE, methylation of APC, ID4, MGMT, RBP1, SFRP1, TIMP3 and TMEFF2 (but not RUNX3 or CDKN2A) occurs as frequently in BE as EAC, suggesting that BE is more like cancer than normal squamous mucosa. I have used DNA methylation as a surrogate measure of the

efficacy of fundoplication and proton pump inhibitor (PPI) treatment for BE. Five or more years after fundoplication there was a significant regression of BE and a reduction in the number of methylated genes in the remaining BE. In contrast, although high-dose PPI for six months significantly reduced inflammation and epithelial cell proliferation, it did not alter methylation. The reduction in methylation may be associated with a decreased risk for the development of dysplasia and adenocarcinoma. Finally, I have suggested extensions to the work published in this thesis. Further understanding of which genes are methylated in BE, EAC and ESCC, the mechanisms responsible for this aberrant methylation, and the function of the genes, would improve our insight into the underlying biology of oesophageal diseases, and potentially lead to new biomarkers or treatment options.

DECLARATION

This work contains no material which has been accepted for the award of any other degree or diploma in any university or other tertiary institution to Eric Smith and, to the best of my knowledge and belief, contains no material previously published or written by another person, except where due reference has been made in the text.

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Eric Smith

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ABBREVIATIONS

BE	Barrett's oesophagus
cDNA	complementary DNA
COBRA	combined bisulfite restriction analysis
COX2	cyclooxygenase 2
CpG	cytosine-phosphate-guanine dinucleotide
DNA	deoxyribonucleic acid
DNMT	DNA methyltransferase
EAC	oesophageal adenocarcinoma
EMR	endoscopic mucosal resection
ESCC	oesophageal squamous cell carcinoma
LOH	loss of heterozygosity
MBD	methyl-CpG-binding domain
MSP	methylation-specific PCR
NSAID	non-steroidal anti-inflammatory drug
PCR	polymerase chain reaction
PPI	proton pump inhibitor
RNA	ribonucleic acid
USA	United States of America

To Catherine and Maddie

In memory of our faithful hounds, Sha and Yasmine